Global reconstruction of the human metabolic network based on genomic and bibliomic data

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Metabolism is a vital cellular process, and its malfunction is a major contributor to human disease. Metabolic networks are complex and highly interconnected, and thus systems-level computational approaches are required to elucidate and understand metabolic genotype–phenotype relationships. We have manually reconstructed the global human metabolic network based on Build 35 of the genome annotation and a comprehensive evaluation of >50 years of legacy data (i.e., bibliomic data). Herein we describe the reconstruction process and demonstrate how the resulting genome-scale (or global) network can be used (*i*) for the discovery of missing information, (*ii*) for the formulation of an *in silico* model, and (*iii*) as a structured context for analyzing high-throughput biological data sets. Our comprehensive evaluation of the literature revealed many gaps in the current understanding of human metabolism that require future experimental investigation. Mathematical analysis of network structure elucidated the implications of intracellular compartmentalization and the potential use of correlated reaction sets for alternative drug target identification. Integrated analysis of high-throughput data sets within the context of the reconstruction enabled a global assessment of functional metabolic states. These results highlight some of the applications enabled by the reconstructed human metabolic network. The establishment of this network represents an important step toward genome-scale human systems biology.

constraint based | metabolism | model | systems biology

An individual's metabolism is determined by one's genetics, environment, and nutrition. With the available human genome sequence and its annotation (1–3), we can hope to define the human body's complement of metabolic enzymes. In addition, numerous metabolic genes and enzymes have been individually studied for decades, resulting in a collective knowledge base, or "bibliome," that includes reaction mechanisms and well characterized interactions. Manual component-by-component (bottom-up) reconstruction of genomic and bibliomic data leads to a biochemically, genetically, and genomically structured (BiGG) reconstruction (4) that can be mathematically represented as an *in silico* model for computing allowable network states under governing chemical and genetic constraints (5). The procedure for integrating these diverse data types to form a network reconstruction and predictive model is well established for microorganisms (4) and has recently been applied to mouse hybridomas (6). Such *in silico* models have enabled hypothesis-driven biology, including the prediction of the outcome of adaptive evolution (7–11) and the identification and discovery of candidates for missing metabolic functions that were subsequently experimentally verified (12). Because metabolic networks are more complex in mammals than in single-celled organisms, there is likely to be an even greater opportunity for the use of computational models to understand the basis of normal and abnormal cellular function.

Here we present the reconstruction of the global human metabolic map. *Homo sapiens* Recon 1 is a comprehensive literature-based genome-scale metabolic reconstruction that accounts for the functions of 1,496 ORFs, 2,004 proteins, 2,766 metabolites, and 3,311 metabolic and transport reactions. This network reconstruction was transformed into an *in silico* model of human metabolism and validated through the simulation of 288 known metabolic functions found in a variety of cell and tissue types. Recon 1 (*i*) enables the identification of gaps in our understanding of human metabolism, (*ii*) facilitates the computational interrogation of the overall properties of the human metabolic network, and (*iii*) provides context for analysis of "-omics" data sets. These examples are described in further detail herein.

Results and Discussion

Reconstruction and Validation of *H. sapiens* Recon 1. A well annotated genome sequence is vital for bottom-up reconstruction because it enables the rapid identification of candidate network components (4) and the assembly of a preliminary network (13) that can be used as a starting point for manual curation [supporting information (SI) Fig. 5]. We used Enzyme Commission numbers (14) and Gene Ontologies (15) to identify an initial set of 1,865 human metabolic genes from the November 2004 annotations (Build 35) of Kyoto Encyclopedia of Genes and Genomes (KEGG) (16), National Center for Biotechnology Information's LocusLink (17) [now EntrezGene (18)], and the H-Invitational Database (19). These genes were mapped to a rudimentary network of 3,623 metabolic enzymes and 3,673 reactions from KEGG's LIGAND database and the compartmentalized yeast metabolic reconstruction (20). In addition to establishing initial network scope, LIGAND's pathway-based organizational structure also facilitated parallel network assembly. A team of researchers simultaneously curated network components by evaluation of >50 years of biological evidence from >1,500 primary literature articles, reviews, and biochemical textbooks. Strict quality control/quality assurance methods were used throughout the reconstruction (see *Materials and Methods*). Manual literature-based reconstruction ensured that the network components and their interactions were based on direct physical evidence and reflected the current knowledge of human metabolism.

Bottom-up reconstructions can be represented mathematically, enabling the computational interrogation of their properties (4, 21). We validated the basic functionality of the human metabolic network by simulating 288 known metabolic functions *in silico* (SI Tables 2–4). Like genome sequence assembly and

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Abbreviations: BiGG, biochemically, genetically, and genomically structured; SVD, singular value decomposition.

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Table 1. *H. sapiens* Recon 1 network statistics

Component	Number
Genes	1,496
Transcripts*	1,905
Proteins	2,004
Complex-associated reactions*	248
Isozyme-associated reactions*	946
Intrasystem reactions	3,311
Metabolic	2,233
Transport†	1,078
Exchange reactions†	432
Compartment-specific metabolites	2,712
Cytoplasm	995
Extracellular space	388
Mitochondrion	383
Golgi apparatus	279
Endoplasmic reticulum	231
Lysosome	207
Peroxisome	139
Nucleus	90
Citations	1,587
Primary literature	1,378
Review articles	188
Textbooks	21
Validated metabolic functions	288
Knowledge gaps‡	356

*See *Materials and Methods* for definitions of transcripts, complexes, and isozymes.

†Transport reactions refer to intrasystem transport across a boundary (organellar and plasma membranes), whereas exchange reactions describe metabolite transport across the system boundary, e.g., into and out of the extracellular space from the surrounding medium.

‡Number of "dead-end" metabolites only produced or consumed.

annotation, network reconstruction is an iterative process, and consequently several rounds of iterative gap analysis (i.e., targeted literature searches to identify metabolic reactions that were missed initially) and comprehensive revalidation were required to achieve a BiGG database and a high-quality network reconstruction (SI Fig. 6).

The result of five iterative rounds of reconstruction and validation is *H. sapiens* Recon 1 and the first human cellular process to be comprehensively modeled at this level of detail and accuracy (Table 1). It was almost entirely constructed from human-specific data and includes many reactions directly extracted from the literature that are not described in any chart or database. Furthermore, Recon 1 represents several hierarchical levels of detail, namely:

- Carefully formulated metabolites and reactions, which account for known reaction stoichiometry, substrate/cofactor specificity, and directionality, as well as overall conservation of mass and charge-based metabolite ionization states at pH 7.2.
- Full compartmentalization of metabolites in and their exchange between seven intracellular locations (cytoplasm, mitochondria, nucleus, endoplasmic reticulum, Golgi apparatus, lysosome, and peroxisome) and the extracellular environment.
- Precise Boolean descriptions of gene–protein relationships such as alternatively spliced variants, protein complexes, and isozymes.
- Confidence scores and literature references based on known biological evidence associated with each gene, protein, and reaction.

The entire contents of *H. sapiens* Recon 1 is freely available in several formats [searchable database, metabolite and reaction lists, human-specific metabolic maps, stoichiometric matrix, and Systems Biology Markup Language (22)] at http://bigg.ucsd.edu and in SI Figs. 7–16 and SI Tables 5–10. We now describe three applications of Recon 1.

Quantitative Characterization of the Human Metabolic Bibliome Reveals an Uneven Knowledge Landscape. Bottom-up reconstruction of Recon 1 required extensive manual surveys of the primary literature to evaluate biological evidence associated with each gene, protein, and reaction. Viewing confidence scores for these individual components at the system level reveals a global knowledge landscape with specific "peaks" and "valleys" in our understanding of human metabolism (Fig. 1). Three categories of metabolic pathways were identified based on the degree of characterization of their corresponding reactions.

Category I pathways are those where extensive primary literature is available. Chondroitin sulfate is a common component of proteoglycans, which are important in cell adhesion, signaling, and connective tissue composition. Catabolism of chondroitin sulfate chains (SI Fig. 15) is a typical example of a Category I pathway in which nearly all of the enzymes have been biochemically characterized and their corresponding genes have been identified. However, the initial steps of chondroitin sulfate catabolism in endosomes (CSBPASEly) and final degradation of the core tetrasaccharide linkage (LINKDEG2ly) are not well known (23).

Category II pathways, such as glyoxylate metabolism (SI Fig. 16), have a roughly equal proportion of highly characterized enzymes and those with moderate biological evidence (see *Materials and Methods*). For instance, although the peroxisomal and mitochondrial degradation of glyoxylate to L-glycine (reactions AGTix and AGTim, respectively) has been extensively studied, the presence of the glycerate kinase reaction (GLYCK2) was inferred based on the observation that individuals with D-glycericaciduria (who lack the enzyme catalyzing this reaction) cannot further metabolize D-glycerate and excrete gram amounts of it in their urine (24).

Category III pathways exhibit a wide range of confidence scores and gene coverage. That some of these pathways have not been completely elucidated is somewhat surprising, and arguably these knowledge deficits may not have been comprehensively identified without a systems approach. For example, the mechanism that cycles the end products of vitamin C degradation back to the glycolytic pathway appear to be poorly understood (SI Fig. 17) despite evidence in human erythrocytes that it may be used as an energy source (25). Furthermore, although most of ubiquinone 10 biosynthesis was inferred from physiological evidence, there are a few well studied enzymes interspersed in the pathway (SI Fig. 18). A large number of intracellular transport reactions are also included in this category, indicating that as a whole they require considerably more investigation to elucidate precise mechanistic reactions. Thus, the reconstruction of *H. sapiens* Recon 1 has resulted in a comprehensive appraisal of our knowledge of human metabolism and has led to direct suggestions where further experimental studies are needed (SI Tables 9 and 10).

Singular Value Decomposition (SVD) of the Stoichiometric Matrix Highlights the Importance of Compartmentalization. Network capabilities are constrained in part by the overall structure of the stoichiometric matrix (**S**), which can be analyzed by using computational approaches (21). SVD (26) can identify the most influential components of a network. We used SVD to calculate the effective dimensionality of the human network to assess the number of network components needed to account for a given percentage of its structure. The cumulative normalized singular value spectrum is shown in Fig. 2 and compared with that of previous reconstructions (20, 27). The human and yeast net-

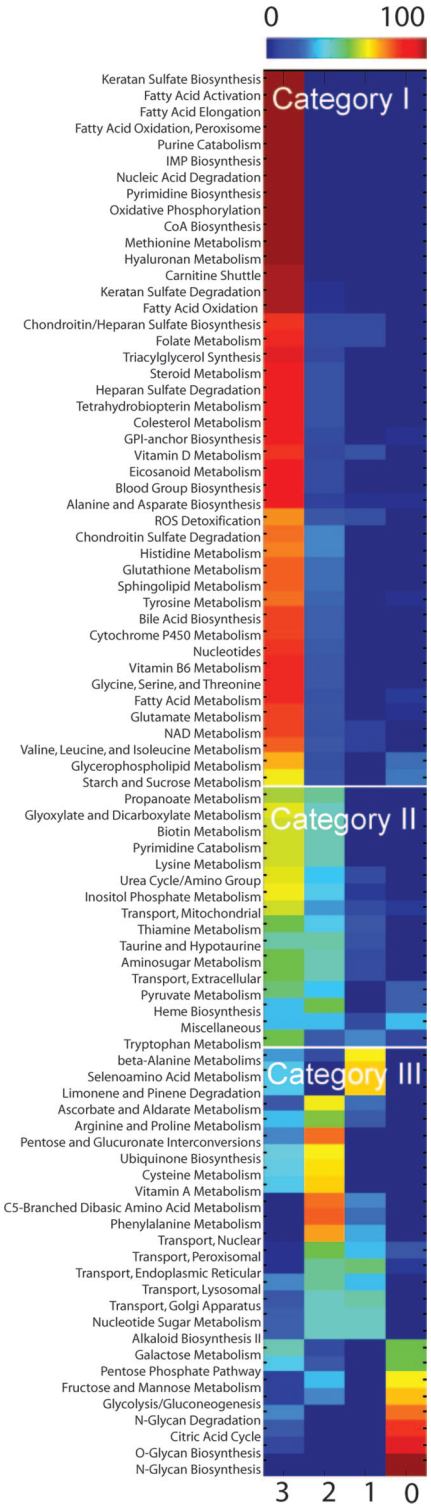
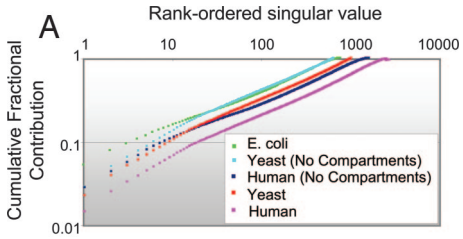


Fig. 1. Human metabolic knowledge landscape. Colors represent the percentage of reactions within a pathway that have a confidence score of 3 (biochemical or genetic evidence), 2 (physiological data or evidence from a nonhuman mammalian cell), 1 (modeling evidence), or 0 (unevaluated). Metabolic pathways (primarily defined by the Kyoto Encyclopedia of Genes and Genomes LIGAND database) were classified into three categories based on their level of characterization as detailed in the text.



B

Mode 1	Mode 2	Mode 3	Mode 4	Mode 5
adp(c)	accoa(m)	h(g)	adp(c)	h(c)
atp(c)	coa(m)	udp(g)	atp(c)	h2o(c)
h(c)	fad(m)	udpgal(g)	h2o(c)	na1(c)
h2o(c)	fadh2(m)		nadp(c)	na1(e)
pi(c)	h(m)		nadph(c)	
	h2o(m)		o2(c)	
	nad(m)		pi(c)	
	nadh(m)		ppi(c)	
	nadp(m)			
	nadph(m)			

Fig. 2. Normalized cumulative singular value spectra for *H. sapiens*, *S. cerevisiae*, and *E. coli* and dominant metabolite modes. (*A*) Compartmentalized networks have a greater effective dimensionality than their noncompartmentalized counterparts, requiring a larger number of singular values to completely reconstruct the network. Each spectrum shows the number of decomposed modes (*x* axis) required to reconstruct a given fraction (*y* axis) of the **S** matrix's content. (*B*) The first five modes of the human metabolite coupling matrix (38) highlight the importance of the production and exchange of energy equivalents and the potentially significant impact of osmotic regulation. c, cytoplasmic; e, extracellular; g, Golgi apparatus; m, mitochondrial.

works are considered with and without metabolite compartmentalization to evaluate its effect on network complexity. We observed that the compartmentalized networks have a significantly larger effective dimensionality, requiring a larger number of independent modes to fully describe their contents. For a functional metabolic model, this result may be interpreted as the expansion of nonredundant metabolic functionality rather than simply a division of linear metabolic pathways across various cellular compartments.

SVD was further applied to demonstrate unbiased systemic links between the metabolites of Recon 1. To minimize any bias arising from differing stoichiometric coefficients and lumped reactions, the metabolite-coupling matrix **M** (28) was constructed and decomposed. The five most dominant modes of the SVD of **M** (Fig. 2) are interpreted as independent groups of interacting metabolites, ordered with monotonically decreasing importance. These have biologically meaningful interpretations as currency exchanges, including high-energy phosphate group transfer (modes 1 and 4), reducing equivalent exchange (mode 2), and sugar transfer (mode 3). Mode 5 is dominated by ions and water, linking biochemical and mechanical relationships in the cell by osmotic force balance. Interestingly, these modes are compartment-specific, highlighting known relationships between compartments and cellular functions. Collectively, these observations highlight some of the implications of compartmentalization in the human metabolic reconstruction and support the notion that compartments may function as independent reaction sets to achieve specific metabolic objectives (29). This finding reinforces the idea that intracellular compartmentalization has functional implications for various metabolites, including glutathione (30), amino acids (31–33), cholesterol and bile acids (34, 35), and sphingolipids (36).

Coupled Reaction Sets Suggest Potential Alternatives to Known Drug Targets. Recon 1 has also enabled *in silico* characterization of the known human metabolic map by using well established constraint-based methods that have been applied extensively to microbial metabolism (37). Coupled reaction sets consist of reactions that are active together in functional states of a network (29, 38). Thus, a flux through one reaction results in a directionally equivalent flux in other reactions in the set. Flux coupling analysis (39) was used to identify coupled reaction sets under aerobic glucose metabolic conditions. One of the largest

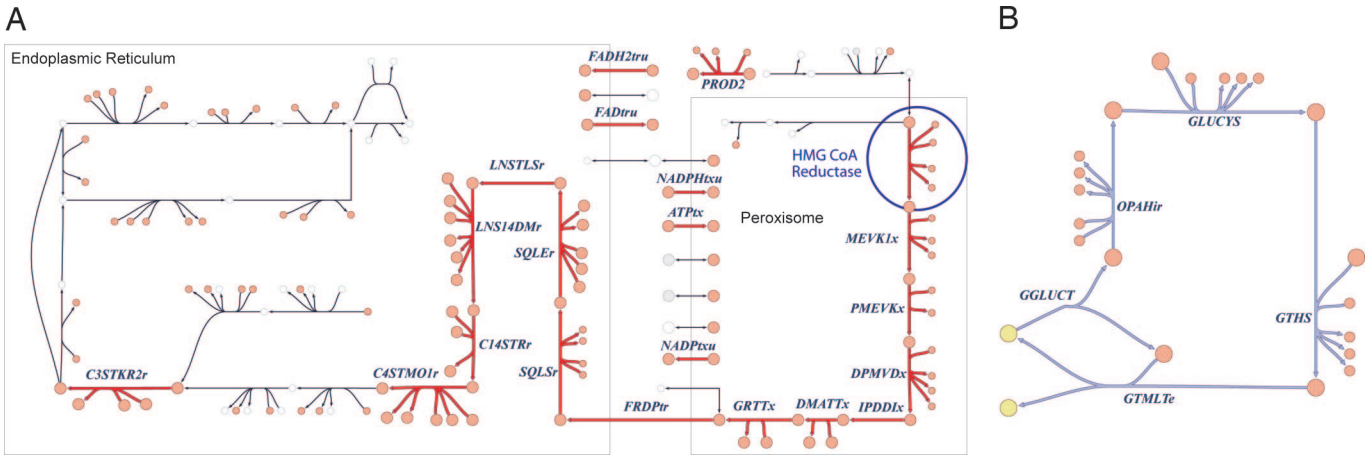


Fig. 3. Coupled reaction sets involving cholesterol biosynthesis and glutathione production and transport. (*A*) The cholesterol biosynthesis coupled set includes all reactions except those shaded in gray. Note that the groups of reactions are not all directly connected and could not be identified by visual inspection alone. (*B*) Reactions in the glutathione reaction set were mapped to disease associations by using Mendelian Inheritance in Man identification tags. Deficiencies in glutathione synthetase (GTHS) or glutamate-cysteine ligase (GLUCYS) both result in hemolytic anemia, supporting the notion that enzyme deficiencies in the same coupled set may have similar phenotypes. Interference with or decreases in GLUCYS activity is associated with an increased risk of myocardial infarctions (MI). A high-resolution version of this figure is available in SI Figs. 19 and 20.

of the >250 coupled reaction sets identified under these metabolic conditions involves two branches of cholesterol biosynthesis (Fig. 3*A* and SI Fig. 19). 3-Hydroxy-3-methylglutaryl-CoA reductase (Entrez Gene ID 3156), a primary metabolic target of the antilipidemic class of statin drugs, is in this coupled reaction set; other members of the set are thus identified as potential alternative drug targets for treating hyperlipidemia. It has been proposed that deficiencies in enzymes belonging to the same functionally coupled reaction set may have similar phenotypes, and examples of this have been reported for the human mitochondria (38). This hypothesis is supported by the example in Fig. 3*B* (SI Fig. 20), which depicts a coupled reaction set involved in the production and transport of glutathione. The Online Mendelian Inheritance in Man (OMIM) (40, 41) identification tags associated with the genes encoding glutathione synthetase (MIM no. 231900; Entrez Gene ID, 2937) and glutamate-cysteine ligase (OMIM no. 230450; Entrez Gene ID, 2729) indicate that both deficiencies result in hemolytic anemia. These examples demonstrate that *in silico* experiments with these models provide an analytical approach to studying the causes and consequences of disease states, which can potentially lead to insights into new drug treatment targets. The use of functionally grouped reactions, such as coupled (39) and correlated reaction sets (42), present a promising approach for the functional analysis of complex networks with applications in elucidating causal relationships in the diseases and potentially identifying new treatment strategies and drug targets (29).

Integrated Analysis of Gene Expression Data Reveals the Effects of Gastric Bypass Surgery on Skeletal Muscle Metabolism. Recon 1 was used as a context for interpreting the effects of gastric bypass surgery on skeletal muscle metabolism. In this study, gene expression data were acquired from the same patients before and after bariatric surgery. Consequently, many genetic factors that might contribute to interindividual differences are not a concern in this analysis. Published gene expression measurements (43) were mapped to the reconstructed network by using gene–transcript–protein–reaction associations (see *Materials and Methods*) and visualized on maps of central metabolism and the electron transport chain (Fig. 4; SI Fig. 21). We observed a general trend of up-regulated anaerobic metabolism and down-regulated oxidative phosphorylation after surgery, with many genes in glycolysis, pentose phosphate pathway, methylglyoxal metabolism, and oxidative phosphorylation showing subtle but consistent overall patterns of expression change (SI Tables 11–15). The relative decrease in mitochondrial bioenergetics is also evident in terms of the smaller number of mitochondrial reactions in the down-regulated network (SI Fig. 22) and is consistent with gene expression changes observed in the skeletal muscle of rhesus monkeys subjected to long-term caloric restriction (44). Comparison of gene expression data in the context of Recon 1 suggests that 1 year after surgery, patients may still be feeling the effects of calorie restriction even after weight stabilization. Thus, Recon 1 represents a versatile and effective integration tool, enabling visualization and analysis of genome-scale context in the context of a highly curated metabolic network.

Conclusions

Reconstruction of the global (or genome-scale) human metabolic network in a standardized, quality-controlled, bottom-up manner is presented. *H. sapiens* Recon 1 is a BiGG reconstruction and represents a milestone in human systems biology. It is a mathematically structured database that enables systematic studies of the human metabolism and its properties. The reconstruction process required comprehensive review of the published human metabolic knowledge base (i.e., bibliomic data), and it led to a global quantitative assessment of network confidence that has highlighted specific areas of limited or poor understanding, such as intracellular transport of metabolites, which need further experimental investigation. The formulation of an *in silico* model from the reconstruction and initial analysis of the network structure highlighted the importance of intracellular compartmentalization. Further analyses demonstrated the potential utility of the model as a tool for discovery and for the analysis and interpretation of high-throughput data. These capabilities will likely be critical in elucidating underlying mechanisms of disease and identifying treatment strategies by developing cell-, tissue-, and context-specific models and building additional layers of complexity (such as gene regulation) into the framework.

Genome-scale microbial metabolic reconstructions have been widely used to successfully perform systems analysis to the point that models resulting from these reconstructions have become tools for hypothesis driven biological discovery (4). We expect that this global human metabolic reconstruc-

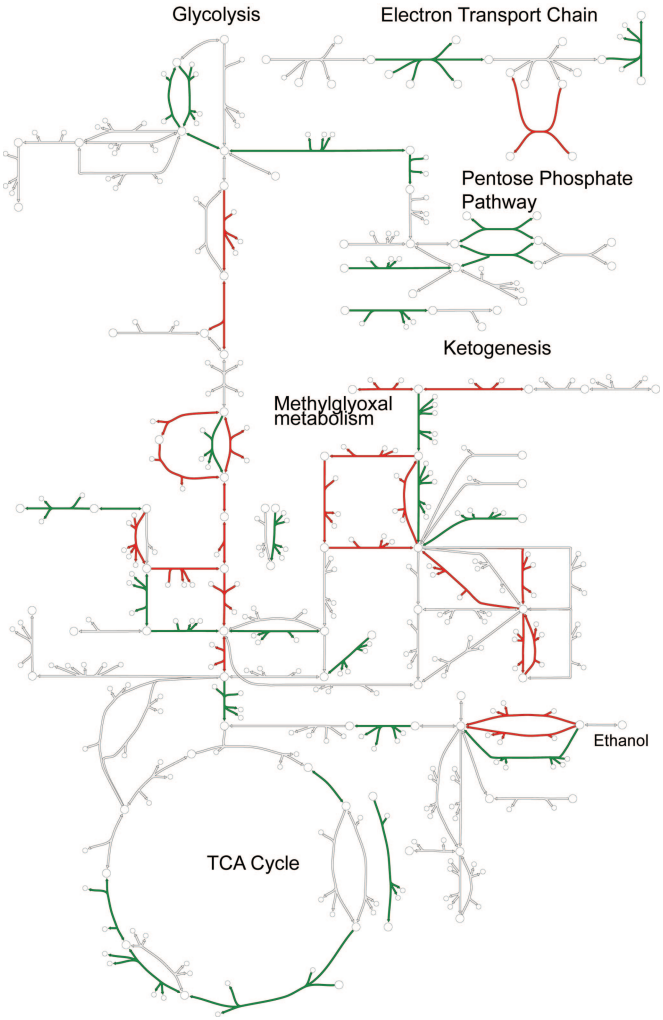


Fig. 4. Integrated analysis of gene expression data from gastric bypass patients before surgery and 1 year afterward. Expression measurements were to reactions in the global human metabolic network and then visualized on Recon 1's comprehensive collection of human metabolic maps. Reactions are color-coded based on their corresponding gene expression changes (green, down-regulated; red, up-regulated; white, no data available or reaction level conflict). Arrows next to reaction abbreviations indicate the magnitude of expression changes on a log10 scale (gray boxes indicate no data available). A high-resolution version of this figure is available in SI Fig. 21.

tion will not only become a prototype for other mammalian reconstructions but will hopefully also enable significant dimensions in the study of in human systems biology, some of which we have described herein. The future promise for individualized medicine and treatment will need a context to integrate and analyze data, and models resulting from these reconstructions can play a significant role in fulfilling this need. However, the development of cell-type or context-specific models will require the integration of various types of data, including transcriptomic, proteomic, fluxomic, and metabolomic measurements. Recon 1 provides the context for integration and analysis of these data into predictive models. For example, the developing field of nutrigenomics requires significant data integration and analysis to elucidate the influence of the diet on an organism's transcriptome, proteome, and metabolome (45). Achieving these ambitious goals will require top–down data sets in conjunction with quantitative bottom-up reconstructions such as *H. sapiens* Recon 1.

Materials and Methods

Reconstruction Procedure. An initial component list was assembled as described in the text. This list was then divided into eight metabolic subsets (amino acids, carbohydrates, energy, glycans, lipids, nucleotides, secondary metabolites/xenobiotics, vitamins, and cofactors) for independent curation by a team of researchers. Putative gene assignments were verified based on evidence collected from genome annotation databases, namely EntrezGene (18), Gene Cards (46), and the scientific literature. Alternative transcripts were identified based on known RefSeq (17) mRNA transcripts for each locus. Substrate and cofactor preferences were identified from the literature and BRENDA (47). Metabolite formula and charge were calculated based on their ionization state at pH 7.2, which for simplicity was presumed to be constant across all compartments. Reaction directionality was determined from thermodynamic data or inferred from legacy data and textbooks. Compartmentalization was determined from protein localization data, sequence targeting signals, and indirect physiological evidence. If these data were unavailable, reactions were modeled as cytoplasmic. The intermembrane space of double-membrane organelles was also modeled as cytoplasmic. Gene–transcript–protein–reaction relationships (5, 6) were manually identified from the literature and formulated as Boolean logic statements. Isozymes (an "or" relationship) were defined as distinct proteins that catalyze the same substrate- and compartment-specific reaction and could arise from one gene due to alternative splicing or could be encoded by independent genes. Cases in which a reaction depended on the presence of more than one gene/protein (an "and" relationship, e.g., proteins with multiple subunits/chains or complexes composed of multiple enzymes) were classified as protein complexes. Confidence scores were assigned based on biological evidence associated with each reaction. Evidence from classical biochemical or genetic experiments, such as gene cloning and protein characterization, was given the highest confidence score (3). Midlevel scores (2) were assigned to reactions based on physiological data or biochemical/genetic evidence from a nonhuman mammalian cell (typically mouse, rat, or rabbit). Reactions with the lowest confidence score (1) were included solely based on *in silico* modeling because, during the process of model validation, they were deemed mandatory for a particular metabolic function. Transport reactions were entirely reconstructed based on literature reports and biochemistry textbooks because the current annotation of transporters is not sufficiently specific with regard to substrates and mechanisms.

Functional Validation and Gap Analysis. The reconstruction was assembled in SimPheny (Genomatica, San Diego, CA), and the stoichiometric matrix was formulated as described (48). Exchange reactions (SI Table 6) were added to enable uptake and secretion of extracellular metabolites for the purpose of simulations. Functional validation was performed by using flux balance analysis (39), allowing recycled cofactor pairs to enter and leave the system as needed (SI Tables 2–4). Comprehensive gap analysis of the stoichiometric matrix was performed after each round of functional validation. Every "dead-end" metabolite that could not be produced or consumed was manually reexamined by returning to the literature to identify possible reactions describing its degradation, production, or transport. A final round of gap analysis was performed upon completion of *H. sapiens* Recon 1, and a description of unresolved gaps is provided in SI Table 9.

Network Analysis. The singular value spectra (26) were computed for *H. sapiens* Recon 1, *Saccharomyces cerevisiae* iND750 (20), and *Escherichia coli* iJR904 (48) as the normalized cumulative sum of the singular values by using Matlab Ver. 6.5 (MathWorks, Natick,

MA). The stoichiometric matrix was not altered or scaled before SVD. The human and yeast networks were decompartmentalized by reassigning all intracellular metabolites to the cytoplasm. Modes were defined as the largest elements (each $>0.25\times$max column value) of the columns of **U** (identical to the columns of **V**), where $\mathbf{U\Sigma V^T} = \hat{\mathbf{S}}\hat{\mathbf{S}}^{\mathbf{T}}$ and $\hat{S}$ is the binary form of **S**. Noncompartmentalized versions of the human and yeast model were created by summing up the rows of the **S** matrix corresponding to the same metabolite in the different intracellular compartments.

Coupled reaction sets were calculated with a bilinear optimization algorithm described by Burgard *et al.* (39) by using LINDO r6.1 (Lindo Systems, Chicago, IL) called from within Matlab Ver. 6.5 for aerobic glucose uptake conditions. Briefly, for all of the fluxes in the network under specified input conditions, if two fluxes always respond in the same manner (both increase or both decrease) to any perturbation or alternative flux distribution, they are said to be coupled.

Gene Expression Analysis. Gene expression data for the gastric bypass study were downloaded from Gene Expression Omnibus (GEO) [GSE5109 (49)]. Expression signals were normalized by the average value for each chip. Log10 ratios of post/pregastric surgery probe expression signals were calculated for all three patients in the gastric bypass data set and mapped to Entrez Gene and RefSeq mRNA identifications (18) in *H. sapiens* Recon 1 based on database identifiers in the Affymetrix (Santa Clara, CA) U133A Plus 2.0 annotation file (50). Probes whose expression ratio was qualitatively inconsistent across all three patients (i.e., not all up or all down) or that conflicted at the gene level were removed from the data set. Average gene expression ratios were then mapped to the reaction network by using Recon 1's gene–transcript–protein–reaction associations.

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Table 2: *H. sapiens* Recon 1 simulation list. A complete list of the 288 simulations used to validate Recon 1. Objective column # refers to the column in SI Table 4 that is optimized in the flux balance analysis simulation.

SIMULATION #	SIMULATION NAME	OBJECTIVE COLUMN #
1	his-L-> glu-L [c]	698
2	hista -> im4ac [c]	761
3	his-L -> hista [c]	750
4	hista -> 3mlda [c]	482
5	pro-L -> glu-L [m]	699
6	glu-L -> pro-L [m]	878
7	arg-L -> glu-L [m]	699
8	ATP[c] max aerobic, glc, v0.05	12
9	arg-L -> no [c]	828
10	asp-L + hco3 -> arg-L [c]	554
11	ptrc -> ala-B [c]	538
12	ura -> ala-B [c]	538
13	carn -> ala-B [c]	538
14	msa -> ala-B [c]	538
15	ala-B -> msa [m]	801
16	ptrc -> spmd [c]	905
17	spmd -> sprm [c]	906
18	ala-L -> ala-D [c]	539
19	ala-D -> pyr [c]	882
20	ATP[c] max, anaerobic glc, v0.05	12
21	gln-L(m) -> glu-L(m)	699
22	glu-L(m) -> akg(m)	536
23	cys-L + glu-L + gly -> gthrd [c]	721
24	gthrd [c] reduces h2o2	720
25	phe-L -> tyr-L [c]	931
26	phe-L -> phpyr [c]	862
27	phe-L -> pheacgln [c]	859
28	phe-L -> peamn [c]	854
29	phe-L -> pacald [c]	843
30	phe-L -> pac [c]	842
31	phe-L -> phaccoa [c]	857
32	selmeth -> selnp [c]	900
33	dna(n) -> dna5mtc(n)	625
34	cys-L -> hyptaur [c]	757
35	hyptaur(c) -> taur(x)	913
36	Lcyst(c) -> taur(x)	913
37	taur(x) -> tchola(x)	914
38	trp-L -> accoa [c]	512
39	trp-L -> srtn [c]	908
40	trp-L -> melatn [c]	792
41	trp-L -> Lfmkynr [c]	496
42	trp-L -> Lkynr [c]	497
43	trp-L -> nformanth [c]	822
44	srtn -> 5moxact [c]	489
45	srtn -> 6hoxmelatn [c]	491
46	srtn -> fna5moxam [c]	660

47	srtn -> nmthsrtn [c]	827
48	srtn -> f5hoxkyn [c]	645
49	trp-L -> quln [c]	888
50	trp-L -> id3acald [c]	758
51	trp-L -> anth [c]	551
52	trp-L -> kynate [c]	775
53	tyr-L -> fum + acac [c]	509
54	tyr-L -> T3 + T4 [c]	925
55	tyr-L -> 34hpp [c]	480
56	tyr-L -> nrpphr [c]	829
57	tyr-L -> adrnl [c]	531
58	tyr-L -> melanin [c]	791
59	tyr-L -> 4hphac [c]	485
60	tyr-L -> dopa [c]	634
61	dopa -> homoval (1) [c]	752
62	dopa -> homoval (2) [c]	752
63	npphr -> 34dhoxpeg [c]	479
64	adrnl -> 34dhoxpeg [c]	479
65	adrnl -> 34dhoxpeg (2) [c]	479
66	arg -> no [c]	828
67	orn -> ptrc [c]	880
68	orn -> spmd [c]	905
69	orn -> sprm [c]	906
70	arg-L -> pcreat [c]	851
71	arg-L -> creat [c]	594
72	glu5sa -> pro-L [c]	877
73	tyr-L -> T3 + T4 (2)	925
74	adrnl -> 34dhoxpeg (3) [c]	479
75	dmpp -> ggdp [c]	692
76	ipdp(x) -> sql(r)	907
77	coke(r) -> pecgoncoa(r)	855
78	acorn -> orn [c]	840
79	4hpro-LT(m) -> glx(m)	703
80	lys-L [c] -->accoa [m] (via saccrp-L pathway)	514
81	akg[c] --> glu-L[c] via ALATA_L	698
82	akg[c] --> glu-L[c] via ASPTA	698
83	akg[m] --> glu-L[m] via ASPTAm	699
84	glu-L-->gln-L[c]	695
85	gln-L[m]-->glu-L[m]	699
86	4abut --> succ [m]	909
87	glu-L-->4abut	484
88	lys-L[x] -->aacoa [m] (via Lpipecol pathway)	514
89	3pg-->ser-L [c]	901
90	3pg-->gly [c]	705
91	gly --> co2 + nh4 (via glycine cleavage system) [m]	583
92	thr-L --> ppcoa [c]	869
93	ser-L-->cys-L [c]	611
94	choline --> betaine --> glycine [m]	706
95	met-L-->cys-L [c]	611
96	cys-L--> 3sala -->so4 [c]	902

97	leu-L --> accoa [m]	514
98	ile-L -->accoa [m]	870
99	val-L --> succoa [m]	911
100	gly -->ser-L --> pyr (via SERD_L) [c]	882
101	cystine -->cys-L [c]	611
102	so4 --> PAPS [c]	848
103	o2- --> h2o2 --> o2 + h2o [m]	831
104	ATP[m] production via electron transport chain	561
105	5aop -->pheme [m]	861
106	asp-L-->asn-L [c]	557
107	asp-L --> oaa [c]	836
108	asn-L --> oaa [c]	836
109	asp-L-->ala-B [c]	538
110	pyr<>ala-L [c]	882
111	ala-L-->pyr [c]	882
112	asp-L-->fum (via dcamp) [c]	668
113	asp-L-->fum (via argsuc) [c]	668
114	pheme-->bilirub [c]	566
115	glc -> pyr [c]	47
116	glc -> lac-D [c]	777
117	glc -> lac + atp + h2o [c]	42
118	pyr -> lac-D [c]	777
119	pyr[c] -> accoa[m] + co2[c] + nadh[m]	8
120	etoh -> acald [c]	511
121	acald -> ac [c]	507
122	lac -> glc [c]	32
123	glyc -> glc [c]	32
124	g6p -> ru5p-D [c]	891
125	g6p -> r5p [c]	890
126	f6p + g3p -> r5p [c]	890
127	udpglcur -> xu5p-D [c]	957
128	fru -> dhap [c]	25
129	fru -> g3p [c]	31
130	gal -> udpgal [c]	943
131	glc -> lcts[g] (2)	778
132	gal -> glc [c]	260
133	pyr -> nad[m] + h[m]	1924
134	pyr -> fad[m] + h[m]	30
135	akg[m[-> oaa[m]	837
136	succoa[m] -> oaa[m]	837
137	fum [m] -> oaa [m]	837
138	ascb -> thrnt [c]	923
139	ascb -> eryth [c]	642
140	ascb -> lyxnt [c]	782
141	ascb -> xylnt [c]	959
142	Tyr-ggn -> glygn2 [c]	714
143	glygn2 -> glc [c]	32
144	glygn2[e] -> glc[e]	261
145	strch1[e] -> glc[e]	261
146	man6p -> kdn [c]	768

147	man -> gdpmann [c]	691
148	fuc -> gdpfuc [c]	689
149	gdpmann -> gdpfuc [c]	689
150	gam6p -> uacgam [c]	55
151	acgal -> udpacgal [c]	939
152	acgam -> cmpacna [c]	579
153	g1p -> dtdprmn [c]	636
154	glc -> inost [c]	763
155	inost -> xu5p-D [c]	957
156	inost -> pail_hs [c]	846
157	inost -> pail4p_hs [c]	845
158	pail45p -> mi145p [c]	796
159	mi145p -> inost [c]	763
160	inost -> pail45p_hs [c]	844
161	itacon[m] -> pyr[m]	883
162	mescon[m] -> pyr[m]	883
163	hpyr -> 2pg [c]	478
164	hpyr -> glyclt [c]	712
165	xylu-D -> glyclt [c]	712
166	glyclt -> gly [c]	705
167	glyx -> oxa [c]	841
168	glx[m] -> glyclt[m]	713
169	hpyr -> glyc-S [c]	710
170	dhap -> mthgxl [c]	802
171	g3p -> mthgxl [c]	802
172	acetone -> mthgxl [c]	802
173	aact -> mthgxl [c]	802
174	mthgxl -> lac-D [c]	777
175	mthgxl -> 12ppd-S [c]	474
176	12ppd-S -> mthgxl [c]	802
177	12ppd-S -> pyr [c]	882
178	ppcoa[m] -> succoa[m]	911
179	acac[m] -> acetone [m]	517
180	acac[m] -> bhb[m]	565
181	hmgcoa(x)->frdp(x)	664
182	hmgcoa(x)->chsterol(r)	2288
183	hmgcoa(x)-chsterol(r)	1886
184	hmgcoa(x)->xoldiolone(r)	3428
185	hmgcoa(x)->xoltriol(c)	1301
186	xoltriol(m)->thcholstoic(m) v0.05	916
187	pmtcoa(c)->crmp_hs(c)	1887
188	pmtcoa(c)->sphmyln_hs(c)	3921
189	galgluside_hs(g) -> gd1c_hs(g)	3986
190	galgluside_hs(g) -> gq1balpha_hs(g)	3975
191	galgluside_hs(g) -> gq1balpha_hs(g) path 2	3974
192	galgluside_hs(g) -> gq1balpha_hs(g) path 3	3980
193	galgluside_hs(g) -> gp1c_hs(g)	3977
194	galgluside_hs(g) -> gd1b2_hs(g)	3973
195	galgluside_hs(g) -> acgagbside_hs(g)	2480
196	galgluside(g) -> galgalgalthcrm_hs(g)	1494

197	galgluside_hs(g) -> acnacngalgbside_hs(g)	3981
198	gluside_hs(g) -> galgluside_hs(g)	1500
199	thcholstoic(x)->gchola(x) v0.05	683
200	thcholstoich(x)->tchola(x) v0.05	914
201	arachd(r) -> txa2(r)	4132
202	glyc(c) + Rtotal(c) -> tag_hs(c) v0.05	912
203	chol(c) + dag_hs(c) -> pe_hs(c)	3654
204	from thm(e) to thmpp(m)	54
205	from thmmp(e) to thmpp(m)	54
206	from thmmp(e) to thmpp(c)	53
207	from thm(c) to thmpp(c)	53
208	from prpp to imp [c]	40
209	from adn(c) to urate(x)	57
210	from imp(c) to urate(x)	57
211	from gsn(c) to urate(x)	57
212	from imp to atp [c]	13
213	from imp to gtp [c]	36
214	from cytd to ala-B [c]	10
215	from cmp to cytd [c]	10
216	from ump to ala-B[c]	10
217	from dcmp to ala-B[c]	10
218	missing dtmp-3aib(c) testing	3
219	from gln-L + HCO3 to UMP(c)	56
220	from ADP(c) to dATP(n)	20
221	from ADP(c) to dATP(n) 2	20
222	from GDP(c) to dGTP(n)	24
223	from CDP(c) to dCTP(n)	22
224	from GDP(c) to dGTP(n) 2	24
225	from UDP(c) to dTTP(n)	28
226	from tyr-L(m) to q10(m)	50
227	val-L-->3aib [m]	481
228	val-L --> succoa [m]	911
229	from pydx(c) to pydx5p(c)	46
230	from hxan(c) to imp(c)	40
231	from gua(c) to gmp(c)	34
232	from ade(c) to amp(c)	11
233	thcholstoic(x) -> gchola(x)	1502
234	thcholstoic(x) -> tchola(x)	1503
235	gln -> nh4(e) v0.05	343
236	R_group	2235
237	arachd(c)->malcoa(m)	2154
238	accoa(c)->pmtcoa(c)->malcoa(m)	43
239	glyc(c) + Rtotal(c) + Rtotal2(c) -> dag_hs(c)	18
240	phytcoa(x)->dmnoncoa(m) v0.05	621
241	frdp -> dolichol_U [c]	628
242	frdp -> dolichol_L [c]	627
243	dolichol_L -> dolmanp_L[r]	630
244	dolichol_U -> dolmanp_U[r]	631
245	dolichol_U -> g3m8mpdol_U[r]	673
246	dolichol_L -> g3m8mpdol_L[r]	671

247	uacgam -> m8masn[r]	785
248	m8masn[r] -> nm4masn[g]	826
249	nm4masn[g] -> l2fn2m2masn[g]	776
250	nm4masn[g] -> s2l2fn2m2masn[g]	892
251	nm4masn[g] -> n2m2nmasn[g]	803
252	s2l2fn2m2masn[l] -> man[l] + acgam[l]	61
253	n2m2nmasn[l] -> man[l] + acgam[l]	61
254	Ser/Thr[g] + udpacgal[g] -> dsTn_antigen[g]	635
255	Ser/Thr[g] + udpacgal[g] -> sTn_antigen[g]	895
256	Ser/Thr[g] + udpacgal[g] -> core2[g]	592
257	Ser/Thr[g] + udpacgal[g] -> core4[g]	593
258	pail_hs -> gpi_prot_hs[r]	716
259	uacgam + udpglcur -> ha[e]	38
260	ha[l] -> acgam[l] + glcur[l]	59
261	Ser-Gly/Ala-X-Gly[er] -> cs_pre[g]	599
262	Ser-Gly/Ala-X-Gly[er] -> cspg_a[g]	600
263	Ser-Gly/Ala-X-Ser[er] -> cspg_b[g]	602
264	Ser-Gly/Ala-X-Gly[er] -> cspg_c[g]	604
265	Ser-Gly/Ala-X-Gly[er] -> cspg_d[g]	606
266	Ser-Gly/Ala-X-Gly[er] -> cspg_e[g]	608
267	core2[g] -> ksii_core2[g]	771
268	core4[g] -> ksii_core4[g]	773
269	l2fn2m2masn[g] -> ksi[g]	769
270	Ser-Gly/Ala-X-Gly[er] -> hspg[g]	754
271	hspg[ly] -> 2 gal[ly] + glcur[ly] + xyl-D[ly]	5
272	cspg_a[ly] -> 2 gal[ly] + glcur[ly] + xyl-D[ly]	5
273	cspg_b[ly] -> 2gal[ly] + glcur[ly] + xyl-D[ly]	5
274	cspg_c[ly] -> 2 gal[ly] + glcur[ly] + xyl-D[ly]	5
275	cspg_d[ly] -> 2 gal[ly] + glcur[ly] + xyl-D[ly]	5
276	cspg_e[ly] -> 2 gal[ly] + glcur[ly] + xyl-D[ly]	5
277	ksi[l] -> man[l] + acgam[l]	61
278	ksii_core2[ly] -> Ser/Thr[ly]	504
279	ksii_core4[ly] -> Ser/Thr[ly]	504
280	Human Recon 1 test mouse biomass 2	4275
281	ATP[c] max, aerobic, citrate v0.05	12
282	ATP[c] max, aerobic, glutamine substrate v0.05	12
283	ATP[c] max, aerobic, EtOH substrate v0.05	12
284	ATP[c] max, aerobic, lactate substrate v0.05	12
285	ATP[c] max, aerobic, glutamate v0.05	12
286	ATP[c] max, aerobic, glycine substrate v0.05	12
287	ATP[c] max, aerobic, proline substrate v0.05	12
288	orn -> nh4(e) v0.05	343

Table 3: Rows of the stoichiometric matrix (metabolites). Ordered list of rows of the stoichiometric matrix used in the debugging simulations (SI Table 2).

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
1	286c	10fthf(c)	10-Formyltetrahydrofolate	Cytosol
2	20786c	10fthf5glu(c)	10-formyltetrahydrofolate-[Glu](5)	Cytosol
3	20787c	10fthf6glu(c)	10-formyltetrahydrofolate-[Glu](6)	Cytosol
4	20788c	10fthf7glu(c)	10-formyltetrahydrofolate-[Glu](7)	Cytosol
5	22812c	11-cis-retfa(c)	fatty acid 11-cis-retinol	Cytosol
6	3407c	11docrtsl(c)	11-Deoxycortisol	Cytosol
7	2404c	11docrtstrn(c)	11-Deoxycorticosterone	Cytosol
8	3552c	12HPET(c)	12-Hydroperoxyeicosa-5,8,10,14-tetraenoate	Cytosol
9	20144c	12RHPET(c)	12R-Hydroperoxyeicosatetraenoate	Cytosol
10	2181c	12ppd-R(c)	(R)-Propane-1,2-diol	Cytosol
11	1889c	12ppd-S(c)	(S)-Propane-1,2-diol	Cytosol
12	22815c	13-cis-oretn(c)	13-cis-oxo-retinoic acid	Cytosol
13	22814c	13-cis-retn(c)	13-cis-retinoate	Cytosol
14	22816c	13-cis-retnglc(c)	13-cis-retinoyl glucuronide	Cytosol
15	812c	13dampp(c)	1,3-Diaminopropane	Cytosol
16	288c	13dpg(c)	3-Phospho-D-glyceroyl phosphate	Cytosol
17	4422c	15HPET(c)	15-Hydroperoxyeicosatetraenoic acid	Cytosol
18	3713c	17ahprgnlone(c)	17alpha-Hydroxypregnenolone	Cytosol
19	769c	17ahprgstrn(c)	17alpha-Hydroxyprogesterone	Cytosol
20	18732c	1mncam(c)	1-Methylnicotinamide	Cytosol
21	4589c	1mpyr(c)	1-Methylpyrrolinium	Cytosol
22	2994c	1pyr5c(c)	1-Pyrroline-5-carboxylate	Cytosol
23	4195c	23doguln(c)	2,3-Dioxo-L-gulonate	Cytosol
24	5576c	23dpg(c)	2,3-Disphospho-D-glycerate	Cytosol
25	20023c	2425dhvitd2(c)	24R,25-Dihyoxyvitamin D2	Cytosol
26	20024c	2425dhvitd3(c)	24R,25-Dihydroxyvitamin D3	Cytosol
27	20412c	24nph(c)	2,4 dihydroxy nitrophenol	Cytosol
28	3554c	25aics(c)	(S)-2-[5-Amino-1-(5-phospho-D-ribosyl)imidazole-4-carboxamido]succinate	Cytosol
29	20014c	25hvitd2(c)	25-Hydroxyvitamin D2	Cytosol
30	20012c	25hvitd3(c)	25-Hydroxyvitamin D3	Cytosol
31	1585c	2amac(c)	2-Aminoacrylate	Cytosol
32	2735c	2ameph(c)	(2-Aminoethyl)phosphonate	Cytosol
33	11252c	2c23dh56dhoxin(c)	2-Carboxy-2,3-dihydro-5,6-dihydroxyindole	Cytosol
34	4321c	2coum(c)	cis-2-Hydroxy cinnamate	Cytosol
35	446c	2dr1p(c)	2-Deoxy-D-ribose 1-phosphate	Cytosol
36	447c	2dr5p(c)	2-Deoxy-D-ribose 5-phosphate	Cytosol
37	4433c	2hb(c)	2-Hydroxybutyrate	Cytosol
38	4332c	2hyoxplac(c)	2-Hydroxyphenylacetate	Cytosol
39	5757c	2kmb(c)	2-keto-4-methylthiobutyrate	Cytosol
40	3219c	2mcacn(c)	cis-2-Methylaconitate	Cytosol
41	1591c	2mcit(c)	2-Methylcitrate	Cytosol
42	1071c	2obut(c)	2-Oxobutanoate	Cytosol
43	9002c	2oxoadp(c)	2-Oxoadipate	Cytosol
44	1120c	2pg(c)	D-Glycerate 2-phosphate	Cytosol
45	813c	2pglyc(c)	2-Phosphoglycolate	Cytosol
46	787c	34dhcinm(c)	3,4-Dihydroxy-trans-cinnamate	Cytosol
47	3465c	34dhmald(c)	3,4-Dihydroxymandelaldehyde	Cytosol
48	4121c	34dhoxmand(c)	3,4-Dihydroxymandelate	Cytosol
49	3464c	34dhoxpeg(c)	3,4-Dihydroxyphenylethyleneglycol	Cytosol
50	3087c	34dhpac(c)	3,4-Dihydroxyphenylacetaldehyde	Cytosol
51	916c	34dhpha(c)	3,4-Dihydroxyphenylacetate	Cytosol

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
52	190c	34dhphe(c)	3,4-Dihydroxy-L-phenylalanine	Cytosol
53	772c	34hpp(c)	3-(4-Hydroxyphenyl)pyruvate	Cytosol
54	9005c	35cgmp(c)	3',5'-Cyclic GMP	Cytosol
55	693c	35diotyr(c)	3,5-Diiodo-L-tyrosine	Cytosol
56	2457c	3aib(c)	L-3-Amino-isobutanoate	Cytosol
57	2444c	3aib-D(c)	D-3-Amino-isobutanoate	Cytosol
58	1111c	3dhguln(c)	3-Dehydro-L-gulonate	Cytosol
59	8537c	3dsphgn(c)	3-Dehydrosphinganine	Cytosol
60	9007c	3hanthrn(c)	3-Hydroxyanthranilate	Cytosol
61	4184c	3hpcoa(c)	3-Hydroxypropionyl-CoA	Cytosol
62	7127c	3hpp(c)	3-Hydroxypropanoate	Cytosol
63	7135c	3htmelys(c)	3-Hydroxy-N6,N6,N6-trimethyl-L-lysine	Cytosol
64	4156c	3hxkynam(c)	3-Hydroxykynurenamine	Cytosol
65	1810c	3ityr-L(c)	3-Iodo-L-tyrosine	Cytosol
66	4123c	3m4hpga(c)	3-Methoxy-4-hydroxyphenylglycolaldehyde	Cytosol
67	10891c	3mlda(c)	3-Methylimidazoleacetic acid	Cytosol
68	4313c	3mldz(c)	3-Methylimidazole acetaldehyde	Cytosol
69	225c	3mob(c)	3-Methyl-2-oxobutanoate	Cytosol
70	445c	3mop(c)	(S)-3-Methyl-2-oxopentanoate	Cytosol
71	4124c	3mox4hoxm(c)	3-Methoxy-4-hydroxymandelate	Cytosol
72	4122c	3mox4hpac(c)	3-Methoxy-4-hydroxyphenylacetaldehyde	Cytosol
73	4126c	3moxtyr(c)	3-Methoxytyramine	Cytosol
74	4211c	3padsel(c)	3'-Phosphoadenylylselenate	Cytosol
75	259c	3pg(c)	3-Phospho-D-glycerate	Cytosol
76	9544c	3php(c)	3-Phosphohydroxypyruvate	Cytosol
77	1105c	3sala(c)	3-Sulfino-L-alanine	Cytosol
78	3427c	3snpyr(c)	3-Sulfinopyruvate	Cytosol
79	15766c	3spyr(c)	3-Sulfopyruvate	Cytosol
80	10517c	3uib(c)	3-Ureidoisobutyrate	Cytosol
81	4163c	42A3HP24DB(c)	4-(2-Amino-3-hydroxyphenyl)-2,4-dioxobutanoate	Cytosol
82	9128c	44mctr(c)	4,4-dimethylcholesta-8,14,24-trienol	Cytosol
83	4159c	46dhoxquin(c)	4,6-Dihydroxyquinoline	Cytosol
84	4157c	48dhoxquin(c)	4,8-Dihydroxyquinoline	Cytosol
85	7924c	4aabutn(c)	4-Acetamidobutanoate	Cytosol
86	176c	4abut(c)	4-Aminobutanoate	Cytosol
87	376c	4abutn(c)	4-Aminobutanal	Cytosol
88	7132c	4aphdob(c)	4-(2-Aminophenyl)-2,4-dioxobutanoate	Cytosol
89	9008c	4fumacac(c)	4-Fumarylacetoacetate	Cytosol
90	896c	4h2oglt(c)	4-Hydroxy-2-oxoglutarate	Cytosol
91	20409c	4hdebrisoquine(c)	4 hydroxy debrisoquine	Cytosol
92	2887c	4hoxpacd(c)	4-Hydroxyphenylacetaldehyde	Cytosol
93	1127c	4hphac(c)	4-Hydroxyphenylacetate	Cytosol
94	2826c	4izp(c)	4-Imidazolone-5-propanoate	Cytosol
95	9010c	4mlacac(c)	4-Maleylacetoacetate	Cytosol
96	285c	4mop(c)	4-Methyl-2-oxopentanoate	Cytosol
97	20411c	4mtolbutamide(c)	4 hydroxy tolbutamide	Cytosol
98	730c	4nph(c)	4-Nitrophenol	Cytosol
99	21119c	4nphsf(c)	4-Nitrophenyl sulfate	Cytosol
100	2022c	4ppan(c)	D-4'-Phosphopantothenate	Cytosol
101	2645c	4ppcys(c)	N-((R)-4-Phosphopantothenoyl)-L-cysteine	Cytosol
102	717c	4pyrdx(c)	4-Pyridoxate	Cytosol

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
103	908c	4tmeabut(c)	4-Trimethylammoniobutanal	Cytosol
104	7131c	4tmeabutn(c)	4-Trimethylammoniobutanoate	Cytosol
105	7551c	56dihindlcrbxlt(c)	5,6-Dihydroxyindole-2-carboxylate	Cytosol
106	751c	56dthm(c)	5,6-Dihydrothymine	Cytosol
107	423c	56dura(c)	5,6-dihydrouracil	Cytosol
108	3862c	5HPET(c)	5-Hydroperoxy-6-trans-8,11,14-cis-eicosatetraenoate	Cytosol
109	10712c	5adtststerone(c)	5alpha-Dihydrotestosterone	Cytosol
110	22786c	5adtststeroneglc(c)	5alpha-Dihydrotestosterone glucuronide	Cytosol
111	26487c	5adtststerones(c)	5alpha-Dihydrotestosterone sulfate	Cytosol
112	10916c	5aizc(c)	5-amino-1-(5-phospho-D-ribosyl)imidazole-4-carboxylate	Cytosol
113	424c	5aop(c)	5-Amino-4-oxopentanoate	Cytosol
114	20783c	5dhf(c)	pentaglutamyl folate (DHF)	Cytosol
115	440c	5forthf(c)	5-Formiminotetrahydrofolate	Cytosol
116	11866c	5fthf(c)	5-Formyltetrahydrofolate	Cytosol
117	20405c	5homeprazole(c)	5 hydroxy omeprazole	Cytosol
118	4155c	5hoxindact(c)	5-Hydroxyindoleacetaldehyde	Cytosol
119	11161c	5hoxindoa(c)	5-Hydroxyindoleacetate	Cytosol
120	4166c	5hoxnfkyn(c)	5-Hydroxy-N-formylkynurenine	Cytosol
121	831c	5htrp(c)	5-Hydroxy-L-tryptophan	Cytosol
122	4169c	5hxkyn(c)	5-Hydroxykynurenine	Cytosol
123	4158c	5hxkynam(c)	5-Hydroxykynurenamine	Cytosol
124	3193c	5mdr1p(c)	5-Methylthio-5-deoxy-D-ribose 1-phosphate	Cytosol
125	3277c	5mdru1p(c)	5-Methylthio-5-deoxy-D-ribulose 1-phosphate	Cytosol
126	4178c	5moxact(c)	5-Methoxyindoleacetate	Cytosol
127	243c	5mta(c)	5-Methylthioadenosine	Cytosol
128	431c	5mthf(c)	5-Methyltetrahydrofolate	Cytosol
129	14013c	5oxpro(c)	5-Oxoproline	Cytosol
130	20780c	5thf(c)	pentaglutamyl folate (THF)	Cytosol
131	20784c	6dhf(c)	haxglutamyl folate (DHF)	Cytosol
132	4162c	6hoxmelatn(c)	6-Hydroxymelatonin	Cytosol
133	20402c	6htststerone(c)	6 beta hydroxy testosterone	Cytosol
134	182c	6pgc(c)	6-Phospho-D-gluconate	Cytosol
135	963c	6pgl(c)	6-phospho-D-glucono-1,5-lactone	Cytosol
136	11000c	6pthp(c)	6-Pyruvoyl-5,6,7,8-tetrahydropterin	Cytosol
137	20781c	6thf(c)	hexaglutamyl folate (THF)	Cytosol
138	834c	7dhchsterol(c)	7-Dehydrocholesterol	Cytosol
139	20785c	7dhf(c)	heptaglutamyl folate (DHF)	Cytosol
140	20782c	7thf(c)	heptaglutamyl folate (THF)	Cytosol
141	22811c	9-cis-retfa(c)	fatty acid 9-cis-retinol	Cytosol
142	69c	ACP(c)	acyl carrier protein	Cytosol
143	7546c	L-dpchrm(c)	L-Dopachrome	Cytosol
144	9011c	L2aadp(c)	L-2-Aminoadipate	Cytosol
145	7588c	L2aadp6sa(c)	L-2-Aminoadipate 6-semialdehyde	Cytosol
146	120c	Lcyst(c)	L-Cysteate	Cytosol
147	105c	Lcystin(c)	L-Cystine	Cytosol
148	7641c	Lfmkynr(c)	L-Formylkynurenine	Cytosol
149	9013c	Lkynr(c)	L-Kynurenine	Cytosol
150	679c	Nacasp(c)	N-Acetyl-L-aspartate	Cytosol
151	10790c	Nacsertn(c)	N-Acetylserotonin	Cytosol
152	18469c	R1coa_hs(c)	R group 1 Coenzyme A homo sapiens	Cytosol

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
153	18470c	R2coa_hs(c)	R group 2 Coenzyme A homo sapiens	Cytosol
154	18471c	R3coa_hs(c)	R group 3 Coenzyme A homo sapiens	Cytosol
155	18493c	R4coa_hs(c)	R group 4 Coenzyme A homo sapiens	Cytosol
156	18494c	R5coa_hs(c)	R group 5 Coenzyme A homo sapiens	Cytosol
157	20277c	R6coa_hs(c)	R group 6 Coenzyme A homo sapiens	Cytosol
158	18523c	Rtotal(c)	R total	Cytosol
159	18525c	Rtotal2(c)	R total 2 position	Cytosol
160	22166c	Rtotal2coa(c)	R total 2 coenzyme A	Cytosol
161	22470c	Rtotal2crn(c)	R total 2 carnitine	Cytosol
162	18526c	Rtotal3(c)	R total 3 position	Cytosol
163	22167c	Rtotal3coa(c)	R total 3 Coenzyme A	Cytosol
164	22471c	Rtotal3crn(c)	R total 3 carnitine	Cytosol
165	22165c	Rtotalcoa(c)	R total Coenzyme A	Cytosol
166	22469c	Rtotalcrn(c)	R total carnitine	Cytosol
167	9015c	Sfglutth(c)	S-Formylglutathione	Cytosol
168	656c	T4hcinnm(c)	trans-4-Hydroxycinnamate	Cytosol
169	18059c	Tyr-ggn(c)	Tyr-194 of apo-glycogenin protein (primer for glycogen synthesis)	Cytosol
170	174c	aacoa(c)	Acetoacetyl-CoA	Cytosol
171	1533c	aact(c)	Aminoacetone	Cytosol
172	360c	abt(c)	L-Arabinitol	Cytosol
173	319c	ac(c)	Acetate	Cytosol
174	5509c	acACP(c)	Acetyl-ACP	Cytosol
175	9016c	acac(c)	Acetoacetate	Cytosol
176	1052c	acald(c)	Acetaldehyde	Cytosol
177	11537c	accoa(c)	Acetyl-CoA	Cytosol
178	3775c	acetol(c)	Acetol	Cytosol
179	266c	acetone(c)	Acetone	Cytosol
180	19739c	acgagbside_hs(c)	alpha GalNAc globoside (homo sapiens)	Cytosol
181	899c	acgal(c)	N-Acetyl-D-galactosamine	Cytosol
182	19195c	acgal1p(c)	N-Acetyl-D-galactosamine 1-phosphate	Cytosol
183	22669c	acgalfucgalacgalfuc12gal14acglcgalgluside_hs(c)	Type IIIA glycolipid	Cytosol
184	22681c	acgalfucgalacgalfucgalacglcgal14acglcgalgluside_hs(c)	Type IIIAb	Cytosol
185	224c	acgam(c)	N-Acetyl-D-glucosamine	Cytosol
186	3247c	acgam1p(c)	N-Acetyl-D-glucosamine 1-phosphate	Cytosol
187	192c	acgam6p(c)	N-Acetyl-D-glucosamine 6-phosphate	Cytosol
188	19740c	acgbgbside_hs(c)	beta GalNAc globoside (homo sapiens)	Cytosol
189	7147c	acgpail_hs(c)	N-Acetyl-D-glucosaminylphosphatidylinositol	Cytosol
190	1617c	ach(c)	Acetylcholine	Cytosol
191	1129c	acmana(c)	N-Acetyl-D-mannosamine	Cytosol
192	11865c	acmanap(c)	N-Acetyl-D-mannosamine 6-phosphate	Cytosol
193	19741c	acn13acngalgbside_hs(c)	sialyl (1,3) sialyl (2,6) galactosylgloboside (homo sapiens)	Cytosol
194	19742c	acn23acngalgbside_hs(c)	sialyl (2,3) sialyl (2,6) galactosylgloboside (homo sapiens)	Cytosol
195	22662c	acnacngal14acglcgalgluside_hs(c)	3',8'-LD1	Cytosol

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
196	19738c	acnacngalgbside_hs(c)	disialyl galactosylgloboside (homo sapiens)	Cytosol
197	134c	acnam(c)	N-Acetylneuraminate	Cytosol
198	4637c	acnamp(c)	N-Acetylneuraminate 9-phosphate	Cytosol
199	22682c	acngalacglcgal14acglcgalgluside_hs(c)	VI3NeuAc-nLc6Cer	Cytosol
200	428c	acorn(c)	N2-Acetyl-L-ornithine	Cytosol
201	7471c	acrn(c)	O-Acetylcarnitine	Cytosol
202	228c	ade(c)	Adenine	Cytosol
203	18534c	adhap_hs(c)	acyl-dihydroxyacetone phosphate	Cytosol
204	270c	adn(c)	Adenosine	Cytosol
205	471c	adp(c)	ADP	Cytosol
206	112c	adpglc(c)	ADPglucose	Cytosol
207	17282c	adpman(c)	ADPmannose	Cytosol
208	2434c	adprbp(c)	ADPribose 2'-phosphate	Cytosol
209	151c	adprib(c)	ADPribose	Cytosol
210	18463c	adrn(c)	adrenic acid	Cytosol
211	18484c	adrncoa(c)	adrenyl coenzyme A	Cytosol
212	25984c	adrncrn(c)	Adrenyl carnitine	Cytosol
213	641c	adrnl(c)	Adrenaline	Cytosol
214	11113c	adsel(c)	Adenylylselenate	Cytosol
215	20413c	aflatoxin(c)	aflatoxin B1	Cytosol
216	247c	agm(c)	Agmatine	Cytosol
217	20819c	ahandrostanglc(c)	Etiocholan-3alpha-ol-17-one 3-glucuronide	Cytosol
218	310c	ahcys(c)	S-Adenosyl-L-homocysteine	Cytosol
219	3611c	ahdt(c)	2-Amino-4-hydroxy-6-(erythro-1,2,3-trihydroxypropyl)dihydropteridine triphosphate	Cytosol
220	3340c	aicar(c)	5-Amino-1-(5-Phospho-D-ribosyl)imidazole-4-carboxamide	Cytosol
221	1941c	air(c)	5-amino-1-(5-phospho-D-ribosyl)imidazole	Cytosol
222	19360c	ak2g_hs(c)	1-alkyl 2-acylglycerol	Cytosol
223	19363c	ak2gchol_hs(c)	1-alkyl 2-acylglycerol 3-phosphocholine	Cytosol
224	19359c	ak2gp_hs(c)	1-alkyl 2-acylglycerol 3-phosphate	Cytosol
225	19361c	ak2gpe_hs(c)	1-alkyl 2-acylglycerol 3-phosphoethanolamine	Cytosol
226	19364c	ak2lgchol_hs(c)	1-alkyl 2-lysoglycerol 3-phosphocholine	Cytosol
227	19357c	akdhap_hs(c)	1-alkyldihydroxyacetone phosphate	Cytosol
228	314c	akg(c)	2-Oxoglutarate	Cytosol
229	19358c	akgp_hs(c)	1-alkylglycerol 3-phosphate (homo sapiens)	Cytosol
230	1063c	ala-B(c)	beta-Alanine	Cytosol
231	1093c	ala-D(c)	D-Alanine	Cytosol
232	11412c	ala-L(c)	L-Alanine	Cytosol
233	73c	alac-S(c)	(S)-2-Acetolactate	Cytosol
234	1447c	aldstrn(c)	Aldosterone	Cytosol
235	18535c	alpa_hs(c)	lysophosphatidic acid (homo sapiens)	Cytosol
236	7642c	am6sa(c)	2-Aminomuconate 6-semialdehyde	Cytosol
237	1086c	amet(c)	S-Adenosyl-L-methionine	Cytosol
238	903c	ametam(c)	S-Adenosylmethioninamine	Cytosol
239	309c	amp(c)	AMP	Cytosol
240	7645c	amuco(c)	2-Aminomuconate	Cytosol
241	352c	andrstrn(c)	Androsterone	Cytosol
242	20815c	andrstrnglc(c)	androsterone glucuronide	Cytosol

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
243	1070c	anth(c)	Anthranilate	Cytosol
244	20406c	antipyrene(c)	antipyrene	Cytosol
245	8976c	ap4a(c)	P1,P4-Bis(5'-adenosyl) tetraphosphate	Cytosol
246	2071c	apnnox(c)	alpha-Pinene-oxide	Cytosol
247	22737c	apoC(c)	Apocarboxlase (no lys residue)	Cytosol
248	22735c	apoC-Lys(c)	Apocarboxylase (Lys residue)	Cytosol
249	22736c	apoC-Lys_btn(c)	Holocarboxylase (biotin covalent bound to Lys residue of apoC)	Cytosol
250	4033c	appnn(c)	(+)-alpha-Pinene	Cytosol
251	3086c	aprgstrn(c)	20alpha-Hydroxyprogesterone	Cytosol
252	7649c	aprut(c)	N-Acetylputrescine	Cytosol
253	279c	aps(c)	Adenosine 5'-phosphosulfate	Cytosol
254	816c	aqcobal(c)	Aquacob(III)alamin	Cytosol
255	307c	arab-L(c)	L-Arabinose	Cytosol
256	5355c	arach(c)	Arachidic acid	Cytosol
257	18483c	arachcoa(c)	arachidyl coenzyme A	Cytosol
258	25967c	arachcrn(c)	arachidyl carnitine	Cytosol
259	11890c	arachd(c)	arachidonic acid	Cytosol
260	11887c	arachdcoa(c)	C20:4-CoA	Cytosol
261	11889c	arachdcrn(c)	C20:4 carnitine	Cytosol
262	337c	arg-L(c)	L-Arginine	Cytosol
263	1962c	argsuc(c)	N(omega)-(L-Arginino)succinate	Cytosol
264	11279c	ascb-L(c)	L-Ascorbate	Cytosol
265	232c	asn-L(c)	L-Asparagine	Cytosol
266	10519c	asp-D(c)	D-Aspartate	Cytosol
267	330c	asp-L(c)	L-Aspartate	Cytosol
268	465c	atp(c)	ATP	Cytosol
269	20142c	avite1(c)	alpha-Tocopherol	Cytosol
270	20141c	avite2(c)	alpha-Tocotrienol	Cytosol
271	4182c	bamppald(c)	beta-Aminopropion aldehyde	Cytosol
272	4322c	bdg2hc(c)	cis-beta-D-Glucosyl-2-hydroxycinnamate	Cytosol
273	392c	betald(c)	Betaine aldehyde	Cytosol
274	870c	bhb(c)	(R)-3-Hydroxybutanoate	Cytosol
275	4279c	bildglcur(c)	Bilirubin beta-diglucuronide	Cytosol
276	1942c	bilglcur(c)	Bilirubin monoglucuronide	Cytosol
277	101c	bilirub(c)	Bilirubin	Cytosol
278	114c	biliverd(c)	Biliverdin	Cytosol
279	4297c	biocyt(c)	Biocytin	Cytosol
280	4584c	btamp(c)	Biotinyl-5'-AMP	Cytosol
281	1079c	btn(c)	Biotin	Cytosol
282	294c	but(c)	Butyrate (n-C4:0)	Cytosol
283	20143c	bvite(c)	beta-tocopherol	Cytosol
284	10989c	bz(c)	Benzoate	Cytosol
285	11888c	c226coa(c)	cervonyl coenzyme A	Cytosol
286	11883c	c226crn(c)	cervonyl carnitine	Cytosol
287	346c	ca2(c)	Calcium	Cytosol
288	11003c	cala(c)	N-Carbamoyl-beta-alanine	Cytosol
289	8980c	camp(c)	cAMP	Cytosol
290	14010c	carn(c)	L-Carnosine	Cytosol
291	19576c	caro(c)	beta-Carotene	Cytosol
292	798c	carveol(c)	(E)-carveol	Cytosol
293	429c	cbasp(c)	N-Carbamoyl-L-aspartate	Cytosol
294	365c	cbl2(c)	Cob(II)alamin	Cytosol

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
295	11004c	cbp(c)	Carbamoyl phosphate	Cytosol
296	20077c	cca_d3(c)	Calcitroic acid (D3)	Cytosol
297	1073c	cdp(c)	CDP	Cytosol
298	9018c	cdpchol(c)	CDPcholine	Cytosol
299	19105c	cdpdag_hs(c)	CDP diacylglycerol (homo sapiens)	Cytosol
300	387c	cdpea(c)	CDPethanolamine	Cytosol
301	7908c	cgly(c)	Cys-Gly	Cytosol
302	14998c	chito2pdol_L(c)	N,N'-Diacetylchitobiosyldiphosphodolichol, human liver homolog	Cytosol
303	14999c	chito2pdol_U(c)	N,N'-Diacetylchitobiosyldiphosphodolichol, human uterine homolog	Cytosol
304	1075c	chol(c)	Choline	Cytosol
305	457c	cholate(c)	Cholate	Cytosol
306	9019c	cholp(c)	Choline phosphate	Cytosol
307	252c	chsterol(c)	Cholesterol	Cytosol
308	26330c	chsterols(c)	cholesterol sulfate	Cytosol
309	19243c	chtn(c)	chitin	Cytosol
310	236c	cit(c)	Citrate	Cytosol
311	169c	citr-L(c)	L-Citrulline	Cytosol
312	5268c	cl(c)	Chloride	Cytosol
313	19386c	clpn_hs(c)	cardiolipin (homo sapiens)	Cytosol
314	18467c	clpnd(c)	clupanodonic acid	Cytosol
315	18488c	clpndcoa(c)	clupanodonyl CoA	Cytosol
316	25990c	clpndcrn(c)	clupanodonyl carnitine	Cytosol
317	11376c	cmp(c)	CMP	Cytosol
318	4188c	cmp2amep(c)	CMP-2-aminoethylphosphonate	Cytosol
319	1088c	cmpacna(c)	CMP-N-acetylneuraminate	Cytosol
320	4189c	cmpntm2amep(c)	CMP-N-trimethyl-2-aminoethylphosphonate	Cytosol
321	7644c	cmusa(c)	2-Amino-3-carboxymuconate semialdehyde	Cytosol
322	12152c	co(c)	Carbon monoxide	Cytosol
323	474c	co2(c)	CO2	Cytosol
324	473c	coa(c)	Coenzyme A	Cytosol
325	4331c	coumarin(c)	coumarin	Cytosol
326	2442c	cpppg3(c)	Coproporphyrinogen III	Cytosol
327	150c	creat(c)	Creatine	Cytosol
328	19478c	crm_hs(c)	ceramide (homo sapiens)	Cytosol
329	2222c	crmp_hs(c)	Ceramide 1-phosphate	Cytosol
330	163c	crn(c)	L-Carnitine	Cytosol
331	643c	crtn(c)	Creatinine	Cytosol
332	11268c	crtsl(c)	Cortisol	Cytosol
333	1737c	crtstrn(c)	Corticosterone	Cytosol
334	11891c	crvnc(c)	cervonic acid, C22:6 n-3	Cytosol
335	212c	csn(c)	Cytosine	Cytosol
336	338c	ctp(c)	CTP	Cytosol
337	245c	cyan(c)	Hydrogen cyanide	Cytosol
338	1062c	cys-L(c)	L-Cysteine	Cytosol
339	14975c	cysam(c)	Cysteamine	Cytosol
340	1150c	cyst-L(c)	L-Cystathionine	Cytosol
341	92c	cytd(c)	Cytidine	Cytosol
342	380c	dad-2(c)	Deoxyadenosine	Cytosol
343	265c	dadp(c)	dADP	Cytosol
344	18537c	dag_hs(c)	diacylglycerol (homo sapiens)	Cytosol

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
345	19362c	dak2gpe_hs(c)	1-alkenyl 2-acylglycerol 3-phosphoethanolamine plasmalogen (homo sapiens)	Cytosol
346	193c	damp(c)	dAMP	Cytosol
347	1091c	datp(c)	dATP	Cytosol
348	3803c	dcacoa(c)	Decanoyl-CoA (n-C10:0CoA)	Cytosol
349	2908c	dcamp(c)	N6-(1,2-Dicarboxyethyl)-AMP	Cytosol
350	5272c	dcdp(c)	dCDP	Cytosol
351	290c	dcmp(c)	dCMP	Cytosol
352	18466c	dcsptn1(c)	docosa-4,7,10,13,16-pentaenoic acid (n-6)	Cytosol
353	18487c	dcsptn1coa(c)	docosa-4,7,10,13,16-pentaenoyl coenzyme A	Cytosol
354	25989c	dcsptn1crn(c)	docosa-4,7,10,13,16-pentaenoyl carnitine	Cytosol
355	78c	dctp(c)	dCTP	Cytosol
356	10918c	dcyt(c)	Deoxycytidine	Cytosol
357	1919c	ddca(c)	Dodecanoate (n-C12:0)	Cytosol
358	10497c	ddcaACP(c)	Dodecanoyl-ACP (n-C12:0ACP)	Cytosol
359	1383c	ddcacoa(c)	Dodecanoyl-CoA (n-C12:0CoA)	Cytosol
360	20408c	debrisoquine(c)	debrisoquine	Cytosol
361	12883c	decdp(c)	all trans Decaprenyl diphosphate	Cytosol
362	15096c	dedol_L(c)	Dehydrodolichol, human liver homolog	Cytosol
363	15100c	dedol_U(c)	Dehydrodolichol, human uterine homolog	Cytosol
364	15085c	dedoldp_L(c)	Dehydrodolichol diphosphate, human liver homolog	Cytosol
365	15086c	dedoldp_U(c)	Dehydrodolichol diphosphate, human uterine homolog	Cytosol
366	15093c	dedolp_L(c)	Dehydrodolichol phosphate, human liver homolog	Cytosol
367	15099c	dedolp_U(c)	Dehydrodolichol phosphate, human uterine homolog	Cytosol
368	3387c	dgchol(c)	Chenodeoxyglycocholate	Cytosol
369	194c	dgdp(c)	dGDP	Cytosol
370	195c	dgmp(c)	dGMP	Cytosol
371	172c	dgsn(c)	Deoxyguanosine	Cytosol
372	143c	dgtp(c)	dGTP	Cytosol
373	251c	dha(c)	Dihydroxyacetone	Cytosol
374	1072c	dhap(c)	Dihydroxyacetone phosphate	Cytosol
375	133c	dhbpt(c)	6,7-Dihydrobiopterin	Cytosol
376	19477c	dhcrm_hs(c)	dihydroceramide (homo sapiens)	Cytosol
377	421c	dhdascb(c)	Dehydroascorbate	Cytosol
378	956c	dhea(c)	Dehydroepiandrosterone	Cytosol
379	3998c	dheas(c)	Dehydroepiandrosterone sulfate	Cytosol
380	10505c	dhf(c)	7,8-Dihydrofolate	Cytosol
381	177c	dhor-S(c)	(S)-Dihydroorotate	Cytosol
382	1032c	didp(c)	dIDP	Cytosol
383	4544c	digalsgalside_hs(c)	Digalactosylceramidesulfate	Cytosol
384	19810c	digalside_hs(c)	Digalactosylceramide	Cytosol
385	9639c	dimp(c)	dIMP	Cytosol
386	3417c	din(c)	Deoxyinosine	Cytosol
387	1033c	ditp(c)	dITP	Cytosol
388	8766c	dkmpp(c)	2,3-diketo-5-methylthio-1-phosphopentane	Cytosol
389	2431c	dlnlcg(c)	dihomo-gamma-linolenic acid (n-6)	Cytosol
390	18491c	dlnlcgcoa(c)	dihomo-gamma-linolenyl coenzyme A	Cytosol
391	25979c	dlnlcgcrn(c)	dihomo-gamma-linolenyl carnitine	Cytosol

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
392	20407c	dmantipyrine(c)	demethylated antipyrine	Cytosol
393	840c	dmgly(c)	N,N-Dimethylglycine	Cytosol
394	21977c	dmhptcoa(c)	2,6 dimethylheptanoyl-CoA	Cytosol
395	26488c	dmhptcrn(c)	2,6 dimethylheptanoyl carnitine	Cytosol
396	21959c	dmnoncoa(c)	4,8 dimethylnonanoyl-CoA	Cytosol
397	38c	dmpp(c)	Dimethylallyl diphosphate	Cytosol
398	724c	dnad(c)	Deamino-NAD+	Cytosol
399	14992c	dolglcp_L(c)	Dolichyl beta-D-glucosyl phosphate, human liver homolog	Cytosol
400	14993c	dolglcp_U(c)	Dolichyl beta-D-glucosyl phosphate, human uterine homolog	Cytosol
401	14986c	dolichol_L(c)	Dolichol, human liver homolog	Cytosol
402	14987c	dolichol_U(c)	Dolichol, human uterine homolog	Cytosol
403	14994c	dolmanp_L(c)	Dolichyl phosphate D-mannose, human liver homolog	Cytosol
404	14995c	dolmanp_U(c)	Dolichyl phosphate D-mannose, human uterine homolog	Cytosol
405	14988c	dolp_L(c)	Dolichol phosphate, human liver homolog	Cytosol
406	14989c	dolp_U(c)	Dolichol phosphate, human uterine homolog	Cytosol
407	2882c	dopa(c)	Dopamine	Cytosol
408	11025c	dopaqn(c)	Dopaquinone	Cytosol
409	21114c	dopasf(c)	Dopamine 3-O-sulfate	Cytosol
410	737c	dpcoa(c)	Dephospho-CoA	Cytosol
411	1462c	drib(c)	Deoxyribose	Cytosol
412	196c	dtdp(c)	dTDP	Cytosol
413	453c	dtdp4d6dg(c)	dTDP-4-dehydro-6-deoxy-D-glucose	Cytosol
414	11394c	dtdp4d6dm(c)	dTDP-4-dehydro-6-deoxy-L-mannose	Cytosol
415	712c	dtdpglu(c)	dTDPglucose	Cytosol
416	2288c	dtdprmn(c)	dTDP-L-rhamnose	Cytosol
417	197c	dtmp(c)	dTMP	Cytosol
418	132c	dtt(c)	Dithiothreitol	Cytosol
419	10551c	dttOX(c)	Oxidized dithiothreitol	Cytosol
420	79c	dttp(c)	dTTP	Cytosol
421	1034c	dudp(c)	dUDP	Cytosol
422	198c	dump(c)	dUMP	Cytosol
423	355c	duri(c)	Deoxyuridine	Cytosol
424	80c	dutp(c)	dUTP	Cytosol
425	18064c	dxtrn(c)	phosphorylase-limit dextrin (glycogenin-1,6{4[1,4-Glc], 4[1,4-Glc]})	Cytosol
426	8301c	e4hglu(c)	L-erythro-4-Hydroxyglutamate	Cytosol
427	10791c	e4p(c)	D-Erythrose 4-phosphate	Cytosol
428	20414c	eaflatoxin(c)	8,9 epxoy aflatoxin B1	Cytosol
429	20367c	ebastine(c)	ebastine	Cytosol
430	20368c	ebastineoh(c)	hydroxylated ebastine	Cytosol
431	18506c	eicostet(c)	eicosatetranoic acid	Cytosol
432	18507c	eicostetcoa(c)	eicosatetranoyl coenzyme A	Cytosol
433	25980c	eicostetcrn(c)	Eicosatetranoyl carnitine	Cytosol
434	588c	elaid(c)	elaidic acid	Cytosol
435	25972c	elaidcrn(c)	Elaidic carnitine	Cytosol
436	1653c	eryth(c)	L-Erythrulose	Cytosol
437	706c	estradiol(c)	Estradiol	Cytosol
438	20817c	estradiolglc(c)	estradiol glucuronide	Cytosol
439	3904c	estriol(c)	estriol	Cytosol

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
440	3415c	estriolglc(c)	16-Glucuronide-estriol	Cytosol
441	86c	estrone(c)	Estrone	Cytosol
442	20814c	estroneglc(c)	estrone glucuronide	Cytosol
443	2601c	estrones(c)	Estrone 3-sulfate	Cytosol
444	254c	etha(c)	Ethanolamine	Cytosol
445	9020c	ethamp(c)	Ethanolamine phosphate	Cytosol
446	87c	etoh(c)	Ethanol	Cytosol
447	2235c	f1p(c)	D-Fructose 1-phosphate	Cytosol
448	441c	f26bp(c)	D-Fructose 2,6-bisphosphate	Cytosol
449	4165c	f5hoxkyn(c)	Formyl-5-hydroxykynurenamine	Cytosol
450	1053c	f6p(c)	D-Fructose 6-phosphate	Cytosol
451	478c	fad(c)	Flavin adenine dinucleotide oxidized	Cytosol
452	42c	fadh2(c)	Flavin adenine dinucleotide reduced	Cytosol
453	340c	fald(c)	Formaldehyde	Cytosol
454	189c	fdp(c)	D-Fructose 1,6-bisphosphate	Cytosol
455	312c	fe2(c)	Fe2+	Cytosol
456	2663c	fgam(c)	N2-Formyl-N1-(5-phospho-D-ribosyl)glycinamide	Cytosol
457	336c	fmn(c)	FMN	Cytosol
458	4161c	fna5moxam(c)	Formyl-N-acetyl-5-methoxykynurenamine	Cytosol
459	118c	fol(c)	Folate	Cytosol
460	334c	for(c)	Formate	Cytosol
461	430c	forglu(c)	N-Formimidoyl-L-glutamate	Cytosol
462	11122c	formcoa(c)	Formyl-CoA	Cytosol
463	3319c	fpram(c)	2-(Formamido)-N1-(5-phospho-D-ribosyl)acetamidine	Cytosol
464	3486c	fprica(c)	5-Formamido-1-(5-phospho-D-ribosyl)imidazole-4-carboxamide	Cytosol
465	10388c	frdp(c)	Farnesyl diphosphate	Cytosol
466	1061c	fru(c)	D-Fructose	Cytosol
467	833c	fuc-L(c)	L-Fucose	Cytosol
468	22691c	fuc13galacglcgal14acglcgalgluside_hs(c)	III3Fuc-nLc6Cer	Cytosol
469	22658c	fuc14galacglcgalgluside_hs(c)	Lea glycolipid	Cytosol
470	2240c	fuc1p-L(c)	L-Fucose 1-phosphate	Cytosol
471	22657c	fucacgalfucgalacglcgalgluside_hs(c)	(Gal)2 (GalNAc)1 (Glc)1 (GlcNAc)1 (LFuc)2 (Cer)1	Cytosol
472	22663c	fucacngal14acglcgalgluside_hs(c)	IV3-a-NeuAc,III3-a-Fuc-nLc4Cer	Cytosol
473	22655c	fucacngalacglcgalgluside_hs(c)	IV3-a-Neu5Ac,III4-a-Fuc-Lc4Cer	Cytosol
474	22665c	fucfuc12gal14acglcgalgluside_hs(c)	Ley glycolipid	Cytosol
475	22693c	fucfuc132galacglcgal14acglcgalgluside_hs(c)	V3Fuc,III3Fuc-nLc6Cer	Cytosol
476	22690c	fucfucfucgalacglc13galacglcgal14acglcgalgluside_hs(c)	(Gal)4 (Glc)1 (GlcNAc)3 (LFuc)3 (Cer)1	Cytosol

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
477	22685c	fucfucfucgalacglcgal14acglcgalgluside_hs(c)	(Gal)3 (Glc)1 (GlcNAc)2 (LFuc)3 (Cer)1	Cytosol
478	22650c	fucfucgalacglcgalgluside_hs(c)	Leb glycolipid	Cytosol
479	22660c	fucgal14acglcgalgluside_hs(c)	Lacto-N-fucopentaosyl III ceramide	Cytosol
480	22652c	fucgalfucgalacglcgalgluside_hs(c)	(Gal)3 (Glc)1 (GlcNAc)1 (LFuc)2 (Cer)1	Cytosol
481	19746c	fucgalgbside_hs(c)	fucosyl galactosylgloboside (homo sapiens)	Cytosol
482	1081c	fum(c)	Fumarate	Cytosol
483	1066c	g1p(c)	D-Glucose 1-phosphate	Cytosol
484	438c	g3p(c)	Glyceraldehyde 3-phosphate	Cytosol
485	444c	g3pc(c)	sn-Glycero-3-phosphocholine	Cytosol
486	765c	g6p(c)	D-Glucose 6-phosphate	Cytosol
487	19963c	gacpail_hs(c)	glucosaminyl-acylphosphatidylinositol	Cytosol
488	1083c	gal(c)	D-Galactose	Cytosol
489	434c	gal1p(c)	alpha-D-Galactose 1-phosphate	Cytosol
490	19744c	galacglcgalgbside_hs(c)	Gal-GlcNAc-Gal globoside (homo sapiens)	Cytosol
491	22670c	galfuc12gal14acglcgalgluside_hs(c)	(Gal)3 (Glc)1 (GlcNAc)1 (LFuc)1 (Cer)1	Cytosol
492	22683c	galfucgalacglcgal14acglcgalgluside_hs(c)	(Gal)4 (Glc)1 (GlcNAc)2 (LFuc)1 (Cer)1	Cytosol
493	22676c	galgalfucfucgalacglcgalacglcgal14acglcgalgluside_hs(c)	(Gal)6 (Glc)1 (GlcNAc)3 (LFuc)2 (Cer)1	Cytosol
494	19735c	galgalgalthcrm_hs(c)	Gal-Gal-Gal-Gal-Gal-Glc-Cer (homo sapiens)	Cytosol
495	19619c	galgluside_hs(c)	galactosyl glucosyl ceramide	Cytosol
496	19614c	galside_hs(c)	galactocerebroside (homo sapiens)	Cytosol
497	1377c	galt(c)	Galactitol	Cytosol
498	171c	gam(c)	D-Glucosamine	Cytosol
499	187c	gam6p(c)	D-Glucosamine 6-phosphate	Cytosol
500	10804c	gar(c)	N1-(5-Phospho-D-ribosyl)glycinamide	Cytosol
501	19624c	gbside_hs(c)	globoside (homo sapiens)	Cytosol
502	10800c	gcald(c)	Glycolaldehyde	Cytosol
503	1554c	gchola(c)	glycocholate	Cytosol
504	19757c	gd1b2_hs(c)	GD1beta (homo sapiens)	Cytosol
505	19754c	gd1c_hs(c)	GD1c (homo sapiens)	Cytosol
506	19759c	gd3_hs(c)	GD3 (homo sapiens)	Cytosol
507	11524c	gdchola(c)	glycochenodeoxycholate	Cytosol
508	321c	gdp(c)	GDP	Cytosol
509	952c	gdpddman(c)	GDP-4-dehydro-6-deoxy-D-mannose	Cytosol
510	168c	gdpfuc(c)	GDP-L-fucose	Cytosol
511	9064c	gdpmann(c)	GDP-D-mannose	Cytosol
512	188c	ggdp(c)	Geranylgeranyl diphosphate	Cytosol
513	18060c	ggn(c)	primed glycogenin (glycogenin-8[1,4-Glc])	Cytosol
514	18308c	glac(c)	D-glucurono-6,3-lactone	Cytosol
515	318c	glc-D(c)	D-Glucose	Cytosol

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
516	632c	glcr(c)	D-Glucarate	Cytosol
517	256c	glcur(c)	D-Glucuronate	Cytosol
518	3887c	glcur1p(c)	D-Glucuronate 1-phosphate	Cytosol
519	11299c	gln-L(c)	L-Glutamine	Cytosol
520	313c	glu-L(c)	L-Glutamate	Cytosol
521	761c	glu5sa(c)	L-Glutamate 5-semialdehyde	Cytosol
522	443c	glucys(c)	gamma-L-Glutamyl-L-cysteine	Cytosol
523	19613c	gluside_hs(c)	glucocerebroside (homo sapiens)	Cytosol
524	329c	glx(c)	Glyoxylate	Cytosol
525	323c	gly(c)	Glycine	Cytosol
526	393c	glyald(c)	D-Glyceraldehyde	Cytosol
527	503c	glyb(c)	Glycine betaine	Cytosol
528	1077c	glyc(c)	Glycerol	Cytosol
529	306c	glyc-R(c)	(R)-Glycerate	Cytosol
530	18741c	glyc-S(c)	(S)-Glycerate	Cytosol
531	55c	glyc3p(c)	Glycerol 3-phosphate	Cytosol
532	237c	glyclt(c)	Glycolate	Cytosol
533	18061c	glygn1(c)	glycogen, structure 1 (glycogenin-11[1,4-Glc])	Cytosol
534	18062c	glygn2(c)	glycogen, structure 2 (glycogenin-1,6-{7[1,4-Glc], 4[1,4-Glc]})	Cytosol
535	18071c	glygn3(c)	glycogen, structure 3 (glycogenin-7[1,4-Glc])	Cytosol
536	226c	gmp(c)	GMP	Cytosol
537	19768c	gp1c_hs(c)	GP1c (homo sapiens)	Cytosol
538	19976c	gp1calpha_hs(c)	GP1c alpha (homo sapiens)	Cytosol
539	3238c	gpail_hs(c)	D-glucosaminylphosphatidylinositol	Cytosol
540	19763c	gq1b_hs(c)	GQ1b (homo sapiens)	Cytosol
541	19771c	gq1balpha_hs(c)	GQ1balpha (homo sapiens)	Cytosol
542	179c	grdp(c)	Geranyl diphosphate	Cytosol
543	5279c	gsn(c)	Guanosine	Cytosol
544	19749c	gt1a_hs(c)	GT1a (homo sapiens)	Cytosol
545	19764c	gt3_hs(c)	GT3 (homo sapiens)	Cytosol
546	1087c	gthox(c)	Oxidized glutathione	Cytosol
547	11388c	gthrd(c)	Reduced glutathione	Cytosol
548	327c	gtp(c)	GTP	Cytosol
549	291c	gua(c)	Guanine	Cytosol
550	10039c	gudac(c)	Guanidinoacetate	Cytosol
551	677c	gullac(c)	L-Gulono-1,4-lactone	Cytosol
552	650c	guln(c)	L-Gulonate	Cytosol
553	1049c	h(c)	H+	Cytosol
554	3c	h2co3(c)	carbonic acid	Cytosol
555	317c	h2o(c)	H2O	Cytosol
556	315c	h2o2(c)	Hydrogen peroxide	Cytosol
557	7643c	hLkynr(c)	3-Hydroxy-L-kynurenine	Cytosol
558	144c	hco3(c)	Bicarbonate	Cytosol
559	20383c	hcoumarin(c)	hydroxy coumarin	Cytosol
560	3844c	hcys-L(c)	L-Homocysteine	Cytosol
561	297c	hdca(c)	Hexadecanoate (n-C16:0)	Cytosol
562	5725c	hdcea(c)	Hexadecenoate (n-C16:1)	Cytosol
563	21857c	hdcecrn(c)	Hexadecenoyl carnitine	Cytosol
564	8780c	hdcoa(c)	Hexadecenoyl-CoA (n-C16:1CoA)	Cytosol
565	3801c	hdd2coa(c)	trans-Hexadec-2-enoyl-CoA	Cytosol
566	26402c	hdd2crn(c)	trans-Hexadec-2-enoyl carnitine	Cytosol

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
567	10496c	hdeACP(c)	cis-hexadec-9-enoyl-[acyl-carrier protein] (n-C16:1)	Cytosol
568	20384c	hestratriol(c)	4,17 dihydroxy estradiol	Cytosol
569	9242c	hexc(c)	hexacosanoate (n-C26:0)	Cytosol
570	11013c	hexccoa(c)	Hexacosanoyl-CoA (n-C26:0CoA)	Cytosol
571	25969c	hexccrn(c)	hexacosanoyl carnitine	Cytosol
572	9021c	hgentis(c)	Homogentisate	Cytosol
573	4128c	hi(c)	HI	Cytosol
574	11120c	his-L(c)	L-Histidine	Cytosol
575	15080c	hista(c)	Histamine	Cytosol
576	838c	hmbil(c)	Hydroxymethylbilane	Cytosol
577	191c	hmgcoa(c)	Hydroxymethylglutaryl-CoA	Cytosol
578	20400c	hnifedipine(c)	hydroxy nifedipine	Cytosol
579	131c	hom-L(c)	L-Homoserine	Cytosol
580	11270c	homoval(c)	Homovanillate	Cytosol
581	6306c	hpdca(c)	heptadecanoate	Cytosol
582	22502c	hpdcacoa(c)	heptadecanoyl coa	Cytosol
583	22758c	hpdcacrn(c)	heptadecanoyl carnitine	Cytosol
584	242c	hpyr(c)	Hydroxypyruvate	Cytosol
585	20388c	hretn(c)	4 hydroxy retinoic acid	Cytosol
586	20376c	htaxol(c)	hydroxylated taxol	Cytosol
587	218c	hxan(c)	Hypoxanthine	Cytosol
588	349c	hyptaur(c)	Hypotaurine	Cytosol
589	464c	i(c)	Iodide	Cytosol
590	158c	icit(c)	Isocitrate	Cytosol
591	1125c	id3acald(c)	Indole-3-acetaldehyde	Cytosol
592	5392c	idour(c)	L-Iduronate	Cytosol
593	1067c	idp(c)	IDP	Cytosol
594	410c	ile-L(c)	L-Isoleucine	Cytosol
595	2132c	im4ac(c)	Imidazole-4-acetate	Cytosol
596	3706c	im4act(c)	Imidazole-4-acetaldehyde	Cytosol
597	1090c	imp(c)	IMP	Cytosol
598	9022c	ind3ac(c)	Indole-3-acetate	Cytosol
599	223c	inost(c)	myo-Inositol	Cytosol
600	147c	ins(c)	Inosine	Cytosol
601	534c	iodine(c)	Iodine	Cytosol
602	1089c	ipdp(c)	Isopentenyl diphosphate	Cytosol
603	1050c	itp(c)	ITP	Cytosol
604	289c	k(c)	potassium	Cytosol
605	19184c	kdn(c)	2-keto-3-deoxy-D-glycero-D-galactononic acid	Cytosol
606	19185c	kdnp(c)	2-keto-3-deoxy-D-glycero-D-galactononic acid 9-phosphate	Cytosol
607	10998c	kynate(c)	4-Hydroxy-2-quinolinecarboxylic acid	Cytosol
608	15670c	l2n2m2mn(c)	de-Fuc, reducing GlcNAc removed, de-Sia form of PA6 (w/o peptide linkage)	Cytosol
609	304c	lac-D(c)	D-Lactate	Cytosol
610	10931c	lac-L(c)	L-Lactate	Cytosol
611	491c	lald-D(c)	D-Lactaldehyde	Cytosol
612	420c	lald-L(c)	L-Lactaldehyde	Cytosol
613	597c	lanost(c)	Lanosterol	Cytosol
614	292c	lcts(c)	Lactose	Cytosol
615	1082c	leu-L(c)	L-Leucine	Cytosol
616	755c	leuktrA4(c)	Leukotriene A4	Cytosol

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
617	1752c	leuktrB4(c)	Leukotriene B4	Cytosol
618	17887c	leuktrC4(c)	Leukotriene C4	Cytosol
619	4410c	leuktrD4(c)	Leukotriene D4	Cytosol
620	26338c	leuktrE4(c)	leukotriene E4	Cytosol
621	26339c	leuktrF4(c)	leukotriene F4	Cytosol
622	18473c	lgnc(c)	lignoceric acid	Cytosol
623	18490c	lgnccoa(c)	lignocericyl coenzyme A	Cytosol
624	25968c	lgnccrn(c)	lignoceryl carnitine	Cytosol
625	2477c	lgt-S(c)	(R)-S-Lactoylglutathione	Cytosol
626	10371c	limnen(c)	Limonene	Cytosol
627	11278c	lipoate(c)	Lipoate	Cytosol
628	18461c	lneldc(c)	linoelaidic acid (all trans C18:2)	Cytosol
629	22137c	lneldcACP(c)	linoelaidic acid ACP (all trans)	Cytosol
630	18482c	lneldccoa(c)	linoelaidyl coenzyme A	Cytosol
631	25975c	lneldccrn(c)	Linoelaidyl carnitine	Cytosol
632	11172c	lnlc(c)	linoleic acid (all cis C18:2) n-6	Cytosol
633	22136c	lnlcACP(c)	linoleic acid ACP (all cis)	Cytosol
634	18481c	lnlccoa(c)	linoleic coenzyme A	Cytosol
635	25976c	lnlccrn(c)	Linoleyl carnitine	Cytosol
636	11152c	lnlnca(c)	alpha-Linolenic acid, C18:3, n-3	Cytosol
637	18480c	lnlncacoa(c)	alpha-Linolenoyl-CoA	Cytosol
638	25978c	lnlncacrn(c)	alpha-linolenyl carnitine	Cytosol
639	5356c	lnlncg(c)	gamma-linolenic acid	Cytosol
640	2277c	lnlncgcoa(c)	gamma-linolenoyl-CoA	Cytosol
641	25977c	lnlncgcrn(c)	gamma-linolenyl carnitine	Cytosol
642	19382c	lpchol_hs(c)	lysophosphatidylcholine (homo sapiens)	Cytosol
643	19998c	lum3(c)	Lumisterol 3	Cytosol
644	328c	lys-L(c)	L-Lysine	Cytosol
645	4198c	lyxnt(c)	L-lyxonate	Cytosol
646	15002c	m1mpdol_L(c)	alpha-D-mannosyl-beta-D-mannosyl-diacylchitobiosyldiphosphodolichol, human liver homolog	Cytosol
647	15003c	m1mpdol_U(c)	alpha-D-mannosyl-beta-D-mannosyl-diacylchitobiosyldiphosphodolichol, human uterine homolog	Cytosol
648	15672c	m2mn(c)	(alpha-D-mannosyl)2-beta-D-mannosyl-N-acetylglucosamine	Cytosol
649	15004c	m2mpdol_L(c)	(alpha-D-mannosyl)2-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human liver homolog	Cytosol
650	15005c	m2mpdol_U(c)	(alpha-D-mannosyl)2-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human uterine homolog	Cytosol
651	15006c	m3mpdol_L(c)	(alpha-D-mannosyl)3-beta-D-mannosyl-diacetylchitodiphosphodolichol, human liver homolog	Cytosol
652	15007c	m3mpdol_U(c)	(alpha-D-mannosyl)3-beta-D-mannosyl-diacetylchitodiphosphodolichol, human uterine homolog	Cytosol
653	15008c	m4mpdol_L(c)	(alpha-D-Mannosyl)4-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human liver homolog	Cytosol

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
654	15009c	m4mpdol_U(c)	(alpha-D-Mannosyl)4-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human uterine homolog	Cytosol
655	18539c	mag_hs(c)	monoacylglycerol 2 (homo sapiens)	Cytosol
656	230c	mal-L(c)	L-Malate	Cytosol
657	50c	malACP(c)	Malonyl-[acyl-carrier protein]	Cytosol
658	11267c	malcoa(c)	Malonyl-CoA	Cytosol
659	267c	malt(c)	Maltose	Cytosol
660	1284c	malttr(c)	Maltotriose	Cytosol
661	11018c	man(c)	D-Mannose	Cytosol
662	2920c	man1p(c)	D-Mannose 1-phosphate	Cytosol
663	137c	man6p(c)	D-Mannose 6-phosphate	Cytosol
664	4139c	melanin(c)	Melanin	Cytosol
665	1013c	melatn(c)	Melatonin	Cytosol
666	1092c	meoh(c)	Methanol	Cytosol
667	11265c	mepi(c)	Metanephrine	Cytosol
668	4310c	mercplac(c)	3-Mercaptolactate	Cytosol
669	26412c	mercplaccys(c)	3-mercaptolactate-cysteine disulfide	Cytosol
670	794c	mercppyr(c)	Mercaptopyruvate	Cytosol
671	343c	met-L(c)	L-Methionine	Cytosol
672	433c	methf(c)	5,10-Methenyltetrahydrofolate	Cytosol
673	3703c	mhista(c)	N-Methylhistamine	Cytosol
674	996c	mi13456p(c)	1D-myo-Inositol 1,3,4,5,6-pentakisphosphate	Cytosol
675	7140c	mi1345p(c)	1D-myo-Inositol 1,3,4,5-tetrakisphosphate	Cytosol
676	11398c	mi1346p(c)	1D-myo-Inositol 1,3,4,6-tetrakisphosphate	Cytosol
677	969c	mi134p(c)	1D-myo-Inositol 1,3,4-trisphosphate	Cytosol
678	3100c	mi13p(c)	1D-myo-Inositol 1,3-bisphosphate	Cytosol
679	8995c	mi145p(c)	1D-myo-Inositol 1,4,5-trisphosphate	Cytosol
680	950c	mi14p(c)	1D-myo-Inositol 1,4-bisphosphate	Cytosol
681	8983c	mi1p-D(c)	1D-myo-Inositol 1-phosphate	Cytosol
682	3981c	mi3456p(c)	1D-myo-Inositol 3,4,5,6-tetrakisphosphate	Cytosol
683	10518c	mi34p(c)	1D-myo-Inositol 3,4-bisphosphate	Cytosol
684	2866c	mi3p-D(c)	1D-myo-Inositol 3-phosphate	Cytosol
685	11166c	mi4p-D(c)	1D-myo-Inositol 4-phosphate	Cytosol
686	3284c	micit(c)	methylisocitrate	Cytosol
687	938c	minohp(c)	myo-Inositol hexakisphosphate	Cytosol
688	11043c	mlthf(c)	5,10-Methylenetetrahydrofolate	Cytosol
689	13998c	mma(c)	monomethylamine	Cytosol
690	451c	mmcoa-S(c)	(S)-Methylmalonyl-CoA	Cytosol
691	15673c	mn(c)	beta-1,4-mannose-N-acetylglucosamine	Cytosol
692	15000c	mpdol_L(c)	beta-D-Mannosyldiacetylchitobiosyldiphosphodolichol, human liver homolog	Cytosol
693	15001c	mpdol_U(c)	beta-D-Mannosyldiacetylchitobiosyldiphosphodolichol, human uterine homolog	Cytosol
694	277c	msa(c)	Malonate semialdehyde	Cytosol
695	370c	mthgxl(c)	Methylglyoxal	Cytosol
696	10495c	myrsACP(c)	Myristoyl-ACP (n-C14:0ACP)	Cytosol
697	15681c	n2m2nm(c)	n2m2nmasn (w/o peptide linkage)	Cytosol
698	15682c	n2m2nmn(c)	reducing GlcNAc removed form of n2m2nmasn (w/o peptide)	Cytosol
699	7923c	n4abutn(c)	N4-Acetylaminobutanal	Cytosol

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
700	1023c	na1(c)	Sodium	Cytosol
701	301c	nac(c)	Nicotinate	Cytosol
702	466c	nad(c)	Nicotinamide adenine dinucleotide	Cytosol
703	467c	nadh(c)	Nicotinamide adenine dinucleotide - reduced	Cytosol
704	469c	nadp(c)	Nicotinamide adenine dinucleotide phosphate	Cytosol
705	468c	nadph(c)	Nicotinamide adenine dinucleotide phosphate - reduced	Cytosol
706	14996c	naglc2p_L(c)	N-Acetyl-D-glucosaminyldiphosphodolichol, human liver homolog	Cytosol
707	14997c	naglc2p_U(c)	N-Acetyl-D-glucosaminyldiphosphodolichol, human uterine homolog	Cytosol
708	233c	ncam(c)	Nicotinamide	Cytosol
709	4171c	nformanth(c)	N-Formylanthranilate	Cytosol
710	476c	nh4(c)	Ammonium	Cytosol
711	10883c	nicrns(c)	Nicotinate D-ribonucleoside	Cytosol
712	776c	nicrnt(c)	Nicotinate D-ribonucleotide	Cytosol
713	20399c	nifedipine(c)	nifedipine	Cytosol
714	77c	nmn(c)	NMN	Cytosol
715	2047c	nmptrc(c)	N-Methylputrescine	Cytosol
716	4614c	nmthsrtn(c)	N-Methylserotonin	Cytosol
717	361c	no(c)	Nitric oxide	Cytosol
718	4127c	normete-L(c)	L-Normetanephrine	Cytosol
719	668c	npthl(c)	Naphthalene	Cytosol
720	371c	nrpphr(c)	Norepinephrine	Cytosol
721	21117c	nrpphrsf(c)	Sulfate derivative of norepinephrine	Cytosol
722	18464c	nrvnc(c)	nervonic acid	Cytosol
723	18485c	nrvnccoa(c)	nervonyl coenzyme A	Cytosol
724	25974c	nrvnccrn(c)	Nervonyl carnitine	Cytosol
725	5380c	ntm2amep(c)	N-Trimethyl-2-aminoethylphosphonate	Cytosol
726	4397c	nwharg(c)	N-(omega)-Hydroxyarginine	Cytosol
727	470c	o2(c)	O2	Cytosol
728	461c	o2s(c)	Superoxide anion	Cytosol
729	322c	oaa(c)	Oxaloacetate	Cytosol
730	20055c	oagd3_hs(c)	9-O-Acetylated GD3 (homo sapiens)	Cytosol
731	20056c	oagt3_hs(c)	9-O-Acetylated GT3 (homo sapiens)	Cytosol
732	10688c	occoa(c)	Octanoyl-CoA (n-C8:0CoA)	Cytosol
733	1249c	ocdca(c)	octadecanoate (n-C18:0)	Cytosol
734	5936c	ocdcaACP(c)	Octadecanoyl-ACP (n-C18:0ACP)	Cytosol
735	8769c	ocdcea(c)	octadecenoate (n-C18:1)	Cytosol
736	8770c	ocdcya(c)	octadecadienoate (n-C18:2)	Cytosol
737	8790c	ocdcyaACP(c)	Octadecynoyl-ACP (n-C18:2ACP)	Cytosol
738	5354c	octa(c)	octanoate (n-C8:0)	Cytosol
739	5871c	octeACP(c)	cis-octadec-11-enoyl-[acyl-carrier protein] (n-C18:1)	Cytosol
740	8401c	od2coa(c)	trans-Octadec-2-enoyl-CoA	Cytosol
741	8782c	odecoa(c)	Octadecenoyl-CoA (n-C18:1CoA)	Cytosol
742	11885c	odecrn(c)	octadecenoyl carnitine	Cytosol
743	1021c	oh1(c)	hydroxide ion	Cytosol
744	20404c	omeprazole(c)	omeprazole	Cytosol
745	20401c	onpthl(c)	naphthalene epoxide	Cytosol
746	22810c	oretn(c)	4-oxo-retonoic acid	Cytosol
747	1304c	orn(c)	Ornithine	Cytosol
748	148c	orot(c)	Orotate	Cytosol

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
749	881c	orot5p(c)	Orotidine 5'-phosphate	Cytosol
750	10901c	oxa(c)	Oxalate	Cytosol
751	18536c	pa_hs(c)	phosphatidic acid (homo sapiens)	Cytosol
752	9657c	pac(c)	Phenylacetic acid	Cytosol
753	1100c	pacald(c)	Phenylacetaldehyde	Cytosol
754	19365c	paf_hs(c)	1-alkyl 2-acteylglycerol 3-phosphocholine (homo sapiens)	Cytosol
755	4431c	pail345p_hs(c)	phosphatidylinositol-3,4,5-trisphosphate (Homo sapiens)	Cytosol
756	19605c	pail34p_hs(c)	phosphatidylinositol-3,4-bisphosphate (Homo sapiens)	Cytosol
757	19704c	pail35p_hs(c)	phosphatidylinositol-3,5-bisphosphate (Homo sapiens)	Cytosol
758	3992c	pail3p_hs(c)	1-Phosphatidyl-1D-myo-inositol 3-phosphate (Homo sapiens)	Cytosol
759	19333c	pail45p_hs(c)	phosphatidylinositol 4,5-bisphosphate (Homo sapiens)	Cytosol
760	19332c	pail4p_hs(c)	1-Phosphatidyl-1D-myo-inositol 4-phosphate (Homo sapiens)	Cytosol
761	19479c	pail5p_hs(c)	1-Phosphatidyl-1D-myo-inositol 5-phosphate (Homo sapiens)	Cytosol
762	19327c	pail_hs(c)	phosphatidylinositol (homo sapiens)	Cytosol
763	5870c	palmACP(c)	Palmitoyl-ACP (n-C16:0ACP)	Cytosol
764	900c	pan4p(c)	Pantetheine 4'-phosphate	Cytosol
765	333c	pap(c)	Adenosine 3',5'-bisphosphate	Cytosol
766	332c	paps(c)	3'-Phosphoadenylyl sulfate	Cytosol
767	19051c	pchol_hs(c)	Phosphatidylcholine (homo sapiens)	Cytosol
768	7124c	pcollg5hlys(c)	Procollagen 5-hydroxy-L-lysine	Cytosol
769	2265c	pcollglys(c)	Procollagen L-lysine	Cytosol
770	10038c	pcreat(c)	Phosphocreatine	Cytosol
771	15675c	pcrn(c)	propionyl-carnitine	Cytosol
772	19999c	pd3(c)	Previtamin D3	Cytosol
773	1116c	pdx5p(c)	Pyridoxine 5'-phosphate	Cytosol
774	19050c	pe_hs(c)	phosphatidylethanolamine (homo sapiens)	Cytosol
775	9637c	peamn(c)	Phenethylamine	Cytosol
776	344c	pep(c)	Phosphoenolpyruvate	Cytosol
777	19700c	peracd(c)	Perillic acid	Cytosol
778	2536c	perillyl(c)	Perillyl alcohol	Cytosol
779	19385c	pglyc_hs(c)	phosphatidylglycerol (homo sapiens)	Cytosol
780	19384c	pgp_hs(c)	phosphatidyl glycerol phosphate (homo sapiens)	Cytosol
781	397c	phaccoa(c)	Phenylacetyl-CoA	Cytosol
782	1048c	phe-L(c)	L-Phenylalanine	Cytosol
783	2972c	pheacgln(c)	alpha-N-Phenylacetyl-L-glutamine	Cytosol
784	11520c	pheme(c)	Protoheme	Cytosol
785	10564c	phom(c)	O-Phospho-L-homoserine	Cytosol
786	240c	phpyr(c)	Phenylpyruvate	Cytosol
787	10509c	phyQ(c)	Phylloquinone	Cytosol
788	1308c	phyt(c)	phytanic acid	Cytosol
789	21953c	phytcoa(c)	phytanyl coa	Cytosol
790	472c	pi(c)	Phosphate	Cytosol
791	11029c	pmtcoa(c)	Palmitoyl-CoA (n-C16:0CoA)	Cytosol
792	2244c	pmtcrn(c)	L-Palmitoylcarnitine	Cytosol
793	10928c	pnto-R(c)	(R)-Pantothenate	Cytosol

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
794	238c	ppa(c)	Propionate (n-C3:0)	Cytosol
795	487c	ppbng(c)	Porphobilinogen	Cytosol
796	1064c	ppcoa(c)	Propanoyl-CoA	Cytosol
797	475c	ppi(c)	Diphosphate	Cytosol
798	19580c	ppmi12346p(c)	5-Diphosphoinositol pentakisphosphate	Cytosol
799	19581c	ppmi1346p(c)	Diphosphoinositol tetrakisphosphate	Cytosol
800	864c	pppg9(c)	Protoporphyrinogen IX	Cytosol
801	2452c	pppi(c)	Inorganic triphosphate	Cytosol
802	2325c	pram(c)	5-Phospho-beta-D-ribosylamine	Cytosol
803	10681c	prgnlone(c)	Pregnenolone	Cytosol
804	26331c	prgnlones(c)	pregnenolone sulfate	Cytosol
805	10510c	prgstrn(c)	Progesterone	Cytosol
806	21954c	prist(c)	pristanic acid	Cytosol
807	21957c	pristanal(c)	pristanal	Cytosol
808	21955c	pristcoa(c)	pristanoyl coa	Cytosol
809	629c	pro-D(c)	D-Proline	Cytosol
810	229c	pro-L(c)	L-Proline	Cytosol
811	3331c	prostg1(c)	(13E)-11alpha-Hydroxy-9,15-dioxoprost-13-enoate	Cytosol
812	11382c	prostgd2(c)	Prostaglandin D2	Cytosol
813	3492c	prostge1(c)	Prostaglandin E1	Cytosol
814	398c	prostge2(c)	Prostaglandin E2	Cytosol
815	1126c	prostgf2(c)	Prostaglandin F2alpha	Cytosol
816	422c	prostgh2(c)	Prostaglandin H2	Cytosol
817	1078c	prpp(c)	5-Phospho-alpha-D-ribose 1-diphosphate	Cytosol
818	19052c	ps_hs(c)	phosphatidylserine (homo sapiens)	Cytosol
819	824c	pser-L(c)	O-Phospho-L-serine	Cytosol
820	6304c	ptdca(c)	pentadecanoate	Cytosol
821	22500c	ptdcacoa(c)	pentadecanoyl Coenzyme A	Cytosol
822	22757c	ptdcacrn(c)	pendtadenoyl carnitine	Cytosol
823	1094c	ptrc(c)	Putrescine	Cytosol
824	670c	ptth(c)	Pantetheine	Cytosol
825	1130c	pyam5p(c)	Pyridoxamine 5'-phosphate	Cytosol
826	362c	pydam(c)	Pyridoxamine	Cytosol
827	298c	pydx(c)	Pyridoxal	Cytosol
828	479c	pydx5p(c)	Pyridoxal 5'-phosphate	Cytosol
829	160c	pydxn(c)	Pyridoxine	Cytosol
830	1851c	pylald(c)	Perillyl aldehyde	Cytosol
831	311c	pyr(c)	Pyruvate	Cytosol
832	406c	q10(c)	Ubiquinone-10	Cytosol
833	11879c	q10h2(c)	Ubiquinol-10	Cytosol
834	2854c	quln(c)	Quinolinate	Cytosol
835	10390c	r1p(c)	alpha-D-Ribose 1-phosphate	Cytosol
836	1999c	r5p(c)	alpha-D-Ribose 5-phosphate	Cytosol
837	156c	rbl-D(c)	D-Ribulose	Cytosol
838	91c	rbt(c)	Ribitol	Cytosol
839	22806c	retfa(c)	fatty acid retinol	Cytosol
840	208c	retinal(c)	Retinal	Cytosol
841	19631c	retinal-11-cis(c)	cis-11-retinal	Cytosol
842	22820c	retinal-cis-13(c)	cis-13-retinal	Cytosol
843	19630c	retinal-cis-9(c)	cis-9-retinal	Cytosol
844	90c	retinol(c)	Retinol	Cytosol
845	19628c	retinol-9-cis(c)	9-cis-retinol	Cytosol
846	19629c	retinol-cis-11(c)	cis-11-retinol	Cytosol

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
847	22819c	retinol-cis-13(c)	cis-13-retinol	Cytosol
848	11153c	retn(c)	Retinoate	Cytosol
849	22809c	retncoa(c)	retinoyl CoA	Cytosol
850	20818c	retnglc(c)	retinoyl glucuronide	Cytosol
851	1080c	rib-D(c)	D-Ribose	Cytosol
852	303c	ribflv(c)	Riboflavin	Cytosol
853	2368c	rnam(c)	N-Ribosylnicotinamide	Cytosol
854	261c	ru5p-D(c)	D-Ribulose 5-phosphate	Cytosol
855	15667c	s2l2n2m2m(c)	de-Fuc form of PA6 (w/o peptide linkage)	Cytosol
856	15669c	s2l2n2m2mn(c)	de-Fuc, reducing GlcNAc removed form of PA6 (w/o peptide linkage)	Cytosol
857	140c	s7p(c)	Sedoheptulose 7-phosphate	Cytosol
858	271c	sarcs(c)	Sarcosine	Cytosol
859	645c	sbt-D(c)	D-Sorbitol	Cytosol
860	4207c	seahcys(c)	Se-Adenosylselenohomocysteine	Cytosol
861	4301c	seasmet(c)	Se-Adenosylselenomethionine	Cytosol
862	4212c	sel(c)	Selenate	Cytosol
863	4389c	selcys(c)	Selenocysteine	Cytosol
864	4214c	selcyst(c)	Selenocystathionine	Cytosol
865	4213c	selhcys(c)	Selenohomocysteine	Cytosol
866	3846c	selmeth(c)	Selenomethionine	Cytosol
867	1247c	seln(c)	Selenide	Cytosol
868	3734c	selnp(c)	Selenophosphate	Cytosol
869	512c	ser-D(c)	D-Serine	Cytosol
870	339c	ser-L(c)	L-Serine	Cytosol
871	19615c	sgalside_hs(c)	sulfatide galactocerebroside (homo sapiens)	Cytosol
872	15786c	sl-L(c)	L-sulfolactate	Cytosol
873	1060c	so3(c)	Sulfite	Cytosol
874	335c	so4(c)	Sulfate	Cytosol
875	26303c	spc_hs(c)	sphingosylphosphorylcholine (homo sapiens)	Cytosol
876	9025c	sph1p(c)	Sphinganine 1-phosphate	Cytosol
877	708c	sphgn(c)	Sphinganine	Cytosol
878	10703c	sphings(c)	Sphingosine	Cytosol
879	19618c	sphmyln_hs(c)	sphingomyelin (homo sapiens)	Cytosol
880	4541c	sphs1p(c)	Sphingosine 1-phosphate	Cytosol
881	161c	spmd(c)	Spermidine	Cytosol
882	518c	sprm(c)	Spermine	Cytosol
883	638c	srtn(c)	Serotonin	Cytosol
884	8781c	stcoa(c)	Stearoyl-CoA (n-C18:0CoA)	Cytosol
885	11884c	stcrn(c)	stearoylcarnitine	Cytosol
886	18462c	strdnc(c)	stearidonic acid C18:4, n-3	Cytosol
887	18492c	strdnccoa(c)	stearidonyl coenzyme A	Cytosol
888	25985c	strdnccrn(c)	stearidonyl carnitine	Cytosol
889	325c	succ(c)	Succinate	Cytosol
890	26271c	tag1p-D(c)	D-Tagatose 1-phosphate	Cytosol
891	18538c	tag_hs(c)	triacylglycerol (homo sapiens)	Cytosol
892	646c	tagat-D(c)	D-Tagatose	Cytosol
893	293c	taur(c)	Taurine	Cytosol
894	20374c	taxol(c)	paclitaxel	Cytosol
895	3700c	tchola(c)	taurocholic acid	Cytosol
896	1428c	tcynt(c)	Thiocyanate	Cytosol
897	3390c	tdchola(c)	taurochenodeoxycholate	Cytosol
898	1862c	tdcoa(c)	Tetradecanoyl-CoA (n-C14:0CoA)	Cytosol

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
899	5939c	tdeACP(c)	cis-tetradec-7-enoyl-[acyl-carrier protein] (n-C14:1)	Cytosol
900	18514c	tethex3(c)	tetracosahexaenoic acid, n-3	Cytosol
901	18515c	tethex3coa(c)	tetracosahexaenoyl coenzyme A	Cytosol
902	18512c	tetpent3(c)	tetracosapentaenoic acid, n-3	Cytosol
903	18513c	tetpent3coa(c)	tetracosapentaenoyl coenzyme A, n-3	Cytosol
904	25991c	tetpent3crn(c)	tetracosapentaenoyl carnitine	Cytosol
905	18508c	tetpent6(c)	tetracosapentaenoic acid, n-6	Cytosol
906	18509c	tetpent6coa(c)	tetracosapentaenoyl coenzyme A, n-6	Cytosol
907	25992c	tetpent6crn(c)	tetracosapentaenoyl carnitine	Cytosol
908	18510c	tettet6(c)	tetracosatetraenoic acid n-6	Cytosol
909	18511c	tettet6coa(c)	tetracosatetraenoyl coenzyme A	Cytosol
910	25986c	tettet6crn(c)	Tetracosatetraenoyl carnitine	Cytosol
911	135c	thbpt(c)	Tetrahydrobiopterin	Cytosol
912	22636c	thbpt4acam(c)	Tetrahydrobiopterin-4a-carbinolamine	Cytosol
913	19623c	thcrm_hs(c)	trihexosyl ceramide (homo sapiens)	Cytosol
914	1483c	thcys(c)	Thiocysteine	Cytosol
915	1065c	thf(c)	5,6,7,8-Tetrahydrofolate	Cytosol
916	210c	thm(c)	Thiamin	Cytosol
917	866c	thmmp(c)	Thiamin monophosphate	Cytosol
918	341c	thmpp(c)	Thiamine diphosphate	Cytosol
919	2271c	thmtp(c)	Thiamin triphosphate	Cytosol
920	75c	thp2c(c)	2,3,4,5-Tetrahydropyridine-2-carboxylate	Cytosol
921	253c	thr-L(c)	L-Threonine	Cytosol
922	1481c	thrnt(c)	L-Threonate	Cytosol
923	246c	thym(c)	Thymine	Cytosol
924	5269c	thymd(c)	Thymidine	Cytosol
925	1482c	thyox-L(c)	L-Thyroxine	Cytosol
926	2907c	tmlys(c)	N6,N6,N6-Trimethyl-L-lysine	Cytosol
927	18465c	tmndnc(c)	timnodonic acid C20:5, n-3	Cytosol
928	18486c	tmndnccoa(c)	timnodonyl coenzyme A	Cytosol
929	25988c	tmndnccrn(c)	Timnodonyl carnitine	Cytosol
930	20410c	tolbutamide(c)	tolbutamide	Cytosol
931	181c	trdox(c)	Oxidized thioredoxin	Cytosol
932	180c	trdrd(c)	Reduced thioredoxin	Cytosol
933	867c	tre(c)	Trehalose	Cytosol
934	2543c	triodthy(c)	Triiodothyronine	Cytosol
935	21120c	triodthysuf(c)	Triiodothyronine sulfate	Cytosol
936	1047c	trp-L(c)	L-Tryptophan	Cytosol
937	405c	trypta(c)	Tryptamine	Cytosol
938	20000c	ts3(c)	Tachysterol 3	Cytosol
939	10622c	tststerone(c)	Testosterone	Cytosol
940	20816c	tststeroneglc(c)	testosterone glucuronide	Cytosol
941	26486c	tststerones(c)	testosterone sulfate	Cytosol
942	164c	tsul(c)	Thiosulfate	Cytosol
943	12382c	ttc-ggdp(c)	trans,trans,cis-Geranylgeranyl diphosphate	Cytosol
944	6302c	ttdca(c)	tetradecanoate (n-C14:0)	Cytosol
945	8772c	ttdcea(c)	tetradecenoate (n-C14:1)	Cytosol
946	26814c	ttdcrn(c)	tetradecanoyl carnitine	Cytosol
947	1777c	txa2(c)	Thromboxane A2	Cytosol
948	100c	tym(c)	Tyramine	Cytosol
949	21118c	tymsf(c)	Tyramine O-sulfate	Cytosol
950	1051c	tyr-L(c)	L-Tyrosine	Cytosol

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
951	326c	uacgam(c)	UDP-N-acetyl-D-glucosamine	Cytosol
952	477c	udp(c)	UDP	Cytosol
953	10912c	udpacgal(c)	UDP-N-acetyl-D-galactosamine	Cytosol
954	316c	udpg(c)	UDPglucose	Cytosol
955	331c	udpgal(c)	UDPgalactose	Cytosol
956	241c	udpglcur(c)	UDP-D-glucuronate	Cytosol
957	255c	udpxyl(c)	UDP-D-xylose	Cytosol
958	1068c	ump(c)	UMP	Cytosol
959	687c	uppg3(c)	Uroporphyrinogen III	Cytosol
960	1069c	ura(c)	Uracil	Cytosol
961	199c	urate(c)	Urate	Cytosol
962	640c	urcan(c)	Urocanate	Cytosol
963	1054c	urea(c)	Urea	Cytosol
964	10727c	uri(c)	Uridine	Cytosol
965	345c	utp(c)	UTP	Cytosol
966	18459c	vacc(c)	vaccenic acid	Cytosol
967	18479c	vacccoa(c)	vaccenyl coenzyme A	Cytosol
968	25973c	vacccrn(c)	Vaccenyl carnitine	Cytosol
969	250c	val-L(c)	L-Valine	Cytosol
970	20013c	vitd2(c)	Vitamin D2	Cytosol
971	20001c	vitd3(c)	Vitamin D3	Cytosol
972	20811c	whddca(c)	omega hydroxy dodecanoate (n-C12:0)	Cytosol
973	20813c	whhdca(c)	omega hydroxy hexadecanoate (n-C16:0)	Cytosol
974	20403c	whtststerone(c)	w hydroxy testosterone	Cytosol
975	20812c	whttdca(c)	omega hydroxy tetradecanoate (n-C14:0)	Cytosol
976	216c	xan(c)	Xanthine	Cytosol
977	436c	xmp(c)	Xanthosine 5'-phosphate	Cytosol
978	3380c	xol7ah(c)	7alpha-Hydroxy-5beta-cholestan-3-one	Cytosol
979	3381c	xol7ah2(c)	3alpha,7alpha-Dihydroxy-5beta-cholestane	Cytosol
980	11535c	xol7aone(c)	7alpha-Hydroxycholest-4-en-3-one	Cytosol
981	3384c	xoldiolone(c)	7alpha,12alpha-Dihydroxycholest-4-en-3-one	Cytosol
982	3382c	xoldioloneh(c)	7alpha,12alpha-Dihydroxy-5beta-cholestan-3-one	Cytosol
983	22732c	xolest2_hs(c)	cholesterol ester (from FULLR2)	Cytosol
984	2593c	xolest_hs(c)	cholesterol ester	Cytosol
985	17068c	xoltri24(c)	7-alpha,24(S)-Dihydroxycholesterol	Cytosol
986	17067c	xoltri25(c)	7-alpha,25-Dihydroxycholesterol	Cytosol
987	4061c	xoltri27(c)	7-alpha,27-Dihydroxycholesterol	Cytosol
988	3383c	xoltriol(c)	3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestane	Cytosol
989	459c	xtp(c)	XTP	Cytosol
990	10906c	xtsn(c)	Xanthosine	Cytosol
991	22281c	xu1p-D(c)	D-Xylulose 1-phosphate	Cytosol
992	283c	xu5p-D(c)	D-Xylulose 5-phosphate	Cytosol
993	248c	xyl-D(c)	D-Xylose	Cytosol
994	4197c	xylnt(c)	L-Xylonate	Cytosol
995	211c	xylt(c)	Xylitol	Cytosol
996	157c	xylu-D(c)	D-Xylulose	Cytosol
997	159c	xylu-L(c)	L-Xylulose	Cytosol
998	20140c	yvite(c)	gamma-Tocopherol	Cytosol
999	286e	10fthf(e)	10-Formyltetrahydrofolate	Extra-organism
1000	20786e	10fthf5glu(e)	10-formyltetrahydrofolate-[Glu](5)	Extra-organism
1001	20787e	10fthf6glu(e)	10-formyltetrahydrofolate-[Glu](6)	Extra-organism
1002	20788e	10fthf7glu(e)	10-formyltetrahydrofolate-[Glu](7)	Extra-organism

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
1003	22812e	11-cis-retfa(e)	fatty acid 11-cis-retinol	Extra-organism
1004	22816e	13-cis-retnglc(e)	13-cis-retinoyl glucuronide	Extra-organism
1005	22325e	1glyc_hs(e)	1 acyl phosphoglycerol	Extra-organism
1006	18732e	1mncam(e)	1-Methylnicotinamide	Extra-organism
1007	20023e	2425dhvitd2(e)	24R,25-Dihyoxyvitamin D2	Extra-organism
1008	20024e	2425dhvitd3(e)	24R,25-Dihydroxyvitamin D3	Extra-organism
1009	20412e	24nph(e)	2,4 dihydroxy nitrophenol	Extra-organism
1010	20014e	25hvitd2(e)	25-Hydroxyvitamin D2	Extra-organism
1011	20012e	25hvitd3(e)	25-Hydroxyvitamin D3	Extra-organism
1012	4433e	2hb(e)	2-Hydroxybutyrate	Extra-organism
1013	1591e	2mcit(e)	2-Methylcitrate	Extra-organism
1014	3464e	34dhoxpeg(e)	3,4-Dihydroxyphenylethyleneglycol	Extra-organism
1015	190e	34dhphe(e)	3,4-Dihydroxy-L-phenylalanine	Extra-organism
1016	9005e	35cgmp(e)	3',5'-Cyclic GMP	Extra-organism
1017	2457e	3aib(e)	L-3-Amino-isobutanoate	Extra-organism
1018	2444e	3aib-D(e)	D-3-Amino-isobutanoate	Extra-organism
1019	10891e	3mlda(e)	3-Methylimidazoleacetic acid	Extra-organism
1020	176e	4abut(e)	4-Aminobutanoate	Extra-organism
1021	20409e	4hdebrisoquine(e)	4 hydroxy debrisoquine	Extra-organism
1022	1127e	4hphac(e)	4-Hydroxyphenylacetate	Extra-organism
1023	20411e	4mtolbutamide(e)	4 hydroxy tolbutamide	Extra-organism
1024	730e	4nph(e)	4-Nitrophenol	Extra-organism
1025	21119e	4nphsf(e)	4-Nitrophenyl sulfate	Extra-organism
1026	717e	4pyrdx(e)	4-Pyridoxate	Extra-organism
1027	10712e	5adtststerone(e)	5alpha-Dihydrotestosterone	Extra-organism
1028	22786e	5adtststeroneglc(e)	5alpha-Dihydrotestosterone glucuronide	Extra-organism
1029	26487e	5adtststerones(e)	5alpha-Dihydrotestosterone sulfate	Extra-organism
1030	20783e	5dhf(e)	pentaglutamyl folate (DHF)	Extra-organism
1031	11866e	5fthf(e)	5-Formyltetrahydrofolate	Extra-organism
1032	20405e	5homeprazole(e)	5 hydroxy omeprazole	Extra-organism
1033	831e	5htrp(e)	5-Hydroxy-L-tryptophan	Extra-organism
1034	431e	5mthf(e)	5-Methyltetrahydrofolate	Extra-organism
1035	20780e	5thf(e)	pentaglutamyl folate (THF)	Extra-organism
1036	20784e	6dhf(e)	haxglutamyl folate (DHF)	Extra-organism
1037	20402e	6htststerone(e)	6 beta hydroxy testosterone	Extra-organism
1038	20781e	6thf(e)	hexaglutamyl folate (THF)	Extra-organism
1039	20785e	7dhf(e)	heptaglutamyl folate (DHF)	Extra-organism
1040	20782e	7thf(e)	heptaglutamyl folate (THF)	Extra-organism
1041	22811e	9-cis-retfa(e)	fatty acid 9-cis-retinol	Extra-organism
1042	105e	Lcystin(e)	L-Cystine	Extra-organism
1043	18523e	Rtotal(e)	R total	Extra-organism
1044	18525e	Rtotal2(e)	R total 2 position	Extra-organism
1045	18526e	Rtotal3(e)	R total 3 position	Extra-organism
1046	18059e	Tyr-ggn(e)	Tyr-194 of apo-glycogenin protein (primer for glycogen synthesis)	Extra-organism
1047	360e	abt(e)	L-Arabinitol	Extra-organism
1048	319e	ac(e)	Acetate	Extra-organism
1049	9016e	acac(e)	Acetoacetate	Extra-organism
1050	1052e	acald(e)	Acetaldehyde	Extra-organism
1051	266e	acetone(e)	Acetone	Extra-organism

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
1052	22669e	acgalfucgalacgalfuc12gal14acglcgalgluside_hs(e)	Type IIIA glycolipid	Extra-organism
1053	22681e	acgalfucgalacgalfucgalacglcgal14acglcgalgluside_hs(e)	Type IIIAb	Extra-organism
1054	224e	acgam(e)	N-Acetyl-D-glucosamine	Extra-organism
1055	1617e	ach(e)	Acetylcholine	Extra-organism
1056	19741e	acn13acngalgbside_hs(e)	sialyl (1,3) sialyl (2,6) galactosylgloboside (homo sapiens)	Extra-organism
1057	19742e	acn23acngalgbside_hs(e)	sialyl (2,3) sialyl (2,6) galactosylgloboside (homo sapiens)	Extra-organism
1058	22662e	acnacngal14acglcgalgluside_hs(e)	3',8'-LD1	Extra-organism
1059	19738e	acnacngalgbside_hs(e)	disialyl galactosylgloboside (homo sapiens)	Extra-organism
1060	22682e	acngalacglcgal14acglcgalgluside_hs(e)	VI3NeuAc-nLc6Cer	Extra-organism
1061	228e	ade(e)	Adenine	Extra-organism
1062	270e	adn(e)	Adenosine	Extra-organism
1063	471e	adp(e)	ADP	Extra-organism
1064	2434e	adprbp(e)	ADPribose 2'-phosphate	Extra-organism
1065	151e	adprib(e)	ADPribose	Extra-organism
1066	18463e	adrn(e)	adrenic acid	Extra-organism
1067	641e	adrnl(e)	Adrenaline	Extra-organism
1068	20413e	aflatoxin(e)	aflatoxin B1	Extra-organism
1069	20819e	ahandrostanglc(e)	Etiocholan-3alpha-ol-17-one 3-glucuronide	Extra-organism
1070	19364e	ak2lgchol_hs(e)	1-alkyl 2-lysoglycerol 3-phosphocholine	Extra-organism
1071	314e	akg(e)	2-Oxoglutarate	Extra-organism
1072	1063e	ala-B(e)	beta-Alanine	Extra-organism
1073	1093e	ala-D(e)	D-Alanine	Extra-organism
1074	11412e	ala-L(e)	L-Alanine	Extra-organism
1075	1447e	aldstrn(e)	Aldosterone	Extra-organism
1076	309e	amp(e)	AMP	Extra-organism
1077	352e	andrstrn(e)	Androsterone	Extra-organism
1078	20815e	andrstrnglc(e)	androsterone glucuronide	Extra-organism
1079	20406e	antipyrene(e)	antipyrene	Extra-organism
1080	2071e	apnnox(e)	alpha-Pinene-oxide	Extra-organism
1081	4033e	appnn(e)	(+)-alpha-Pinene	Extra-organism
1082	3086e	aprgstrn(e)	20alpha-Hydroxyprogesterone	Extra-organism
1083	816e	aqcobal(e)	Aquacob(III)alamin	Extra-organism
1084	307e	arab-L(e)	L-Arabinose	Extra-organism
1085	5355e	arach(e)	Arachidic acid	Extra-organism
1086	11890e	arachd(e)	arachidonic acid	Extra-organism
1087	337e	arg-L(e)	L-Arginine	Extra-organism
1088	11279e	ascb-L(e)	L-Ascorbate	Extra-organism
1089	232e	asn-L(e)	L-Asparagine	Extra-organism
1090	10519e	asp-D(e)	D-Aspartate	Extra-organism
1091	330e	asp-L(e)	L-Aspartate	Extra-organism
1092	465e	atp(e)	ATP	Extra-organism

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
1093	20142e	avite1(e)	alpha-Tocopherol	Extra-organism
1094	20141e	avite2(e)	alpha-Tocotrienol	Extra-organism
1095	870e	bhb(e)	(R)-3-Hydroxybutanoate	Extra-organism
1096	4279e	bildglcur(e)	Bilirubin beta-diglucuronide	Extra-organism
1097	1942e	bilglcur(e)	Bilirubin monoglucuronide	Extra-organism
1098	101e	bilirub(e)	Bilirubin	Extra-organism
1099	4297e	biocyt(e)	Biocytin	Extra-organism
1100	1079e	btn(e)	Biotin	Extra-organism
1101	294e	but(e)	Butyrate (n-C4:0)	Extra-organism
1102	20143e	bvite(e)	beta-tocopherol	Extra-organism
1103	10989e	bz(e)	Benzoate	Extra-organism
1104	346e	ca2(e)	Calcium	Extra-organism
1105	8980e	camp(e)	cAMP	Extra-organism
1106	19576e	caro(e)	beta-Carotene	Extra-organism
1107	798e	carveol(e)	(E)-carveol	Extra-organism
1108	20077e	cca_d3(e)	Calcitroic acid (D3)	Extra-organism
1109	7908e	cgly(e)	Cys-Gly	Extra-organism
1110	1075e	chol(e)	Choline	Extra-organism
1111	457e	cholate(e)	Cholate	Extra-organism
1112	252e	chsterol(e)	Cholesterol	Extra-organism
1113	19243e	chtn(e)	chitin	Extra-organism
1114	236e	cit(e)	Citrate	Extra-organism
1115	5268e	cl(e)	Chloride	Extra-organism
1116	18467e	clpnd(e)	clupanodonic acid	Extra-organism
1117	11376e	cmp(e)	CMP	Extra-organism
1118	12152e	co(e)	Carbon monoxide	Extra-organism
1119	474e	co2(e)	CO2	Extra-organism
1120	4331e	coumarin(e)	coumarin	Extra-organism
1121	150e	creat(e)	Creatine	Extra-organism
1122	2222e	crmp_hs(e)	Ceramide 1-phosphate	Extra-organism
1123	163e	crn(e)	L-Carnitine	Extra-organism
1124	11891e	crvnc(e)	cervonic acid, C22:6 n-3	Extra-organism
1125	212e	csn(e)	Cytosine	Extra-organism
1126	20541e	cspg_a(e)	chondroitin sulfate A (GalNAc4S-GlcA) proteoglycan	Extra-organism
1127	20599e	cspg_b(e)	chondroitin sulfate B / dermatan sulfate (IdoA2S-GalNAc4S) proteoglycan	Extra-organism
1128	20545e	cspg_c(e)	chondroitin sulfate C (GalNAc6S-GlcA) proteoglycan	Extra-organism
1129	20554e	cspg_d(e)	chondroitin sulfate D (GlcNAc6S-GlcA2S) proteoglycan	Extra-organism
1130	20549e	cspg_e(e)	chondroitin sulfate E (GalNAc4,6diS-GlcA) proteoglycan	Extra-organism
1131	245e	cyan(e)	Hydrogen cyanide	Extra-organism
1132	1062e	cys-L(e)	L-Cysteine	Extra-organism
1133	92e	cytd(e)	Cytidine	Extra-organism
1134	380e	dad-2(e)	Deoxyadenosine	Extra-organism
1135	3751e	dad-5(e)	5'-Deoxyadenosine	Extra-organism
1136	18537e	dag_hs(e)	diacylglycerol (homo sapiens)	Extra-organism
1137	18466e	dcsptn1(e)	docosa-4,7,10,13,16-pentaenoic acid (n-6)	Extra-organism
1138	10918e	dcyt(e)	Deoxycytidine	Extra-organism
1139	20408e	debrisoquine(e)	debrisoquine	Extra-organism
1140	3387e	dgchol(e)	Chenodeoxyglycocholate	Extra-organism

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
1141	172e	dgsn(e)	Deoxyguanosine	Extra-organism
1142	421e	dhdascb(e)	Dehydroascorbate	Extra-organism
1143	3998e	dheas(e)	Dehydroepiandrosterone sulfate	Extra-organism
1144	10505e	dhf(e)	7,8-Dihydrofolate	Extra-organism
1145	4544e	digalsgalside_hs(e)	Digalactosylceramidesulfate	Extra-organism
1146	3417e	din(e)	Deoxyinosine	Extra-organism
1147	2431e	dlnlcg(e)	dihomo-gamma-linolenic acid (n-6)	Extra-organism
1148	20407e	dmantipyrine(e)	demethylated antipyrine	Extra-organism
1149	26488e	dmhptcrn(e)	2,6 dimethylheptanoyl carnitine	Extra-organism
1150	2882e	dopa(e)	Dopamine	Extra-organism
1151	21114e	dopasf(e)	Dopamine 3-O-sulfate	Extra-organism
1152	1462e	drib(e)	Deoxyribose	Extra-organism
1153	355e	duri(e)	Deoxyuridine	Extra-organism
1154	20414e	eaflatoxin(e)	8,9 epxoy aflatoxin B1	Extra-organism
1155	20367e	ebastine(e)	ebastine	Extra-organism
1156	20368e	ebastineoh(e)	hydroxylated ebastine	Extra-organism
1157	18506e	eicostet(e)	eicosatetranoic acid	Extra-organism
1158	588e	elaid(e)	elaidic acid	Extra-organism
1159	20817e	estradiolglc(e)	estradiol glucuronide	Extra-organism
1160	3415e	estriolglc(e)	16-Glucuronide-estriol	Extra-organism
1161	20814e	estroneglc(e)	estrone glucuronide	Extra-organism
1162	2601e	estrones(e)	Estrone 3-sulfate	Extra-organism
1163	87e	etoh(e)	Ethanol	Extra-organism
1164	312e	fe2(e)	Fe2+	Extra-organism
1165	5267e	fe3(e)	Fe3+	Extra-organism
1166	118e	fol(e)	Folate	Extra-organism
1167	334e	for(e)	Formate	Extra-organism
1168	1061e	fru(e)	D-Fructose	Extra-organism
1169	833e	fuc-L(e)	L-Fucose	Extra-organism
1170	22691e	fuc13galacglcgal14acglcgalgluside_hs(e)	III3Fuc-nLc6Cer	Extra-organism
1171	22658e	fuc14galacglcgalgluside_hs(e)	Lea glycolipid	Extra-organism
1172	22657e	fucacgalfucgalacglcgalgluside_hs(e)	(Gal)2 (GalNAc)1 (Glc)1 (GlcNAc)1 (LFuc)2 (Cer)1	Extra-organism
1173	22663e	fucacngal14acglcgalgluside_hs(e)	IV3-a-NeuAc,III3-a-Fuc-nLc4Cer	Extra-organism
1174	22655e	fucacngalacglcgalgluside_hs(e)	IV3-a-Neu5Ac,III4-a-Fuc-Lc4Cer	Extra-organism
1175	22665e	fucfuc12gal14acglcgalgluside_hs(e)	Ley glycolipid	Extra-organism
1176	22693e	fucfuc132galacglcgal14acglcgalgluside_hs(e)	V3Fuc,III3Fuc-nLc6Cer	Extra-organism
1177	22690e	fucfucfucgalacglc13galacglcgal14acglcgalgluside_hs(e)	(Gal)4 (Glc)1 (GlcNAc)3 (LFuc)3 (Cer)1	Extra-organism

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
1178	22685e	fucfucfucgalacglcgal14acglcgalgluside_hs(e)	(Gal)3 (Glc)1 (GlcNAc)2 (LFuc)3 (Cer)1	Extra-organism
1179	22650e	fucfucgalacglcgalgluside_hs(e)	Leb glycolipid	Extra-organism
1180	22660e	fucgal14acglcgalgluside_hs(e)	Lacto-N-fucopentaosyl III ceramide	Extra-organism
1181	22652e	fucgalfucgalacglcgalgluside_hs(e)	(Gal)3 (Glc)1 (GlcNAc)1 (LFuc)2 (Cer)1	Extra-organism
1182	19746e	fucgalgbside_hs(e)	fucosyl galactosylgloboside (homo sapiens)	Extra-organism
1183	1083e	gal(e)	D-Galactose	Extra-organism
1184	19744e	galacglcgalgbside_hs(e)	Gal-GlcNAc-Gal globoside (homo sapiens)	Extra-organism
1185	22670e	galfuc12gal14acglcgalgluside_hs(e)	(Gal)3 (Glc)1 (GlcNAc)1 (LFuc)1 (Cer)1	Extra-organism
1186	22683e	galfucgalacglcgal14acglcgalgluside_hs(e)	(Gal)4 (Glc)1 (GlcNAc)2 (LFuc)1 (Cer)1	Extra-organism
1187	22676e	galgalfucfucgalacglcgalacglcgal14acglcgalgluside_hs(e)	(Gal)6 (Glc)1 (GlcNAc)3 (LFuc)2 (Cer)1	Extra-organism
1188	19735e	galgalgalthcrm_hs(e)	Gal-Gal-Gal-Gal-Gal-Glc-Cer (homo sapiens)	Extra-organism
1189	171e	gam(e)	D-Glucosamine	Extra-organism
1190	19624e	gbside_hs(e)	globoside (homo sapiens)	Extra-organism
1191	1554e	gchola(e)	glycocholate	Extra-organism
1192	19757e	gd1b2_hs(e)	GD1beta (homo sapiens)	Extra-organism
1193	19754e	gd1c_hs(e)	GD1c (homo sapiens)	Extra-organism
1194	11524e	gdchola(e)	glycochenodeoxycholate	Extra-organism
1195	321e	gdp(e)	GDP	Extra-organism
1196	318e	glc-D(e)	D-Glucose	Extra-organism
1197	11299e	gln-L(e)	L-Glutamine	Extra-organism
1198	313e	glu-L(e)	L-Glutamate	Extra-organism
1199	7925e	gluala(e)	5-L-Glutamyl-L-alanine	Extra-organism
1200	323e	gly(e)	Glycine	Extra-organism
1201	503e	glyb(e)	Glycine betaine	Extra-organism
1202	1077e	glyc(e)	Glycerol	Extra-organism
1203	18741e	glyc-S(e)	(S)-Glycerate	Extra-organism
1204	18062e	glygn2(e)	glycogen, structure 2 (glycogenin-1,6-{7[1,4-Glc], 4[1,4-Glc]})	Extra-organism
1205	18142e	glygn4(e)	glycogen, structure 4 (glycogenin-1,6-{2[1,4-Glc], [1,4-Glc]})	Extra-organism
1206	18148e	glygn5(e)	glycogen, structure 5 (glycogenin-2[1,4-Glc])	Extra-organism
1207	226e	gmp(e)	GMP	Extra-organism
1208	19768e	gp1c_hs(e)	GP1c (homo sapiens)	Extra-organism
1209	19976e	gp1calpha_hs(e)	GP1c alpha (homo sapiens)	Extra-organism
1210	19763e	gq1b_hs(e)	GQ1b (homo sapiens)	Extra-organism
1211	19771e	gq1balpha_hs(e)	GQ1balpha (homo sapiens)	Extra-organism
1212	5279e	gsn(e)	Guanosine	Extra-organism
1213	19749e	gt1a_hs(e)	GT1a (homo sapiens)	Extra-organism
1214	1087e	gthox(e)	Oxidized glutathione	Extra-organism

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
1215	11388e	gthrd(e)	Reduced glutathione	Extra-organism
1216	327e	gtp(e)	GTP	Extra-organism
1217	291e	gua(e)	Guanine	Extra-organism
1218	1049e	h(e)	H+	Extra-organism
1219	317e	h2o(e)	H2O	Extra-organism
1220	315e	h2o2(e)	Hydrogen peroxide	Extra-organism
1221	9554e	ha(e)	hyaluronan	Extra-organism
1222	22610e	ha_pre1(e)	hyaluronan biosynthesis, precursor 1	Extra-organism
1223	144e	hco3(e)	Bicarbonate	Extra-organism
1224	20383e	hcoumarin(e)	hydroxy coumarin	Extra-organism
1225	297e	hdca(e)	Hexadecanoate (n-C16:0)	Extra-organism
1226	5725e	hdcea(e)	Hexadecenoate (n-C16:1)	Extra-organism
1227	20384e	hestratriol(e)	4,17 dihydroxy estradiol	Extra-organism
1228	9242e	hexc(e)	hexacosanoate (n-C26:0)	Extra-organism
1229	11120e	his-L(e)	L-Histidine	Extra-organism
1230	15080e	hista(e)	Histamine	Extra-organism
1231	131e	hom-L(e)	L-Homoserine	Extra-organism
1232	6306e	hpdca(e)	heptadecanoate	Extra-organism
1233	20638e	hspg(e)	heparan sulfate proteoglycan	Extra-organism
1234	20376e	htaxol(e)	hydroxylated taxol	Extra-organism
1235	218e	hxan(e)	Hypoxanthine	Extra-organism
1236	464e	i(e)	Iodide	Extra-organism
1237	1067e	idp(e)	IDP	Extra-organism
1238	410e	ile-L(e)	L-Isoleucine	Extra-organism
1239	1090e	imp(e)	IMP	Extra-organism
1240	223e	inost(e)	myo-Inositol	Extra-organism
1241	147e	ins(e)	Inosine	Extra-organism
1242	289e	k(e)	potassium	Extra-organism
1243	20192e	ksi(e)	keratan sulfate I	Extra-organism
1244	22553e	ksi_deg1(e)	keratan sulfate I, degradation product 1	Extra-organism
1245	20156e	ksii_core2(e)	keratan sulfate II (core 2-linked)	Extra-organism
1246	20342e	ksii_core4(e)	keratan sulfate II (core 4-linked)	Extra-organism
1247	304e	lac-D(e)	D-Lactate	Extra-organism
1248	10931e	lac-L(e)	L-Lactate	Extra-organism
1249	292e	lcts(e)	Lactose	Extra-organism
1250	1082e	leu-L(e)	L-Leucine	Extra-organism
1251	17887e	leuktrC4(e)	Leukotriene C4	Extra-organism
1252	18473e	lgnc(e)	lignoceric acid	Extra-organism
1253	10371e	limnen(e)	Limonene	Extra-organism
1254	11278e	lipoate(e)	Lipoate	Extra-organism
1255	18461e	lneldc(e)	linoelaidic acid (all trans C18:2)	Extra-organism
1256	11172e	lnlc(e)	linoleic acid (all cis C18:2) n-6	Extra-organism
1257	11152e	lnlnca(e)	alpha-Linolenic acid, C18:3, n-3	Extra-organism
1258	5356e	lnlncg(e)	gamma-linolenic acid	Extra-organism
1259	19382e	lpchol_hs(e)	lysophosphatidylcholine (homo sapiens)	Extra-organism
1260	328e	lys-L(e)	L-Lysine	Extra-organism
1261	18539e	mag_hs(e)	monoacylglycerol 2 (homo sapiens)	Extra-organism
1262	267e	malt(e)	Maltose	Extra-organism
1263	1284e	malttr(e)	Maltotriose	Extra-organism
1264	11018e	man(e)	D-Mannose	Extra-organism
1265	137e	man6p(e)	D-Mannose 6-phosphate	Extra-organism
1266	1092e	meoh(e)	Methanol	Extra-organism
1267	11265e	mepi(e)	Metanephrine	Extra-organism

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
1268	26412e	mercplaccys(e)	3-mercaptolactate-cysteine disulfide	Extra-organism
1269	343e	met-L(e)	L-Methionine	Extra-organism
1270	370e	mthgxl(e)	Methylglyoxal	Extra-organism
1271	3649e	n2m2nmasn(e)	N-Acetyl-beta-D-glucosaminyl-1,2-alpha-D-mannosyl-1,3-(N-acetyl-beta-D-glucosaminyl-1,2-alpha-D-mannosyl-1,6)-(N-acetyl-beta-D-glucosaminyl-1,4)-beta-D-mannosyl-1,4-N-acetyl-beta-D-glucosaminyl-R	Extra-organism
1272	1023e	na1(e)	Sodium	Extra-organism
1273	301e	nac(e)	Nicotinate	Extra-organism
1274	466e	nad(e)	Nicotinamide adenine dinucleotide	Extra-organism
1275	469e	nadp(e)	Nicotinamide adenine dinucleotide phosphate	Extra-organism
1276	233e	ncam(e)	Nicotinamide	Extra-organism
1277	476e	nh4(e)	Ammonium	Extra-organism
1278	20399e	nifedipine(e)	nifedipine	Extra-organism
1279	361e	no(e)	Nitric oxide	Extra-organism
1280	668e	npthl(e)	Naphthalene	Extra-organism
1281	371e	nrpphr(e)	Norepinephrine	Extra-organism
1282	21117e	nrpphrsf(e)	Sulfate derivative of norepinephrine	Extra-organism
1283	18464e	nrvnc(e)	nervonic acid	Extra-organism
1284	470e	o2(e)	O2	Extra-organism
1285	461e	o2s(e)	Superoxide anion	Extra-organism
1286	20055e	oagd3_hs(e)	9-O-Acetylated GD3 (homo sapiens)	Extra-organism
1287	20056e	oagt3_hs(e)	9-O-Acetylated GT3 (homo sapiens)	Extra-organism
1288	1249e	ocdca(e)	octadecanoate (n-C18:0)	Extra-organism
1289	8769e	ocdcea(e)	octadecenoate (n-C18:1)	Extra-organism
1290	5354e	octa(e)	octanoate (n-C8:0)	Extra-organism
1291	1021e	oh1(e)	hydroxide ion	Extra-organism
1292	20404e	omeprazole(e)	omeprazole	Extra-organism
1293	20401e	onpthl(e)	naphthalene epoxide	Extra-organism
1294	1304e	orn(e)	Ornithine	Extra-organism
1295	10901e	oxa(e)	Oxalate	Extra-organism
1296	19365e	paf_hs(e)	1-alkyl 2-acteylglycerol 3-phosphocholine (homo sapiens)	Extra-organism
1297	19051e	pchol_hs(e)	Phosphatidylcholine (homo sapiens)	Extra-organism
1298	19050e	pe_hs(e)	phosphatidylethanolamine (homo sapiens)	Extra-organism
1299	5307e	peplys(e)	Peptidyl-L-lysine	Extra-organism
1300	2536e	perillyl(e)	Perillyl alcohol	Extra-organism
1301	19385e	pglyc_hs(e)	phosphatidylglycerol (homo sapiens)	Extra-organism
1302	1048e	phe-L(e)	L-Phenylalanine	Extra-organism
1303	2972e	pheacgln(e)	alpha-N-Phenylacetyl-L-glutamine	Extra-organism
1304	11520e	pheme(e)	Protoheme	Extra-organism
1305	10509e	phyQ(e)	Phylloquinone	Extra-organism
1306	1308e	phyt(e)	phytanic acid	Extra-organism
1307	472e	pi(e)	Phosphate	Extra-organism
1308	10928e	pnto-R(e)	(R)-Pantothenate	Extra-organism
1309	238e	ppa(e)	Propionate (n-C3:0)	Extra-organism
1310	629e	pro-D(e)	D-Proline	Extra-organism
1311	229e	pro-L(e)	L-Proline	Extra-organism
1312	11382e	prostgd2(e)	Prostaglandin D2	Extra-organism
1313	3492e	prostge1(e)	Prostaglandin E1	Extra-organism
1314	398e	prostge2(e)	Prostaglandin E2	Extra-organism
1315	1126e	prostgf2(e)	Prostaglandin F2alpha	Extra-organism

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
1316	19052e	ps_hs(e)	phosphatidylserine (homo sapiens)	Extra-organism
1317	6304e	ptdca(e)	pentadecanoate	Extra-organism
1318	362e	pydam(e)	Pyridoxamine	Extra-organism
1319	298e	pydx(e)	Pyridoxal	Extra-organism
1320	160e	pydxn(e)	Pyridoxine	Extra-organism
1321	311e	pyr(e)	Pyruvate	Extra-organism
1322	91e	rbt(e)	Ribitol	Extra-organism
1323	22806e	retfa(e)	fatty acid retinol	Extra-organism
1324	90e	retinol(e)	Retinol	Extra-organism
1325	19628e	retinol-9-cis(e)	9-cis-retinol	Extra-organism
1326	19629e	retinol-cis-11(e)	cis-11-retinol	Extra-organism
1327	11153e	retn(e)	Retinoate	Extra-organism
1328	20818e	retnglc(e)	retinoyl glucuronide	Extra-organism
1329	19574e	retpalm [deleted 10/09/2005 06:18:49 PM](e)	Retinyl palminate	Extra-organism
1330	1080e	rib-D(e)	D-Ribose	Extra-organism
1331	303e	ribflv(e)	Riboflavin	Extra-organism
1332	15207e	s2l2fn2m2masn(e)	PA6	Extra-organism
1333	15665e	s2l2n2m2masn(e)	de-Fuc form of PA6	Extra-organism
1334	271e	sarcs(e)	Sarcosine	Extra-organism
1335	4212e	sel(e)	Selenate	Extra-organism
1336	512e	ser-D(e)	D-Serine	Extra-organism
1337	339e	ser-L(e)	L-Serine	Extra-organism
1338	15786e	sl-L(e)	L-sulfolactate	Extra-organism
1339	335e	so4(e)	Sulfate	Extra-organism
1340	26303e	spc_hs(e)	sphingosylphosphorylcholine (homo sapiens)	Extra-organism
1341	9025e	sph1p(e)	Sphinganine 1-phosphate	Extra-organism
1342	4541e	sphs1p(e)	Sphingosine 1-phosphate	Extra-organism
1343	638e	srtn(e)	Serotonin	Extra-organism
1344	18126e	strch1(e)	starch, structure 1 (1,6-{7[1,4-Glc], 4[1,4-Glc]})	Extra-organism
1345	18141e	strch2(e)	starch, structure 2 (1,6-{2[1,4-Glc], [1,4-Glc]})	Extra-organism
1346	18462e	strdnc(e)	stearidonic acid C18:4, n-3	Extra-organism
1347	325e	succ(e)	Succinate	Extra-organism
1348	1056e	sucr(e)	Sucrose	Extra-organism
1349	18538e	tag_hs(e)	triacylglycerol (homo sapiens)	Extra-organism
1350	646e	tagat-D(e)	D-Tagatose	Extra-organism
1351	293e	taur(e)	Taurine	Extra-organism
1352	20374e	taxol(e)	paclitaxel	Extra-organism
1353	3700e	tchola(e)	taurocholic acid	Extra-organism
1354	1428e	tcynt(e)	Thiocyanate	Extra-organism
1355	3390e	tdchola(e)	taurochenodeoxycholate	Extra-organism
1356	18514e	tethex3(e)	tetracosahexaenoic acid, n-3	Extra-organism
1357	18512e	tetpent3(e)	tetracosapentaenoic acid, n-3	Extra-organism
1358	18508e	tetpent6(e)	tetracosapentaenoic acid, n-6	Extra-organism
1359	18510e	tettet6(e)	tetracosatetraenoic acid n-6	Extra-organism
1360	1065e	thf(e)	5,6,7,8-Tetrahydrofolate	Extra-organism
1361	210e	thm(e)	Thiamin	Extra-organism
1362	866e	thmmp(e)	Thiamin monophosphate	Extra-organism
1363	2271e	thmtp(e)	Thiamin triphosphate	Extra-organism
1364	253e	thr-L(e)	L-Threonine	Extra-organism
1365	246e	thym(e)	Thymine	Extra-organism
1366	5269e	thymd(e)	Thymidine	Extra-organism

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
1367	1482e	thyox-L(e)	L-Thyroxine	Extra-organism
1368	18465e	tmndnc(e)	timnodonic acid C20:5, n-3	Extra-organism
1369	20410e	tolbutamide(e)	tolbutamide	Extra-organism
1370	867e	tre(e)	Trehalose	Extra-organism
1371	2543e	triodthy(e)	Triiodothyronine	Extra-organism
1372	21120e	triodthysuf(e)	Triiodothyronine sulfate	Extra-organism
1373	1047e	trp-L(e)	L-Tryptophan	Extra-organism
1374	20816e	tststeroneglc(e)	testosterone glucuronide	Extra-organism
1375	26486e	tststerones(e)	testosterone sulfate	Extra-organism
1376	164e	tsul(e)	Thiosulfate	Extra-organism
1377	6302e	ttdca(e)	tetradecanoate (n-C14:0)	Extra-organism
1378	1777e	txa2(e)	Thromboxane A2	Extra-organism
1379	21118e	tymsf(e)	Tyramine O-sulfate	Extra-organism
1380	1051e	tyr-L(e)	L-Tyrosine	Extra-organism
1381	477e	udp(e)	UDP	Extra-organism
1382	1068e	ump(e)	UMP	Extra-organism
1383	1069e	ura(e)	Uracil	Extra-organism
1384	199e	urate(e)	Urate	Extra-organism
1385	1054e	urea(e)	Urea	Extra-organism
1386	10727e	uri(e)	Uridine	Extra-organism
1387	345e	utp(e)	UTP	Extra-organism
1388	18459e	vacc(e)	vaccenic acid	Extra-organism
1389	250e	val-L(e)	L-Valine	Extra-organism
1390	20013e	vitd2(e)	Vitamin D2	Extra-organism
1391	20001e	vitd3(e)	Vitamin D3	Extra-organism
1392	20811e	whddca(e)	omega hydroxy dodecanoate (n-C12:0)	Extra-organism
1393	20813e	whhdca(e)	omega hydroxy hexadecanoate (n-C16:0)	Extra-organism
1394	20403e	whtststerone(e)	w hydroxy testosterone	Extra-organism
1395	20812e	whttdca(e)	omega hydroxy tetradecanoate (n-C14:0)	Extra-organism
1396	22732e	xolest2_hs(e)	cholesterol ester (from FULLR2)	Extra-organism
1397	2593e	xolest_hs(e)	cholesterol ester	Extra-organism
1398	17068e	xoltri24(e)	7-alpha,24(S)-Dihydroxycholesterol	Extra-organism
1399	17067e	xoltri25(e)	7-alpha,25-Dihydroxycholesterol	Extra-organism
1400	4061e	xoltri27(e)	7-alpha,27-Dihydroxycholesterol	Extra-organism
1401	248e	xyl-D(e)	D-Xylose	Extra-organism
1402	211e	xylt(e)	Xylitol	Extra-organism
1403	20140e	yvite(e)	gamma-Tocopherol	Extra-organism
1404	9005g	35cgmp(g)	3',5'-Cyclic GMP	Golgi Apparatus
1405	15787g	Ser/Thr(g)	protein-linked serine or threonine residue (O-glycosylation site)	Golgi Apparatus
1406	15792g	T_antigen(g)	T antigen (core 1)	Golgi Apparatus
1407	15788g	Tn_antigen(g)	Tn antigen	Golgi Apparatus
1408	319g	ac(g)	Acetate	Golgi Apparatus
1409	11537g	accoa(g)	Acetyl-CoA	Golgi Apparatus
1410	19739g	acgagbside_hs(g)	alpha GalNAc globoside (homo sapiens)	Golgi Apparatus
1411	899g	acgal(g)	N-Acetyl-D-galactosamine	Golgi Apparatus
1412	22666g	acgalfuc12gal14acglcgalgluside_hs(g)	(Gal)2 (GalNAc)1 (Glc)1 (GlcNAc)1 (LFuc)1 (Cer)1	Golgi Apparatus
1413	22669g	acgalfucgalacgalfuc12gal14acglcgalgluside_hs(g)	Type IIIA glycolipid	Golgi Apparatus

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
1414	22681g	acgalfucgalacgalfucgalacglcgal14acglcgalgluside_hs(g)	Type IIIAb	Golgi Apparatus
1415	22678g	acgalfucgalacglcgal14acglcgalgluside_hs(g)	(Gal)3 (GalNAc)1 (Glc)1 (GlcNAc)2 (LFuc)1 (Cer)1	Golgi Apparatus
1416	22656g	acgalfucgalacglcgalgluside_hs(g)	Type IA glycolipid	Golgi Apparatus
1417	19740g	acgbgbside_hs(g)	beta GalNAc globoside (homo sapiens)	Golgi Apparatus
1418	22686g	acglc13galacglcgal14acglcgalgluside_hs(g)	nLc7Cer	Golgi Apparatus
1419	22671g	acglcgal14acglcgalgluside_hs(g)	nLc5Cer	Golgi Apparatus
1420	22673g	acglcgalacglcgal14acglcgalgluside_hs(g)	(Gal)3 (Glc)1 (GlcNAc)3 (Cer)1	Golgi Apparatus
1421	19743g	acglcgalgbside_hs(g)	GlcNAc-Gal globoside (homo sapiens)	Golgi Apparatus
1422	22647g	acglcgalgluside_hs(g)	(Gal)1 (Glc)1 (GlcNAc)1 (Cer)1	Golgi Apparatus
1423	19741g	acn13acngalgbside_hs(g)	sialyl (1,3) sialyl (2,6) galactosylgloboside (homo sapiens)	Golgi Apparatus
1424	19742g	acn23acngalgbside_hs(g)	sialyl (2,3) sialyl (2,6) galactosylgloboside (homo sapiens)	Golgi Apparatus
1425	22662g	acnacngal14acglcgalgluside_hs(g)	3',8'-LD1	Golgi Apparatus
1426	19738g	acnacngalgbside_hs(g)	disialyl galactosylgloboside (homo sapiens)	Golgi Apparatus
1427	22661g	acngal14acglcgalgluside_hs(g)	Sialyl-3-paragloboside	Golgi Apparatus
1428	22682g	acngalacglcgal14acglcgalgluside_hs(g)	VI3NeuAc-nLc6Cer	Golgi Apparatus
1429	22654g	acngalacglcgalgluside_hs(g)	(Gal)3 (Glc)1 (GlcNAc)1 (Cer)1	Golgi Apparatus
1430	19737g	acngalgbside_hs(g)	sialyl galactosylgloboside (homo sapiens)	Golgi Apparatus
1431	309g	amp(g)	AMP	Golgi Apparatus
1432	8980g	camp(g)	cAMP	Golgi Apparatus
1433	1075g	chol(g)	Choline	Golgi Apparatus
1434	9019g	cholp(g)	Choline phosphate	Golgi Apparatus
1435	252g	chsterol(g)	Cholesterol	Golgi Apparatus
1436	11376g	cmp(g)	CMP	Golgi Apparatus
1437	1088g	cmpacna(g)	CMP-N-acetylneuraminate	Golgi Apparatus
1438	474g	co2(g)	CO2	Golgi Apparatus
1439	473g	coa(g)	Coenzyme A	Golgi Apparatus
1440	15793g	core2(g)	Core 2	Golgi Apparatus
1441	15796g	core3(g)	Core 3	Golgi Apparatus
1442	15797g	core4(g)	Core 4	Golgi Apparatus
1443	15887g	core5(g)	Core 5	Golgi Apparatus

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
1444	15798g	core6(g)	Core 6	Golgi Apparatus
1445	15888g	core7(g)	Core 7	Golgi Apparatus
1446	15886g	core8(g)	Core 8	Golgi Apparatus
1447	19478g	crm_hs(g)	ceramide (homo sapiens)	Golgi Apparatus
1448	20499g	cs,hs_linkage(g)	chondroitin sulfate/heparan sulfate linkage region (GlcA-(Gal)2-Xyl-L-Ser (protein))	Golgi Apparatus
1449	20538g	cs_a,b,e_pre1(g)	chondroitin sulfate A (GalNAc4S-GlcA), B (IdoA2S-GalNAc4S), and E (GalNAc4,6diS-GlcA), precursor 1	Golgi Apparatus
1450	20539g	cs_a,b_pre2(g)	chondroitin sulfate A (GalNAc4S-GlcA) and B (IdoA2S-GalNAc4S), precursor 2	Golgi Apparatus
1451	20540g	cs_a,b_pre3(g)	chondroitin sulfate A (GalNAc4S-GlcA) and B (IdoA2S-GalNAc4S), precursor 3	Golgi Apparatus
1452	20597g	cs_b_pre4(g)	chondroitin sulfate B (IdoA2S-GalNAc4S), precursor 4	Golgi Apparatus
1453	20598g	cs_b_pre5(g)	chondroitin sulfate B (IdoA2S-GalNAc4s), precursor 5	Golgi Apparatus
1454	20542g	cs_c,d,e_pre1(g)	chondroitin sulfate C (GalNAc6S-GlcA) and D (GlcNAc6S-GlcA2S), precursor 1	Golgi Apparatus
1455	20543g	cs_c_pre2(g)	chondroitin sulfate C (GalNAc6S-GlcA), precursor 2	Golgi Apparatus
1456	20544g	cs_c_pre3(g)	chondroitin sulfate C (GalNAc6S-GlcA), precursor 3	Golgi Apparatus
1457	20550g	cs_d_pre2(g)	chondroitin sulfate D (GlcNAc6S-GlcA2S) precursor 2	Golgi Apparatus
1458	20551g	cs_d_pre3(g)	chondroitin sulfate D (GlcNAc6S-GlcA2S), precursor 3	Golgi Apparatus
1459	20552g	cs_d_pre4(g)	chondroitin sulfate D (GlcNAc6S-GlcA2S), precursor 4	Golgi Apparatus
1460	20553g	cs_d_pre5(g)	chondroitin sulfate D (GlcNAc6S-GlcA2S), precursor 5	Golgi Apparatus
1461	20546g	cs_e_pre2(g)	chondroitin sulfate E (GalNAc4,6diS-GlcA), precursor 2	Golgi Apparatus
1462	20547g	cs_e_pre3(g)	chondroitin sulfate E (GalNAc4,6diS-GlcA), precursor 3	Golgi Apparatus
1463	20548g	cs_e_pre4(g)	chondroitin sulfate E (GalNAc4,6diS-GlcA), precursor 4	Golgi Apparatus
1464	20591g	cs_e_pre5a(g)	chondroitin sulfate E (GalNAc4,6diS-GlcA), precursor 5a	Golgi Apparatus
1465	20594g	cs_e_pre5b(g)	chondroitin sulfate E (GalNAc4,6diS-GlcA), precursor 5b	Golgi Apparatus
1466	20537g	cs_pre(g)	chondroitin sulfate precursor (GalNAc-GlcA-(Gal)2-Xyl-L-Ser (protein))	Golgi Apparatus
1467	20541g	cspg_a(g)	chondroitin sulfate A (GalNAc4S-GlcA) proteoglycan	Golgi Apparatus
1468	20599g	cspg_b(g)	chondroitin sulfate B / dermatan sulfate (IdoA2S-GalNAc4S) proteoglycan	Golgi Apparatus
1469	20545g	cspg_c(g)	chondroitin sulfate C (GalNAc6S-GlcA) proteoglycan	Golgi Apparatus
1470	20554g	cspg_d(g)	chondroitin sulfate D (GlcNAc6S-GlcA2S) proteoglycan	Golgi Apparatus
1471	20549g	cspg_e(g)	chondroitin sulfate E (GalNAc4,6diS-GlcA) proteoglycan	Golgi Apparatus

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
1472	4544g	digalsgalside_hs(g)	Digalactosylceramidesulfate	Golgi Apparatus
1473	19810g	digalside_hs(g)	Digalactosylceramide	Golgi Apparatus
1474	14993g	dolglcp_U(g)	Dolichyl beta-D-glucosyl phosphate, human uterine homolog	Golgi Apparatus
1475	14989g	dolp_U(g)	Dolichol phosphate, human uterine homolog	Golgi Apparatus
1476	15795g	dsT_antigen(g)	disialyl-T antigen	Golgi Apparatus
1477	15885g	f1a(g)	F1alpha	Golgi Apparatus
1478	15195g	fn2m2masn(g)	N4-{N-Acetyl-beta-D-glucosaminyl-(1,2)-alpha-D-mannosyl-(1,3)-[N-acetyl-beta-D-glucosaminyl-(1,2)-alpha-D-mannosyl-(1,6)]-beta-D-mannosyl-(1,4)-N-acetyl-beta-D-glucosaminyl-(1,4)-[alpha-L-fucosyl-(1,6)]-N-acetyl-beta-D-glucosaminyl}asparagine	Golgi Apparatus
1479	22664g	fuc12gal14acglcgalgluside_hs(g)	Type IIH glycolipid	Golgi Apparatus
1480	22692g	fuc132galacglcgal14acglcgalgluside_hs(g)	V3Fuc-nLc6Cer	Golgi Apparatus
1481	22691g	fuc13galacglcgal14acglcgalgluside_hs(g)	III3Fuc-nLc6Cer	Golgi Apparatus
1482	22658g	fuc14galacglcgalgluside_hs(g)	Lea glycolipid	Golgi Apparatus
1483	22657g	fucacgalfucgalacglcgalgluside_hs(g)	(Gal)2 (GalNAc)1 (Glc)1 (GlcNAc)1 (LFuc)2 (Cer)1	Golgi Apparatus
1484	22663g	fucacngal14acglcgalgluside_hs(g)	IV3-a-NeuAc,III3-a-Fuc-nLc4Cer	Golgi Apparatus
1485	22655g	fucacngalacglcgalgluside_hs(g)	IV3-a-Neu5Ac,III4-a-Fuc-Lc4Cer	Golgi Apparatus
1486	22665g	fucfuc12gal14acglcgalgluside_hs(g)	Ley glycolipid	Golgi Apparatus
1487	22693g	fucfuc132galacglcgal14acglcgalgluside_hs(g)	V3Fuc,III3Fuc-nLc6Cer	Golgi Apparatus
1488	22690g	fucfucfucgalacglc13galacglcgal14acglcgalgluside_hs(g)	(Gal)4 (Glc)1 (GlcNAc)3 (LFuc)3 (Cer)1	Golgi Apparatus
1489	22685g	fucfucfucgalacglcgal14acglcgalgluside_hs(g)	(Gal)3 (Glc)1 (GlcNAc)2 (LFuc)3 (Cer)1	Golgi Apparatus
1490	22689g	fucfucgalacglc13galacglcgal14acglcgalgluside_hs(g)	(Gal)4 (Glc)1 (GlcNAc)3 (LFuc)2 (Cer)1	Golgi Apparatus
1491	22684g	fucfucgalacglcgal14acglcgalgluside_hs(g)	(Gal)3 (Glc)1 (GlcNAc)2 (LFuc)2 (Cer)1	Golgi Apparatus
1492	22675g	fucfucgalacglcgalacglcgal14acglcgalgluside_hs(g)	(Gal)4 (Glc)1 (GlcNAc)3 (LFuc)2 (Cer)1	Golgi Apparatus

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
1493	22650g	fucfucgalacglcgalglluside_hs(g)	Leb glycolipid	Golgi Apparatus
1494	22660g	fucgal14acglcgalglluside_hs(g)	Lacto-N-fucopentaosyl III ceramide	Golgi Apparatus
1495	22668g	fucgalacgalfuc12gal14acglcgalgluside_hs(g)	Type IIIH glycolipid	Golgi Apparatus
1496	22680g	fucgalacgalfucgalacglcgal14acglcgalgluside_hs(g)	(Gal)4 (GalNAc)1 (Glc)1 (GlcNAc)2 (LFuc)2 (Cer)1	Golgi Apparatus
1497	22688g	fucgalacglc13galacglcgal14acglcgalgluside_hs(g)	(Gal)4 (Glc)1 (GlcNAc)3 (LFuc)1 (Cer)1	Golgi Apparatus
1498	22677g	fucgalacglcgal14acglcgalgluside_hs(g)	VI2Fuc-nLc6	Golgi Apparatus
1499	22649g	fucgalacglcgalglside_hs(g)	Type IH glycolipid	Golgi Apparatus
1500	22652g	fucgalfucgalacglcgalgluside_hs(g)	(Gal)3 (Glc)1 (GlcNAc)1 (LFuc)2 (Cer)1	Golgi Apparatus
1501	19746g	fucgalgbside_hs(g)	fucosyl galactosylgloboside (homo sapiens)	Golgi Apparatus
1502	15443g	g1m6masnB1(g)	glucosyl-(alpha-D-mannosyl)6-beta-D-mannosyl-diacetylchitobiosyl-L-asparagine (protein)	Golgi Apparatus
1503	15442g	g1m7masnB(g)	glucosyl-(alpha-D-mannosyl)7-beta-D-mannosyl-diacetylchitobiosyl-L-asparagine, isoform B (protein)	Golgi Apparatus
1504	15441g	g1m7masnC(g)	glucosyl-(alpha-D-mannosyl)7-beta-D-mannosyl-diacetylchitobiosyl-L-asparagine, isoform C (protein)	Golgi Apparatus
1505	15142g	g1m8masn(g)	(alpha-D-Glucosyl)-(alpha-D-mannosyl)8-beta-D-mannosyl-diacetylchitobiosyl-L-asparagine (protein)	Golgi Apparatus
1506	15138g	g2m8masn(g)	(alpha-D-Glucosyl)2-(alpha-D-mannosyl)8-beta-D-mannosyl-diacetylchitobiosyl-L-asparagine (protein)	Golgi Apparatus
1507	15115g	g3m8masn(g)	(alpha-D-Glucosyl)3-(alpha-D-mannosyl)8-beta-D-mannosyl-diacetylchitobiosyl-L-asparagine (protein)	Golgi Apparatus
1508	15024g	g3m8mpdol_U(g)	(alpha-D-Glucosyl)3-(alpha-D-mannosyl)8-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human uterine homolog	Golgi Apparatus
1509	19751g	ga1_hs(g)	GA1 (homo sapiens)	Golgi Apparatus
1510	19750g	ga2_hs(g)	GA2 (homo sapiens)	Golgi Apparatus
1511	22659g	gal14acglcgalglside_hs(g)	Lactoneotetraosylceramide	Golgi Apparatus
1512	22667g	galacgalfuc12gal14acglcgalgluside_hs(g)	(Gal)3 (GalNAc)1 (Glc)1 (GlcNAc)1 (LFuc)1 (Cer)1	Golgi Apparatus
1513	22679g	galacgalfucgalacglcgal14acglcgalglside_hs(g)	(Gal)4 (GalNAc)1 (Glc)1 (GlcNAc)2 (LFuc)1 (Cer)1	Golgi Apparatus

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
1514	22687g	galacglc13galacglcgal14acglcgalgluside_hs(g)	nLc8Cer	Golgi Apparatus
1515	22672g	galacglcgal14acglcgalgluside_hs(g)	i-antigen	Golgi Apparatus
1516	22674g	galacglcgalacglcgal14acglcgalgluside_hs(g)	I-antigen	Golgi Apparatus
1517	19744g	galacglcgalgbside_hs(g)	Gal-GlcNAc-Gal globoside (homo sapiens)	Golgi Apparatus
1518	22648g	galacglcgalgluside_hs(g)	Lc4Cer	Golgi Apparatus
1519	22670g	galfuc12gal14acglcgalgluside_hs(g)	(Gal)3 (Glc)1 (GlcNAc)1 (LFuc)1 (Cer)1	Golgi Apparatus
1520	22683g	galfucgalacglcgal14acglcgalgluside_hs(g)	(Gal)4 (Glc)1 (GlcNAc)2 (LFuc)1 (Cer)1	Golgi Apparatus
1521	22651g	galfucgalacglcgalgluside_hs(g)	Type IB glycolipid	Golgi Apparatus
1522	22676g	galgalfucfucgalacglcgalacglcgal14acglcgalgluside_hs(g)	(Gal)6 (Glc)1 (GlcNAc)3 (LFuc)2 (Cer)1	Golgi Apparatus
1523	19735g	galgalgalthcrm_hs(g)	Gal-Gal-Gal-Gal-Gal-Glc-Cer (homo sapiens)	Golgi Apparatus
1524	19734g	galgalthcrm_hs(g)	Gal-Gal-Gal-Gal-Glc-Cer (homo sapiens)	Golgi Apparatus
1525	19736g	galgbside_hs(g)	galactosylgloboside (homo sapiens)	Golgi Apparatus
1526	19619g	galgluside_hs(g)	galactosyl glucosyl ceramide	Golgi Apparatus
1527	19614g	galside_hs(g)	galactocerebroside (homo sapiens)	Golgi Apparatus
1528	19733g	galthcrm_hs(g)	Gal-Gal-Gal-Glc-Cer (homo sapiens)	Golgi Apparatus
1529	19624g	gbside_hs(g)	globoside (homo sapiens)	Golgi Apparatus
1530	19747g	gd1a_hs(g)	GD1a (homo sapiens)	Golgi Apparatus
1531	19769g	gd1alpha_hs(g)	GD1a (homo sapiens)	Golgi Apparatus
1532	19757g	gd1b2_hs(g)	GD1beta (homo sapiens)	Golgi Apparatus
1533	19761g	gd1b_hs(g)	GD1b (homo sapiens)	Golgi Apparatus
1534	19754g	gd1c_hs(g)	GD1c (homo sapiens)	Golgi Apparatus
1535	19760g	gd2_hs(g)	GD2 (homo sapiens)	Golgi Apparatus
1536	19759g	gd3_hs(g)	GD3 (homo sapiens)	Golgi Apparatus
1537	321g	gdp(g)	GDP	Golgi Apparatus
1538	168g	gdpfuc(g)	GDP-L-fucose	Golgi Apparatus
1539	318g	glc-D(g)	D-Glucose	Golgi Apparatus
1540	15438g	glc1man(g)	glucose-1,3-mannose oligosaccharide	Golgi Apparatus
1541	15437g	glc2man(g)	(2)[glucose-1,3]-mannose oligosaccharide	Golgi Apparatus
1542	15433g	glc3man(g)	glucose-1,2-(2)[glucose-1,3]-mannose oligosaccharide	Golgi Apparatus
1543	19613g	gluside_hs(g)	glucocerebroside (homo sapiens)	Golgi Apparatus
1544	19622g	gm1_hs(g)	ganglioside GM1 (homo sapiens)	Golgi Apparatus
1545	19756g	gm1a_hs(g)	GM1alpha (homo sapiens)	Golgi Apparatus
1546	19752g	gm1b_hs(g)	GM1b (homo sapiens)	Golgi Apparatus
1547	19621g	gm2_hs(g)	ganglioside GM2 (homo sapiens)	Golgi Apparatus
1548	19755g	gm2a_hs(g)	GM2alpha (homo sapiens)	Golgi Apparatus
1549	19620g	gm3_hs(g)	ganglioside GM3 (homo sapiens)	Golgi Apparatus

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
1550	226g	gmp(g)	GMP	Golgi Apparatus
1551	15935g	gncore1(g)	GlcNAc-alpha-1,4-Core 1	Golgi Apparatus
1552	15932g	gncore2(g)	GlcNAc-alpha-1,4-Core 2	Golgi Apparatus
1553	19768g	gp1c_hs(g)	GP1c (homo sapiens)	Golgi Apparatus
1554	19976g	gp1calpha_hs(g)	GP1c alpha (homo sapiens)	Golgi Apparatus
1555	19763g	gq1b_hs(g)	GQ1b (homo sapiens)	Golgi Apparatus
1556	19771g	gq1balpha_hs(g)	GQ1balpha (homo sapiens)	Golgi Apparatus
1557	19767g	gq1c_hs(g)	GQ1c (homo sapiens)	Golgi Apparatus
1558	19749g	gt1a_hs(g)	GT1a (homo sapiens)	Golgi Apparatus
1559	19770g	gt1alpha_hs(g)	GT1aalpha (homo sapiens)	Golgi Apparatus
1560	19762g	gt1b_hs(g)	GT1b (homo sapiens)	Golgi Apparatus
1561	19766g	gt1c_hs(g)	GT1c (homo sapiens)	Golgi Apparatus
1562	19765g	gt2_hs(g)	GT2 (homo sapiens)	Golgi Apparatus
1563	19764g	gt3_hs(g)	GT3 (homo sapiens)	Golgi Apparatus
1564	1049g	h(g)	H+	Golgi Apparatus
1565	317g	h2o(g)	H2O	Golgi Apparatus
1566	3844g	hcys-L(g)	L-Homocysteine	Golgi Apparatus
1567	20618g	hs_pre1(g)	heparan sulfate, precursor 1	Golgi Apparatus
1568	20627g	hs_pre10(g)	heparan sulfate, precursor 10	Golgi Apparatus
1569	20628g	hs_pre11(g)	heparan sulfate, precursor 11	Golgi Apparatus
1570	20629g	hs_pre12(g)	heparan sulfate, precursor 12	Golgi Apparatus
1571	20630g	hs_pre13(g)	heparan sulfate, precursor 13	Golgi Apparatus
1572	20718g	hs_pre14(g)	heparan sulfate, precursor 14	Golgi Apparatus
1573	20719g	hs_pre15(g)	heparan sulfate, precursor 15	Golgi Apparatus
1574	20619g	hs_pre2(g)	heparan sulfate, precursor 2	Golgi Apparatus
1575	20620g	hs_pre3(g)	heparan sulfate, precursor 3	Golgi Apparatus
1576	20621g	hs_pre4(g)	heparan sulfate, precursor 4	Golgi Apparatus
1577	20622g	hs_pre5(g)	heparan sulfate, precursor 5	Golgi Apparatus
1578	20623g	hs_pre6(g)	heparan sulfate, precursor 6	Golgi Apparatus
1579	20624g	hs_pre7(g)	heparan sulfate, precursor 7	Golgi Apparatus
1580	20625g	hs_pre8(g)	heparan sulfate, precursor 8	Golgi Apparatus
1581	20626g	hs_pre9(g)	heparan sulfate, precursor 9	Golgi Apparatus
1582	20638g	hspg(g)	heparan sulfate proteoglycan	Golgi Apparatus
1583	289g	k(g)	potassium	Golgi Apparatus
1584	20192g	ksi(g)	keratan sulfate I	Golgi Apparatus
1585	20131g	ksi_pre1(g)	keratan sulfate I biosynthesis, precursor 1	Golgi Apparatus
1586	20165g	ksi_pre10(g)	keratan sulfate I biosynthesis, precursor 10	Golgi Apparatus
1587	20166g	ksi_pre11(g)	keratan sulfate I biosynthesis, precursor 11	Golgi Apparatus
1588	20167g	ksi_pre12(g)	keratan sulfate I biosynthesis, precursor 12	Golgi Apparatus
1589	20168g	ksi_pre13(g)	keratan sulfate I biosynthesis, precursor 13	Golgi Apparatus
1590	20169g	ksi_pre14(g)	keratan sulfate I biosynthesis, precursor 14	Golgi Apparatus
1591	20170g	ksi_pre15(g)	keratan sulfate I biosynthesis, precursor 15	Golgi Apparatus
1592	20171g	ksi_pre16(g)	keratan sulfate I biosynthesis, precursor 16	Golgi Apparatus
1593	20172g	ksi_pre17(g)	keratan sulfate I biosynthesis, precursor 17	Golgi Apparatus
1594	20173g	ksi_pre18(g)	keratan sulfate I biosynthesis, precursor 18	Golgi Apparatus
1595	20174g	ksi_pre19(g)	keratan sulfate I biosynthesis, precursor 19	Golgi Apparatus
1596	20132g	ksi_pre2(g)	keratan sulfate I biosynthesis, precursor 2	Golgi Apparatus
1597	20175g	ksi_pre20(g)	keratan sulfate I biosynthesis, precursor 20	Golgi Apparatus
1598	20176g	ksi_pre21(g)	keratan sulfate I biosynthesis, precursor 21	Golgi Apparatus
1599	20177g	ksi_pre22(g)	keratan sulfate I biosynthesis, precursor 22	Golgi Apparatus
1600	20178g	ksi_pre23(g)	keratan sulfate I biosynthesis, precursor 23	Golgi Apparatus
1601	20179g	ksi_pre24(g)	keratan sulfate I biosynthesis, precursor 24	Golgi Apparatus
1602	20180g	ksi_pre25(g)	keratan sulfate I biosynthesis, precursor 25	Golgi Apparatus

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
1603	20181g	ksi_pre26(g)	keratan sulfate I biosynthesis, precursor 26	Golgi Apparatus
1604	20182g	ksi_pre27(g)	keratan sulfate I biosynthesis, precursor 27	Golgi Apparatus
1605	20183g	ksi_pre28(g)	keratan sulfate I biosynthesis, precursor 28	Golgi Apparatus
1606	20184g	ksi_pre29(g)	keratan sulfate I biosynthesis, precursor 29	Golgi Apparatus
1607	20133g	ksi_pre3(g)	keratan sulfate I biosynthesis, precursor 3	Golgi Apparatus
1608	20185g	ksi_pre30(g)	keratan sulfate I biosynthesis, precursor 30	Golgi Apparatus
1609	20186g	ksi_pre31(g)	keratan sulfate I biosynthesis, precursor 31	Golgi Apparatus
1610	20187g	ksi_pre32(g)	keratan sulfate I biosynthesis, precursor 32	Golgi Apparatus
1611	20188g	ksi_pre33(g)	keratan sulfate I biosynthesis, precursor 33	Golgi Apparatus
1612	20189g	ksi_pre34(g)	keratan sulfate I biosynthesis, precursor 34	Golgi Apparatus
1613	20190g	ksi_pre35(g)	keratan sulfate I biosynthesis, precursor 35	Golgi Apparatus
1614	20191g	ksi_pre36(g)	keratan sulfate I biosynthesis, precursor 36	Golgi Apparatus
1615	20159g	ksi_pre4(g)	keratan sulfate I biosynthesis, precursor 4	Golgi Apparatus
1616	20160g	ksi_pre5(g)	keratan sulfate I biosynthesis, precursor 5	Golgi Apparatus
1617	20161g	ksi_pre6(g)	keratan sulfate I biosynthesis, precursor 6	Golgi Apparatus
1618	20162g	ksi_pre7(g)	keratan sulfate I biosynthesis, precursor 7	Golgi Apparatus
1619	20163g	ksi_pre8(g)	keratan sulfate I biosynthesis, precursor 8	Golgi Apparatus
1620	20164g	ksi_pre9(g)	keratan sulfate I biosynthesis, precursor 9	Golgi Apparatus
1621	20156g	ksii_core2(g)	keratan sulfate II (core 2-linked)	Golgi Apparatus
1622	20079g	ksii_core2_pre1(g)	keratan sulfate II biosynthesis, precursor 1	Golgi Apparatus
1623	20155g	ksii_core2_pre10(g)	keratan sulfate II biosynthesis, precursor 10	Golgi Apparatus
1624	20085g	ksii_core2_pre2(g)	keratan sulfate II biosynthesis, precursor 2	Golgi Apparatus
1625	20134g	ksii_core2_pre3(g)	keratan sulfate II biosynthesis, precursor 3	Golgi Apparatus
1626	20135g	ksii_core2_pre4(g)	keratan sulfate II biosynthesis, precursor 4	Golgi Apparatus
1627	20149g	ksii_core2_pre5(g)	keratan sulfate II biosynthesis, precursor 5	Golgi Apparatus
1628	20150g	ksii_core2_pre6(g)	keratan sulfate II biosynthesis, precursor 6	Golgi Apparatus
1629	20151g	ksii_core2_pre7(g)	keratan sulfate II biosynthesis, precursor 7	Golgi Apparatus
1630	20153g	ksii_core2_pre8(g)	keratan sulfate II biosynthesis, precursor 8	Golgi Apparatus
1631	20154g	ksii_core2_pre9(g)	keratan sulfate II biosynthesis, precursor 9	Golgi Apparatus
1632	20342g	ksii_core4(g)	keratan sulfate II (core 4-linked)	Golgi Apparatus
1633	20332g	ksii_core4_pre1(g)	keratan sulfate II biosynthesis, precursor 1	Golgi Apparatus
1634	20341g	ksii_core4_pre10(g)	keratan sulfate II biosynthesis, precursor 10	Golgi Apparatus
1635	20333g	ksii_core4_pre2(g)	keratan sulfate II boisynthesis, precursor 2	Golgi Apparatus
1636	20334g	ksii_core4_pre3(g)	keratan sulfate II biosynthesis, precursor 3	Golgi Apparatus
1637	20335g	ksii_core4_pre4(g)	keratan sulfate II biosynthesis, precursor 4	Golgi Apparatus
1638	20336g	ksii_core4_pre5(g)	keratan sulfate II biosynthesis, precursor 5	Golgi Apparatus

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
1639	20337g	ksii_core4_pre6(g)	keratan sulfate II biosynthesis, precursor 6	Golgi Apparatus
1640	20338g	ksii_core4_pre7(g)	keratan sulfate II biosynthesis, precursor 7	Golgi Apparatus
1641	20339g	ksii_core4_pre8(g)	keratan sulfate II biosynthesis, precursor 8	Golgi Apparatus
1642	20340g	ksii_core4_pre9(g)	keratan sulfate II biosynthesis, precursor 9	Golgi Apparatus
1643	15198g	l2fn2m2masn(g)	{[galactosyl-(1,4)-N-Acetyl-glucosaminyl-(1,2)-mannosyl-(1,3)-],[N-acetyl-glucosaminyl-(1,2)-mannosyl-(1,6)-]mannosyl-(1,4)-N-acetyl-glucosaminyl-(1,4)-[fucosyl-(1,6)]-N-acetyl-glucosaminyl}asparagine	Golgi Apparatus
1644	20459g	l2xser(g)	(Gal)2-Xyl-L-Ser (protein)	Golgi Apparatus
1645	292g	lcts(g)	Lactose	Golgi Apparatus
1646	20364g	lxser(g)	Gal-Xyl-L-Ser (protein)	Golgi Apparatus
1647	15154g	m4masn(g)	(alpha-D-mannosyl)4-beta-D-mannosyl-diacetylchitobiosyl-L-asparagine (protein)	Golgi Apparatus
1648	15170g	m5masnB1(g)	(alpha-D-mannosyl)5-beta-D-mannosyl-diacetylchitobiosyl-L-asparagine (protein)	Golgi Apparatus
1649	15171g	m5masnB2(g)	(alpha-D-mannosyl)5-beta-D-mannosyl-diacetylchitobiosyl-L-asparagine (protein)	Golgi Apparatus
1650	15161g	m5masnC(g)	(alpha-D-mannosyl)5-beta-D-mannosyl-diacetylchitobiosyl-L-asparagine (protein)	Golgi Apparatus
1651	15167g	m6masnA(g)	(alpha-D-mannosyl)6-beta-D-mannosyl-diacetylchitobiosyl-L-asparagine (protein)	Golgi Apparatus
1652	15168g	m6masnB1(g)	(alpha-D-mannosyl)6-beta-D-mannosyl-diacetylchitobiosyl-L-asparagine (protein)	Golgi Apparatus
1653	15169g	m6masnB2(g)	(alpha-D-mannosyl)6-beta-D-mannosyl-diacetylchitobiosyl-L-asparagine (protein)	Golgi Apparatus
1654	15160g	m6masnC(g)	(alpha-D-mannosyl)6-beta-D-mannosyl-diacetylchitobiosyl-L-asparagine (protein)	Golgi Apparatus
1655	15165g	m7masnA(g)	(alpha-D-mannosyl)7-beta-D-mannosyl-diacetylchitobiosyl-L-asparagine, isoform A (protein)	Golgi Apparatus
1656	15159g	m7masnB(g)	(alpha-D-mannosyl)7-beta-D-mannosyl-diacetylchitobiosyl-L-asparagine, isoform B (protein)	Golgi Apparatus
1657	15166g	m7masnC(g)	(alpha-D-mannosyl)7-beta-D-mannosyl-diacetylchitobiosyl-L-asparagine, isoform C (protein)	Golgi Apparatus
1658	15144g	m8masn(g)	(alpha-D-mannosyl)8-beta-D-mannosyl-diacetylchitobiosyl-L-asparagine (protein)	Golgi Apparatus
1659	11018g	man(g)	D-Mannose	Golgi Apparatus
1660	15192g	n2m2masn(g)	((N-acetyl-D-glucosaminyl)2-(alpha-D-mannosyl)2-beta-D-mannosyl-diacetylchitobiosyl)-L-asparagine (protein)	Golgi Apparatus
1661	3649g	n2m2nmasn(g)	N-Acetyl-beta-D-glucosaminyl-1,2-alpha-D-mannosyl-1,3-(N-acetyl-beta-D-glucosaminyl-1,2-alpha-D-mannosyl-1,6)-(N-acetyl-beta-D-glucosaminyl-1,4)-beta-D-mannosyl-1,4-N-acetyl-beta-D-glucosaminyl-R	Golgi Apparatus

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
1662	15212g	n3m2masn(g)	((N-acetyl-D-glucosaminyl)3-(alpha-D-mannosyl)2-beta-D-mannosyl-diacetylchitobiosyl)-L-asparagine (protein)	Golgi Apparatus
1663	15213g	n4m2masn(g)	((N-acetyl-D-glucosaminyl)4-(alpha-D-mannosyl)2-beta-D-mannosyl-diacetylchitobiosyl)-L-asparagine (protein)	Golgi Apparatus
1664	15214g	n5m2masn(g)	((N-acetyl-D-glucosaminyl)5-(alpha-D-mannosyl)2-beta-D-mannosyl-diacetylchitobiosyl)-L-asparagine (protein)	Golgi Apparatus
1665	1023g	na1(g)	Sodium	Golgi Apparatus
1666	4360g	nm2masn(g)	(N-acetyl-D-glucosaminyl-(alpha-D-mannosyl)2-beta-D-mannosyl-diacetylchitobiosyl)-L-asparagine (protein)	Golgi Apparatus
1667	4358g	nm4masn(g)	(N-acetyl-D-glucosaminyl-(alpha-D-mannosyl)4-beta-D-mannosyl-diacetylchitobiosyl)-L-asparagine (protein)	Golgi Apparatus
1668	20055g	oagd3_hs(g)	9-O-Acetylated GD3 (homo sapiens)	Golgi Apparatus
1669	20056g	oagt3_hs(g)	9-O-Acetylated GT3 (homo sapiens)	Golgi Apparatus
1670	18536g	pa_hs(g)	phosphatidic acid (homo sapiens)	Golgi Apparatus
1671	333g	pap(g)	Adenosine 3',5'-bisphosphate	Golgi Apparatus
1672	332g	paps(g)	3'-Phosphoadenylyl sulfate	Golgi Apparatus
1673	19051g	pchol_hs(g)	Phosphatidylcholine (homo sapiens)	Golgi Apparatus
1674	19050g	pe_hs(g)	phosphatidylethanolamine (homo sapiens)	Golgi Apparatus
1675	472g	pi(g)	Phosphate	Golgi Apparatus
1676	19052g	ps_hs(g)	phosphatidylserine (homo sapiens)	Golgi Apparatus
1677	15207g	s2l2fn2m2masn(g)	PA6	Golgi Apparatus
1678	15794g	sT_antigen(g)	sialyl-T antigen	Golgi Apparatus
1679	15789g	sTn_antigen(g)	sialyl-Tn antigen	Golgi Apparatus
1680	19615g	sgalside_hs(g)	sulfatide galactocerebroside (homo sapiens)	Golgi Apparatus
1681	19618g	sphmyln_hs(g)	sphingomyelin (homo sapiens)	Golgi Apparatus
1682	19623g	thcrm_hs(g)	trihexosyl ceramide (homo sapiens)	Golgi Apparatus
1683	326g	uacgam(g)	UDP-N-acetyl-D-glucosamine	Golgi Apparatus
1684	477g	udp(g)	UDP	Golgi Apparatus
1685	10912g	udpacgal(g)	UDP-N-acetyl-D-galactosamine	Golgi Apparatus
1686	316g	udpg(g)	UDPglucose	Golgi Apparatus
1687	331g	udpgal(g)	UDPgalactose	Golgi Apparatus
1688	241g	udpglcur(g)	UDP-D-glucuronate	Golgi Apparatus
1689	255g	udpxyl(g)	UDP-D-xylose	Golgi Apparatus
1690	1068g	ump(g)	UMP	Golgi Apparatus
1691	20363g	xser(g)	Xyl-L-Ser (protein)	Golgi Apparatus
1692	286l	10fthf(l)	10-Formyltetrahydrofolate	Lysosome
1693	20786l	10fthf5glu(l)	10-formyltetrahydrofolate-[Glu](5)	Lysosome
1694	20787l	10fthf6glu(l)	10-formyltetrahydrofolate-[Glu](6)	Lysosome
1695	20788l	10fthf7glu(l)	10-formyltetrahydrofolate-[Glu](7)	Lysosome
1696	18604l	3amp(l)	3'-AMP	Lysosome
1697	176l	4abut(l)	4-Aminobutanoate	Lysosome
1698	20783l	5dhf(l)	pentaglutamyl folate (DHF)	Lysosome
1699	20780l	5thf(l)	pentaglutamyl folate (THF)	Lysosome
1700	20784l	6dhf(l)	haxglutamyl folate (DHF)	Lysosome
1701	20781l	6thf(l)	hexaglutamyl folate (THF)	Lysosome
1702	20785l	7dhf(l)	heptaglutamyl folate (DHF)	Lysosome
1703	20782l	7thf(l)	heptaglutamyl folate (THF)	Lysosome

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
1704	15102l	Asn-X-Ser/Thr(l)	protein-linked asparagine residue (N-glycosylation site)	Lysosome
1705	18523l	Rtotal(l)	R total	Lysosome
1706	20362l	Ser-Gly/Ala-X-Gly(l)	protein-linked serine residue (glycosaminoglycan attachment site)	Lysosome
1707	15787l	Ser/Thr(l)	protein-linked serine or threonine residue (O-glycosylation site)	Lysosome
1708	15788l	Tn_antigen(l)	Tn antigen	Lysosome
1709	11537l	accoa(l)	Acetyl-CoA	Lysosome
1710	19739l	acgagbside_hs(l)	alpha GalNAc globoside (homo sapiens)	Lysosome
1711	899l	acgal(l)	N-Acetyl-D-galactosamine	Lysosome
1712	224l	acgam(l)	N-Acetyl-D-glucosamine	Lysosome
1713	19740l	acgbgbside_hs(l)	beta GalNAc globoside (homo sapiens)	Lysosome
1714	134l	acnam(l)	N-Acetylneuraminate	Lysosome
1715	228l	ade(l)	Adenine	Lysosome
1716	270l	adn(l)	Adenosine	Lysosome
1717	1093l	ala-D(l)	D-Alanine	Lysosome
1718	11412l	ala-L(l)	L-Alanine	Lysosome
1719	309l	amp(l)	AMP	Lysosome
1720	9019l	cholp(l)	Choline phosphate	Lysosome
1721	252l	chsterol(l)	Cholesterol	Lysosome
1722	11376l	cmp(l)	CMP	Lysosome
1723	473l	coa(l)	Coenzyme A	Lysosome
1724	15798l	core6(l)	Core 6	Lysosome
1725	19478l	crm_hs(l)	ceramide (homo sapiens)	Lysosome
1726	22508l	cs_a(l)	chondroitin sulfate A (GalNAc4S-GlcA), free chain	Lysosome
1727	22507l	cs_a_deg1(l)	chondroitin sulfate A (GalNAc4S-GlcA), degradation product 1	Lysosome
1728	22513l	cs_a_deg2(l)	chondroitin sulfate A (GalNAc4S-GlcA), degradation product 2	Lysosome
1729	22514l	cs_a_deg3(l)	chondroitin sulfate A (GalNAc4S-GlcA), degradation product 3	Lysosome
1730	22515l	cs_a_deg4(l)	chondroitin sulfate A (GalNAc4S-GlcA), degradation product 4	Lysosome
1731	22516l	cs_a_deg5(l)	chondroitin sulfate A (GalNAc4S-GlcA), degradation product 5	Lysosome
1732	22511l	cs_b(l)	chondroitin sulfate B / dermatan sulfate (IdoA2S-GalNAc4S), free chain	Lysosome
1733	22517l	cs_b_deg1(l)	chondroitin sulfate B / dermatan sulfate (IdoA2S-GalNAc4S), degradation product 1	Lysosome
1734	22518l	cs_b_deg2(l)	chondroitin sulfate B / dermatan sulfate (IdoA2S-GalNAc4S), degradation product 2	Lysosome
1735	22519l	cs_b_deg3(l)	chondroitin sulfate B / dermatan sulfate (IdoA2S-GalNAc4S), degradation product 3	Lysosome
1736	22509l	cs_c(l)	chondroitin sulfate C (GalNAc6S-GlcA), free chain	Lysosome
1737	22520l	cs_c_deg1(l)	chondroitin sulfate C (GalNAc6S-GlcA), degradation product 1	Lysosome
1738	22521l	cs_c_deg2(l)	chondroitin sulfate C (GalNAc6S-GlcA), degradation product 2	Lysosome
1739	22522l	cs_c_deg3(l)	chondroitin sulfate C (GalNAc6S-GlcA), degradation product 3	Lysosome

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
1740	22523l	cs_c_deg4(l)	chondroitin sulfate C (GalNAc6S-GlcA), degradation product 4	Lysosome
1741	22524l	cs_c_deg5(l)	chondroitin sulfate C (GalNAc6S-GlcA), degradation product 5	Lysosome
1742	22510l	cs_d(l)	chondroitin sulfate D (GlcNAc6S-GlcA2S), free chain	Lysosome
1743	22525l	cs_d_deg1(l)	chondroitin sulfate D (GlcNAc6S-GlcA2S), degradation product 1	Lysosome
1744	22526l	cs_d_deg2(l)	chondroitin sulfate D (GlcNAc6S-GlcA2S), degradation product 2	Lysosome
1745	22527l	cs_d_deg3(l)	chondroitin sulfate D (GlcNAc6S-GlcA2S), degradation product 3	Lysosome
1746	22528l	cs_d_deg4(l)	chondroitin sulfate D (GlcNAc6S-GlcA2S), degradation product 4	Lysosome
1747	22529l	cs_d_deg5(l)	chondroitin sulfate D (GlcNAc6S-GlcA2S), degradation product 5	Lysosome
1748	22530l	cs_d_deg6(l)	chondroitin sulfate D (GlcNAc6S-GlcA2S), degradation product 6	Lysosome
1749	22512l	cs_e(l)	chondroitin sulfate E (GalNAc4,6diS-GlcA), free chain	Lysosome
1750	22532l	cs_e_deg1(l)	chondroitin sulfate E (GalNAc4,6diS-GlcA), degradation product 1	Lysosome
1751	22533l	cs_e_deg2(l)	chondroitin sulfate E (GalNAc4,6diS-GlcA), degradation product 2	Lysosome
1752	22534l	cs_e_deg3(l)	chondroitin sulfate E (GalNAc4,6diS-GlcA), degradation product 3	Lysosome
1753	22535l	cs_e_deg4(l)	chondroitin sulfate E (GalNAc4,6diS-GlcA), degradation product 4	Lysosome
1754	22536l	cs_e_deg5(l)	chondroitin sulfate E (GalNAc4,6diS-GlcA), degradation product 5	Lysosome
1755	22537l	cs_e_deg6(l)	chondroitin sulfate E (GalNAc4,6diS-GlcA), degradation product 6	Lysosome
1756	22538l	cs_e_deg7(l)	chondroitin sulfate E (GalNAc4,6diS-GlcA), degradation product 7	Lysosome
1757	20541l	cspg_a(l)	chondroitin sulfate A (GalNAc4S-GlcA) proteoglycan	Lysosome
1758	20599l	cspg_b(l)	chondroitin sulfate B / dermatan sulfate (IdoA2S-GalNAc4S) proteoglycan	Lysosome
1759	20545l	cspg_c(l)	chondroitin sulfate C (GalNAc6S-GlcA) proteoglycan	Lysosome
1760	20554l	cspg_d(l)	chondroitin sulfate D (GlcNAc6S-GlcA2S) proteoglycan	Lysosome
1761	20549l	cspg_e(l)	chondroitin sulfate E (GalNAc4,6diS-GlcA) proteoglycan	Lysosome
1762	92l	cytd(l)	Cytidine	Lysosome
1763	380l	dad-2(l)	Deoxyadenosine	Lysosome
1764	193l	damp(l)	dAMP	Lysosome
1765	290l	dcmp(l)	dCMP	Lysosome
1766	10918l	dcyt(l)	Deoxycytidine	Lysosome
1767	195l	dgmp(l)	dGMP	Lysosome
1768	172l	dgsn(l)	Deoxyguanosine	Lysosome
1769	10505l	dhf(l)	7,8-Dihydrofolate	Lysosome
1770	19810l	digalside_hs(l)	Digalactosylceramide	Lysosome

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
1771	737l	dpcoa(l)	Dephospho-CoA	Lysosome
1772	197l	dtmp(l)	dTMP	Lysosome
1773	15885l	f1a(l)	F1alpha	Lysosome
1774	340l	fald(l)	Formaldehyde	Lysosome
1775	833l	fuc-L(l)	L-Fucose	Lysosome
1776	1083l	gal(l)	D-Galactose	Lysosome
1777	19619l	galgluside_hs(l)	galactosyl glucosyl ceramide	Lysosome
1778	19614l	galside_hs(l)	galactocerebroside (homo sapiens)	Lysosome
1779	19624l	gbside_hs(l)	globoside (homo sapiens)	Lysosome
1780	318l	glc-D(l)	D-Glucose	Lysosome
1781	256l	glcur(l)	D-Glucuronate	Lysosome
1782	313l	glu-L(l)	L-Glutamate	Lysosome
1783	19613l	gluside_hs(l)	glucocerebroside (homo sapiens)	Lysosome
1784	323l	gly(l)	Glycine	Lysosome
1785	226l	gmp(l)	GMP	Lysosome
1786	5279l	gsn(l)	Guanosine	Lysosome
1787	1049l	h(l)	H+	Lysosome
1788	317l	h2o(l)	H2O	Lysosome
1789	315l	h2o2(l)	Hydrogen peroxide	Lysosome
1790	9554l	ha(l)	hyaluronan	Lysosome
1791	22611l	ha_deg1(l)	hyaluronan degradation product 1	Lysosome
1792	22610l	ha_pre1(l)	hyaluronan biosynthesis, precursor 1	Lysosome
1793	20796l	hs(l)	heparan sulfate, free chain	Lysosome
1794	20755l	hs_deg1(l)	heparan sulfate, degradation product 1	Lysosome
1795	20764l	hs_deg10(l)	heparan sulfate, degradation product 10	Lysosome
1796	20765l	hs_deg11(l)	heparan sulfate, degradation product 11	Lysosome
1797	20766l	hs_deg12(l)	heparan sulfate, degradation product 12	Lysosome
1798	20767l	hs_deg13(l)	heparan sulfate, degradation product 13	Lysosome
1799	20768l	hs_deg14(l)	heparan sulfate, degradation product 14	Lysosome
1800	20769l	hs_deg15(l)	heparan sulfate, degradation product 15	Lysosome
1801	20770l	hs_deg16(l)	heparan sulfate, degradation product 16	Lysosome
1802	20771l	hs_deg17(l)	heparan sulfate, degradation product 17	Lysosome
1803	20772l	hs_deg18(l)	heparan sulfate, degradation product 18	Lysosome
1804	20773l	hs_deg19(l)	heparan sulfate, degradation product 19	Lysosome
1805	20756l	hs_deg2(l)	heparan sulfate, degradation product 2	Lysosome
1806	20774l	hs_deg20(l)	heparan sulfate, degradation product 20	Lysosome
1807	20775l	hs_deg21(l)	heparan sulfate, degradation product 21	Lysosome
1808	20776l	hs_deg22(l)	heparan sulfate, degradation product 22	Lysosome
1809	20777l	hs_deg23(l)	heparan sulfate, degradation product 23	Lysosome
1810	20795l	hs_deg24(l)	heparan sulfate, degradation product 24	Lysosome
1811	20794l	hs_deg25(l)	heparan sulfate, degradation product 25	Lysosome
1812	20757l	hs_deg3(l)	heparan sulfate, degradation product 3	Lysosome
1813	20758l	hs_deg4(l)	heparan sulfate, degradation product 4	Lysosome
1814	20759l	hs_deg5(l)	heparan sulfate, degradation product 5	Lysosome
1815	20760l	hs_deg6(l)	heparan sulfate, degradation product 6	Lysosome
1816	20761l	hs_deg7(l)	heparan sulfate, degradation product 7	Lysosome
1817	20762l	hs_deg8(l)	heparan sulfate, degradation product 8	Lysosome
1818	20763l	hs_deg9(l)	heparan sulfate, degradation product 9	Lysosome
1819	20638l	hspg(l)	heparan sulfate proteoglycan	Lysosome
1820	218l	hxan(l)	Hypoxanthine	Lysosome
1821	5392l	idour(l)	L-Iduronate	Lysosome
1822	147l	ins(l)	Inosine	Lysosome
1823	20192l	ksi(l)	keratan sulfate I	Lysosome

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
1824	22553l	ksi_deg1(l)	keratan sulfate I, degradation product 1	Lysosome
1825	22562l	ksi_deg10(l)	keratan sulfate I, degradation product 10	Lysosome
1826	22563l	ksi_deg11(l)	keratan sulfate I, degradation product 11	Lysosome
1827	22564l	ksi_deg12(l)	keratan sulfate I, degradation product 12	Lysosome
1828	22565l	ksi_deg13(l)	keratan sulfate I, degradation product 13	Lysosome
1829	22566l	ksi_deg14(l)	keratan sulfate I, degradation product 14	Lysosome
1830	22567l	ksi_deg15(l)	keratan sulfate I, degradation product 15	Lysosome
1831	22575l	ksi_deg16(l)	keratan sulfate I, degradation product 16	Lysosome
1832	22583l	ksi_deg17(l)	keratan sulfate I, degradation product 17	Lysosome
1833	22568l	ksi_deg18(l)	keratan sulfate I, degradation product 18	Lysosome
1834	22576l	ksi_deg19(l)	keratan sulfate I, degradation product 19	Lysosome
1835	22554l	ksi_deg2(l)	keratan sulfate I, degradation product 2	Lysosome
1836	22584l	ksi_deg20(l)	keratan sulfate I, degradation product 20	Lysosome
1837	22569l	ksi_deg21(l)	keratan sulfate I, degradation product 21	Lysosome
1838	22577l	ksi_deg22(l)	keratan sulfate I, degradation product 22	Lysosome
1839	22585l	ksi_deg23(l)	keratan sulfate I, degradation product 23	Lysosome
1840	22570l	ksi_deg24(l)	keratan sulfate I, degradation product 24	Lysosome
1841	22578l	ksi_deg25(l)	keratan sulfate I, degradation product 25	Lysosome
1842	22586l	ksi_deg26(l)	keratan sulfate I, degradation product 26	Lysosome
1843	22571l	ksi_deg27(l)	keratan sulfate I, degradation product 27	Lysosome
1844	22579l	ksi_deg28(l)	keratan sulfate I, degradation product 28	Lysosome
1845	22587l	ksi_deg29(l)	keratan sulfate I, degradation product 29	Lysosome
1846	22555l	ksi_deg3(l)	keratan sulfate I, degradation product 3	Lysosome
1847	22572l	ksi_deg30(l)	keratan sulfate I, degradation product 30	Lysosome
1848	22580l	ksi_deg31(l)	keratan sulfate I, degradation product 31	Lysosome
1849	22588l	ksi_deg32(l)	keratan sulfate I, degradation product 32	Lysosome
1850	22573l	ksi_deg33(l)	keratan sulfate I, degradation product 33	Lysosome
1851	22581l	ksi_deg34(l)	keratan sulfate I, degradation product 34	Lysosome
1852	22589l	ksi_deg35(l)	keratan sulfate I, degradation product 35	Lysosome
1853	22574l	ksi_deg36(l)	keratan sulfate I, degradation product 36	Lysosome
1854	22582l	ksi_deg37(l)	keratan sulfate I, degradation product 37	Lysosome
1855	22590l	ksi_deg38(l)	keratan sulfate I, degradation product 38	Lysosome
1856	22591l	ksi_deg39(l)	keratan sulfate I, degradation product 39	Lysosome
1857	22556l	ksi_deg4(l)	keratan sulfate I, degradation product 4	Lysosome
1858	22592l	ksi_deg40(l)	keratan sulfate I, degradation product 40	Lysosome
1859	22593l	ksi_deg41(l)	keratan sulfate I, degradation product 41	Lysosome
1860	22557l	ksi_deg5(l)	keratan sulfate I, degradation product 5	Lysosome
1861	22558l	ksi_deg6(l)	keratan sulfate I, degradation product 6	Lysosome
1862	22559l	ksi_deg7(l)	keratan sulfate I, degradation product 7	Lysosome
1863	22560l	ksi_deg8(l)	keratan sulfate I, degradation product 8	Lysosome
1864	22561l	ksi_deg9(l)	keratan sulfate I, degradation product 9	Lysosome
1865	20156l	ksii_core2(l)	keratan sulfate II (core 2-linked)	Lysosome
1866	22594l	ksii_core2_deg1(l)	keratan sulfate II (core 2-linked), degradation product 1	Lysosome
1867	22595l	ksii_core2_deg2(l)	keratan sulfate II (core 2-linked), degradation product 2	Lysosome
1868	22596l	ksii_core2_deg3(l)	keratan sulfate II (core 2-linked), degradation product 3	Lysosome
1869	22597l	ksii_core2_deg4(l)	keratan sulfate II (core 2-linked), degradation product 4	Lysosome
1870	22598l	ksii_core2_deg5(l)	keratan sulfate II (core 2-linked), degradation product 5	Lysosome

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
1871	22599l	ksii_core2_deg6(l)	keratan sulfate II (core 2-linked), degradation product 6	Lysosome
1872	22600l	ksii_core2_deg7(l)	keratan sulfate II (core 2-linked), degradation product 7	Lysosome
1873	22601l	ksii_core2_deg8(l)	keratan sulfate II (core 2-linked), degradation product 8	Lysosome
1874	22602l	ksii_core2_deg9(l)	keratan sulfate II (core 2-linked), degradation product 9	Lysosome
1875	20342l	ksii_core4(l)	keratan sulfate II (core 4-linked)	Lysosome
1876	22605l	ksii_core4_deg1(l)	keratan sulfate II (core 4-linked), degradation product 1	Lysosome
1877	22606l	ksii_core4_deg2(l)	keratan sulfate II (core 4-linked), degradation product 2	Lysosome
1878	22607l	ksii_core4_deg3(l)	keratan sulfate II (core 4-linked), degradation product 3	Lysosome
1879	22608l	ksii_core4_deg4(l)	keratan sulfate II (core 4-linked), degradation product 4	Lysosome
1880	15670l	l2n2m2mn(l)	de-Fuc, reducing GlcNAc removed, de-Sia form of PA6 (w/o peptide linkage)	Lysosome
1881	292l	lcts(l)	Lactose	Lysosome
1882	15672l	m2mn(l)	(alpha-D-mannosyl)2-beta-D-mannosyl-N-acetylglucosamine	Lysosome
1883	267l	malt(l)	Maltose	Lysosome
1884	1284l	malttr(l)	Maltotriose	Lysosome
1885	11018l	man(l)	D-Mannose	Lysosome
1886	1092l	meoh(l)	Methanol	Lysosome
1887	15673l	mn(l)	beta-1,4-mannose-N-acetylglucosamine	Lysosome
1888	15671l	n2m2mn(l)	de-Fuc, reducing GlcNAc removed, de-Sia, de-Gal form of PA6 (w/o peptide linkage)	Lysosome
1889	15681l	n2m2nm(l)	n2m2nmasn (w/o peptide linkage)	Lysosome
1890	3649l	n2m2nmasn(l)	N-Acetyl-beta-D-glucosaminyl-1,2-alpha-D-mannosyl-1,3-(N-acetyl-beta-D-glucosaminyl-1,2-alpha-D-mannosyl-1,6)-(N-acetyl-beta-D-glucosaminyl-1,4)-beta-D-mannosyl-1,4-N-acetyl-beta-D-glucosaminyl-R	Lysosome
1891	15682l	n2m2nmn(l)	reducing GlcNAc removed form of n2m2nmasn (w/o peptide)	Lysosome
1892	472l	pi(l)	Phosphate	Lysosome
1893	629l	pro-D(l)	D-Proline	Lysosome
1894	229l	pro-L(l)	L-Proline	Lysosome
1895	15207l	s2l2fn2m2masn(l)	PA6	Lysosome
1896	15667l	s2l2n2m2m(l)	de-Fuc form of PA6 (w/o peptide linkage)	Lysosome
1897	15665l	s2l2n2m2masn(l)	de-Fuc form of PA6	Lysosome
1898	15669l	s2l2n2m2mn(l)	de-Fuc, reducing GlcNAc removed form of PA6 (w/o peptide linkage)	Lysosome
1899	19615l	sgalside_hs(l)	sulfatide galactocerebroside (homo sapiens)	Lysosome
1900	335l	so4(l)	Sulfate	Lysosome
1901	10703l	sphings(l)	Sphingosine	Lysosome
1902	19618l	sphmyln_hs(l)	sphingomyelin (homo sapiens)	Lysosome
1903	1065l	thf(l)	5,6,7,8-Tetrahydrofolate	Lysosome
1904	5269l	thymd(l)	Thymidine	Lysosome
1905	477l	udp(l)	UDP	Lysosome
1906	10912l	udpacgal(l)	UDP-N-acetyl-D-galactosamine	Lysosome

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
1907	1068l	ump(l)	UMP	Lysosome
1908	10727l	uri(l)	Uridine	Lysosome
1909	248l	xyl-D(l)	D-Xylose	Lysosome
1910	286m	10fthf(m)	10-Formyltetrahydrofolate	Mitochondria
1911	20786m	10fthf5glu(m)	10-formyltetrahydrofolate-[Glu](5)	Mitochondria
1912	20787m	10fthf6glu(m)	10-formyltetrahydrofolate-[Glu](6)	Mitochondria
1913	20788m	10fthf7glu(m)	10-formyltetrahydrofolate-[Glu](7)	Mitochondria
1914	3407m	11docrtsl(m)	11-Deoxycortisol	Mitochondria
1915	2404m	11docrtstrn(m)	11-Deoxycorticosterone	Mitochondria
1916	20075m	1a2425thvitd2(m)	1-alpha,24R,25-Trihydroxyvitamin D2	Mitochondria
1917	20076m	1a2425thvitd3(m)	1-alpha,24R,25-Trihydroxyvitamin D3	Mitochondria
1918	20018m	1a25dhvitd2(m)	1-alpha,25-Dihydroxyvitamin D2	Mitochondria
1919	20017m	1a25dhvitd3(m)	1-alpha,25-Dihydroxyvitamin D3	Mitochondria
1920	3261m	1p3h5c(m)	L-1-Pyrroline-3-hydroxy-5-carboxylate	Mitochondria
1921	2994m	1pyr5c(m)	1-Pyrroline-5-carboxylate	Mitochondria
1922	7532m	20ahchsterol(m)	20alpha-hydroxy cholesterol	Mitochondria
1923	20023m	2425dhvitd2(m)	24R,25-Dihyoxyvitamin D2	Mitochondria
1924	20024m	2425dhvitd3(m)	24R,25-Dihydroxyvitamin D3	Mitochondria
1925	20014m	25hvitd2(m)	25-Hydroxyvitamin D2	Mitochondria
1926	20012m	25hvitd3(m)	25-Hydroxyvitamin D3	Mitochondria
1927	2707m	2aobut(m)	L-2-Amino-3-oxobutanoate	Mitochondria
1928	19793m	2dp6mep(m)	2-Decaprenyl-6-methoxyphenol	Mitochondria
1929	19804m	2dp6mobq(m)	2-Decaprenyl-6-methoxy-1,4-benzoquinone	Mitochondria
1930	19805m	2dp6mobq_me(m)	2-Decaprenyl-3-methyl-6-methoxy-1,4-benzoquinone	Mitochondria
1931	19808m	2dpmhobq(m)	2-Decaprenyl-3-methyl-5-hydroxy-6-methoxy-1,4-benzoquinone	Mitochondria
1932	2497m	2maacoa(m)	2-Methyl-3-acetoacetyl-CoA	Mitochondria
1933	2498m	2mb2coa(m)	trans-2-Methylbut-2-enoyl-CoA	Mitochondria
1934	844m	2mbcoa(m)	2-Methylbutanoyl-CoA	Mitochondria
1935	186m	2mop(m)	2-Methyl-3-oxopropanoate	Mitochondria
1936	2388m	2mp2coa(m)	2-Methylprop-2-enoyl-CoA	Mitochondria
1937	9002m	2oxoadp(m)	2-Oxoadipate	Mitochondria
1938	22485m	34hpl(m)	3-(4-Hydroxyphenyl)lactate	Mitochondria
1939	772m	34hpp(m)	3-(4-Hydroxyphenyl)pyruvate	Mitochondria
1940	2457m	3aib(m)	L-3-Amino-isobutanoate	Mitochondria
1941	2444m	3aib-D(m)	D-3-Amino-isobutanoate	Mitochondria
1942	19791m	3dpdhb(m)	3-Decaprenyl-4,5-dihdydroxybenzoate	Mitochondria
1943	19792m	3dpdhb_me(m)	3-Decaprenyl-4-hydroxy-5-methoxybenzoate	Mitochondria
1944	19772m	3dphb(m)	3-Decaprenyl-4-hydroxybenzoate	Mitochondria
1945	19703m	3h26dm5coa(m)	3-Hydroxy-2,6-dimethyl-5-methylene-heptanoyl-CoA	Mitochondria
1946	905m	3hbcoa(m)	(S)-3-Hydroxybutanoyl-CoA	Mitochondria
1947	2736m	3hbcoa-R(m)	(R)-3-Hydroxybutanoyl-CoA	Mitochondria
1948	4444m	3hibutcoa(m)	(S)-3-Hydroxyisobutyryl-CoA	Mitochondria
1949	3162m	3hmbcoa(m)	(S)-3-Hydroxy-2-methylbutyryl-CoA	Mitochondria
1950	779m	3hmp(m)	3-Hydroxy-2-methylpropanoate	Mitochondria
1951	4184m	3hpcoa(m)	3-Hydroxypropionyl-CoA	Mitochondria
1952	7135m	3htmelys(m)	3-Hydroxy-N6,N6,N6-trimethyl-L-lysine	Mitochondria
1953	2308m	3mb2coa(m)	3-Methylbut-2-enoyl-CoA	Mitochondria
1954	2423m	3mgcoa(m)	3-Methylglutaconyl-CoA	Mitochondria
1955	225m	3mob(m)	3-Methyl-2-oxobutanoate	Mitochondria
1956	445m	3mop(m)	(S)-3-Methyl-2-oxopentanoate	Mitochondria

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1957	1105m	3sala(m)	3-Sulfino-L-alanine	Mitochondria
1958	3427m	3snpyr(m)	3-Sulfinopyruvate	Mitochondria
1959	15766m	3spyr(m)	3-Sulfopyruvate	Mitochondria
1960	7924m	4aabutn(m)	4-Acetamidobutanoate	Mitochondria
1961	176m	4abut(m)	4-Aminobutanoate	Mitochondria
1962	896m	4h2oglt(m)	4-Hydroxy-2-oxoglutarate	Mitochondria
1963	234m	4hbz(m)	4-Hydroxybenzoate	Mitochondria
1964	22487m	4hbzcoa(m)	4-hydroxybenoyl-CoA	Mitochondria
1965	8300m	4hglusa(m)	L-4-Hydroxyglutamate semialdehyde	Mitochondria
1966	913m	4hpro-LT(m)	trans-4-Hydroxy-L-proline	Mitochondria
1967	285m	4mop(m)	4-Methyl-2-oxopentanoate	Mitochondria
1968	1711m	4mptnl(m)	4-Methylpentanal	Mitochondria
1969	2022m	4ppan(m)	D-4'-Phosphopantothenate	Mitochondria
1970	908m	4tmeabut(m)	4-Trimethylammoniobutanal	Mitochondria
1971	424m	5aop(m)	5-Amino-4-oxopentanoate	Mitochondria
1972	20783m	5dhf(m)	pentaglutamyl folate (DHF)	Mitochondria
1973	4155m	5hoxindact(m)	5-Hydroxyindoleacetaldehyde	Mitochondria
1974	11161m	5hoxindoa(m)	5-Hydroxyindoleacetate	Mitochondria
1975	20780m	5thf(m)	pentaglutamyl folate (THF)	Mitochondria
1976	20784m	6dhf(m)	haxglutamyl folate (DHF)	Mitochondria
1977	20781m	6thf(m)	hexaglutamyl folate (THF)	Mitochondria
1978	20785m	7dhf(m)	heptaglutamyl folate (DHF)	Mitochondria
1979	20782m	7thf(m)	heptaglutamyl folate (THF)	Mitochondria
1980	69m	ACP(m)	acyl carrier protein	Mitochondria
1981	9011m	L2aadp(m)	L-2-Aminoadipate	Mitochondria
1982	7588m	L2aadp6sa(m)	L-2-Aminoadipate 6-semialdehyde	Mitochondria
1983	120m	Lcyst(m)	L-Cysteate	Mitochondria
1984	679m	Nacasp(m)	N-Acetyl-L-aspartate	Mitochondria
1985	22166m	Rtotal2coa(m)	R total 2 coenzyme A	Mitochondria
1986	22470m	Rtotal2crn(m)	R total 2 carnitine	Mitochondria
1987	22167m	Rtotal3coa(m)	R total 3 Coenzyme A	Mitochondria
1988	22471m	Rtotal3crn(m)	R total 3 carnitine	Mitochondria
1989	22165m	Rtotalcoa(m)	R total Coenzyme A	Mitochondria
1990	22469m	Rtotalcrn(m)	R total carnitine	Mitochondria
1991	656m	T4hcinnm(m)	trans-4-Hydroxycinnamate	Mitochondria
1992	174m	aacoa(m)	Acetoacetyl-CoA	Mitochondria
1993	1533m	aact(m)	Aminoacetone	Mitochondria
1994	319m	ac(m)	Acetate	Mitochondria
1995	9016m	acac(m)	Acetoacetate	Mitochondria
1996	1052m	acald(m)	Acetaldehyde	Mitochondria
1997	11537m	accoa(m)	Acetyl-CoA	Mitochondria
1998	266m	acetone(m)	Acetone	Mitochondria
1999	2957m	acg5p(m)	N-Acetyl-L-glutamyl 5-phosphate	Mitochondria
2000	975m	acg5sa(m)	N-Acetyl-L-glutamate 5-semialdehyde	Mitochondria
2001	1115m	acglu(m)	N-Acetyl-L-glutamate	Mitochondria
2002	7471m	acrn(m)	O-Acetylcarnitine	Mitochondria
2003	270m	adn(m)	Adenosine	Mitochondria
2004	10925m	adocbl(m)	Adenosylcobalamin	Mitochondria
2005	471m	adp(m)	ADP	Mitochondria
2006	151m	adprib(m)	ADPribose	Mitochondria
2007	18484m	adrncoa(m)	adrenyl coenzyme A	Mitochondria
2008	25984m	adrncrn(m)	Adrenyl carnitine	Mitochondria
2009	247m	agm(m)	Agmatine	Mitochondria

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2010	310m	ahcys(m)	S-Adenosyl-L-homocysteine	Mitochondria
2011	314m	akg(m)	2-Oxoglutarate	Mitochondria
2012	1063m	ala-B(m)	beta-Alanine	Mitochondria
2013	11412m	ala-L(m)	L-Alanine	Mitochondria
2014	1447m	aldstrn(m)	Aldosterone	Mitochondria
2015	18535m	alpa_hs(m)	lysophosphatidic acid (homo sapiens)	Mitochondria
2016	7690m	alpam(m)	S-aminomethyldihydrolipoamide	Mitochondria
2017	10354m	alpro(m)	S-Aminomethyldihydrolipoylprotein	Mitochondria
2018	1086m	amet(m)	S-Adenosyl-L-methionine	Mitochondria
2019	309m	amp(m)	AMP	Mitochondria
2020	22737m	apoC(m)	Apocarboxlase (no lys residue)	Mitochondria
2021	22735m	apoC-Lys(m)	Apocarboxylase (Lys residue)	Mitochondria
2022	22736m	apoC-Lys_btn(m)	Holocarboxylase (biotin covalent bound to Lys residue of apoC)	Mitochondria
2023	18483m	arachcoa(m)	arachidyl coenzyme A	Mitochondria
2024	25967m	arachcrn(m)	arachidyl carnitine	Mitochondria
2025	11887m	arachdcoa(m)	C20:4-CoA	Mitochondria
2026	11889m	arachdcrn(m)	C20:4 carnitine	Mitochondria
2027	337m	arg-L(m)	L-Arginine	Mitochondria
2028	232m	asn-L(m)	L-Asparagine	Mitochondria
2029	330m	asp-L(m)	L-Aspartate	Mitochondria
2030	465m	atp(m)	ATP	Mitochondria
2031	733m	b2coa(m)	Crotonoyl-CoA	Mitochondria
2032	4182m	bamppald(m)	beta-Aminopropion aldehyde	Mitochondria
2033	392m	betald(m)	Betaine aldehyde	Mitochondria
2034	870m	bhb(m)	(R)-3-Hydroxybutanoate	Mitochondria
2035	4297m	biocyt(m)	Biocytin	Mitochondria
2036	4584m	btamp(m)	Biotinyl-5'-AMP	Mitochondria
2037	222m	btcoa(m)	Butanoyl-CoA	Mitochondria
2038	1079m	btn(m)	Biotin	Mitochondria
2039	294m	but(m)	Butyrate (n-C4:0)	Mitochondria
2040	11888m	c226coa(m)	cervonyl coenzyme A	Mitochondria
2041	11883m	c226crn(m)	cervonyl carnitine	Mitochondria
2042	19701m	c2m26dcoa(m)	cis-2-Methyl-5-isopropylhexa-2,5-dienoyl-CoA	Mitochondria
2043	10988m	cbl1(m)	Cob(I)alamin	Mitochondria
2044	365m	cbl2(m)	Cob(II)alamin	Mitochondria
2045	11004m	cbp(m)	Carbamoyl phosphate	Mitochondria
2046	20077m	cca_d3(m)	Calcitroic acid (D3)	Mitochondria
2047	1073m	cdp(m)	CDP	Mitochondria
2048	19105m	cdpdag_hs(m)	CDP diacylglycerol (homo sapiens)	Mitochondria
2049	1075m	chol(m)	Choline	Mitochondria
2050	252m	chsterol(m)	Cholesterol	Mitochondria
2051	236m	cit(m)	Citrate	Mitochondria
2052	828m	citmcoa-L(m)	L-Citramalyl-CoA	Mitochondria
2053	169m	citr-L(m)	L-Citrulline	Mitochondria
2054	18488m	clpndcoa(m)	clupanodonyl CoA	Mitochondria
2055	25990m	clpndcrn(m)	clupanodonyl carnitine	Mitochondria
2056	11376m	cmp(m)	CMP	Mitochondria
2057	474m	co2(m)	CO2	Mitochondria
2058	473m	coa(m)	Coenzyme A	Mitochondria
2059	22486m	coucoa(m)	p-coumaroyl-CoA	Mitochondria
2060	150m	creat(m)	Creatine	Mitochondria
2061	163m	crn(m)	L-Carnitine	Mitochondria

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2062	11268m	crtsl(m)	Cortisol	Mitochondria
2063	1737m	crtstrn(m)	Corticosterone	Mitochondria
2064	338m	ctp(m)	CTP	Mitochondria
2065	245m	cyan(m)	Hydrogen cyanide	Mitochondria
2066	1062m	cys-L(m)	L-Cysteine	Mitochondria
2067	92m	cytd(m)	Cytidine	Mitochondria
2068	265m	dadp(m)	dADP	Mitochondria
2069	1091m	datp(m)	dATP	Mitochondria
2070	5272m	dcdp(m)	dCDP	Mitochondria
2071	290m	dcmp(m)	dCMP	Mitochondria
2072	18487m	dcsptn1coa(m)	docosa-4,7,10,13,16-pentaenoyl coenzyme A	Mitochondria
2073	25989m	dcsptn1crn(m)	docosa-4,7,10,13,16-pentaenoyl carnitine	Mitochondria
2074	78m	dctp(m)	dCTP	Mitochondria
2075	10918m	dcyt(m)	Deoxycytidine	Mitochondria
2076	2416m	dd2coa(m)	trans-Dodec-2-enoyl-CoA	Mitochondria
2077	12055m	dd3coa(m)	3-dodecenoyl CoA	Mitochondria
2078	12883m	decdp(m)	all trans Decaprenyl diphosphate	Mitochondria
2079	194m	dgdp(m)	dGDP	Mitochondria
2080	195m	dgmp(m)	dGMP	Mitochondria
2081	172m	dgsn(m)	Deoxyguanosine	Mitochondria
2082	143m	dgtp(m)	dGTP	Mitochondria
2083	3997m	dhcholestanate(m)	3alpha,7alpha-Dihydroxy-5beta-cholestanate	Mitochondria
2084	10505m	dhf(m)	7,8-Dihydrofolate	Mitochondria
2085	394m	dhlam(m)	Dihydrolipoamide	Mitochondria
2086	56m	dhlpro(m)	Dihydrolipolprotein	Mitochondria
2087	1032m	didp(m)	dIDP	Mitochondria
2088	1033m	ditp(m)	dITP	Mitochondria
2089	18491m	dlnlcgcoa(m)	dihomo-gamma-linolenyl coenzyme A	Mitochondria
2090	25979m	dlnlcgcrn(m)	dihomo-gamma-linolenyl carnitine	Mitochondria
2091	840m	dmgly(m)	N,N-Dimethylglycine	Mitochondria
2092	21977m	dmhptcoa(m)	2,6 dimethylheptanoyl-CoA	Mitochondria
2093	26488m	dmhptcrn(m)	2,6 dimethylheptanoyl carnitine	Mitochondria
2094	21959m	dmnoncoa(m)	4,8 dimethylnonanoyl-CoA	Mitochondria
2095	21976m	dmnoncrn(m)	4,8 dimethylnonanoyl carnitine	Mitochondria
2096	724m	dnad(m)	Deamino-NAD+	Mitochondria
2097	196m	dtdp(m)	dTDP	Mitochondria
2098	197m	dtmp(m)	dTMP	Mitochondria
2099	79m	dttp(m)	dTTP	Mitochondria
2100	1034m	dudp(m)	dUDP	Mitochondria
2101	198m	dump(m)	dUMP	Mitochondria
2102	355m	duri(m)	Deoxyuridine	Mitochondria
2103	80m	dutp(m)	dUTP	Mitochondria
2104	8301m	e4hglu(m)	L-erythro-4-Hydroxyglutamate	Mitochondria
2105	18507m	eicostetcoa(m)	eicosatetranoyl coenzyme A	Mitochondria
2106	25980m	eicostetcrn(m)	Eicosatetranoyl carnitine	Mitochondria
2107	25972m	elaidcrn(m)	Elaidic carnitine	Mitochondria
2108	20557m	etfox(m)	Electron transfer flavoprotein oxidized	Mitochondria
2109	20558m	etfrd(m)	Electron transfer flavoprotein reduced	Mitochondria
2110	478m	fad(m)	Flavin adenine dinucleotide oxidized	Mitochondria
2111	42m	fadh2(m)	Flavin adenine dinucleotide reduced	Mitochondria
2112	340m	fald(m)	Formaldehyde	Mitochondria
2113	312m	fe2(m)	Fe2+	Mitochondria

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
2114	10041m	ficytC(m)	Ferricytochrome c	Mitochondria
2115	1084m	ficytc(m)	Ferricytochrome c	Mitochondria
2116	10042m	focytC(m)	Ferrocytochrome C	Mitochondria
2117	1085m	focytc(m)	Ferrocytochrome c	Mitochondria
2118	334m	for(m)	Formate	Mitochondria
2119	1081m	fum(m)	Fumarate	Mitochondria
2120	10800m	gcald(m)	Glycolaldehyde	Mitochondria
2121	321m	gdp(m)	GDP	Mitochondria
2122	18308m	glac(m)	D-glucurono-6,3-lactone	Mitochondria
2123	632m	glcr(m)	D-Glucarate	Mitochondria
2124	661m	gln-D(m)	D-Glutamine	Mitochondria
2125	11299m	gln-L(m)	L-Glutamine	Mitochondria
2126	273m	glu-D(m)	D-Glutamate	Mitochondria
2127	313m	glu-L(m)	L-Glutamate	Mitochondria
2128	2458m	glu5p(m)	L-Glutamate 5-phosphate	Mitochondria
2129	761m	glu5sa(m)	L-Glutamate 5-semialdehyde	Mitochondria
2130	356m	glutcoa(m)	Glutaryl-CoA	Mitochondria
2131	329m	glx(m)	Glyoxylate	Mitochondria
2132	323m	gly(m)	Glycine	Mitochondria
2133	503m	glyb(m)	Glycine betaine	Mitochondria
2134	1077m	glyc(m)	Glycerol	Mitochondria
2135	55m	glyc3p(m)	Glycerol 3-phosphate	Mitochondria
2136	237m	glyclt(m)	Glycolate	Mitochondria
2137	226m	gmp(m)	GMP	Mitochondria
2138	5279m	gsn(m)	Guanosine	Mitochondria
2139	1087m	gthox(m)	Oxidized glutathione	Mitochondria
2140	11388m	gthrd(m)	Reduced glutathione	Mitochondria
2141	327m	gtp(m)	GTP	Mitochondria
2142	1049m	h(m)	H+	Mitochondria
2143	3m	h2co3(m)	carbonic acid	Mitochondria
2144	317m	h2o(m)	H2O	Mitochondria
2145	315m	h2o2(m)	Hydrogen peroxide	Mitochondria
2146	144m	hco3(m)	Bicarbonate	Mitochondria
2147	21857m	hdcecrn(m)	Hexadecenoyl carnitine	Mitochondria
2148	8780m	hdcoa(m)	Hexadecenoyl-CoA (n-C16:1CoA)	Mitochondria
2149	3801m	hdd2coa(m)	trans-Hexadec-2-enoyl-CoA	Mitochondria
2150	26402m	hdd2crn(m)	trans-Hexadec-2-enoyl carnitine	Mitochondria
2151	11013m	hexccoa(m)	Hexacosanoyl-CoA (n-C26:0CoA)	Mitochondria
2152	25969m	hexccrn(m)	hexacosanoyl carnitine	Mitochondria
2153	191m	hmgcoa(m)	Hydroxymethylglutaryl-CoA	Mitochondria
2154	22502m	hpdcacoa(m)	heptadecanoyl coa	Mitochondria
2155	22758m	hpdcacrn(m)	heptadecanoyl carnitine	Mitochondria
2156	242m	hpyr(m)	Hydroxypyruvate	Mitochondria
2157	1119m	ibcoa(m)	Isobutyryl-CoA	Mitochondria
2158	158m	icit(m)	Isocitrate	Mitochondria
2159	1125m	id3acald(m)	Indole-3-acetaldehyde	Mitochondria
2160	1067m	idp(m)	IDP	Mitochondria
2161	410m	ile-L(m)	L-Isoleucine	Mitochondria
2162	2132m	im4ac(m)	Imidazole-4-acetate	Mitochondria
2163	3706m	im4act(m)	Imidazole-4-acetaldehyde	Mitochondria
2164	1090m	imp(m)	IMP	Mitochondria
2165	9022m	ind3ac(m)	Indole-3-acetate	Mitochondria
2166	147m	ins(m)	Inosine	Mitochondria

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
2167	359m	itaccoa(m)	Itaconyl-CoA	Mitochondria
2168	104m	itacon(m)	Itaconate	Mitochondria
2169	1050m	itp(m)	ITP	Mitochondria
2170	1908m	ivcoa(m)	Isovaleryl-CoA	Mitochondria
2171	304m	lac-D(m)	D-Lactate	Mitochondria
2172	10931m	lac-L(m)	L-Lactate	Mitochondria
2173	491m	lald-D(m)	D-Lactaldehyde	Mitochondria
2174	420m	lald-L(m)	L-Lactaldehyde	Mitochondria
2175	1082m	leu-L(m)	L-Leucine	Mitochondria
2176	18490m	lgnccoa(m)	lignocericyl coenzyme A	Mitochondria
2177	25968m	lgnccrn(m)	lignoceryl carnitine	Mitochondria
2178	2477m	lgt-S(m)	(R)-S-Lactoylglutathione	Mitochondria
2179	18482m	lneldccoa(m)	linoelaidyl coenzyme A	Mitochondria
2180	25975m	lneldccrn(m)	Linoelaidyl carnitine	Mitochondria
2181	18481m	lnlccoa(m)	linoleic coenzyme A	Mitochondria
2182	25976m	lnlccrn(m)	Linoleyl carnitine	Mitochondria
2183	18480m	lnlncacoa(m)	alpha-Linolenoyl-CoA	Mitochondria
2184	25978m	lnlncacrn(m)	alpha-linolenyl carnitine	Mitochondria
2185	2277m	lnlncgcoa(m)	gamma-linolenoyl-CoA	Mitochondria
2186	25977m	lnlncgcrn(m)	gamma-linolenyl carnitine	Mitochondria
2187	296m	lpam(m)	Lipoamide	Mitochondria
2188	1657m	lpro(m)	Lipoylprotein	Mitochondria
2189	328m	lys-L(m)	L-Lysine	Mitochondria
2190	230m	mal-L(m)	L-Malate	Mitochondria
2191	50m	malACP(m)	Malonyl-[acyl-carrier protein]	Mitochondria
2192	11267m	malcoa(m)	Malonyl-CoA	Mitochondria
2193	794m	mercppyr(m)	Mercaptopyruvate	Mitochondria
2194	4468m	mescoa(m)	Mesaconyl-CoA	Mitochondria
2195	1409m	mescon(m)	Mesaconate	Mitochondria
2196	433m	methf(m)	5,10-Methenyltetrahydrofolate	Mitochondria
2197	11043m	mlthf(m)	5,10-Methylenetetrahydrofolate	Mitochondria
2198	943m	mmcoa-R(m)	(R)-Methylmalonyl-CoA	Mitochondria
2199	451m	mmcoa-S(m)	(S)-Methylmalonyl-CoA	Mitochondria
2200	277m	msa(m)	Malonate semialdehyde	Mitochondria
2201	7923m	n4abutn(m)	N4-Acetylaminobutanal	Mitochondria
2202	466m	nad(m)	Nicotinamide adenine dinucleotide	Mitochondria
2203	467m	nadh(m)	Nicotinamide adenine dinucleotide - reduced	Mitochondria
2204	469m	nadp(m)	Nicotinamide adenine dinucleotide phosphate	Mitochondria
2205	468m	nadph(m)	Nicotinamide adenine dinucleotide phosphate - reduced	Mitochondria
2206	476m	nh4(m)	Ammonium	Mitochondria
2207	776m	nicrnt(m)	Nicotinate D-ribonucleotide	Mitochondria
2208	77m	nmn(m)	NMN	Mitochondria
2209	18485m	nrvnccoa(m)	nervonyl coenzyme A	Mitochondria
2210	25974m	nrvnccrn(m)	Nervonyl carnitine	Mitochondria
2211	470m	o2(m)	O2	Mitochondria
2212	461m	o2s(m)	Superoxide anion	Mitochondria
2213	322m	oaa(m)	Oxaloacetate	Mitochondria
2214	10688m	occoa(m)	Octanoyl-CoA (n-C8:0CoA)	Mitochondria
2215	8401m	od2coa(m)	trans-Octadec-2-enoyl-CoA	Mitochondria
2216	8782m	odecoa(m)	Octadecenoyl-CoA (n-C18:1CoA)	Mitochondria
2217	11885m	odecrn(m)	octadecenoyl carnitine	Mitochondria
2218	1021m	oh1(m)	hydroxide ion	Mitochondria

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
2219	1304m	orn(m)	Ornithine	Mitochondria
2220	18536m	pa_hs(m)	phosphatidic acid (homo sapiens)	Mitochondria
2221	19051m	pchol_hs(m)	Phosphatidylcholine (homo sapiens)	Mitochondria
2222	10038m	pcreat(m)	Phosphocreatine	Mitochondria
2223	15675m	pcrn(m)	propionyl-carnitine	Mitochondria
2224	19050m	pe_hs(m)	phosphatidylethanolamine (homo sapiens)	Mitochondria
2225	344m	pep(m)	Phosphoenolpyruvate	Mitochondria
2226	19700m	peracd(m)	Perillic acid	Mitochondria
2227	1048m	phe-L(m)	L-Phenylalanine	Mitochondria
2228	11520m	pheme(m)	Protoheme	Mitochondria
2229	240m	phpyr(m)	Phenylpyruvate	Mitochondria
2230	472m	pi(m)	Phosphate	Mitochondria
2231	11029m	pmtcoa(m)	Palmitoyl-CoA (n-C16:0CoA)	Mitochondria
2232	2244m	pmtcrn(m)	L-Palmitoylcarnitine	Mitochondria
2233	10928m	pnto-R(m)	(R)-Pantothenate	Mitochondria
2234	238m	ppa(m)	Propionate (n-C3:0)	Mitochondria
2235	1064m	ppcoa(m)	Propanoyl-CoA	Mitochondria
2236	475m	ppi(m)	Diphosphate	Mitochondria
2237	1772m	ppp9(m)	Protoporphyrin	Mitochondria
2238	864m	pppg9(m)	Protoporphyrinogen IX	Mitochondria
2239	2452m	pppi(m)	Inorganic triphosphate	Mitochondria
2240	10681m	prgnlone(m)	Pregnenolone	Mitochondria
2241	229m	pro-L(m)	L-Proline	Mitochondria
2242	744m	prpncoa(m)	Propenoyl-CoA	Mitochondria
2243	19052m	ps_hs(m)	phosphatidylserine (homo sapiens)	Mitochondria
2244	22500m	ptdcacoa(m)	pentadecanoyl Coenzyme A	Mitochondria
2245	22757m	ptdcacrn(m)	pendtadenoyl carnitine	Mitochondria
2246	1094m	ptrc(m)	Putrescine	Mitochondria
2247	1130m	pyam5p(m)	Pyridoxamine 5'-phosphate	Mitochondria
2248	479m	pydx5p(m)	Pyridoxal 5'-phosphate	Mitochondria
2249	1851m	pylald(m)	Perillyl aldehyde	Mitochondria
2250	311m	pyr(m)	Pyruvate	Mitochondria
2251	406m	q10(m)	Ubiquinone-10	Mitochondria
2252	11879m	q10h2(m)	Ubiquinol-10	Mitochondria
2253	1999m	r5p(m)	alpha-D-Ribose 5-phosphate	Mitochondria
2254	8994m	saccrp-L(m)	L-Saccharopine	Mitochondria
2255	271m	sarcs(m)	Sarcosine	Mitochondria
2256	339m	ser-L(m)	L-Serine	Mitochondria
2257	15786m	sl-L(m)	L-sulfolactate	Mitochondria
2258	1060m	so3(m)	Sulfite	Mitochondria
2259	335m	so4(m)	Sulfate	Mitochondria
2260	8781m	stcoa(m)	Stearoyl-CoA (n-C18:0CoA)	Mitochondria
2261	11884m	stcrn(m)	stearoylcarnitine	Mitochondria
2262	18492m	strdnccoa(m)	stearidonyl coenzyme A	Mitochondria
2263	25985m	strdnccrn(m)	stearidonyl carnitine	Mitochondria
2264	325m	succ(m)	Succinate	Mitochondria
2265	1058m	succoa(m)	Succinyl-CoA	Mitochondria
2266	284m	sucsal(m)	Succinic semialdehyde	Mitochondria
2267	19702m	t2m26dcoa(m)	trans-2-Methyl-5-isopropylhexa-2,5-dienoyl-CoA	Mitochondria
2268	1428m	tcynt(m)	Thiocyanate	Mitochondria
2269	1862m	tdcoa(m)	Tetradecanoyl-CoA (n-C14:0CoA)	Mitochondria
2270	18513m	tetpent3coa(m)	tetracosapentaenoyl coenzyme A, n-3	Mitochondria
2271	25991m	tetpent3crn(m)	tetracosapentaenoyl carnitine	Mitochondria

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
2272	18509m	tetpent6coa(m)	tetracosapentaenoyl coenzyme A, n-6	Mitochondria
2273	25992m	tetpent6crn(m)	tetracosapentaenoyl carnitine	Mitochondria
2274	18511m	tettet6coa(m)	tetracosatetraenoyl coenzyme A	Mitochondria
2275	25986m	tettet6crn(m)	Tetracosatetraenoyl carnitine	Mitochondria
2276	852m	thcholst(m)	3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestan-26-al	Mitochondria
2277	3477m	thcholstoic(m)	3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestanoate	Mitochondria
2278	1065m	thf(m)	5,6,7,8-Tetrahydrofolate	Mitochondria
2279	210m	thm(m)	Thiamin	Mitochondria
2280	866m	thmmp(m)	Thiamin monophosphate	Mitochondria
2281	341m	thmpp(m)	Thiamine diphosphate	Mitochondria
2282	5269m	thymd(m)	Thymidine	Mitochondria
2283	18486m	tmndnccoa(m)	timnodonyl coenzyme A	Mitochondria
2284	25988m	tmndnccrn(m)	Timnodonyl carnitine	Mitochondria
2285	181m	trdox(m)	Oxidized thioredoxin	Mitochondria
2286	180m	trdrd(m)	Reduced thioredoxin	Mitochondria
2287	164m	tsul(m)	Thiosulfate	Mitochondria
2288	26814m	ttdcrn(m)	tetradecanoyl carnitine	Mitochondria
2289	1051m	tyr-L(m)	L-Tyrosine	Mitochondria
2290	477m	udp(m)	UDP	Mitochondria
2291	1068m	ump(m)	UMP	Mitochondria
2292	1054m	urea(m)	Urea	Mitochondria
2293	10727m	uri(m)	Uridine	Mitochondria
2294	345m	utp(m)	UTP	Mitochondria
2295	18479m	vacccoa(m)	vaccenyl coenzyme A	Mitochondria
2296	25973m	vacccrn(m)	Vaccenyl carnitine	Mitochondria
2297	250m	val-L(m)	L-Valine	Mitochondria
2298	20013m	vitd2(m)	Vitamin D2	Mitochondria
2299	20001m	vitd3(m)	Vitamin D3	Mitochondria
2300	4060m	xol27oh(m)	27-Hydroxycholesterol	Mitochondria
2301	3381m	xol7ah2(m)	3alpha,7alpha-Dihydroxy-5beta-cholestane	Mitochondria
2302	3375m	xol7ah2al(m)	3alpha,7alpha-Dihydroxy-5beta-cholestan-26-al	Mitochondria
2303	3374m	xol7ah3(m)	3alpha,7alpha,26-Trihydroxy-5beta-cholestane	Mitochondria
2304	3384m	xoldiolone(m)	7alpha,12alpha-Dihydroxycholest-4-en-3-one	Mitochondria
2305	3379m	xoltetrol(m)	3alpha,7alpha,12alpha,26-Tetrahydroxy-5beta-cholestane	Mitochondria
2306	3383m	xoltriol(m)	3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestane	Mitochondria
2307	22815n	13-cis-oretn(n)	13-cis-oxo-retinoic acid	Nucleus
2308	22814n	13-cis-retn(n)	13-cis-retinoate	Nucleus
2309	9005n	35cgmp(n)	3',5'-Cyclic GMP	Nucleus
2310	11000n	6pthp(n)	6-Pyruvoyl-5,6,7,8-tetrahydropterin	Nucleus
2311	4292n	Ndmelys(n)	Protein N6,N6-dimethyl-L-lysine	Nucleus
2312	10936n	Nmelys(n)	Histone N6-methyl-L-lysine	Nucleus
2313	4293n	Ntmelys(n)	Protein N6,N6,N6-trimethyl-L-lysine	Nucleus
2314	11537n	accoa(n)	Acetyl-CoA	Nucleus
2315	1617n	ach(n)	Acetylcholine	Nucleus
2316	134n	acnam(n)	N-Acetylneuraminate	Nucleus
2317	471n	adp(n)	ADP	Nucleus
2318	310n	ahcys(n)	S-Adenosyl-L-homocysteine	Nucleus
2319	3611n	ahdt(n)	2-Amino-4-hydroxy-6-(erythro-1,2,3-trihydroxypropyl)dihydropteridine triphosphate	Nucleus

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
2320	1086n	amet(n)	S-Adenosyl-L-methionine	Nucleus
2321	465n	atp(n)	ATP	Nucleus
2322	4297n	biocyt(n)	Biocytin	Nucleus
2323	1079n	btn(n)	Biotin	Nucleus
2324	1073n	cdp(n)	CDP	Nucleus
2325	1075n	chol(n)	Choline	Nucleus
2326	11376n	cmp(n)	CMP	Nucleus
2327	1088n	cmpacna(n)	CMP-N-acetylneuraminate	Nucleus
2328	474n	co2(n)	CO2	Nucleus
2329	473n	coa(n)	Coenzyme A	Nucleus
2330	338n	ctp(n)	CTP	Nucleus
2331	92n	cytd(n)	Cytidine	Nucleus
2332	265n	dadp(n)	dADP	Nucleus
2333	18537n	dag_hs(n)	diacylglycerol (homo sapiens)	Nucleus
2334	1091n	datp(n)	dATP	Nucleus
2335	5272n	dcdp(n)	dCDP	Nucleus
2336	290n	dcmp(n)	dCMP	Nucleus
2337	78n	dctp(n)	dCTP	Nucleus
2338	10918n	dcyt(n)	Deoxycytidine	Nucleus
2339	194n	dgdp(n)	dGDP	Nucleus
2340	143n	dgtp(n)	dGTP	Nucleus
2341	1032n	didp(n)	dIDP	Nucleus
2342	1033n	ditp(n)	dITP	Nucleus
2343	18424n	dna(n)	DNA	Nucleus
2344	18425n	dna5mtc(n)	DNA 5-methylcytosine	Nucleus
2345	724n	dnad(n)	Deamino-NAD+	Nucleus
2346	196n	dtdp(n)	dTDP	Nucleus
2347	79n	dttp(n)	dTTP	Nucleus
2348	1034n	dudp(n)	dUDP	Nucleus
2349	198n	dump(n)	dUMP	Nucleus
2350	355n	duri(n)	Deoxyuridine	Nucleus
2351	80n	dutp(n)	dUTP	Nucleus
2352	334n	for(n)	Formate	Nucleus
2353	321n	gdp(n)	GDP	Nucleus
2354	226n	gmp(n)	GMP	Nucleus
2355	327n	gtp(n)	GTP	Nucleus
2356	1049n	h(n)	H+	Nucleus
2357	317n	h2o(n)	H2O	Nucleus
2358	315n	h2o2(n)	Hydrogen peroxide	Nucleus
2359	20388n	hretn(n)	4 hydroxy retinoic acid	Nucleus
2360	1067n	idp(n)	IDP	Nucleus
2361	1050n	itp(n)	ITP	Nucleus
2362	328n	lys-L(n)	L-Lysine	Nucleus
2363	996n	mi13456p(n)	1D-myo-Inositol 1,3,4,5,6-pentakisphosphate	Nucleus
2364	7140n	mi1345p(n)	1D-myo-Inositol 1,3,4,5-tetrakisphosphate	Nucleus
2365	11398n	mi1346p(n)	1D-myo-Inositol 1,3,4,6-tetrakisphosphate	Nucleus
2366	19579n	mi1456p(n)	1D-myo-Inositol 1,4,5,6-tetrakisphosphate	Nucleus
2367	8995n	mi145p(n)	1D-myo-Inositol 1,4,5-trisphosphate	Nucleus
2368	950n	mi14p(n)	1D-myo-Inositol 1,4-bisphosphate	Nucleus
2369	8983n	mi1p-D(n)	1D-myo-Inositol 1-phosphate	Nucleus
2370	938n	minohp(n)	myo-Inositol hexakisphosphate	Nucleus
2371	466n	nad(n)	Nicotinamide adenine dinucleotide	Nucleus
2372	469n	nadp(n)	Nicotinamide adenine dinucleotide phosphate	Nucleus

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
2373	468n	nadph(n)	Nicotinamide adenine dinucleotide phosphate - reduced	Nucleus
2374	476n	nh4(n)	Ammonium	Nucleus
2375	776n	nicrnt(n)	Nicotinate D-ribonucleotide	Nucleus
2376	77n	nmn(n)	NMN	Nucleus
2377	470n	o2(n)	O2	Nucleus
2378	461n	o2s(n)	Superoxide anion	Nucleus
2379	22810n	oretn(n)	4-oxo-retonoic acid	Nucleus
2380	18536n	pa_hs(n)	phosphatidic acid (homo sapiens)	Nucleus
2381	4431n	pail345p_hs(n)	phosphatidylinositol-3,4,5-trisphosphate (Homo sapiens)	Nucleus
2382	19605n	pail34p_hs(n)	phosphatidylinositol-3,4-bisphosphate (Homo sapiens)	Nucleus
2383	3992n	pail3p_hs(n)	1-Phosphatidyl-1D-myo-inositol 3-phosphate (Homo sapiens)	Nucleus
2384	19333n	pail45p_hs(n)	phosphatidylinositol 4,5-bisphosphate (Homo sapiens)	Nucleus
2385	19332n	pail4p_hs(n)	1-Phosphatidyl-1D-myo-inositol 4-phosphate (Homo sapiens)	Nucleus
2386	19479n	pail5p_hs(n)	1-Phosphatidyl-1D-myo-inositol 5-phosphate (Homo sapiens)	Nucleus
2387	19327n	pail_hs(n)	phosphatidylinositol (homo sapiens)	Nucleus
2388	5307n	peplys(n)	Peptidyl-L-lysine	Nucleus
2389	472n	pi(n)	Phosphate	Nucleus
2390	475n	ppi(n)	Diphosphate	Nucleus
2391	19580n	ppmi12346p(n)	5-Diphosphoinositol pentakisphosphate	Nucleus
2392	19581n	ppmi1346p(n)	Diphosphoinositol tetrakisphosphate	Nucleus
2393	2452n	pppi(n)	Inorganic triphosphate	Nucleus
2394	11153n	retn(n)	Retinoate	Nucleus
2395	4207n	seahcys(n)	Se-Adenosylselenohomocysteine	Nucleus
2396	4301n	seasmet(n)	Se-Adenosylselenomethionine	Nucleus
2397	135n	thbpt(n)	Tetrahydrobiopterin	Nucleus
2398	477n	udp(n)	UDP	Nucleus
2399	1068n	ump(n)	UMP	Nucleus
2400	10727n	uri(n)	Uridine	Nucleus
2401	345n	utp(n)	UTP	Nucleus
2402	3407r	11docrtsl(r)	11-Deoxycortisol	Endoplasmic Reticulum
2403	2404r	11docrtstrn(r)	11-Deoxycorticosterone	Endoplasmic Reticulum
2404	20447r	12harachd(r)	12 hydroxy arachidonic acid	Endoplasmic Reticulum
2405	22814r	13-cis-retn(r)	13-cis-retinoate	Endoplasmic Reticulum
2406	22816r	13-cis-retnglc(r)	13-cis-retinoyl glucuronide	Endoplasmic Reticulum
2407	3713r	17ahprgnlone(r)	17alpha-Hydroxypregnenolone	Endoplasmic Reticulum
2408	769r	17ahprgstrn(r)	17alpha-Hydroxyprogesterone	Endoplasmic Reticulum
2409	20446r	18harachd(r)	18 hydroxy arachidonic acid	Endoplasmic Reticulum

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
2410	9128r	44mctr(r)	4,4-dimethylcholesta-8,14,24-trienol	Endoplasmic Reticulum
2411	3689r	44mzym(r)	4,4-dimethylzymosterol	Endoplasmic Reticulum
2412	913r	4hpro-LT(r)	trans-4-Hydroxy-L-proline	Endoplasmic Reticulum
2413	9129r	4mzym_int1(r)	4-Methylzymosterol intermediate 1	Endoplasmic Reticulum
2414	9130r	4mzym_int2(r)	4-Methylzymosterol intermediate 2	Endoplasmic Reticulum
2415	10712r	5adtststerone(r)	5alpha-Dihydrotestosterone	Endoplasmic Reticulum
2416	22786r	5adtststeroneglc(r)	5alpha-Dihydrotestosterone glucuronide	Endoplasmic Reticulum
2417	20402r	6htststerone(r)	6 beta hydroxy testosterone	Endoplasmic Reticulum
2418	182r	6pgc(r)	6-Phospho-D-gluconate	Endoplasmic Reticulum
2419	963r	6pgl(r)	6-phospho-D-glucono-1,5-lactone	Endoplasmic Reticulum
2420	834r	7dhchsterol(r)	7-Dehydrocholesterol	Endoplasmic Reticulum
2421	15102r	Asn-X-Ser/Thr(r)	protein-linked asparagine residue (N-glycosylation site)	Endoplasmic Reticulum
2422	4293r	Ntmelys(r)	Protein N6,N6,N6-trimethyl-L-lysine	Endoplasmic Reticulum
2423	18469r	R1coa_hs(r)	R group 1 Coenzyme A homo sapiens	Endoplasmic Reticulum
2424	18470r	R2coa_hs(r)	R group 2 Coenzyme A homo sapiens	Endoplasmic Reticulum
2425	20362r	Ser-Gly/Ala-X-Gly(r)	protein-linked serine residue (glycosaminoglycan attachment site)	Endoplasmic Reticulum
2426	689r	Ssq23epx(r)	(S)-Squalene-2,3-epoxide	Endoplasmic Reticulum
2427	1052r	acald(r)	Acetaldehyde	Endoplasmic Reticulum
2428	11537r	accoa(r)	Acetyl-CoA	Endoplasmic Reticulum
2429	7471r	acrn(r)	O-Acetylcarnitine	Endoplasmic Reticulum
2430	471r	adp(r)	ADP	Endoplasmic Reticulum
2431	2661r	ahandrostan(r)	3alpha-Hydroxy-5beta-androstan-17-one	Endoplasmic Reticulum
2432	20819r	ahandrostanglc(r)	Etiocholan-3alpha-ol-17-one 3-glucuronide	Endoplasmic Reticulum
2433	310r	ahcys(r)	S-Adenosyl-L-homocysteine	Endoplasmic Reticulum
2434	314r	akg(r)	2-Oxoglutarate	Endoplasmic Reticulum
2435	1086r	amet(r)	S-Adenosyl-L-methionine	Endoplasmic Reticulum

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
2436	309r	amp(r)	AMP	Endoplasmic Reticulum
2437	2893r	andrstandn(r)	androstanedione	Endoplasmic Reticulum
2438	17675r	andrstndn(r)	Androstenedione	Endoplasmic Reticulum
2439	352r	andrstrn(r)	Androsterone	Endoplasmic Reticulum
2440	20815r	andrstrnglc(r)	androsterone glucuronide	Endoplasmic Reticulum
2441	11890r	arachd(r)	arachidonic acid	Endoplasmic Reticulum
2442	465r	atp(r)	ATP	Endoplasmic Reticulum
2443	4279r	bildglcur(r)	Bilirubin beta-diglucuronide	Endoplasmic Reticulum
2444	1942r	bilglcur(r)	Bilirubin monoglucuronide	Endoplasmic Reticulum
2445	101r	bilirub(r)	Bilirubin	Endoplasmic Reticulum
2446	10989r	bz(r)	Benzoate	Endoplasmic Reticulum
2447	11004r	cbp(r)	Carbamoyl phosphate	Endoplasmic Reticulum
2448	3369r	chlstol(r)	Cholesta-7,24-dien-3beta-ol	Endoplasmic Reticulum
2449	1075r	chol(r)	Choline	Endoplasmic Reticulum
2450	3507r	cholcoar(r)	3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestanoyl-CoA	Endoplasmic Reticulum
2451	17159r	cholcoas(r)	3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestanoyl-CoA(S)	Endoplasmic Reticulum
2452	252r	chsterol(r)	Cholesterol	Endoplasmic Reticulum
2453	26330r	chsterols(r)	cholesterol sulfate	Endoplasmic Reticulum
2454	474r	co2(r)	CO2	Endoplasmic Reticulum
2455	473r	coa(r)	Coenzyme A	Endoplasmic Reticulum
2456	559r	coke(r)	cocaine	Endoplasmic Reticulum
2457	11168r	cortsn(r)	Cortisone	Endoplasmic Reticulum
2458	19478r	crm_hs(r)	ceramide (homo sapiens)	Endoplasmic Reticulum
2459	163r	crn(r)	L-Carnitine	Endoplasmic Reticulum
2460	11268r	crtsl(r)	Cortisol	Endoplasmic Reticulum
2461	1737r	crtstrn(r)	Corticosterone	Endoplasmic Reticulum

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
2462	18537r	dag_hs(r)	diacylglycerol (homo sapiens)	Endoplasmic Reticulum
2463	3688r	ddsmsterol(r)	7-Dehydrodesmosterol	Endoplasmic Reticulum
2464	20042r	dem2emgacpail_prot_hs(r)	deacylated-(phosphoethanolaminyl-dimannosyl),(phosphoethanolaminyl)-mannosyl-glucosaminyl-acylphosphatidylinositol	Endoplasmic Reticulum
2465	20041r	dgpi_prot_hs(r)	deacylated-glycophosphatidylinositol (GPI)-anchored protein	Endoplasmic Reticulum
2466	3997r	dhcholestanate(r)	3alpha,7alpha-Dihydroxy-5beta-cholestanate	Endoplasmic Reticulum
2467	3322r	dhcholestancoa(r)	3alpha,7alpha-Dihydroxy-5beta-cholestanoyl-CoA	Endoplasmic Reticulum
2468	3377r	dhcholoylcoa(r)	3alpha,7alpha-Dihydroxy-5beta-cholest-24-enoyl-CoA	Endoplasmic Reticulum
2469	956r	dhea(r)	Dehydroepiandrosterone	Endoplasmic Reticulum
2470	3998r	dheas(r)	Dehydroepiandrosterone sulfate	Endoplasmic Reticulum
2471	14990r	doldp_L(r)	Dolichol diphosphate, human liver homolog	Endoplasmic Reticulum
2472	14991r	doldp_U(r)	Dolichol diphosphate, human uterine homolog	Endoplasmic Reticulum
2473	14992r	dolglcp_L(r)	Dolichyl beta-D-glucosyl phosphate, human liver homolog	Endoplasmic Reticulum
2474	14993r	dolglcp_U(r)	Dolichyl beta-D-glucosyl phosphate, human uterine homolog	Endoplasmic Reticulum
2475	14986r	dolichol_L(r)	Dolichol, human liver homolog	Endoplasmic Reticulum
2476	14987r	dolichol_U(r)	Dolichol, human uterine homolog	Endoplasmic Reticulum
2477	14994r	dolmanp_L(r)	Dolichyl phosphate D-mannose, human liver homolog	Endoplasmic Reticulum
2478	14995r	dolmanp_U(r)	Dolichyl phosphate D-mannose, human uterine homolog	Endoplasmic Reticulum
2479	14988r	dolp_L(r)	Dolichol phosphate, human liver homolog	Endoplasmic Reticulum
2480	14989r	dolp_U(r)	Dolichol phosphate, human uterine homolog	Endoplasmic Reticulum
2481	1463r	dsmsterol(r)	Desmosterol	Endoplasmic Reticulum
2482	3714r	eandrstrn(r)	epiandrosterone	Endoplasmic Reticulum
2483	20367r	ebastine(r)	ebastine	Endoplasmic Reticulum
2484	20368r	ebastineoh(r)	hydroxylated ebastine	Endoplasmic Reticulum
2485	19820r	ecgon(r)	ecgonine	Endoplasmic Reticulum
2486	19809r	egme(r)	ecgonine methyl ester	Endoplasmic Reticulum

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
2487	19995r	em2emgacpail_hs(r)	(phosphoethanolaminyl-dimannosyl),(phosphoethanolaminyl)-mannosyl-glucosaminyl-acylphosphatidylinositol (H7)	Endoplasmic Reticulum
2488	20040r	em2emgacpail_prot_hs(r)	(phosphoethanolaminyl-dimannosyl),(phosphoethanolaminyl)-mannosyl-glucosaminyl-acylphosphatidylinositol	Endoplasmic Reticulum
2489	19993r	em3gacpail_hs(r)	phosphoethanolaminyl-trimannosyl-glucosaminyl-acylphosphatidylinositol (H6')	Endoplasmic Reticulum
2490	19994r	emem2gacpail_hs(r)	(phosphoethanolaminyl-mannosyl),(phosphoethanolaminyl)-dimannosyl-glucosaminyl-acylphosphatidylinositol (H7')	Endoplasmic Reticulum
2491	19989r	emgacpail_hs(r)	phosphoethanolaminyl-mannosyl-glucosylaminyl-acylphosphatidylinositol (H5)	Endoplasmic Reticulum
2492	706r	estradiol(r)	Estradiol	Endoplasmic Reticulum
2493	20817r	estradiolglc(r)	estradiol glucuronide	Endoplasmic Reticulum
2494	3904r	estriol(r)	estriol	Endoplasmic Reticulum
2495	3415r	estriolglc(r)	16-Glucuronide-estriol	Endoplasmic Reticulum
2496	86r	estrone(r)	Estrone	Endoplasmic Reticulum
2497	20814r	estroneglc(r)	estrone glucuronide	Endoplasmic Reticulum
2498	2601r	estrones(r)	Estrone 3-sulfate	Endoplasmic Reticulum
2499	9020r	ethamp(r)	Ethanolamine phosphate	Endoplasmic Reticulum
2500	478r	fad(r)	Flavin adenine dinucleotide oxidized	Endoplasmic Reticulum
2501	42r	fadh2(r)	Flavin adenine dinucleotide reduced	Endoplasmic Reticulum
2502	334r	for(r)	Formate	Endoplasmic Reticulum
2503	10388r	frdp(r)	Farnesyl diphosphate	Endoplasmic Reticulum
2504	15443r	g1m6masnB1(r)	glucosyl-(alpha-D-mannosyl)6-beta-D-mannosyl-diacetylchitobiosyl-L-asparagine (protein)	Endoplasmic Reticulum
2505	15442r	g1m7masnB(r)	glucosyl-(alpha-D-mannosyl)7-beta-D-mannosyl-diacetylchitobiosyl-L-asparagine, isoform B (protein)	Endoplasmic Reticulum
2506	15441r	g1m7masnC(r)	glucosyl-(alpha-D-mannosyl)7-beta-D-mannosyl-diacetylchitobiosyl-L-asparagine, isoform C (protein)	Endoplasmic Reticulum
2507	15142r	g1m8masn(r)	(alpha-D-Glucosyl)-(alpha-D-mannosyl)8-beta-D-mannosyl-diacetylchitobiosyl-L-asparagine (protein)	Endoplasmic Reticulum
2508	15019r	g1m8mpdol_L(r)	alpha-D-Glucosyl-(alpha-D-mannosyl)8-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human liver homolog	Endoplasmic Reticulum

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
2509	15020r	g1m8mpdol_U(r)	alpha-D-Glucosyl-(alpha-D-mannosyl)8-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human uterine homolog	Endoplasmic Reticulum
2510	15138r	g2m8masn(r)	(alpha-D-Glucosyl)2-(alpha-D-mannosyl)8-beta-D-mannosyl-diacetylchitobiosyl-L-asparagine (protein)	Endoplasmic Reticulum
2511	15021r	g2m8mpdol_L(r)	(alpha-D-Glucosyl)2-(alpha-D-mannosyl)8-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human liver homolog	Endoplasmic Reticulum
2512	15022r	g2m8mpdol_U(r)	(alpha-D-Glucosyl)2-(alpha-D-mannosyl)8-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human uterine homolog	Endoplasmic Reticulum
2513	15115r	g3m8masn(r)	(alpha-D-Glucosyl)3-(alpha-D-mannosyl)8-beta-D-mannosyl-diacetylchitobiosyl-L-asparagine (protein)	Endoplasmic Reticulum
2514	15023r	g3m8mpdol_L(r)	(alpha-D-Glucosyl)3-(alpha-D-mannosyl)8-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human liver homolog	Endoplasmic Reticulum
2515	15024r	g3m8mpdol_U(r)	(alpha-D-Glucosyl)3-(alpha-D-mannosyl)8-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human uterine homolog	Endoplasmic Reticulum
2516	765r	g6p(r)	D-Glucose 6-phosphate	Endoplasmic Reticulum
2517	19963r	gacpail_hs(r)	glucosaminyl-acylphosphatidylinositol	Endoplasmic Reticulum
2518	18308r	glac(r)	D-glucurono-6,3-lactone	Endoplasmic Reticulum
2519	318r	glc-D(r)	D-Glucose	Endoplasmic Reticulum
2520	256r	glcur(r)	D-Glucuronate	Endoplasmic Reticulum
2521	313r	glu-L(r)	L-Glutamate	Endoplasmic Reticulum
2522	19613r	gluside_hs(r)	glucocerebroside (homo sapiens)	Endoplasmic Reticulum
2523	19996r	gpi_hs(r)	glycophosphatidylinositol (GPI) anchor precursor (3-(phosphoethanolaminyl-mannosyl)-glucosaminyl-acylphosphatidylinositol) (H8)	Endoplasmic Reticulum
2524	20035r	gpi_prot_hs(r)	glycophosphatidylinositol (GPI)-anchored protein	Endoplasmic Reticulum
2525	20039r	gpi_sig(r)	glycophosphatidylinositol (GPI) signal sequence (C-terminal peptide)	Endoplasmic Reticulum
2526	11388r	gthrd(r)	Reduced glutathione	Endoplasmic Reticulum
2527	677r	gullac(r)	L-Gulono-1,4-lactone	Endoplasmic Reticulum
2528	650r	guln(r)	L-Gulonate	Endoplasmic Reticulum
2529	1049r	h(r)	H+	Endoplasmic Reticulum
2530	317r	h2o(r)	H2O	Endoplasmic Reticulum

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
2531	297r	hdca(r)	Hexadecanoate (n-C16:0)	Endoplasmic Reticulum
2532	17864r	hemeBo(r)	Heme B oxidized	Endoplasmic Reticulum
2533	17865r	hemeBr(r)	Heme B reduced	Endoplasmic Reticulum
2534	20384r	hestratriol(r)	4,17 dihydroxy estradiol	Endoplasmic Reticulum
2535	191r	hmgcoa(r)	Hydroxymethylglutaryl-CoA	Endoplasmic Reticulum
2536	399r	hxdcal(r)	Hexadecanal	Endoplasmic Reticulum
2537	597r	lanost(r)	Lanosterol	Endoplasmic Reticulum
2538	755r	leuktrA4(r)	Leukotriene A4	Endoplasmic Reticulum
2539	1752r	leuktrB4(r)	Leukotriene B4	Endoplasmic Reticulum
2540	26340r	leuktrB4wcooh(r)	w-carboxy leukotriene B4	Endoplasmic Reticulum
2541	20365r	leuktrB4woh(r)	w-hydroxyl leukotriene B4	Endoplasmic Reticulum
2542	17887r	leuktrC4(r)	Leukotriene C4	Endoplasmic Reticulum
2543	4410r	leuktrD4(r)	Leukotriene D4	Endoplasmic Reticulum
2544	780r	lthstrl(r)	5alpha-Cholest-7-en-3beta-ol	Endoplasmic Reticulum
2545	20047r	m(em)3gacpail_hs(r)	mannosyl-3-(phosphoethanolaminyl-mannosyl)-glucosaminyl-acylphosphatidylinositol (M4A)	Endoplasmic Reticulum
2546	20052r	m(em)3gacpail_prot_hs(r)	mannosyl-3-(phosphoethanolaminyl-mannosyl)-glucosaminyl-acylphosphatidylinositol-Protein (M4A)	Endoplasmic Reticulum
2547	19991r	m2emgacpail_hs(r)	(dimannosyl),(phosphoethanolaminyl)-mannosyl-glucosylaminyl-acylphosphatidylinositol (H6)	Endoplasmic Reticulum
2548	19968r	m2gacpail_hs(r)	dimannosyl-glucosaminyl-acylphosphatidylinositol (H3)	Endoplasmic Reticulum
2549	20045r	m3emgacpail_hs(r)	(trimannosyl),(phosphoethanolaminyl)-mannosyl-glucosaminyl-acylphosphatidylinositol (M4C)	Endoplasmic Reticulum
2550	19992r	m3gacpail_hs(r)	trimannosyl-glucosaminyl-acylphosphatidylinositol (H4)	Endoplasmic Reticulum
2551	15008r	m4mpdol_L(r)	(alpha-D-Mannosyl)4-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human liver homolog	Endoplasmic Reticulum
2552	15009r	m4mpdol_U(r)	(alpha-D-Mannosyl)4-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human uterine homolog	Endoplasmic Reticulum
2553	15010r	m5mpdol_L(r)	(alpha-D-Mannosyl)5-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human liver homolog	Endoplasmic Reticulum
2554	15011r	m5mpdol_U(r)	(alpha-D-Mannosyl)5-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human uterine homolog	Endoplasmic Reticulum

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
2555	15012r	m6mpdol_L(r)	(alpha-D-Mannosyl)6-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human liver homolog	Endoplasmic Reticulum
2556	15013r	m6mpdol_U(r)	(alpha-D-Mannosyl)6-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human uterine homolog	Endoplasmic Reticulum
2557	15159r	m7masnB(r)	(alpha-D-mannosyl)7-beta-D-mannosyl-diacetylchitobiosyl-L-asparagine, isoform B (protein)	Endoplasmic Reticulum
2558	15014r	m7mpdol_L(r)	(alpha-D-Mannosyl)7-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human liver homolog	Endoplasmic Reticulum
2559	15016r	m7mpdol_U(r)	(alpha-D-Mannosyl)7-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human uterine homolog	Endoplasmic Reticulum
2560	15144r	m8masn(r)	(alpha-D-mannosyl)8-beta-D-mannosyl-diacetylchitobiosyl-L-asparagine (protein)	Endoplasmic Reticulum
2561	15017r	m8mpdol_L(r)	(alpha-D-Mannosyl)8-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human liver homolog	Endoplasmic Reticulum
2562	15018r	m8mpdol_U(r)	(alpha-D-Mannosyl)8-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human uterine homolog	Endoplasmic Reticulum
2563	11018r	man(r)	D-Mannose	Endoplasmic Reticulum
2564	20046r	mem2emgacpail_hs(r)	({[(mannosyl),(phosphoethanolaminyl)]-dimannosyl},{phosphoethanolaminyl})-mannosyl-glucosaminyl-acylphosphatidylinositol (M4B)	Endoplasmic Reticulum
2565	20051r	mem2emgacpail_prot_hs(r)	({[(mannosyl),(phosphoethanolaminyl)]-dimannosyl},{phosphoethanolaminyl})-mannosyl-glucosaminyl-acylphosphatidylinositol-Protein (M4B)	Endoplasmic Reticulum
2566	19990r	memgacpail_hs(r)	(mannosyl),(phosphoethanolaminyl)-mannosyl-glucosylaminyl-acylphosphatidylinositol (B)	Endoplasmic Reticulum
2567	1092r	meoh(r)	Methanol	Endoplasmic Reticulum
2568	418r	mev-R(r)	(R)-Mevalonate	Endoplasmic Reticulum
2569	19966r	mgacpail_hs(r)	mannosyl-glucosaminyl-acylphosphatidylinositiol (H2)	Endoplasmic Reticulum
2570	466r	nad(r)	Nicotinamide adenine dinucleotide	Endoplasmic Reticulum
2571	467r	nadh(r)	Nicotinamide adenine dinucleotide - reduced	Endoplasmic Reticulum
2572	469r	nadp(r)	Nicotinamide adenine dinucleotide phosphate	Endoplasmic Reticulum
2573	468r	nadph(r)	Nicotinamide adenine dinucleotide phosphate - reduced	Endoplasmic Reticulum
2574	476r	nh4(r)	Ammonium	Endoplasmic Reticulum
2575	470r	o2(r)	O2	Endoplasmic Reticulum

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
2576	18536r	pa_hs(r)	phosphatidic acid (homo sapiens)	Endoplasmic Reticulum
2577	19605r	pail34p_hs(r)	phosphatidylinositol-3,4-bisphosphate (Homo sapiens)	Endoplasmic Reticulum
2578	19704r	pail35p_hs(r)	phosphatidylinositol-3,5-bisphosphate (Homo sapiens)	Endoplasmic Reticulum
2579	3992r	pail3p_hs(r)	1-Phosphatidyl-1D-myo-inositol 3-phosphate (Homo sapiens)	Endoplasmic Reticulum
2580	19332r	pail4p_hs(r)	1-Phosphatidyl-1D-myo-inositol 4-phosphate (Homo sapiens)	Endoplasmic Reticulum
2581	19479r	pail5p_hs(r)	1-Phosphatidyl-1D-myo-inositol 5-phosphate (Homo sapiens)	Endoplasmic Reticulum
2582	19327r	pail_hs(r)	phosphatidylinositol (homo sapiens)	Endoplasmic Reticulum
2583	19051r	pchol_hs(r)	Phosphatidylcholine (homo sapiens)	Endoplasmic Reticulum
2584	19050r	pe_hs(r)	phosphatidylethanolamine (homo sapiens)	Endoplasmic Reticulum
2585	19967r	pecgon(r)	pseudoecgonine	Endoplasmic Reticulum
2586	19969r	pecgoncoa(r)	Pseudoecgonyl-CoA	Endoplasmic Reticulum
2587	22613r	pepslys(r)	peptide sans lysine	Endoplasmic Reticulum
2588	472r	pi(r)	Phosphate	Endoplasmic Reticulum
2589	475r	ppi(r)	Diphosphate	Endoplasmic Reticulum
2590	20038r	pre_prot(r)	glycophosphatidylinositol (GPI)-anchored protein precursor	Endoplasmic Reticulum
2591	10681r	prgnlone(r)	Pregnenolone	Endoplasmic Reticulum
2592	26331r	prgnlones(r)	pregnenolone sulfate	Endoplasmic Reticulum
2593	10510r	prgstrn(r)	Progesterone	Endoplasmic Reticulum
2594	229r	pro-L(r)	L-Proline	Endoplasmic Reticulum
2595	11382r	prostgd2(r)	Prostaglandin D2	Endoplasmic Reticulum
2596	398r	prostge2(r)	Prostaglandin E2	Endoplasmic Reticulum
2597	422r	prostgh2(r)	Prostaglandin H2	Endoplasmic Reticulum
2598	856r	prostgi2(r)	Prostaglandin I2	Endoplasmic Reticulum
2599	19052r	ps_hs(r)	phosphatidylserine (homo sapiens)	Endoplasmic Reticulum
2600	11153r	retn(r)	Retinoate	Endoplasmic Reticulum
2601	20818r	retnglc(r)	retinoyl glucuronide	Endoplasmic Reticulum

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
2602	261r	ru5p-D(r)	D-Ribulose 5-phosphate	Endoplasmic Reticulum
2603	335r	so4(r)	Sulfate	Endoplasmic Reticulum
2604	9025r	sph1p(r)	Sphinganine 1-phosphate	Endoplasmic Reticulum
2605	708r	sphgn(r)	Sphinganine	Endoplasmic Reticulum
2606	10703r	sphings(r)	Sphingosine	Endoplasmic Reticulum
2607	4541r	sphs1p(r)	Sphingosine 1-phosphate	Endoplasmic Reticulum
2608	519r	sql(r)	Squalene	Endoplasmic Reticulum
2609	325r	succ(r)	Succinate	Endoplasmic Reticulum
2610	3477r	thcholstoic(r)	3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestanoate	Endoplasmic Reticulum
2611	2907r	tmlys(r)	N6,N6,N6-Trimethyl-L-lysine	Endoplasmic Reticulum
2612	10622r	tststerone(r)	Testosterone	Endoplasmic Reticulum
2613	20816r	tststeroneglc(r)	testosterone glucuronide	Endoplasmic Reticulum
2614	1777r	txa2(r)	Thromboxane A2	Endoplasmic Reticulum
2615	477r	udp(r)	UDP	Endoplasmic Reticulum
2616	10912r	udpacgal(r)	UDP-N-acetyl-D-galactosamine	Endoplasmic Reticulum
2617	316r	udpg(r)	UDPglucose	Endoplasmic Reticulum
2618	241r	udpglcur(r)	UDP-D-glucuronate	Endoplasmic Reticulum
2619	255r	udpxyl(r)	UDP-D-xylose	Endoplasmic Reticulum
2620	1068r	ump(r)	UMP	Endoplasmic Reticulum
2621	20366r	wharachd(r)	w-hydroxyl arachidonic acid	Endoplasmic Reticulum
2622	20403r	whtststerone(r)	w hydroxy testosterone	Endoplasmic Reticulum
2623	17046r	xol24oh(r)	24-Hydroxycholesterol	Endoplasmic Reticulum
2624	17047r	xol25oh(r)	25-Hydroxycholesterol	Endoplasmic Reticulum
2625	4060r	xol27oh(r)	27-Hydroxycholesterol	Endoplasmic Reticulum
2626	11131r	xol7a(r)	7 alpha-Hydroxycholesterol	Endoplasmic Reticulum
2627	3381r	xol7ah2(r)	3alpha,7alpha-Dihydroxy-5beta-cholestane	Endoplasmic Reticulum

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
2628	11535r	xol7aone(r)	7alpha-Hydroxycholest-4-en-3-one	Endoplasmic Reticulum
2629	3384r	xoldiolone(r)	7alpha,12alpha-Dihydroxycholest-4-en-3-one	Endoplasmic Reticulum
2630	2593r	xolest_hs(r)	cholesterol ester	Endoplasmic Reticulum
2631	17068r	xoltri24(r)	7-alpha,24(S)-Dihydroxycholesterol	Endoplasmic Reticulum
2632	17067r	xoltri25(r)	7-alpha,25-Dihydroxycholesterol	Endoplasmic Reticulum
2633	4061r	xoltri27(r)	7-alpha,27-Dihydroxycholesterol	Endoplasmic Reticulum
2634	3383r	xoltriol(r)	3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestane	Endoplasmic Reticulum
2635	20363r	xser(r)	Xyl-L-Ser (protein)	Endoplasmic Reticulum
2636	9132r	zym_int2(r)	zymosterol intermediate 2	Endoplasmic Reticulum
2637	3367r	zymst(r)	zymosterol	Endoplasmic Reticulum
2638	10801r	zymstnl(r)	Zymostenol	Endoplasmic Reticulum
2639	11156x	1p2cbxl(x)	1-Pyrroline-2-carboxylate	Peroxisome
2640	3121x	1pipdn2c(x)	delta1-Piperideine-2-carboxylate	Peroxisome
2641	19703x	3h26dm5coa(x)	3-Hydroxy-2,6-dimethyl-5-methylene-heptanoyl-CoA	Peroxisome
2642	905x	3hbcoa(x)	(S)-3-Hydroxybutanoyl-CoA	Peroxisome
2643	4184x	3hpcoa(x)	3-Hydroxypropionyl-CoA	Peroxisome
2644	3794x	3odcoa(x)	3-Oxodecanoyl-CoA	Peroxisome
2645	3792x	3oddcoa(x)	3-Oxododecanoyl-CoA	Peroxisome
2646	3788x	3ohdcoa(x)	3-Oxohexadecanoyl-CoA	Peroxisome
2647	8402x	3ohodcoa(x)	3-Oxooctadecanoyl-CoA	Peroxisome
2648	9236x	3ohxccoa(x)	3-Oxohexacosyl-CoA	Peroxisome
2649	3790x	3otdcoa(x)	3-Oxotetradecanoyl-CoA	Peroxisome
2650	10559x	5a2opntn(x)	5-Amino-2-oxopentanoate	Peroxisome
2651	10525x	5dpmev(x)	(R)-5-Diphosphomevalonate	Peroxisome
2652	2892x	5g2oxpt(x)	5-Guanidino-2-oxopentanoate	Peroxisome
2653	883x	5pmev(x)	(R)-5-Phosphomevalonate	Peroxisome
2654	2428x	6a2ohxnt(x)	6-Amino-2-oxohexanoate	Peroxisome
2655	411x	Lpipecol(x)	L-Pipecolate	Peroxisome
2656	18523x	Rtotal(x)	R total	Peroxisome
2657	22165x	Rtotalcoa(x)	R total Coenzyme A	Peroxisome
2658	174x	aacoa(x)	Acetoacetyl-CoA	Peroxisome
2659	9016x	acac(x)	Acetoacetate	Peroxisome
2660	1052x	acald(x)	Acetaldehyde	Peroxisome
2661	11537x	accoa(x)	Acetyl-CoA	Peroxisome
2662	7471x	acrn(x)	O-Acetylcarnitine	Peroxisome
2663	18534x	adhap_hs(x)	acyl-dihydroxyacetone phosphate	Peroxisome
2664	471x	adp(x)	ADP	Peroxisome
2665	18463x	adrn(x)	adrenic acid	Peroxisome
2666	18484x	adrncoa(x)	adrenyl coenzyme A	Peroxisome
2667	19357x	akdhap_hs(x)	1-alkyldihydroxyacetone phosphate	Peroxisome
2668	314x	akg(x)	2-Oxoglutarate	Peroxisome

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
2669	1093x	ala-D(x)	D-Alanine	Peroxisome
2670	11412x	ala-L(x)	L-Alanine	Peroxisome
2671	19356x	alkylR1oh(x)	hydroxy alkyl chain	Peroxisome
2672	309x	amp(x)	AMP	Peroxisome
2673	18483x	arachcoa(x)	arachidyl coenzyme A	Peroxisome
2674	11887x	arachdcoa(x)	C20:4-CoA	Peroxisome
2675	644x	arg-D(x)	D-Arginine	Peroxisome
2676	10519x	asp-D(x)	D-Aspartate	Peroxisome
2677	465x	atp(x)	ATP	Peroxisome
2678	733x	b2coa(x)	Crotonoyl-CoA	Peroxisome
2679	11888x	c226coa(x)	cervonyl coenzyme A	Peroxisome
2680	19701x	c2m26dcoa(x)	cis-2-Methyl-5-isopropylhexa-2,5-dienoyl-CoA	Peroxisome
2681	10881x	cholcoa(x)	Choloyl-CoA	Peroxisome
2682	3386x	cholcoads(x)	3alpha,7alpha,12alpha-Trihydroxy-5beta-cholest-24-enoyl-CoA	Peroxisome
2683	3391x	cholcoaone(x)	3alpha,7alpha,12alpha-Trihydroxy-5beta-24-oxocholestanoyl-CoA	Peroxisome
2684	3507x	cholcoar(x)	3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestanoyl-CoA	Peroxisome
2685	17159x	cholcoas(x)	3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestanoyl-CoA(S)	Peroxisome
2686	18488x	clpndcoa(x)	clupanodonyl CoA	Peroxisome
2687	474x	co2(x)	CO2	Peroxisome
2688	473x	coa(x)	Coenzyme A	Peroxisome
2689	163x	crn(x)	L-Carnitine	Peroxisome
2690	3803x	dcacoa(x)	Decanoyl-CoA (n-C10:0CoA)	Peroxisome
2691	3848x	dcholcoa(x)	chenodeoxycholoyl coenzyme a	Peroxisome
2692	18487x	dcsptn1coa(x)	docosa-4,7,10,13,16-pentaenoyl coenzyme A	Peroxisome
2693	1383x	ddcacoa(x)	Dodecanoyl-CoA (n-C12:0CoA)	Peroxisome
2694	3387x	dgchol(x)	Chenodeoxyglycocholate	Peroxisome
2695	11531x	dgcholcoa(x)	Chenodeoxyglycocholoyl-CoA	Peroxisome
2696	1072x	dhap(x)	Dihydroxyacetone phosphate	Peroxisome
2697	3997x	dhcholestanate(x)	3alpha,7alpha-Dihydroxy-5beta-cholestanate	Peroxisome
2698	3322x	dhcholestancoa(x)	3alpha,7alpha-Dihydroxy-5beta-cholestanoyl-CoA	Peroxisome
2699	3377x	dhcholoylcoa(x)	3alpha,7alpha-Dihydroxy-5beta-cholest-24-enoyl-CoA	Peroxisome
2700	3376x	dhocholoylcoa(x)	3alpha,7alpha,12alpha,26-Tetrahydroxy-5beta-cholestane	Peroxisome
2701	21959x	dmnoncoa(x)	4,8 dimethylnonanoyl-CoA	Peroxisome
2702	21976x	dmnoncrn(x)	4,8 dimethylnonanoyl carnitine	Peroxisome
2703	38x	dmpp(x)	Dimethylallyl diphosphate	Peroxisome
2704	87x	etoh(x)	Ethanol	Peroxisome
2705	478x	fad(x)	Flavin adenine dinucleotide oxidized	Peroxisome
2706	42x	fadh2(x)	Flavin adenine dinucleotide reduced	Peroxisome
2707	340x	fald(x)	Formaldehyde	Peroxisome
2708	11122x	formcoa(x)	Formyl-CoA	Peroxisome
2709	10388x	frdp(x)	Farnesyl diphosphate	Peroxisome
2710	1554x	gchola(x)	glycocholate	Peroxisome
2711	11524x	gdchola(x)	glycochenodeoxycholate	Peroxisome
2712	329x	glx(x)	Glyoxylate	Peroxisome
2713	323x	gly(x)	Glycine	Peroxisome
2714	237x	glyclt(x)	Glycolate	Peroxisome

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
2715	179x	grdp(x)	Geranyl diphosphate	Peroxisome
2716	1049x	h(x)	H+	Peroxisome
2717	317x	h2o(x)	H2O	Peroxisome
2718	315x	h2o2(x)	Hydrogen peroxide	Peroxisome
2719	297x	hdca(x)	Hexadecanoate (n-C16:0)	Peroxisome
2720	3801x	hdd2coa(x)	trans-Hexadec-2-enoyl-CoA	Peroxisome
2721	11013x	hexccoa(x)	Hexacosanoyl-CoA (n-C26:0CoA)	Peroxisome
2722	191x	hmgcoa(x)	Hydroxymethylglutaryl-CoA	Peroxisome
2723	242x	hpyr(x)	Hydroxypyruvate	Peroxisome
2724	218x	hxan(x)	Hypoxanthine	Peroxisome
2725	158x	icit(x)	Isocitrate	Peroxisome
2726	1089x	ipdp(x)	Isopentenyl diphosphate	Peroxisome
2727	18490x	lgnccoa(x)	lignocericyl coenzyme A	Peroxisome
2728	2277x	lnlncgcoa(x)	gamma-linolenoyl-CoA	Peroxisome
2729	328x	lys-L(x)	L-Lysine	Peroxisome
2730	11267x	malcoa(x)	Malonyl-CoA	Peroxisome
2731	418x	mev-R(x)	(R)-Mevalonate	Peroxisome
2732	451x	mmcoa-S(x)	(S)-Methylmalonyl-CoA	Peroxisome
2733	1023x	na1(x)	Sodium	Peroxisome
2734	466x	nad(x)	Nicotinamide adenine dinucleotide	Peroxisome
2735	467x	nadh(x)	Nicotinamide adenine dinucleotide - reduced	Peroxisome
2736	469x	nadp(x)	Nicotinamide adenine dinucleotide phosphate	Peroxisome
2737	468x	nadph(x)	Nicotinamide adenine dinucleotide phosphate - reduced	Peroxisome
2738	476x	nh4(x)	Ammonium	Peroxisome
2739	18485x	nrvnccoa(x)	nervonyl coenzyme A	Peroxisome
2740	470x	o2(x)	O2	Peroxisome
2741	461x	o2s(x)	Superoxide anion	Peroxisome
2742	322x	oaa(x)	Oxaloacetate	Peroxisome
2743	10688x	occoa(x)	Octanoyl-CoA (n-C8:0CoA)	Peroxisome
2744	8782x	odecoa(x)	Octadecenoyl-CoA (n-C18:1CoA)	Peroxisome
2745	19415x	orn-D(x)	D-Ornithine	Peroxisome
2746	10901x	oxa(x)	Oxalate	Peroxisome
2747	15675x	pcrn(x)	propionyl-carnitine	Peroxisome
2748	1308x	phyt(x)	phytanic acid	Peroxisome
2749	21956x	phyt2ohcoa(x)	2-Hydroxyphytanoyl-CoA	Peroxisome
2750	21953x	phytcoa(x)	phytanyl coa	Peroxisome
2751	472x	pi(x)	Phosphate	Peroxisome
2752	11029x	pmtcoa(x)	Palmitoyl-CoA (n-C16:0CoA)	Peroxisome
2753	1064x	ppcoa(x)	Propanoyl-CoA	Peroxisome
2754	475x	ppi(x)	Diphosphate	Peroxisome
2755	21954x	prist(x)	pristanic acid	Peroxisome
2756	21957x	pristanal(x)	pristanal	Peroxisome
2757	21955x	pristcoa(x)	pristanoyl coa	Peroxisome
2758	629x	pro-D(x)	D-Proline	Peroxisome
2759	744x	prpncoa(x)	Propenoyl-CoA	Peroxisome
2760	311x	pyr(x)	Pyruvate	Peroxisome
2761	271x	sarcs(x)	Sarcosine	Peroxisome
2762	339x	ser-L(x)	L-Serine	Peroxisome
2763	8781x	stcoa(x)	Stearoyl-CoA (n-C18:0CoA)	Peroxisome
2764	18492x	strdnccoa(x)	stearidonyl coenzyme A	Peroxisome
2765	325x	succ(x)	Succinate	Peroxisome
2766	19702x	t2m26dcoa(x)	trans-2-Methyl-5-isopropylhexa-2,5-dienoyl-CoA	Peroxisome

Row	Metabolite #	Abbreviation	Metabolite Name	Compartment
2767	293x	taur(x)	Taurine	Peroxisome
2768	3700x	tchola(x)	taurocholic acid	Peroxisome
2769	3390x	tdchola(x)	taurochenodeoxycholate	Peroxisome
2770	1862x	tdcoa(x)	Tetradecanoyl-CoA (n-C14:0CoA)	Peroxisome
2771	18515x	tethex3coa(x)	tetracosahexaenoyl coenzyme A	Peroxisome
2772	18513x	tetpent3coa(x)	tetracosapentaenoyl coenzyme A, n-3	Peroxisome
2773	18509x	tetpent6coa(x)	tetracosapentaenoyl coenzyme A, n-6	Peroxisome
2774	18511x	tettet6coa(x)	tetracosatetraenoyl coenzyme A	Peroxisome
2775	3378x	thcholoylcoa(x)	3alpha,7alpha,24-Trihydroxy-5beta-cholestanoyl-CoA	Peroxisome
2776	3477x	thcholstoic(x)	3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestanoate	Peroxisome
2777	75x	thp2c(x)	2,3,4,5-Tetrahydropyridine-2-carboxylate	Peroxisome
2778	18486x	tmndnccoa(x)	timnodonyl coenzyme A	Peroxisome
2779	8904x	ttccoa(x)	tetracosanoyl-CoA (n-C24:0CoA)	Peroxisome
2780	199x	urate(x)	Urate	Peroxisome
2781	216x	xan(x)	Xanthine	Peroxisome

Table 4: Columns of the stoichiometric matrix (reactions). Ordered list of reactions in the stoichiometric matrix used in the debugging simulations (SI Table 2). Reaction # is a nonredundant identifier used to denote each reaction.

Column	Reaction #	Abbreviation	Reaction Name
1	19551	DM_13-cis-oretn(n)	13-cis-oxo-retinoic acid demand
2	19552	DM_13-cis-retn(n)	13-cis-retinoate demand
3	14122	DM_3aib(c)	DM_3aib(c)
4	20466	DM_Asn-X-Ser/Thr(ly)	DM_Asn-X-Ser/Thr(ly)
5	15019	DM_LINKDEGly	demand reaction for lysosomal degradation of proteoglycan linkage
6	20471	DM_Ser-Gly/Ala-X-Gly(ly)	DM_Ser-Gly/Ala-X-Gly(ly)
7	20470	DM_Ser/Thr(ly)	DM_Ser/Thr(ly)
8	13303	DM_accoa/nadh/co2	pyruvate decarboxylation
9	13304	DM_accoa/nadh/co2(m)	pyruvate decarboxylation
10	14117	DM_ala-B(c)	DM_ala-B(c)
11	2318	DM_amp	DM_amp
12	1012	DM_atp(c)	atp demand
13	4317	DM_atp2(c)	atp demand
14	20250	DM_avite1(c)	alpha-Tocopherol demand
15	20251	DM_avite2(c)	alpha-Tocotrienol demand
16	20252	DM_bvite(c)	beta-tocopherol demand
17	923	DM_coa(c)	Coenzyme A demand
18	14811	DM_dag_hs	dag_hs demand
19	19371	DM_datp(m)	dATP demand
20	14129	DM_datp(n)	DM_datp(n)
21	19372	DM_dctp(m)	dCTP demand
22	14128	DM_dctp(n)	DM_dctp(n)
23	14152	DM_dgtp(m)	DM_dgtp(m)
24	14130	DM_dgtp(n)	DM_dgtp(n)
25	941	DM_dhap(c)	Dihydroxyacetone phosphate demand
26	20467	DM_dsT_antigen(g)	DM_dsT_antigen(g)
27	19373	DM_dttp(m)	dTTP demand
28	14131	DM_dttp(n)	DM_dttp(n)
29	20347	DM_ethamp(r)	Ethanolamine phosphate demand
30	13542	DM_fadh(m)	fadh demand
31	13502	DM_g3p(c)	DM_g3p(c)
32	13381	DM_glc(c)	glucose demand
33	13438	DM_glcur	glucuronate demand
34	2319	DM_gmp(c)	DM_gmp(c)
35	20468	DM_gpi_sig(er)	DM_gpi_sig(er)
36	9284	DM_gtp2	gtp demand 2
37	13437	DM_guln	gulonate demand
38	14928	DM_ha(e)	DM_ha(e)
39	19553	DM_hretn(n)	4 hydroxy retinoic acid demand
40	9272	DM_imp	imp demand
41	20469	DM_kdn(c)	DM_kdn(c)
42	13300	DM_lac-D/atp/h2o	anaerobic glycolysis demand
43	14742	DM_malcoa(m)	malcoa demand
44	20464	DM_melanin(c)	DM_melanin(c)
45	19554	DM_oretn(n)	4-oxo-retonoic acid demand
46	14576	DM_pydx5p(c)	DM_pydx5p(c)
47	945	DM_pyr(c)	Pyruvate demand
48	10039	DM_pyr(m)	Pyruvate demand
49	14230	DM_q10(c)	DM_q10(c)
50	14233	DM_q10(m)	DM_q10(m)
51	20472	DM_sTn_antigen(g)	DM_sTn_antigen(g)
52	20463	DM_sprm(c)	DM_sprm(c)
53	14076	DM_thmpp(c)	Thiamin pyrophosphate demand
54	14071	DM_thmpp(m)	Thiamin pyrophosphate demand
55	3013	DM_uacgam(c)	uacgam demand

Column	Reaction #	Abbreviation	Reaction Name
56	2321	DM_ump(c)	DM_cmp(c)
57	14086	DM_urate(x)	DM_urate(x)
58	20253	DM_yvite(c)	gamma-Tocopherol demand
59	14932	HADEGly	hyaluronan degradation demand function
60	13327	M_amet	amet maintenance reaction
61	14801	NGLYDEGly	N-glycan degradation optimization function, lysosomal
62	10533	sink_urea	sink_urea
63	12730	EX_10fthf(e)	10-Formyltetrahydrofolate exchange
64	14905	EX_10fthf5glu(e)	10-formyltetrahydrofolate-[Glu](5) exchange
65	14906	EX_10fthf6glu(e)	10-formyltetrahydrofolate-[Glu](6) exchange
66	14907	EX_10fthf7glu(e)	10-formyltetrahydrofolate-[Glu](7) exchange
67	15122	EX_11-cis-retfa(e)	fatty acid 11-cis-retinol exchange
68	20388	EX_13-cis-retnglc(e)	13-cis-retinoyl glucuronide exchange
69	14077	EX_1glyc_hs(e)	1 acyl phosphoglycerol exchange
70	10938	EX_1mncam(e)	1-Methylnicotinamide exchange
71	11640	EX_2425dhvitd2(e)	24R,25-Dihyoxyvitamin D2 exchange
72	11641	EX_2425dhvitd3(e)	24R,25-Dihydroxyvitamin D3 exchange
73	20437	EX_24nph(e)	2,4 dihydroxy nitrophenol exchange
74	11642	EX_25hvitd2(e)	25-Hydroxyvitamin D2 exchange
75	11643	EX_25hvitd3(e)	25-Hydroxyvitamin D3 exchange
76	12491	EX_2hb(e)	2-Hydroxybutyrate exchange
77	20839	EX_2mcit(e)	2-Methylcitrate exchange
78	14613	EX_34dhoxpeg(e)	3,4-Dihydroxyphenylethyleneglycol exchange
79	12585	EX_34dhphe(e)	3,4-Dihydroxy-L-phenylalanine exchange
80	12627	EX_35cgmp(e)	3',5'-Cyclic GMP exchange
81	12085	EX_3aib(e)	L-3-Amino-isobutanoate exchange
82	20419	EX_3aib-D(e)	D-3-Amino-isobutanoate exchange
83	14614	EX_3mlda(e)	3-Methylimidazoleacetic acid exchange
84	827	EX_4abut(e)	4-Aminobutanoate exchange
85	20408	EX_4hdebrisoquine(e)	4 hydroxy debrisoquine exchange
86	9538	EX_4hphac(e)	4-Hydroxyphenylacetate exchange
87	20425	EX_4mtolbutamide(e)	4 hydroxy tolbutamide exchange
88	20431	EX_4nph(e)	4-Nitrophenol exchange
89	20432	EX_4nphsf(e)	4-Nitrophenyl sulfate exchange
90	11003	EX_4pyrdx(e)	4-Pyridoxate exchange
91	20374	EX_5adtststerone(e)	5alpha-Dihydrotestosterone exchange
92	20377	EX_5adtststeroneglc(e)	5alpha-Dihydrotestosterone glucuronide exchange
93	20387	EX_5adtststerones(e)	5alpha-Dihydrotestosterone sulfate exchange
94	14908	EX_5dhf(e)	pentaglutamyl folate (DHF) exchange
95	14840	EX_5fthf(e)	5-Formyltetrahydrofolate exchange
96	20414	EX_5homeprazole(e)	5 hydroxy omeprazole exchange
97	12034	EX_5htrp(e)	5-Hydroxy-L-tryptophan exchange
98	14841	EX_5mthf(e)	5-Methyltetrahydrofolate exchange
99	14909	EX_5thf(e)	pentaglutamyl folate (THF) exchange
100	14910	EX_6dhf(e)	haxglutamyl folate (DHF) exchange
101	20433	EX_6htststerone(e)	6 beta hydroxy testosterone exchange
102	14911	EX_6thf(e)	hexaglutamyl folate (THF) exchange
103	14912	EX_7dhf(e)	heptaglutamyl folate (DHF) exchange
104	14913	EX_7thf(e)	heptaglutamyl folate (THF) exchange
105	15123	EX_9-cis-retfa(e)	fatty acid 9-cis-retinol exchange
106	12499	EX_CLPND(e)	clupanodonic acid (docosapentaenoic (n-3)) exchange
107	12035	EX_Lcystin(e)	L-Cystine exchange
108	14078	EX_Rtotal(e)	R total exchange
109	12138	EX_Rtotal2(e)	R total 2 position exchange
110	12139	EX_Rtotal3(e)	R total 3 position exchange

Column	Reaction #	Abbreviation	Reaction Name
111	10421	EX_Tyr-ggn(e)	Tyr-194 of apo-glycogenin protein (primer for glycogen synthesis) exchange
112	2300	EX_abt(e)	L-Arabinitol exchange
113	828	EX_ac(e)	Acetate exchange
114	3659	EX_acac(e)	Acetoacetate exchange
115	1456	EX_acald(e)	Acetaldehyde exchange
116	12492	EX_acetone(e)	Acetone exchange
117	20442	EX_acgalfucgalacgalfuc12gal14acglcgalgluside_hs(e)	Type IIIA glycolipid exchange
118	20356	EX_acgalfucgalacgalfucgalacglcgal14acglcgalgluside_hs(e)	Type IIIAb exchange
119	1045	EX_acgam(e)	N-Acetyl-D-glucosamine exchange
120	12036	EX_ach(e)	Acetylcholine exchange
121	20380	EX_acn13acngalgbside_hs(e)	sialyl (1,3) sialyl (2,6) galactosylgloboside (homo sapiens) exchange
122	20381	EX_acn23acngalgbside_hs(e)	sialyl (2,3) sialyl (2,6) galactosylgloboside (homo sapiens) exchange
123	20383	EX_acnacngal14acglcgalgluside_hs(e)	3',8'-LD1 exchange
124	20385	EX_acnacngalgbside_hs(e)	disialyl galactosylgloboside (homo sapiens) exchange
125	20386	EX_acngalacglcgal14acglcgalgluside_hs(e)	VI3NeuAc-nLc6Cer exchange
126	826	EX_ade(e)	Adenine exchange
127	758	EX_adn(e)	Adenosine exchange
128	4069	EX_adp	adp exchange
129	15038	EX_adprbp(e)	ADPribose 2'-phosphate exchange
130	15039	EX_adprib(e)	ADPribose exchange
131	12493	EX_adrn(e)	adrenic acid exchange
132	12037	EX_adrnl(e)	Adrenaline exchange
133	20427	EX_aflatoxin(e)	aflatoxin B1 exchange
134	20430	EX_ahandrostanglc(e)	Etiocholan-3alpha-ol-17-one 3-glucuronide exchange
135	15040	EX_ak2lgchol_hs(e)	1-alkyl 2-lysoglycerol 3-phosphocholine exchange
136	829	EX_akg(e)	2-Oxoglutarate exchange
137	8154	EX_ala-B(e)	beta-Alanine exchange
138	1064	EX_ala-D(e)	D-Alanine exchange
139	830	EX_ala-L(e)	L-Alanine exchange
140	20353	EX_aldstrn(e)	Aldosterone exchange
141	2026	EX_amp(e)	AMP exchange
142	20357	EX_andrstrn(e)	Androsterone exchange
143	20359	EX_andrstrnglc(e)	androsterone glucuronide exchange
144	20361	EX_antipyrene(e)	antipyrene exchange
145	20364	EX_apnnox(e)	alpha-Pinene-oxide exchange
146	20365	EX_appnn(e)	(+)-alpha-Pinene exchange
147	20368	EX_aprgstrn(e)	20alpha-Hydroxyprogesterone exchange
148	14705	EX_aqcobal(e)	Aquacob(III)alamin exchange
149	680	EX_arab-L(e)	L-Arabinose exchange
150	12494	EX_arach(e)	Arachidic acid exchange
151	4039	EX_arachd(e)	nC20:4 exchange
152	831	EX_arg-L(e)	L-Arginine exchange
153	8153	EX_ascb-L(e)	L-Ascorbate exchange
154	832	EX_asn-L(e)	L-Asparagine exchange
155	12038	EX_asp-D(e)	D-Aspartate exchange
156	833	EX_asp-L(e)	L-Aspartate exchange

Column	Reaction #	Abbreviation	Reaction Name
157	4147	EX_atp(e)	ATP exchange
158	11644	EX_avite1(e)	alpha-Tocopherol exchange
159	11645	EX_avite2(e)	alpha-Tocotrienol exchange
160	5492	EX_bhb(e)	(R)-3-Hydroxybutanoate transport via H+ symport
161	12495	EX_bildglcur(e)	Bilirubin beta-diglucuronide exchange
162	12496	EX_bilglcur(e)	Bilirubin monoglucuronide exchange
163	8476	EX_bilirub(e)	Bilirubin exchange
164	10939	EX_biocyt(e)	Biocytin exchange
165	1608	EX_btn(e)	Biotin exchange
166	2629	EX_but(e)	Butyrate (n-C4:0) exchange
167	11646	EX_bvite(e)	beta-tocopherol exchange
168	20920	EX_bz(e)	Benzoate exchange
169	8748	EX_ca2(e)	Calcium exchange
170	12628	EX_camp(e)	cAMP exchange
171	11004	EX_caro(e)	beta-Carotene exchange
172	20348	EX_carveol(e)	(E)-carveol exchange
173	11647	EX_cca_d3(e)	Calcitroic acid (D3) exchange
174	10940	EX_cgly(e)	Cys-Gly exchange
175	1047	EX_chol(e)	Choline exchange
176	12497	EX_cholate(e)	Cholate exchange
177	12629	EX_chsterol(e)	Cholesterol exchange
178	10942	EX_chtn(e)	chitin exchange
179	1048	EX_cit(e)	Citrate exchange
180	9537	EX_cl(e)	Chloride exchange
181	10943	EX_cmp(e)	CMP exchange
182	8580	EX_co(e)	Carbon monoxide exchange
183	805	EX_co2(e)	CO2 exchange
184	20382	EX_coumarin(e)	coumarin exchange
185	12039	EX_creat(e)	Creatine exchange
186	20384	EX_crmp_hs(e)	Ceramide 1-phosphate exchange
187	706	EX_crn(e)	L-Carnitine exchange
188	4040	EX_crvnc(e)	nC22:6 exchange
189	835	EX_csn(e)	Cytosine exchange
190	14974	EX_cspg_a(e)	chondroitin sulfate A (GalNAc4S-GlcA) proteoglycan exchange
191	14975	EX_cspg_b(e)	chondroitin sulfate B / dermatan sulfate (IdoA2S-GalNAc4S) proteoglycan exchange
192	14976	EX_cspg_c(e)	chondroitin sulfate C (GalNAc6S-GlcA) proteoglycan exchange
193	14979	EX_cspg_d(e)	chondroitin sulfate D (GlcNAc6S-GlcA2S) proteoglycan exchange
194	14973	EX_cspg_e(e)	chondroitin sulfate E (GalNAc4,6diS-GlcA) proteoglycan exchange
195	13944	EX_cyan(e)	Hydrogen cyanide exchange
196	1065	EX_cys-L(e)	L-Cysteine exchange
197	836	EX_cytd(e)	Cytidine exchange
198	4137	EX_dad-2(e)	Deoxyadenosine exchange
199	10422	EX_dad-5(e)	5'-Deoxyadenosine exchange
200	12133	EX_dag_hs(e)	diacylglycerol (homo sapiens) exchange
201	12498	EX_dcsptn1(e)	docosa-4,7,10,13,16-pentaenoic acid (n-6) exchange
202	837	EX_dcyt(e)	Deoxycytidine exchange
203	12500	EX_debrisoquine(e)	debrisoquine exchange
204	20446	EX_dgchol(e)	Chenodeoxyglycocholate exchange
205	1610	EX_dgsn(e)	Deoxyguanosine exchange
206	12040	EX_dhdascb(e)	Dehydroascorbate exchange
207	12501	EX_dheas(e)	Dehydroepiandrosterone sulfate exchange

Column	Reaction #	Abbreviation	Reaction Name
208	14914	EX_dhf(e)	7,8-Dihydrofolate exchange
209	20358	EX_digalsgalside_hs(e)	Digalactosylceramidesulfate exchange
210	1611	EX_din(e)	Deoxyinosine exchange
211	12502	EX_dlnlcg(e)	dihomo-gamma-linolenic acid (n-6) exchange
212	20362	EX_dmantipyrine(e)	demethylated antipyrine exchange
213	20363	EX_dmhptcrn(e)	2,6 dimethylheptanoyl carnitine exchange
214	12041	EX_dopa(e)	Dopamine exchange
215	19506	EX_dopasf(e)	Dopamine 3-O-sulfate exchange
216	20366	EX_drib(e)	Deoxyribose exchange
217	1066	EX_duri(e)	Deoxyuridine exchange
218	20369	EX_eaflatoxin(e)	8,9 epxoy aflatoxin B1 exchange
219	20372	EX_ebastine(e)	ebastine exchange
220	20373	EX_ebastineoh(e)	hydroxylated ebastine exchange
221	12503	EX_eicostet(e)	eicosatetranoic acid exchange
222	12504	EX_elaid(e)	elaidic acid exchange
223	12505	EX_estradiolglc(e)	estradiol glucuronide exchange
224	20379	EX_estriolglc(e)	16-Glucuronide-estriol exchange
225	14079	EX_estroneglc(e)	estrone glucuronide exchange
226	12506	EX_estrones(e)	Estrone 3-sulfate exchange
227	839	EX_etoh(e)	Ethanol exchange
228	1310	EX_fe2(e)	Fe2+ exchange
229	707	EX_fe3(e)	Fe3+ exchange
230	8752	EX_fol(e)	Folate exchange
231	1067	EX_for(e)	Formate exchange
232	681	EX_fru(e)	D-Fructose exchange
233	2028	EX_fuc-L(e)	L-Fucose exchange
234	20389	EX_fuc13galacglcgal14acglcgalgluside_hs(e)	III3Fuc-nLc6Cer exchange
235	20390	EX_fuc14galacglcgalgluside_hs(e)	Lea glycolipid exchange
236	20393	EX_fucacgalfucgalacglcgalgluside_hs(e)	(Gal)2 (GalNAc)1 (Glc)1 (GlcNAc)1 (LFuc)2 (Cer)1 exchange
237	20394	EX_fucacngal14acglcgalgluside_hs(e)	IV3-a-NeuAc,III3-a-Fuc-nLc4Cer exchange
238	20395	EX_fucacngalacglcgalgluside_hs(e)	IV3-a-Neu5Ac,III4-a-Fuc-Lc4Cer exchange
239	20396	EX_fucfuc12gal14acglcgalgluside_hs(e)	Ley glycolipid exchange
240	20397	EX_fucfuc132galacglcgal14acglcgalgluside_hs(e)	V3Fuc,III3Fuc-nLc6Cer exchange
241	20398	EX_fucfucfucgalacglc13galacglcgal14acglcgalgluside_hs(e)	(Gal)4 (Glc)1 (GlcNAc)3 (LFuc)3 (Cer)1 exchange
242	20401	EX_fucfucfucgalacglcgal14acglcgalgluside_hs(e)	(Gal)3 (Glc)1 (GlcNAc)2 (LFuc)3 (Cer)1 exchange
243	20403	EX_fucfucgalacglcgalgluside_hs(e)	Leb glycolipid exchange
244	20405	EX_fucgal14acglcgalgluside_hs(e)	Lacto-N-fucopentaosyl III ceramide exchange
245	20406	EX_fucgalfucgalacglcgalgluside_hs(e)	(Gal)3 (Glc)1 (GlcNAc)1 (LFuc)2 (Cer)1 exchange
246	20407	EX_fucgalgbside_hs(e)	fucosyl galactosylgloboside (homo sapiens) exchange
247	682	EX_gal(e)	D-Galactose exchange
248	20409	EX_galacglcgalgbside_hs(e)	Gal-GlcNAc-Gal globoside (homo sapiens) exchange

Column	Reaction #	Abbreviation	Reaction Name
249	20410	EX_galfuc12gal14acglcgalgluside_hs(e)	(Gal)3 (Glc)1 (GlcNAc)1 (LFuc)1 (Cer)1 exchange
250	20411	EX_galfucgalacglcgal14acglcgalgluside_hs(e)	(Gal)4 (Glc)1 (GlcNAc)2 (LFuc)1 (Cer)1 exchange
251	20412	EX_galgalfucfucgalacglcgalacglcgal14acglcgalgluside_hs(e)	(Gal)6 (Glc)1 (GlcNAc)3 (LFuc)2 (Cer)1 exchange
252	20413	EX_galgalgalthcrm_hs(e)	Gal-Gal-Gal-Gal-Gal-Glc-Cer (homo sapiens) exchange
253	708	EX_gam(e)	D-Glucosamine exchange
254	20417	EX_gbside_hs(e)	globoside (homo sapiens) exchange
255	12507	EX_gchola(e)	glycocholate exchange
256	20420	EX_gd1b2_hs(e)	GD1beta (homo sapiens) exchange
257	20421	EX_gd1c_hs(e)	GD1c (homo sapiens) exchange
258	20422	EX_gdchola(e)	glycochenodeoxycholate exchange
259	8166	EX_gdp(e)	GDP exchange
260	13047	EX_glc(c)	D-Glucose exchange
261	99	EX_glc(e)	D-Glucose exchange
262	710	EX_gln-L(e)	L-Glutamine exchange
263	841	EX_glu-L(e)	L-Glutamate exchange
264	10944	EX_gluala(e)	5-L-Glutamyl-L-alanine exchange
265	1068	EX_gly(e)	Glycine exchange
266	4150	EX_glyb(e)	Glycine betaine exchange
267	711	EX_glyc(e)	Glycerol exchange
268	20434	EX_glyc-S(e)	(S)-Glycerate exchange
269	10423	EX_glygn2(e)	glycogen, structure 2 (glycogenin-1,6-{7[1,4-Glc], 4[1,4-Glc]}) exchange
270	10424	EX_glygn4(e)	glycogen, structure 4 (glycogenin-1,6-{2[1,4-Glc], [1,4-Glc]}) exchange
271	10425	EX_glygn5(e)	glycogen, structure 5 (glycogenin-2[1,4-Glc]) exchange
272	10945	EX_gmp(e)	GMP exchange
273	20349	EX_gp1c_hs(e)	GP1c (homo sapiens) exchange
274	20350	EX_gp1calpha_hs(e)	GP1c alpha (homo sapiens) exchange
275	20351	EX_gq1b_hs(e)	GQ1b (homo sapiens) exchange
276	20352	EX_gq1balpha_hs(e)	GQ1balpha (homo sapiens) exchange
277	1069	EX_gsn(e)	Guanosine exchange
278	20355	EX_gt1a_hs(e)	GT1a (homo sapiens) exchange
279	1614	EX_gthox(e)	Oxidized glutathione exchange
280	2571	EX_gthrd(e)	Reduced glutathione exchange
281	8167	EX_gtp(e)	GTP exchange
282	842	EX_gua(e)	Guanine exchange
283	104	EX_h(e)	H+ exchange
284	100	EX_h2o(e)	H2O exchange
285	10946	EX_h2o2(e)	Hydrogen peroxide exchange
286	14615	EX_ha(e)	hyaluronan exchange
287	14616	EX_ha_pre1(e)	hyaluronan biosynthesis, precursor 1 exchange
288	12134	EX_hco3(e)	Bicarbonate exchange
289	20367	EX_hcoumarin(e)	hydroxy coumarin exchange
290	4143	EX_hdca(e)	Hexadecanoate (n-C16:0) exchange
291	2040	EX_hdcea(e)	hexadecenoate (n-C16:1) exchange
292	20371	EX_hestratriol(e)	4,17 dihydroxy estradiol exchange
293	12508	EX_hexc(e)	hexacosanoate (n-C26:0) exchange
294	843	EX_his-L(e)	L-Histidine exchange
295	12042	EX_hista(e)	Histamine exchange
296	12043	EX_hom-L(e)	L-Homoserine exchange
297	20376	EX_hpdca(e)	heptadecanoate exchange
298	14972	EX_hspg(e)	heparan sulfate proteoglycan exchange

Column	Reaction #	Abbreviation	Reaction Name
299	20378	EX_htaxol(e)	hydroxylated taxol exchange
300	844	EX_hxan(e)	Hypoxanthine exchange
301	12135	EX_i(e)	Iodide exchange
302	11255	EX_idp(e)	IDP exchange
303	845	EX_ile-L(e)	L-Isoleucine exchange
304	11256	EX_imp(e)	IMP exchange
305	712	EX_inost(e)	myo-Inositol exchange
306	759	EX_ins(e)	Inosine exchange
307	846	EX_k(e)	K+ exchange
308	14617	EX_ksi(e)	keratan sulfate I exchange
309	14618	EX_ksi_deg1(e)	keratan sulfate I, degradation product 1 exchange
310	14977	EX_ksii_core2(e)	keratan sulfate II (core 2-linked) exchange
311	14978	EX_ksii_core4(e)	keratan sulfate II (core 4-linked) exchange
312	3075	EX_lac-D(e)	D-lactate exchange
313	847	EX_lac-L(e)	L-Lactate exchange
314	2032	EX_lcts(e)	Lactose exchange
315	848	EX_leu-L(e)	L-Leucine exchange
316	12509	EX_leuktrC4(e)	Leukotriene C4 exchange
317	12510	EX_lgnc(e)	lignoceric acid exchange
318	20399	EX_limnen(e)	Limonene exchange
319	9487	EX_lipoate(e)	Lipoate exchange
320	12511	EX_lneldc(e)	linoelaidic acid exchange
321	14080	EX_lnlc(e)	linoleic acid (all cis C18:2) exchange
322	12512	EX_lnlc(e) [deleted 08/16/2005 05:23:37 PM]	linoleic acid exchange
323	12513	EX_lnlnca(e)	alpha-Linolenic acid exchange
324	12514	EX_lnlncg(e)	gamma-linolenic acid exchange
325	12136	EX_lpchol_hs(e)	lysophosphatidylcholine (homo sapiens) exchange
326	1072	EX_lys-L(e)	L-Lysine exchange
327	14081	EX_mag_hs(e)	monoacylglycerol 2 (homo sapiens) exchange
328	713	EX_malt(e)	Maltose exchange
329	3253	EX_malttr(e)	Maltotriose exchange
330	714	EX_man(e)	D-Mannose exchange
331	2631	EX_man6p(e)	D-Mannose 6-phosphate exchange
332	7746	EX_meoh(e)	methanol exchange
333	20415	EX_mepi(e)	Metanephrine exchange
334	20416	EX_mercplaccys(e)	3-mercaptolactate-cysteine disulfide exchange
335	1120	EX_met-L(e)	L-Methionine exchange
336	14823	EX_mthgxl(e)	Methylglyoxal exchange
337	20919	EX_n2m2nmasn(e)	N-Acetyl-beta-D-glucosaminyl-1,2-alpha-D-mannosyl-1,3-(N-acetyl-beta-D-glucosaminyl-1,2-alpha-D-mannosyl-1,6)-(N-acetyl-beta-D-glucosaminyl-1,4)-beta-D-mannosyl-1,4-N-acetyl-beta-D-glucosaminyl-R exchange
338	850	EX_na1(e)	Sodium exchange
339	2033	EX_nac(e)	Nicotinate exchange
340	2034	EX_nad(e)	Nicotinamide adenine dinucleotide exchange
341	10111	EX_nadp(e)	Nicotinamide adenine dinucleotide phosphate exchange
342	8203	EX_ncam(e)	Nicotinamide exchange
343	892	EX_nh4(e)	Ammonia exchange
344	20428	EX_nifedipine(e)	nifedipine exchange
345	6011	EX_no(e)	Nitric oxide exchange
346	20429	EX_npthl(e)	Naphthalene exchange
347	12044	EX_nrpphr(e)	Norepinephrine exchange
348	19507	EX_nrpphrsf(e)	Sulfate derivative of norepinephrine exchange
349	12515	EX_nrvnc(e)	nervonic acid exchange
350	804	EX_o2(e)	O2 exchange

Column	Reaction #	Abbreviation	Reaction Name
351	12318	EX_o2s(e)	Superoxide anion exchange
352	20435	EX_oagd3_hs(e)	9-O-Acetylated GD3 (homo sapiens) exchange
353	20436	EX_oagt3_hs(e)	9-O-Acetylated GT3 (homo sapiens) exchange
354	2035	EX_ocdca(e)	octadecanoate (n-C18:0) exchange
355	4144	EX_ocdcea(e)	octadecenoate (n-C18:1) exchange
356	8163	EX_octa(e)	octanoate (n-C8:0) exchange
357	3809	EX_oh1	OH1 Exchange
358	20447	EX_omeprazole(e)	omeprazole exchange
359	20448	EX_onpthl(e)	naphthalene epoxide exchange
360	852	EX_orn(e)	Ornithine exchange
361	12516	EX_oxa(e)	Oxalate exchange
362	15041	EX_paf_hs(e)	1-alkyl 2-acteylglycerol 3-phosphocholine (homo sapiens) exchange
363	12137	EX_pchol_hs(e)	Phosphatidylcholine (homo sapiens) exchange
364	15042	EX_pe_hs(e)	phosphatidylethanolamine (homo sapiens) exchange
365	14824	EX_peplys(e)	Peptidyl-L-lysine exchange
366	20354	EX_perillyl(e)	Perillyl alcohol exchange
367	14082	EX_pglyc_hs(e)	phosphatidylglycerol (homo sapiens) exchange
368	853	EX_phe-L(e)	L-Phenylalanine exchange
369	14619	EX_pheacgln(e)	alpha-N-Phenylacetyl-L-glutamine exchange
370	7833	EX_pheme(e)	Protoheme exchange
371	10947	EX_phyQ(e)	Phylloquinone exchange
372	20360	EX_phyt(e)	phytanic acid exchange
373	101	EX_pi(e)	Phosphate exchange
374	1616	EX_pnto-R(e)	(R)-Pantothenate exchange
375	8443	EX_ppa(e)	Propionate exchange
376	11702	EX_pro-D(e)	D-Proline exchange
377	854	EX_pro-L(e)	L-Proline exchange
378	12517	EX_prostgd2(e)	Prostaglandin D2 exchange
379	12518	EX_prostge1(e)	Prostaglandin E1 exchange
380	12519	EX_prostge2(e)	Prostaglandin E2 exchange
381	12520	EX_prostgf2(e)	Prostaglandin F2alpha exchange
382	15043	EX_ps_hs(e)	phosphatidylserine (homo sapiens) exchange
383	20370	EX_ptdca(e)	pentadecanoate exchange
384	11005	EX_pydam(e)	Pyridoxamine exchange
385	11006	EX_pydx(e)	Pyridoxal exchange
386	11007	EX_pydxn(e)	Pyridoxine exchange
387	855	EX_pyr(e)	Pyruvate exchange
388	20375	EX_rbt(e)	Ribitol exchange
389	15070	EX_retfa(e)	fatty acid retinol exchange
390	11008	EX_retinol(e)	Retinol exchange
391	15125	EX_retinol-9-cis(e)	9-cis-retinol exchange
392	15126	EX_retinol-cis-11(e)	cis-11-retinol exchange
393	15127	EX_retn(e)	Retinoate exchange
394	15128	EX_retnglc(e)	retinoyl glucuronide exchange
395	15129	EX_retpalm [deleted 10/09/2005 06:18:49 PM](e)	Retinyl palminate exchange
396	11009	EX_retpalm(e) [deleted 10/09/2005 06:38:54 PM]	Retinyl palminate exchange
397	717	EX_rib-D(e)	D-Ribose exchange
398	991	EX_ribflv(e)	Riboflavin exchange
399	10032	EX_s2l2fn2m2masn(e)	PA6 exchange
400	10033	EX_s2l2n2m2masn(e)	de-Fuc form of PA6 exchange
401	14706	EX_sarcs(e)	Sarcosine exchange
402	12521	EX_sel(e)	Selenate exchange
403	4138	EX_ser-D(e)	D-Serine exchange

Column	Reaction #	Abbreviation	Reaction Name
404	1074	EX_ser-L(e)	L-Serine exchange
405	14620	EX_sl-L(e)	L-sulfolactate exchange
406	719	EX_so4(e)	Sulfate exchange
407	20921	EX_spc_hs(e)	sphingosylphosphorylcholine (homo sapiens) exchange
408	20391	EX_sph1p(e)	Sphinganine 1-phosphate exchange
409	20392	EX_sphs1p(e)	Sphingosine 1-phosphate exchange
410	12522	EX_srtn(e)	Serotonin exchange
411	10426	EX_strch1(e)	starch, structure 1 (1,6-{7[1,4-Glc], 4[1,4-Glc]}) exchange
412	10427	EX_strch2(e)	starch, structure 2 (1,6-{2[1,4-Glc], [1,4-Glc]}) exchange
413	12523	EX_strdnc(e)	stearidonic acid exchange
414	856	EX_succ(e)	Succinate exchange
415	720	EX_sucr(e)	Sucrose exchange
416	12140	EX_tag_hs(e)	triacylglycerol (homo sapiens) exchange
417	20400	EX_tagat-D(e)	D-Tagatose exchange
418	2634	EX_taur(e)	Taurine exchange
419	20402	EX_taxol(e)	paclitaxel exchange
420	12524	EX_tchola(e)	Taurocholic acid exchange
421	13954	EX_tcynt(e)	Thiocyanate exchange
422	20404	EX_tdchola(e)	taurochenodeoxycholate exchange
423	12525	EX_tethex3(e)	tetracosahexaenoic acid, n-3 exchange
424	12526	EX_tetpent3(e)	tetracosapentaenoic acid, n-3 exchange
425	12527	EX_tetpent6(e)	tetracosapentaenoic acid, n-6 exchange
426	12528	EX_tettet6(e)	tetracosatetraenoic acid n-6 exchange
427	12733	EX_thf(e)	5,6,7,8-Tetrahydrofolate exchange
428	1075	EX_thm(e)	Thiamin exchange
429	2298	EX_thmmp(e)	Thiamin monophosphate exchange
430	14083	EX_thmtp(e)	Thiamin triphosphate exchange
431	857	EX_thr-L(e)	L-Threonine exchange
432	1621	EX_thym(e)	Thymine exchange
433	858	EX_thymd(e)	Thymidine exchange
434	12529	EX_thyox-L(e)	L-Thyroxine exchange
435	12530	EX_tmndnc(e)	timnodonic acid exchange
436	20418	EX_tolbutamide(e)	tolbutamide exchange
437	721	EX_tre(e)	Trehalose exchange
438	12531	EX_triodthy(e)	Triiodothyronine exchange
439	19508	EX_triodthysuf(e)	Triiodothyronine sulfate exchange
440	1076	EX_trp-L(e)	L-Tryptophan exchange
441	20423	EX_tststeroneglc(e)	testosterone glucuronide exchange
442	20424	EX_tststerones(e)	testosterone sulfate exchange
443	2635	EX_tsul(e)	Thiosulfate exchange
444	2037	EX_ttdca(e)	tetradecanoate (n-C14:0) exchange
445	20426	EX_txa2(e)	Thromboxane A2 exchange
446	19509	EX_tymsf(e)	Tyramine O-sulfate exchange
447	859	EX_tyr-L(e)	L-Tyrosine exchange
448	11257	EX_udp(e)	UDP exchange
449	10948	EX_ump(e)	UMP exchange
450	860	EX_ura(e)	Uracil exchange
451	19510	EX_urate(e)	Urate exchange
452	2925	EX_urea(e)	Urea exchange
453	861	EX_uri(e)	Uridine exchange
454	11258	EX_utp(e)	UTP exchange
455	12532	EX_vacc(e)	vaccenic acid exchange
456	862	EX_val-L(e)	L-Valine exchange
457	11648	EX_vitd2(e)	Vitamin D2 exchange
458	11649	EX_vitd3(e)	Vitamin D3 exchange
459	20438	EX_whddca(e)	omega hydroxy dodecanoate (n-C12:0) exchange

Column	Reaction #	Abbreviation	Reaction Name
460	20439	EX_whhdca(e)	omega hydroxy hexadecanoate (n-C16:0) exchange
461	20440	EX_whtststerone(e)	w hydroxy testosterone exchange
462	20441	EX_whttdca(e)	omega hydroxy tetradecanoate (n-C14:0) exchange
463	14825	EX_xolest2_hs(e)	cholesterol ester (from FULLR2) exchange
464	14826	EX_xolest_hs(e)	cholesterol ester exchange
465	20443	EX_xoltri24(e)	7-alpha,24(S)-Dihydroxycholesterol exchange
466	20444	EX_xoltri25(e)	7-alpha,25-Dihydroxycholesterol exchange
467	20445	EX_xoltri27(e)	7-alpha,27-Dihydroxycholesterol exchange
468	684	EX_xyl-D(e)	D-Xylose exchange
469	4145	EX_xylt(e)	Xylitol exchange
470	11650	EX_yvite(e)	gamma-Tocopherol exchange
471	3153	IN_glc(er)	IN_glc(er)
472	3158	IN_glc(g)	IN_glc
473	6061	sink_10fthf	sink_10fthf
474	14185	sink_12ppd-S(c)	sink_12ppd-S(c)
475	13461	sink_2amac(c)	sink_2amac(c)
476	10599	sink_2dr1p(c)	sink_2dr1p(c)
477	6027	sink_2obut(c)	sink_2obut(c)
478	14024	sink_2pg(c)	sink_2pg(c)
479	13479	sink_34dhoxpeg	sink_34dhoxpeg
480	13462	sink_34hpp	sink_34hpp
481	14235	sink_3aib(m)	sink_3aib(m)
482	12688	sink_3mlda	sink_3mlda
483	978	sink_3pg(c)	sink_3pg(c)
484	12760	sink_4abut	sink_4abut
485	13475	sink_4hphac(c)	sink_4hphac(c)
486	13919	sink_4hpro-LT(m)	sink_4hpro-LT(m)
487	14109	sink_5aop(c)	sink_5aop(c)
488	12232	sink_5forthf(c)	5forthf sink
489	13445	sink_5moxact(c)	sink_5moxact(c)
490	12825	sink_5mta(c)	sink_5mta(c)
491	13446	sink_6hoxmelatn(c)	sink_6hoxmelatn(c)
492	14796	sink_Asn-X-Ser/Thr(ly)	sink_Asn-X-Ser/Thr(ly)
493	14733	sink_Asn-X-Ser/Thr(r)	sink_Asn-X-Ser/Thr(r)
494	13420	sink_Lcyst(c)	sink_Lcyst(c)
495	13499	sink_Lcystin(c)	sink_Lcystin(c)
496	13442	sink_Lfmkynr(c)	sink_Lfmkynr(c)
497	13443	sink_Lkynr(c)	sink_Lkynr(c)
498	13333	sink_Rtotal(c)	sink_Rtotal(c)
499	13370	sink_Rtotal2(c)	sink_Rtotal2(c)
500	13374	sink_Rtotal3(c)	sink_Rtotal3(c)
501	14934	sink_Ser-Gly/Ala-X-Gly(er)	sink_Ser-Gly/Ala-X-Gly(er)
502	15014	sink_Ser-Gly/Ala-X-Gly(ly)	sink_Ser-Gly/Ala-X-Gly(ly)
503	14804	sink_Ser/Thr(g)	sink_Ser/Thr(g)
504	15030	sink_Ser/Thr(ly)	sink_Ser/Thr(ly)
505	13699	sink_Tyr-ggn	sink_Tyr-ggn
506	14092	sink_aact(c)	sink_aact(c)
507	1291	sink_ac(c)	sink_ac(c)
508	14970	sink_ac(g)	sink_ac(g)
509	5808	sink_acac(c)	sink_acac(c)
510	13452	sink_acac(m)	sink_acac(m)
511	13357	sink_acald(c)	Acetaldehyde exchange
512	3815	sink_accoa(c)	sink_accoa(c)
513	15017	sink_accoa(ly)	sink_accoa(ly)
514	4300	sink_accoa(m)	sink_accoa(m)
515	15138	sink_accoa(x)	sink_accoa(x)

Column	Reaction #	Abbreviation	Reaction Name
516	14091	sink_acetone(c)	sink_acetone(c)
517	14201	sink_acetone(m)	sink_acetone(m)
518	13349	sink_acgagbside_hs(g)	sink_acgagbside_hs(g)
519	13735	sink_acgal(c)	sink_acgal(c)
520	15023	sink_acgal(ly)	sink_acgal(ly)
521	13740	sink_acgam	sink_acgam
522	14798	sink_acgam(ly)	sink_acgam(ly)
523	13352	sink_acnacngalgbside_hs(g)	sink_acnacngalgbside_hs(g)
524	14799	sink_acnam(ly)	sink_acnam(ly)
525	13869	sink_acorn(c)	sink_acorn(c)
526	6032	sink_ade(c)	sink_ade(c)
527	6066	sink_adn(c)	sink_adn(c)
528	888	sink_adp(c)	sink_adp(c)
529	965	sink_adp(m)	sink_adp(m)
530	13246	sink_adp(x)	sink_adp(x)
531	13465	sink_adrnl(c)	sink_adrnl(c)
532	12759	sink_agm(c)	sink_agm(c)
533	7791	sink_ahcys(c)	sink_ahcys(c)
534	14232	sink_ahcys(m)	sink_ahcys(m)
535	4622	sink_akg(c)	sink_akg(c)
536	967	sink_akg(m)	sink_akg(m)
537	15136	sink_akg(x)	sink_akg(x)
538	12821	sink_ala-B(c)	sink_ala-B(c)
539	12862	sink_ala-D(c)	sink_ala-D(c)
540	14027	sink_ala-D(x)	sink_ala-D(x)
541	7980	sink_ala-L(c)	sink_ala-L(c)
542	14032	sink_ala-L(x)	sink_ala-L(x)
543	924	sink_alac-S(c)	sink_alac-S(c)
544	4932	sink_amet	sink_amet
545	14231	sink_amet(m)	sink_amet(m)
546	12823	sink_ametam	sink_ametam
547	1131	sink_amp(c)	sink_amp(c)
548	4292	sink_amp(m)	sink_amp(m)
549	13764	sink_amp(r)	sink_amp(r)
550	13278	sink_amp(x)	sink_amp(x)
551	13453	sink_anth(c)	sink_anth(c)
552	14741	sink_arachd(c)	sink_arachd(c)
553	13366	sink_arachd(er)	sink_arachd(er)
554	7982	sink_arg(c)	sink_arg(c)
555	12743	sink_arg(m)	sink_arg(m)
556	13633	sink_ascb-L(c)	L-Ascorbate sink
557	7983	sink_asn(c)	sink_asn(c)
558	4625	sink_asp(c)	sink_asp(c)
559	12861	sink_asp(m)	sink_asp(m)
560	933	sink_atp(c)	sink_atp(c)
561	13104	sink_atp(m)	sink_atp(m)
562	13762	sink_atp(r)	sink_atp(r)
563	13245	sink_atp(x)	sink_atp(x)
564	13319	sink_betald(m)	sink_betald(m)
565	14203	sink_bhb(m)	sink_bhb(m)
566	14195	sink_bilirub(c)	sink_bilirub(c)
567	13760	sink_bz(r)	sink_bz(r)
568	12843	sink_carn(c)	sink_carn(c)
569	14136	sink_cdp(c)	sink_cdp(c)
570	13789	sink_cdpdag(c)	sink_cdpdag(c)

Column	Reaction #	Abbreviation	Reaction Name
571	13096	sink_chol(c)	sink_chol(c)
572	13320	sink_chol(m)	sink_chol(m)
573	13421	sink_cholcoa(x)	sink_cholcoa(x)
574	14746	sink_chsterol(c)	sink_chsterol(c)
575	13263	sink_chsterol(r)	sink_chsterol(r)
576	14190	sink_citr(c)	sink_citr(c)
577	4024	sink_cmp(c)	sink_cmp(c)
578	13343	sink_cmp(g)	sink_cmp(g)
579	13741	sink_cmpacna(c)	sink_cmpacna(c)
580	13345	sink_cmpacna(g)	sink_cmpacna(g)
581	14197	sink_co(c)	sink_co(c)
582	1289	sink_co2(c)	sink_co2(c)
583	7817	sink_co2(m)	sink_co2(m)
584	13258	sink_co2(r)	sink_co2(r)
585	13247	sink_co2(x)	sink_co2(x)
586	922	sink_coa(c)	sink_coa(c)
587	15018	sink_coa(ly)	sink_coa(ly)
588	964	sink_coa(m)	sink_coa(m)
589	13763	sink_coa(r)	sink_coa(r)
590	13251	sink_coa(x)	sink_coa(x)
591	13758	sink_coke(r)	sink_coke(r)
592	14809	sink_core2(g)	sink_core2(g)
593	14810	sink_core4(g)	sink_core4(g)
594	13486	sink_creat(c)	sink_creat(c)
595	13335	sink_crmp_hs(c)	sink_crmp_hs(c)
596	4291	sink_crn(c)	sink_crn(c)
597	14739	sink_crn(m)	sink_crn(m)
598	15139	sink_crn(x)	sink_crn(x)
599	14938	sink_cs_pre(g)	sink_cs_pre(g)
600	14941	sink_cspg_a(g)	sink_cspg_a(g)
601	15022	sink_cspg_a(ly)	sink_cspg_a(ly)
602	14942	sink_cspg_b(g)	sink_cspg_b(g)
603	15024	sink_cspg_b(ly)	sink_cspg_b(ly)
604	14943	sink_cspg_c(g)	sink_cspg_c(g)
605	15025	sink_cspg_c(ly)	sink_cspg_c(ly)
606	14944	sink_cspg_d(g)	sink_cspg_d(g)
607	15026	sink_cspg_d(ly)	sink_cspg_d(ly)
608	14945	sink_cspg_e(g)	sink_cspg_e(g)
609	15027	sink_cspg_e(ly)	sink_cspg_e(ly)
610	1915	sink_ctp(c)	sink_ctp(c)
611	7986	sink_cys-L(c)	L-Cys sink
612	14115	sink_cytd(c)	sink_cytd(c)
613	13332	sink_dag_hs(c)	sink_dag_hs(c)
614	14830	sink_dag_hs(er)	sink_dag_hs(er)
615	14118	sink_dcmp(c)	sink_dcmp(c)
616	14229	sink_decdp(m)	sink_decdp(m)
617	14026	sink_dhap(c)	sink_dhap(c)
618	13180	sink_dhbpt(c)	sink_dhbpt(c)
619	5085	sink_dhf(c)	sink_dhf(c)
620	15134	sink_dmhptcoa(m)	sink_dmhptcoa(m)
621	15142	sink_dmnoncoa(m)	sink_dmnoncoa(m)
622	15141	sink_dmnoncoa(x)	sink_dmnoncoa(x)
623	13745	sink_dmpp	sink_dmpp
624	13309	sink_dna(n)	sink_dna(n)
625	13310	sink_dna5mtc(n)	sink_dna5mtc(n)
626	14727	sink_dolglcp_U(g)	sink_dolglcp_U(g)

Column	Reaction #	Abbreviation	Reaction Name
627	14719	sink_dolichol_L(c)	sink_dolichol_L(c)
628	14718	sink_dolichol_U(c)	sink_dolichol_U(c)
629	14720	sink_dolmanp_L(c)	sink_dolmanp_L(c)
630	14721	sink_dolmanp_L(r)	sink_dolmanp_L(r)
631	14722	sink_dolmanp_U(r)	sink_dolmanp_U(r)
632	14729	sink_dolp_U(g)	sink_dolp_U(g)
633	14732	sink_dolp_U(r)	sink_dolp_U(r)
634	13476	sink_dopa(c)	sink_dopa(c)
635	14807	sink_dsT_antigen(g)	sink_dsT_antigen(g)
636	13744	sink_dtdprmn(c)	sink_dtdprmn(c)
637	14123	sink_dtmp(c)	sink_dtmp(c)
638	13311	sink_dtt(c)	sink_dtt(c)
639	13312	sink_dttOX(c)	sink_dttOX(c)
640	7991	sink_dttp(c)	sink_dttp(c)
641	14119	sink_dump(c)	sink_dump(c)
642	13641	sink_eryth	sink_eryth
643	1272	sink_etha	ethanolamine sink
644	13356	sink_etoh(c)	Ethanol exchange
645	13449	sink_f5hoxkyn(c)	sink_f5hoxkyn(c)
646	1135	sink_f6p(c)	sink_f6p(c)
647	4305	sink_fad(c)	sink_fad(c)
648	4296	sink_fad(m)	sink_fad(m)
649	13262	sink_fad(r)	sink_fad(r)
650	13286	sink_fad(x)	sink_fad(x)
651	4303	sink_fadh2(c)	sink_fadh2(c)
652	4295	sink_fadh2(m)	sink_fadh2(m)
653	13261	sink_fadh2(r)	sink_fadh2(r)
654	13285	sink_fadh2(x)	sink_fadh2(x)
655	13485	sink_fald(c)	sink_fald(c)
656	13324	sink_fald(m)	sink_fald(m)
657	14194	sink_fe2(c)	sink_fe2(c)
658	14113	sink_fe2(m)	sink_fe2(m)
659	4307	sink_ficytc(m)	sink_ficytc(m)
660	13447	sink_fna5moxam(c)	sink_fna5moxam(c)
661	4309	sink_focytc(m)	sink_focytc(m)
662	13259	sink_for(r)	sink_for(r)
663	14717	sink_frdp(c)	sink_frdp(c)
664	13249	sink_frdp(x)	sink_frdp(x)
665	13500	sink_fru(c)	D-Fructose sink
666	5827	sink_fuc-L	sink_fuc-L
667	14795	sink_fuc-L(ly)	sink_fuc-L(ly)
668	5027	sink_fum	sink_fum
669	966	sink_fum(m)	sink_fum(m)
670	1455	sink_g1p(c)	g1p Input
671	14784	sink_g3m8mpdol_L(r)	sink_g3m8mpdol_L(r)
672	14726	sink_g3m8mpdol_U(g)	sink_g3m8mpdol_U(g)
673	14730	sink_g3m8mpdol_U(r)	sink_g3m8mpdol_U(r)
674	977	sink_g3p(c)	sink_g3p(c)
675	959	sink_g6p(c)	sink_g6p(c)
676	13380	sink_g6p(r)	sink_g6p(r)
677	14828	sink_gacpail_hs(c)	sink_gacpail_hs(c)
678	5749	sink_gal(c)	sink_gal(c)
679	14800	sink_gal(ly)	sink_gal(ly)
680	13351	sink_galgalgalthcrm_hs(g)	sink_galgalgalthcrm_hs(g)
681	13337	sink_galgluside_hs(g)	sink_galgluside_hs(g)
682	13733	sink_gam6p(c)	sink_gam6p(c)

Column	Reaction #	Abbreviation	Reaction Name
683	13282	sink_gchola(x)	sink_gchola(x)
684	13348	sink_gd1b2_hs(g)	sink_gd1b2_hs(g)
685	13346	sink_gd1c_hs(g)	sink_gd1c_hs(g)
686	4079	sink_gdp(c)	sink_gdp(c)
687	14790	sink_gdp(g)	sink_gdp(g)
688	4080	sink_gdp(m)	sink_gdp(m)
689	13728	sink_gdpfuc(c)	sink_gdpfuc(c)
690	14789	sink_gdpfuc(g)	sink_gdpfuc(g)
691	13727	sink_gdpmann(c)	sink_gdpmann(c)
692	13746	sink_ggdp	sink_ggdp
693	15020	sink_glcur(ly)	sink_glcur(ly)
694	13168	sink_gln-D(m)	sink_gln-D(m)
695	7993	sink_gln-L(c)	sink_gln-L(c)
696	12864	sink_gln-L(m)	sink_gln-L(m)
697	13169	sink_glu-D(m)	sink_glu-D(m)
698	4547	sink_glu-L(c)	sink_glu-L(c)
699	12712	sink_glu-L(m)	sink_glu-L(m)
700	13488	sink_glu5sa(c)	sink_glu5sa(c)
701	13353	sink_gluside_hs(g)	sink_gluside_hs(g)
702	14033	sink_glx(c)	sink_glx(c)
703	13920	sink_glx(m)	sink_glx(m)
704	14031	sink_glx(x)	sink_glx(x)
705	7994	sink_gly(c)	sink_gly(c)
706	13290	sink_gly(m)	sink_gly(m)
707	13281	sink_gly(x)	sink_gly(x)
708	13373	sink_glyc(c)	sink_glyc(c)
709	4001	sink_glyc(m)	sink_glyc(m)
710	14037	sink_glyc-S(c)	sink_glyc-S(c)
711	13393	sink_glyc3p(c)	Glycerol 3-phosphate sink
712	8275	sink_glyclt(c)	sink_glyclt(c)
713	14036	sink_glyclt(m)	sink_glyclt(m)
714	13700	sink_glygn2(c)	sink_glygn2(c)
715	13347	sink_gp1c_hs(g)	sink_gp1c_hs(g)
716	14833	sink_gpi_prot_hs(er)	sink_gpi_prot_hs(er)
717	14832	sink_gpi_sig(er)	sink_gpi_sig(er)
718	13339	sink_gq1balpha_hs(g)	sink_gq1balpha_hs(g)
719	14093	sink_gsn(c)	sink_gsn(c)
720	13177	sink_gthox(c)	sink_gthox(c)
721	13176	sink_gthrd(c)	sink_gthrd(c)
722	1916	sink_gtp(c)	sink_gtp(c)
723	4082	sink_gtp(m)	sink_gtp(m)
724	5131	sink_gua(c)	sink_gua(c)
725	934	sink_h(c)	sink_h(c)
726	2162	sink_h(er)	sink_h(er)
727	2164	sink_h(g)	sink_h(g)
728	15012	sink_h(ly)	sink_h(ly)
729	1004	sink_h(m)	sink_h(m)
730	2163	sink_h(n)	sink_h(n)
731	2161	sink_h(p)	sink_h(p)
732	1877	sink_h2o(c)	sink_h2o(c)
733	1302	sink_h2o(g)	sink_h2o(g)
734	14794	sink_h2o(ly)	sink_h2o(ly)
735	4301	sink_h2o(m)	sink_h2o(m)
736	13253	sink_h2o(r)	sink_h2o(r)
737	12941	sink_h2o(x)	sink_h2o(x)
738	8600	sink_h2o2(c)	sink_h2o2(c)

Column	Reaction #	Abbreviation	Reaction Name
739	14105	sink_h2o2(m)	sink_h2o2(m)
740	12944	sink_h2o2(x)	sink_h2o2(x)
741	14933	sink_ha(ly)	sink_ha(ly)
742	911	sink_hco3(c)	sink_hco3(c)
743	12784	sink_hco3(m)	sink_hco3(m)
744	5781	sink_hcys-L	sink_hcys-L
745	13301	sink_hcys-L(c)	sink_hcys-L(c)
746	13368	sink_hemeBo(er)	sink_hemeBo(er)
747	13369	sink_hemeBr(er)	sink_hemeBr(er)
748	13459	sink_hi(c)	sink_hi(c)
749	7996	sink_his-L	sink_his-L
750	12686	sink_hista	sink_hista
751	13250	sink_hmgcoa(x)	sink_hmgcoa(x)
752	13478	sink_homoval(c)	sink_homoval(c)
753	14023	sink_hpyr(c)	sink_hpyr(c)
754	14969	sink_hspg(g)	sink_hspg(g)
755	15011	sink_hspg(ly)	sink_hspg(ly)
756	5133	sink_hxan(c)	sink_hxan(c)
757	13418	sink_hyptaur(c)	sink_hyptaur(c)
758	13451	sink_id3acald(c)	sink_id3acald(c)
759	15015	sink_idour(ly)	sink_idour(ly)
760	13457	sink_ile(m)	sink_ile(m)
761	12687	sink_im4ac	sink_im4ac
762	6062	sink_imp	sink_imp
763	13371	sink_inost(c)	sink_inost(c)
764	13458	sink_iodine(c)	sink_iodine(c)
765	13747	sink_ipdp	sink_ipdp
766	13750	sink_ipdp(x)	sink_ipdp(x)
767	13792	sink_itacon(m)	sink_itacon(m)
768	13725	sink_kdn(c)	sink_kdn(c)
769	14948	sink_ksi(g)	sink_ksi(g)
770	15028	sink_ksi(ly)	sink_ksi(ly)
771	14946	sink_ksii_core2(g)	sink_ksii_core2(g)
772	15029	sink_ksii_core2(ly)	sink_ksii_core2(ly)
773	14947	sink_ksii_core4(g)	sink_ksii_core4(g)
774	15033	sink_ksii_core4(ly)	sink_ksii_core4(ly)
775	13454	sink_kynate(c)	sink_kynate(c)
776	14788	sink_l2fn2m2masn(g)	sink_l2fn2m2masn(g)
777	10522	sink_lac-D	D-lactate sink
778	13518	sink_lcts(g)	sink_lcts(g)
779	13450	sink_leu(m)	sink_leu(m)
780	8000	sink_lys(c)	sink_lys(c)
781	12949	sink_lys(x)	sink_lys(x)
782	13642	sink_lyxnt(c)	sink_lyxnt(c)
783	14725	sink_m4mpdol_U(c)	sink_m4mpdol_U(c)
784	14724	sink_m8masn(g)	sink_m8masn(g)
785	14772	sink_m8masn(r)	sink_m8masn(r)
786	4623	sink_mal(c)	sink_mal(c)
787	14740	sink_malcoa(m)	sink_malcoa(m)
788	13726	sink_man(c)	sink_man(c)
789	14787	sink_man(g)	sink_man(g)
790	13724	sink_man6p(c)	sink_man6p(c)
791	13466	sink_melanin(c)	sink_melanin(c)
792	13441	sink_melatn(c)	sink_melatn(c)
793	13761	sink_meoh(r)	sink_meoh(r)
794	13793	sink_mescon(m)	sink_mescon(m)

Column	Reaction #	Abbreviation	Reaction Name
795	5782	sink_met(c)	sink_met(c)
796	13791	sink_mi145p(c)	sink_mi145p(c)
797	6064	sink_mlthf(c)	sink_mlthf(c)
798	13296	sink_mlthf(m)	sink_mlthf(m)
799	13480	sink_mma(c)	sink_mma(c)
800	12847	sink_msa(c)	sink_msa(c)
801	20459	sink_msa(m)	sink_msa(m)
802	14090	sink_mthgxl(c)	sink_mthgxl(c)
803	14792	sink_n2m2nmasn(g)	sink_n2m2nmasn(g)
804	14803	sink_n2m2nmasn(ly)	sink_n2m2nmasn(ly)
805	13419	sink_na1(x)	sink_na1(x)
806	4071	sink_nad(c)	sink_nad(c)
807	1575	sink_nad(m)	sink_nad(m)
808	13254	sink_nad(r)	sink_nad(r)
809	12945	sink_nad(x)	sink_nad(x)
810	1965	sink_nadh(c)	sink_nadh(c)
811	4075	sink_nadh(m)	sink_nadh(m)
812	13255	sink_nadh(r)	sink_nadh(r)
813	12946	sink_nadh(x)	sink_nadh(x)
814	1132	sink_nadp(c)	nadp sink
815	4921	sink_nadp(m)	nadph sink
816	13257	sink_nadp(r)	nadp sink
817	13248	sink_nadp(x)	nadph sink
818	1133	sink_nadph(c)	nadph sink
819	4920	sink_nadph(m)	nadph sink
820	13256	sink_nadph(r)	nadph sink
821	13242	sink_nadph(x)	nadph sink
822	13444	sink_nformanth(c)	sink_nformanth(c)
823	12923	sink_nh3(m)	sink_nh3(m)
824	12943	sink_nh3(x)	sink_nh3(x)
825	1292	sink_nh4(c)	sink_nh4(c)
826	14785	sink_nm4masn(g)	sink_nm4masn(g)
827	13448	sink_nmthsrtn(c)	sink_nmthsrtn(c)
828	12762	sink_no(c)	sink_no(c)
829	13464	sink_nrpphr(c)	sink_nrpphr(c)
830	7977	sink_o2(c)	sink_o2(c)
831	13237	sink_o2(m)	sink_o2(m)
832	13260	sink_o2(r)	sink_o2(r)
833	12940	sink_o2(x)	sink_o2(x)
834	13640	sink_o2s(c)	sink_o2s(c)
835	4925	sink_o2s(m)	sink_o2s(m)
836	4076	sink_oaa(c)	sink_oaa(c)
837	980	sink_oaa(m)	sink_oaa(m)
838	14073	sink_oh1	OH1 sink
839	14074	sink_oh1(m)	OH1 sink
840	1700	sink_orn(c)	sink_orn(c)
841	13635	sink_oxa(c)	sink_oxa(c)
842	13201	sink_pac(c)	sink_pac(c)
843	13198	sink_pacald(c)	sink_pacald(c)
844	13372	sink_pail45p_hs(c)	sink_pail45p_hs(c)
845	13790	sink_pail4p_hs(c)	sink_pail4p_hs(c)
846	13787	sink_pail_hs(c)	sink_pail_hs(c)
847	14940	sink_pap(g)	sink_pap(g)
848	14099	sink_paps(c)	sink_paps(c)
849	14939	sink_paps(g)	sink_paps(g)
850	13331	sink_pchol_hs(c)	sink_pchol_hs(c)

Column	Reaction #	Abbreviation	Reaction Name
851	13487	sink_pcreat(c)	sink_pcreat(c)
852	13376	sink_pe_hs(c)	sink_pe_hs(c)
853	14829	sink_pe_hs(er)	sink_pe_hs(er)
854	13192	sink_peamn(c)	sink_peamn(c)
855	13759	sink_pecgoncoa(r)	sink_pecgoncoa(r)
856	979	sink_pep(c)	sink_pep(c)
857	13202	sink_phaccoa(c)	sink_phaccoa(c)
858	8004	sink_phe-L(c)	sink_phe-L(c)
859	13191	sink_pheacgln(c)	sink_pheacgln(c)
860	14196	sink_pheme(c)	sink_pheme(c)
861	14110	sink_pheme(m)	sink_pheme(m)
862	13185	sink_phpyr(c)	sink_phpyr(c)
863	15135	sink_phytcoa(c)	sink_phytcoa(c)
864	932	sink_pi(c)	sink_pi(c)
865	13325	sink_pi(er)	sink_pi(er)
866	7816	sink_pi(m)	sink_pi(m)
867	13243	sink_pi(x)	sink_pi(x)
868	920	sink_pmtcoa(c)	sink_pmtcoa(c)
869	13298	sink_ppcoa(c)	sink_ppcoa(c)
870	13460	sink_ppcoa(m)	sink_ppcoa(m)
871	13365	sink_ppcoa(x)	sink_ppcoa(x)
872	931	sink_ppi(c)	sink_ppi(c)
873	4310	sink_ppi(m)	sink_ppi(m)
874	13264	sink_ppi(r)	sink_ppi(r)
875	13244	sink_ppi(x)	sink_ppi(x)
876	14831	sink_pre_prot(er)	sink_pre_prot(er)
877	8006	sink_pro-L(c)	sink_pro-L(c)
878	12740	sink_pro-L(m)	sink_pro-L(m)
879	1963	sink_prpp(c)	sink_prpp(c)
880	8008	sink_ptrc(c)	sink_ptrc(c)
881	14573	sink_pydx(c)	sink_pydx(c)
882	1288	sink_pyr(c)	sink_pyr(c)
883	960	sink_pyr(m)	sink_pyr(m)
884	14028	sink_pyr(x)	sink_pyr(x)
885	14124	sink_q10(c)	sink_q10(c)
886	4286	sink_q10(m)	sink_q10(m)
887	14125	sink_q10h2(m)	sink_q10h2(m)
888	13172	sink_quln	sink_quln
889	13203	sink_r1p	sink_r1p
890	975	sink_r5p(c)	sink_r5p(c)
891	3657	sink_ru5p-D	sink_ru5p-D
892	14791	sink_s2l2fn2m2masn(g)	sink_s2l2fn2m2masn(g)
893	14793	sink_s2l2fn2m2masn(ly)	sink_s2l2fn2m2masn(ly)
894	14806	sink_sT_antigen(g)	sink_sT_antigen(g)
895	14808	sink_sTn_antigen(g)	sink_sTn_antigen(g)
896	12711	sink_saccrp-L(m)	sink_saccrp-L(m)
897	13416	sink_seahcys(n)	sink_seahcys(n)
898	13417	sink_seasmet(n)	sink_seasmet(n)
899	13305	sink_selmeth(c)	sink_selmeth(c)
900	13306	sink_selnp(c)	sink_selnp(c)
901	8009	sink_ser-L(c)	sink_ser-L(c)
902	1701	sink_so4(c)	sink_so4(c)
903	15013	sink_so4(ly)	sink_so4(ly)
904	13334	sink_sphmyln_hs(c)	sink_sphmyln_hs(c)
905	8010	sink_spmd(c)	sink_spmd(c)
906	12860	sink_sprm(c)	sink_sprm(c)

Column	Reaction #	Abbreviation	Reaction Name
907	13751	sink_sql(r)	sink_sql(r)
908	13440	sink_srtn(c)	sink_srtn(c)
909	968	sink_succ(m)	sink_succ(m)
910	15137	sink_succ(x)	sink_succ(x)
911	981	sink_succoa(m)	sink_succoa(m)
912	13375	sink_tag_hs(c)	sink_tag_hs(c)
913	13280	sink_taur(x)	sink_taur(x)
914	13283	sink_tchola(x)	sink_tchola(x)
915	13179	sink_thbpt(c)	sink_thbpt(c)
916	13277	sink_thcholstoic(m)	sink_thcholstoic(m)
917	13284	sink_thcholstoic(x)	sink_thcholstoic(x)
918	3821	sink_thf(c)	sink_thf(c)
919	13295	sink_thf(m)	sink_thf(m)
920	5903	sink_thm(c)	sink_thm(c)
921	14075	sink_thmmp(c)	sink_thmmp(c)
922	8012	sink_thr-L(c)	sink_thr-L(c)
923	13634	sink_thrnt(c)	sink_thrnt(c)
924	937	sink_thym(c)	sink_thym(c)
925	13455	sink_thyox-L(c)	sink_thyox-L(c)
926	10600	sink_trdox(c)	sink_trdox(c)
927	10601	sink_trdrd(c)	sink_trdrd(c)
928	13456	sink_triodthy(c)	sink_triodthy(c)
929	8015	sink_trp-L(c)	sink_trp-L(c)
930	13367	sink_txa2(er)	sink_txa2(er)
931	8016	sink_tyr-L(c)	sink_tyr-L(c)
932	14228	sink_tyr-L(m)	sink_tyr-L(m)
933	5829	sink_uacgam	sink_uacgam
934	14786	sink_uacgam(g)	sink_uacgam(g)
935	13436	sink_udp(c)	sink_udp(c)
936	14936	sink_udp(er)	sink_udp(er)
937	13340	sink_udp(g)	sink_udp(g)
938	15031	sink_udp(ly)	sink_udp(ly)
939	13736	sink_udpacgal(c)	sink_udpacgal(c)
940	13341	sink_udpacgal(g)	sink_udpacgal(g)
941	15032	sink_udpacgal(ly)	sink_udpacgal(ly)
942	5787	sink_udpg(c)	sink_udpg(c)
943	13517	sink_udpgal(c)	sink_udpgal(c)
944	13344	sink_udpgal(g)	sink_udpgal(g)
945	10615	sink_udpglcur(c)	sink_udpglcur(c)
946	14937	sink_udpglcur(g)	sink_udpglcur(g)
947	14935	sink_udpxyl(er)	sink_udpxyl(er)
948	10627	sink_ump(c)	sink_ump(c)
949	13519	sink_ump(g)	sink_ump(g)
950	12837	sink_ura(c)	sink_ura(c)
951	14085	sink_urate(x)	sink_urate(x)
952	1917	sink_utp(c)	sink_utp(c)
953	13463	sink_val-L(m)	sink_val-L(m)
954	13273	sink_xoldiolone(r)	sink_xoldiolone(r)
955	13275	sink_xoltriol(c)	sink_xoltriol(c)
956	13276	sink_xoltriol(m)	sink_xoltriol(m)
957	1910	sink_xu5p-D	sink xu5p-D
958	15021	sink_xyl-D(ly)	sink_xyl-D(ly)
959	13643	sink_xylnt(c)	sink_xylnt(c)
960	14025	sink_xylu-D(c)	sink_xylu-D(c)
961	14894	10FTHF5GLUtl	5-glutamyl-10FTHF transport, lysosomal
962	14901	10FTHF5GLUtm	5-glutamyl-10FTHF transport, mitochondrial

Column	Reaction #	Abbreviation	Reaction Name
963	14896	10FTHF6GLUtl	6-glutamyl-10FTHF transport, lysosomal
964	14900	10FTHF6GLUtm	6-glutamyl-10FTHF transport, mitochondrial
965	14895	10FTHF7GLUtl	7-glutamyl-10FTHF transport, lysosomal
966	14899	10FTHF7GLUtm	7-glutamyl-10FTHF transport, mitochondrial
967	14902	10FTHFtl	10-Formyltetrahydrofolate lysosomal transport via diffusion
968	3763	10FTHFtm	10-Formyltetrahydrofolate mitochondrial transport via diffusion
969	19788	11DOCRTSLtm	11-deoxycortisol intracellular transport
970	19787	11DOCRTSLtr	11-deoxycortisol intracellular transport
971	19790	11DOCRTSTRNtm	11-deoxycorticosterone intracellular transport
972	19789	11DOCRTSTRNtr	11-deoxycorticosterone intracellular transport
973	10534	13DAMPPOX	1,3-Diaminopropane:oxygen oxidoreductase (deaminating)
974	10513	1MNCAMti	N1-Methylnicotinamide transport
975	12671	1PPDCRp	delta1-piperideine-2-carboxylate reductase, perixosomal
976	11378	1a,24,25VITD2Hm	1-alpha-Vitamin D-24,25-hydroxylase (D2)
977	11379	1a,24,25VITD3Hm	1-alpha-Vitamin D-24,25-hydroxylase (D3)
978	11380	1a,25VITD2Hm	1-alpha,24R,25-Vitamin D-hydroxylase (D2)
979	11381	1a,25VITD3Hm	1-alpha,24R,25-Vitamin D-hydroxylase (D3)
980	11367	24,25DHVITD2t	24,25-Dihydroxyvitamin D2 transport from cytoplasm
981	11366	24,25DHVITD2tm	24,25-Dihydroxyvitamin D2 transport from mitochondria
982	11368	24,25DHVITD3t	24,25-Dihydroxyvitamin D3 transport from cytoplasm
983	11369	24,25DHVITD3tm	24,25-Dihydroxyvitamin D3 transport from mitochondria
984	11329	24,25VITD2Hm	24R-Vitamin D-25-hydroxylase (D2)
985	11331	24,25VITD3Hm	24R-Vitamin D-25-hydroxylase (D3)
986	19709	24NPHte	xenobiotic transport
987	11370	25HVITD2t	25-hydroxyvitamin D2 transport from cytoplasm
988	11371	25HVITD2tin	25-hydroxyvitamin D2 transport in cytoplasm
989	11373	25HVITD2tin-m	25-hydroxyvitamin D2 transport in mitochondria
990	11372	25HVITD2tm	25-hydroxyvitamin D2 transport from mitochondria
991	11374	25HVITD3t	25-hydroxyvitamin D3 transport from cytoplasm
992	11375	25HVITD3tin	25-hydroxyvitamin D3 transport in cytoplasm
993	11376	25HVITD3tin-m	25-hydroxyvitamin D3 transport in mitochondria
994	11377	25HVITD3tm	25-hydroxyvitamin D3 transport from mitochondria
995	11328	25VITD2Hm	1-alpha-Vitamin D-25-hydroxylase (D2)
996	11327	25VITD3Hm	1-alpha-Vitamin D-25-hydroxylase (D3)
997	13555	2AMACHYD	2-Aminoacrylate hydrolysis
998	14558	2AMACSULT	2-Aminoacrylate sulfotransferase
999	11294	2AMADPTm	L-2-aminoadipate shuttle (cytosol/mitochondria)
1000	20139	2DR1PP	2-deoxy-D-ribose 1-phosphate phosphorylase
1001	10742	2HBO	2-Hydroxybutyrate:NAD+ oxidoreductase
1002	12476	2HBt2	2-hydroxybutyrate cotransport with proton
1003	12047	2HCO3_NAt	bicarbonate transport (Na/HCO3 1:2 cotransport)
1004	20838	2MCITt	2-methylcitrate transport via diffusion
1005	9498	2OXOADOXm	2-Oxoadipate:lipoamde 2-oxidoreductase(decarboxylating and acceptor-succinylating) (mitochondria)
1006	11293	2OXOADPTm	2-oxoadipate shuttle (cytosol/mitochondria)
1007	9453	34DHOXPEGOX	3,4-Dihydroxyphenylethyleneglycol:NAD+ oxidoreductase
1008	14589	34DHOXPEGt	3,4-Dihydroxyphenylethyleneglycol transport (diffusion)
1009	11389	34DHPHAMT	3,4-Dihydroxyphenylacetate:amet O-methyltransferase
1010	12564	34DHPHEt	3,4-Dihydroxy-L-phenylalanine transport
1011	11585	34DHPLACOX	3,4-Dihydroxyphenylacetaldehyde:NAD+ oxidoreductase
1012	9441	34DHPLACOX(NADP)	3,4-Dihydroxyphenylacetaldehyde:NADP+ oxidoreductase
1013	11582	34DHXMANDACOX	3,4-Dihydroxymandelaldehyde:NAD+ oxidoreductase
1014	9448	34DHXMANDACOX(NADP)	3,4-Dihydroxymandelaldehyde:NADP+ oxidoreductase

Column	Reaction #	Abbreviation	Reaction Name
1015	14223	34HPLFM	3-(4-hydroxyphenyl-)lactate formation
1016	2388	34HPPOR	4-Hydroxyphenylpyruvate:oxygen oxidoreductase
1017	19548	35CGMPtn	35cGMP nuclear transport
1018	14094	3AIBTm	L-3-aminoisobutyrate transaminase, mitochondrial
1019	12083	3AIBt	3-amino-isobutyrate transport
1020	14971	3AIBtm	3-amino-isobutyrate transport, mitochondrial
1021	11091	3DPHBH1	Hydroxylation of 3-Decaprenyl-4-hydroxybenzoate (NADH)
1022	11092	3DPHBH2	Hydroxylation of 3-Decaprenyl-4-hydroxybenzoate (NADPH)
1023	1879	3DSPHR	3-Dehydrosphinganine reductase
1024	3260	3HAO	3-hydroxyanthranilate 3,4-dioxygenase
1025	10779	3HBCDm	3-hydroxybutyryl-CoA dehydratase, mitochondrial
1026	10911	3HBCOAHLm	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial
1027	12048	3HCO3_NAt	bicarbonate transport (Na/HCO3 1:3 cotransport)
1028	9508	3HKYNAKGAT	3-Hydroxy-L-kynurenine:2-oxoglutarate aminotransferase
1029	9391	3HLYTCL	3-Hydroxy-L-tyrosine carboxy-lyase
1030	9803	3HPCOAHYD	3-hydroxyisobutyryl-Coenzyme A hydrolase
1031	10754	3HPPD	3-hydroxypropionate dehydrogenase
1032	9578	3HXKYNDCL	3-Hydroxykynurenamine decarboxy-lyase
1033	9582	3HXKYNOXDA	3-Hydroxykynurenamine:oxygen oxidoreductase(deaminating)(flavin-containing)
1034	9434	3M4HDXPAC	3-Methoxy-4-hydroxyphenylacetaldehyde:NAD+ oxidoreductase
1035	14512	3MLDAt	3MLDA extracellular transport via diffusion
1036	13267	3MOBt2im	3-methyl-2-oxobutanoate mitochondrial transport via proton symport
1037	13265	3MOPt2im	3-Methyl-2-oxopentanoate mitochondrial transport via proton symport
1038	11598	3MOX4HOXPGALDOX	3-Methoxy-4-hydroxyphenylglycolaldehyde:NAD+ oxidoreductase
1039	9450	3MOX4HOXPGALDOX(NADP)	3-Methoxy-4-hydroxyphenylglycolaldehyde:NADP+ oxidoreductase
1040	11387	3MOXTYROX	3-Methoxytyramine:oxygen oxidoreductase (deaminating)
1041	12645	3NTD7l	3'-nucleotidase (AMP), lysosome
1042	14612	3SALAASPm	cysteinesulfinate-aspartate mitochondrial shuttle
1043	9859	3SALACBOXL	3-Sulfino-L-alanine carboxy-lyase
1044	14770	3SALAOX	cysteinesulfinic acid oxidase
1045	14567	3SALATAi	3-sulfino-alanine transaminase (irreversible)
1046	14566	3SALATAim	3-sulfino-alanine transaminase (irreversible), mitochondrial
1047	11474	3SPYRSP	3-sulfinopyruvate hydrolase (spotaneous reaction)
1048	14771	3SPYRSPm	3-sulfinopyruvate hydrolase (spotaneous reaction), mitochondrial
1049	9406	41R1H2MAE12BOOX	4-[(1R)-1-Hydroxy-2-(methylamino)ethyl]-1,2-benzenediol:oxygen oxidoreductase(deaminating)(flavin-containing)
1050	12098	41R2A1H12BOOX	4-[(1R)-2-Amino-1-hydroxyethyl]-1,2-benzenediol:oxygen oxidoreductase(deaminating)(flavin-containing)
1051	9431	42A12BOOX	4-(2-Aminoethyl)-1,2-benzenediol:oxygen oxidoreductase(deaminating)(flavin-containing)
1052	1683	4ABUTtm	4-aminobutanoate mitochondrial transport via diffusion
1053	14222	4HBZCOAFm	4-hydroxybenzoyl-CoA formation
1054	14227	4HBZFm	4-hydroxybenzoate formation
1055	19710	4HDEBRISOQUINEte	xenobiotic transport
1056	1845	4HGLSDm	L-4-hydroxyglutamate semialdehyde dehydrogenase, mitochondrial

Column	Reaction #	Abbreviation	Reaction Name
1057	9452	4HOXPACDOX(NADP)	4-Hydroxyphenylacetaldehyde:NADP+ oxidoreductase
1058	13266	4MOPt2im	4-methyl-2-oxopentanoate mitochondrial transport via proton symport
1059	19711	4MTOLBUTAMIDEte	xenobiotic transport
1060	19712	4NPHSFte	xenobiotic transport
1061	12105	4NPHSULT	4-Nitrophenol Sulfotransferase
1062	19700	4NPHte	xenobiotic transport
1063	10954	4PYRDX	4-Pyridoxal secretion
1064	19767	5ADTSTSTERONEGLCte	glucuronidated compound transport
1065	19744	5ADTSTSTERONEGLCtr	glucuronidated compound transport
1066	20336	5ADTSTSTERONESULT	5alpha-Dihydrotestosterone sulfotransferase
1067	20338	5ADTSTSTERONESte	sulfonated testosterone transport
1068	20021	5ADTSTSTERONEte	5 alpha dihydrotesterone transport
1069	14985	5ADTSTSTERONEtr	5 alpha dihydrotesterone intracellular transport
1070	1760	5AOPtm	5-Aminolevulinate mitochondrial transport
1071	14888	5DHFtl	5-glutamyl-DHF transport, lysosomal
1072	14839	5FTHFt2	5-formyltetrahydrofolate transport via anion exchange
1073	9579	5HLTDL	5-Hydroxy-L-tryptophan decarboxy-lyase
1074	19713	5HOMEPRAZOLEte	xenobiotic transport
1075	9604	5HOXINDACTO2OX	5-Hydroxyindoleacetaldehyde:oxygen oxidoreductase
1076	9586	5HOXINDACTOX	5-Hydroxyindoleacetaldehyde:NAD+ oxidoreductase
1077	9587	5HOXINDACTOXm	5-Hydroxyindoleacetaldehyde:NAD+ oxidoreductase (mito)
1078	9584	5HOXINOXDA	5-Hydroxytryptamine:oxygen oxidoreductase(deaminating)(flavin-containing)
1079	9610	5HTRPDOX	5-Hydroxy-L-tryptophan:oxygen 2,3-dioxygenase (indole-decyclizing)
1080	11930	5HTRPVESSEC	5-hydroxy-L-tryptophan secretion via secretory vesicle (ATP driven)
1081	9577	5HXKYNDCL	5-Hydroxykynurenamine decarboxy-lyase
1082	9581	5HXKYNOXDA	5-Hydroxykynurenamine:oxygen oxidoreductase(deaminating)(flavin-containing)
1083	14835	5MTHFt	5-Methyltetrahydrofolate transport via receptor binding and protolysis
1084	14838	5MTHFt2	5-methyltetrahydrofolate transport via anion exchange
1085	14891	5THFtl	5-glutamyl-THF transport, lysosomal
1086	14884	5THFtm	5-glutamyl-THF transport,m mitochondrial
1087	14889	6DHFtl	6-glutamyl-DHF transport, lysosomal
1088	14885	6DHFtm	6-glutamyl-DHF transport,m mitochondrial
1089	19747	6HTSTSTERONEte	hydroxylated testosterone transport
1090	19746	6HTSTSTERONEtr	hydroxylated testosterone transport
1091	14893	6THFtl	6-glutamyl-THF transport, lysosomal
1092	14883	6THFtm	6-glutamyl-THF transport,m mitochondrial
1093	14707	7DHCHSTEROLtr	cholesterol precursor intracellular transport
1094	14890	7DHFtl	7-glutamyl-DHF transport, lysosomal
1095	14882	7DHFtm	7-glutamyl-DHF transport,m mitochondrial
1096	14892	7THFtl	7-glutamyl-THF transport, lysosomal
1097	14881	7THFtm	7-glutamyl-THF transport,m mitochondrial
1098	11392	A4GALTc	Lactosylceramide 4-alpha-galactosyltransferase
1099	11071	A4GALTg	Lactosylceramide 4-alpha-galactosyltransferase
1100	8691	A4GNT1g	alpha 1,4-N-acetylglucosaminyltransferase, Golgi apparatus
1101	8689	A4GNT2g	alpha 1,4-N-acetylglucosaminyltransferase, Golgi apparatus
1102	10757	AACOAT	Acetoacetyl-CoA:acetate CoA-transferase

Column	Reaction #	Abbreviation	Reaction Name
1103	11706	AACTOOR	Aminoacetone:oxygen oxidoreductase(deaminating)(flavin-containing)
1104	14676	AACTtm	Aminoacetone transport (mitochondrial)
1105	10901	AAPSAS	AAPSAS
1106	10886	AASAD3	L-aminoadipate-semialdehyde dehydrogenase (NADH)
1107	11477	AASAD3m	L-aminoadipate-semialdehyde dehydrogenase (NADH), mitochondrial
1108	10888	AATAi	2-aminoadipate transaminase, irreversible
1109	14603	ABO1g	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase)
1110	14609	ABO2g	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase)
1111	14629	ABO3g	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase)
1112	14630	ABO4g	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase)
1113	14637	ABO5g	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase)
1114	14643	ABO6g	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase)
1115	14647	ABO7g	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase)
1116	14649	ABO8g	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase)
1117	14664	ABO9g	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase)
1118	9373	ABTArm	4-aminobutyrate transaminase, reversible (mitochondrial)
1119	10157	ABTD	L-arabinitol 4-dehydrogenase
1120	19569	ABTti	L-arabinitol transport via passive diffusion
1121	1267	ABUTD	Aminobutyraldehyde dehydrogenase
1122	11687	ABUTt2r	4-aminobutyrate reversible transport in via proton symport
1123	11688	ABUTt2rL	4-aminobutyrate reversible transport in via proton symport (lysosome)
1124	11936	ABUTt4(2)r	4-aminobutyrate reversible transport in via sodium symport (1:2)
1125	2	ACACT1	acetyl-CoA C-acetyltransferase
1126	10919	ACACT10m	acetyl-CoA C-acetyltransferase, mitochondrial
1127	1498	ACACT1r	acetyl-CoA C-acetyltransferase
1128	3474	ACACT1rm	acetyl-CoA C-acetyltransferase, mitochondrial
1129	9730	ACACT1x	acetyl-CoA C-acetyltransferase, mitochondrial
1130	3081	ACACT4p	acetyl-CoA C-acetyltransferase (octanoyl-CoA), peroxisomal
1131	2077	ACACT5p	acetyl-CoA C-acyltransferase (decanoyl-CoA), peroxisomal
1132	2076	ACACT6p	acetyl-CoA C-acetyltransferase (dodecanoyl), peroxisomal
1133	3078	ACACT7p	acetyl-CoA acyltransferase (tetradecanoyl-CoA), peroxisomal

Column	Reaction #	Abbreviation	Reaction Name
1134	2074	ACACT8p	acetyl-CoA acyltransferase (hexadecanoyl-CoA), peroxisomal
1135	3077	ACACT9p	acetyl-CoA acyltransferase (tetracosanoyl-CoA), peroxisomal
1136	2375	ACACt2	acetoacetate transport via proton symport
1137	5495	ACACt2m	Acetoacetate mitochondrial transport via H+ symport
1138	20150	ACACtx	acetoacetate intracellular transport unknown mechanism
1139	1564	ACALDt	acetaldehyde reversible transport
1140	5533	ACALDtm	acetaldehyde mitochondrial diffusion
1141	19463	ACALDtx	acetaldehyde peroxisomal diffusion
1142	32	ACCOAC	acetyl-CoA carboxylase
1143	8385	ACCOACm	Acetyl-Coa carboxylase, beta isoform
1144	3258	ACCOAL	acetate-CoA ligase (ADP-forming)
1145	8420	ACCOALm	acetate-CoA ligase (AMP-forming)
1146	12539	ACCOAgt	acetyl-coa transport
1147	1534	ACCOAtn	acetyl-CoA transport, nuclear
1148	12540	ACCOAtr	acetyl-coa transport
1149	12480	ACETONEt2	acetone transport via proton symport
1150	14988	ACETONEt2m	acetone mitochondrial transport via proton symport
1151	20126	ACGAGBSIDEtg	acgagbside_hs intracellular transport
1152	20127	ACGAGBSIDEtl	acgagbside_hs intracellular transport
1153	19660	ACGALFUCGALACGALFUC12GAL14ACGLCGALGLUSIDEte	blood group intracellular transport
1154	20162	ACGALFUCGALACGALFUC12GAL14ACGLCGALGLUSIDEtg	blood group intracellular transport
1155	19661	ACGALFUCGALACGALFUCGALACGLCGAL14ACGLCGALGLUSIDEte	blood group intracellular transport
1156	20163	ACGALFUCGALACGALFUCGALACGLCGAL14ACGLCGALGLUSIDEtg	blood group intracellular transport
1157	10648	ACGALK	N-acetylgalactosamine kinase
1158	10649	ACGALK2	N-acetylgalactosamine kinase (ITP)
1159	20149	ACGALtlg	N-acetyl-galactosamine intracellular transport
1160	14918	ACGALtly	N-acetyl-galactosamine lysosomal efflux
1161	10642	ACGAM2E	N-acetylglucosamine 2-epimerase
1162	10569	ACGAM6PSi	N-acetylglucosamine-6-phosphate synthase
1163	9377	ACGAMK	N-acetylglucosamine kinase
1164	1447	ACGAMPM	phosphoacetylglucosamine mutase
1165	14919	ACGAMtly	N-acetyl-glucosamine lysosomal efflux
1166	20128	ACGBGBSIDEtg	acgbgbside_hs intracellular transport
1167	20129	ACGBGBSIDEtl	acgbgbside_hs intracellular transport
1168	11054	ACGPID	N-acetylglucosaminylphosphatidylinositol deacetylase
1169	3464	ACGSm	N-acteylglutamate synthase, mitochondrial
1170	11897	ACHEe	Acetylcholinesterase
1171	11935	ACHVESSEC	Acetylcholine secretion via secretory vesicle (ATP driven)
1172	19523	ACHtn	Acetylcholin transport, nuclear trhough pores
1173	9535	ACITL	ATP-Citrate lyase
1174	20223	ACN13ACNGALGBSIDEte	acn13acngalgbside_hs transport
1175	20207	ACN13ACNGALGBSIDEtg	acn13acngalgbside_hs intracellular transport
1176	20224	ACN23ACNGALGBSIDEte	acn23acngalgbside transport
1177	20208	ACN23ACNGALGBSIDEtg	acn23acngalgbside intracellular transport

Column	Reaction #	Abbreviation	Reaction Name
1178	19663	ACNACNGAL14ACGLCGALGLUSIDEte	blood group intracellular transport
1179	20164	ACNACNGAL14ACGLCGALGLUSIDEtg	blood group intracellular transport
1180	20225	ACNACNGALGBSIDEte	acnacngalgbside_hs transport
1181	20209	ACNACNGALGBSIDEtg	acnacngalgbside_hs intracellular transport
1182	10595	ACNAM9PL	N-Acetylneuraminate 9-phosphate pyruvate-lyase (pyruvate-phosphorylating)
1183	10634	ACNAM9PL2	N-Acetylneuraminate 9-phosphate pyruvate-lyase (pyruvate-phosphorylating)
1184	10644	ACNAMPH	N-Acetylneuraminate 9-phosphate phosphohydrolase
1185	13785	ACNAMlt	N-acetylneuraminate transport into lysososme
1186	15230	ACNAMtn	N-acetylneuraminate nuclear import
1187	19665	ACNGALACGLCGAL14ACGLCGALGLUSIDEte	blood group intracellular transport
1188	20165	ACNGALACGLCGAL14ACGLCGALGLUSIDEtg	blood group intracellular transport
1189	10637	ACNMLr	N-Acetylneuraminate lyase (reversible)
1190	10914	ACOAD10m	acyl-CoA dehydrogenase (2-methylbutanoyl-CoA), mitochondrial
1191	10437	ACOAD1fm	acyl-CoA dehydrogenase (butanoyl-CoA), mitochondrial
1192	10333	ACOAD8m	acyl-CoA dehydrogenase (isovaleryl-CoA), mitochondrial
1193	10916	ACOAD9m	acyl-CoA dehydrogenase (isobutyryl-CoA), mitochondrial
1194	9596	ACOAHi	acetyl-CoA hydrolase
1195	2063	ACOAO7p	acyl-CoA oxidase (hexadecanoyl-CoA), peroxisomal
1196	3280	ACOATA	Acetyl-CoA ACP transacylase
1197	3511	ACODA	acetylornithine deacetylase
1198	285	ACONT	aconitase
1199	241	ACONTm	Aconitate hydratase
1200	13931	ACOX22x	acyl-Coenzyme A oxidase 2, branched chain
1201	9713	ACOX2x	acyl-Coenzyme A oxidase 2, branched chain
1202	120	ACP1(FMN)	acid phosphatase (FMN)
1203	2996	ACRNtm	O-acetylcarnintine transport into mitochondria via diffusion
1204	291	ACS	acetyl-CoA synthetase
1205	7891	ACS2	acetyl-CoA synthase (propionate)
1206	9605	ACSOMT	S-Adenosyl-L-methionine:N-acetylserotonin O-methyltransferase
1207	9606	ACSRTNMT	S-Adenosyl-L-homocysteine:N-acetylserotonin O-methyltransferase
1208	699	ACSm	acetyl-CoA synthetase
1209	14068	ACTLMO	acetol monooxygenase
1210	14063	ACTNMO	acetone monooxygenase
1211	7129	ACYP	acylphosphatase
1212	2190	ACt2m	acetate mitochondrial transport via proton symport
1213	1557	ACt2r	acetate reversible transport via proton symport
1214	20295	ACtg	acetate transport, Golgi apparatus
1215	3513	ADA	Adenosine deaminase
1216	9856	ADAe	Adenosine deaminase, extracellular
1217	10758	ADCim	Acetoacetate decarboxylation (irreversible), mitochondrial
1218	12546	ADEt	adenine reversible transport, cytosol
1219	12575	ADEtl	adenine facilated transport from lysosome
1220	19740	ADHAPtx	intracellular transport (peroxisome)
1221	181	ADK1	adenylate kinase
1222	1572	ADK1m	adenylate kinase, mitochondrial
1223	4682	ADK3	adentylate kinase (GTP)

Column	Reaction #	Abbreviation	Reaction Name
1224	1573	ADK3m	adentylate kinase (GTP)
1225	6806	ADKd	adenylate kinase (d form)
1226	303	ADMDC	adenosylmethionine decarboxylase
1227	2539	ADNCYC	adenylate cyclase
1228	179	ADNK1	adenosine kinase
1229	20320	ADNK1m	adenosine kinase, mitochondrial
1230	12541	ADNt	adenosine facilated transport in cytosol
1231	12054	ADNt4	adenosine transport (Na/Adn cotransport)
1232	12090	ADNt5	adenosine transport (1:2 Na/Adn cotransport)
1233	12579	ADNtl	adenosine facilated transport from lysosome
1234	12146	ADNtm	adenosine facilated transport in mitochondria
1235	9700	ADPGLC	ADPglucose diphosphatase
1236	9701	ADPMAN	ADPmannose diphosphatase
1237	2835	ADPRDP	ADPribose diphosphatase
1238	9699	ADPRDPm	ADPribose diphosphatase (mitochondrial)
1239	15046	ADPRIBt	ADPribose transport
1240	178	ADPT	adenine phosphoribosyltransferase
1241	13546	ADPtx	ADP transporter, peroxisomal
1242	14279	ADRNCOAtx	fatty acid intracellular transport
1243	19102	ADRNCPT1	carnitine O-palmitoyltransferase
1244	19121	ADRNCPT2	carnitine transferase
1245	19083	ADRNCRNt	transport into the mitochondria (carnitine)
1246	11932	ADRNLPVESSEC	Adrenaline secretion via secretory vesicle (ATP driven)
1247	12457	ADRNt	fatty acid transport via diffusion
1248	10024	ADSELK	adenylyl-selenate kinase
1249	2867	ADSK	adenylyl-sulfate kinase
1250	393	ADSL1	adenylosuccinate lyase
1251	394	ADSL2	adenylosuccinate lyase
1252	3516	ADSS	adenylosuccinate synthase
1253	19701	AFLATOXINte	xenobiotic transport
1254	11444	AG13T10g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus
1255	11445	AG13T11g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus
1256	11446	AG13T12g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus
1257	11447	AG13T13g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus
1258	11448	AG13T14g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus
1259	11449	AG13T15g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus
1260	11521	AG13T16g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus
1261	11524	AG13T17g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus
1262	11527	AG13T18g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus
1263	11424	AG13T1g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus
1264	11426	AG13T2g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus
1265	11430	AG13T3g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus
1266	11408	AG13T4g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus

Column	Reaction #	Abbreviation	Reaction Name
1267	11437	AG13T5g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus
1268	11440	AG13T6g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus
1269	11441	AG13T7g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus
1270	11442	AG13T8g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus
1271	11443	AG13T9g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus
1272	3518	AGDC	N-acetylglucosamine-6-phosphate deacetylase
1273	10803	AGLPC	alkyl acylglycerol phosphocholine transferase
1274	10800	AGLPED	alkyl acyl glycerophosphoethanolamine desaturase
1275	14715	AGLPET	alkyl acylglycerol phosphoethanolamine transferase
1276	10790	AGLPH	alkyl glycerol phosphate hydrolase
1277	10787	AGLPR	alkyl glycerol phosphate reductase
1278	10789	AGLPT	alkyl glycerol phosphate acyltransferase
1279	20198	AGMTm	agmatinase (m)
1280	14783	AGPAT1	1-acylglycerol-3-phosphate O-acyltransferase 1
1281	1338	AGPRim	N-acetyl-g-glutamyl-phosphate reductase, irreversible, mitochondrial
1282	10783	AGPSx	alkylglycerone phosphate synthase
1283	10786	AGPex	alkyl glycerol phosphate transport
1284	14006	AGTim	alanine-glyoxylate transaminase (irreversible), mitochondrial
1285	14008	AGTix	alanine-glyoxylate transaminase (irreversible), (peroxisomal)
1286	19766	AHANDROSTANGLCte	glucuronidated compound transport
1287	19748	AHANDROSTANGLCtr	glucuronidated compound transport
1288	366	AHC	adenosylhomocysteinase
1289	2264	AHCYStn	S-adenosyl-L-homocysteine nuclear transport
1290	20879	AHCYStr	S-Adenosyl-L-homocysteine intracellular diffusion
1291	8534	AHEXASE2ly	beta-N-acetylhexosaminidase, lysosomal
1292	8535	AHEXASEly	beta-N-acetylhexosaminidase, lysosomal
1293	396	AICART	phosphoribosylaminoimidazolecarboxamide formyltransferase
1294	1429	AIRCr	phosphoribosylaminoimidazole carboxylase
1295	4072	AKGDm	2-oxoglutarate dehydrogenase
1296	4314	AKGMALtm	alpha-ketoglutarate/malate transporter
1297	12174	AKGt4_3	AKG transport via sodium symport
1298	15151	AKGtp	AKG transporter, peroxisome
1299	13839	AKR1C1	aldo-keto reductase family 1, member C1 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihydrodiol dehydrogenase 4)
1300	9654	AKR1C41	aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihydrodiol dehydrogenase 4)
1301	9656	AKR1C42	aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihydrodiol dehydrogenase 4)
1302	9652	AKR1D	aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase)
1303	9653	AKR1D2	aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase)
1304	11849	ALAASNNaEx	L-alanine/L-asparagine Na-dependent exchange (Ala-L in)
1305	11836	ALACYSNaEx	L-alanine/L-cysteine Na-dependent exchange (Ala-L in)

Column	Reaction #	Abbreviation	Reaction Name
1306	11798	ALADGLNexR	L-alanine/glutamine reversible exchange
1307	11797	ALADGLYexR	D-alanine/glycine reversible exchange
1308	11847	ALAGLNNaEx	L-alanine/L-glutamine Na-dependent exchange (Ala-L in)
1309	11796	ALAGLNexR	L-alanine/glutamine reversible exchange
1310	11795	ALAGLYexR	L-alanine/glycine reversible exchange
1311	298	ALAR	alanine racemase
1312	11834	ALASERNaEx	L-alanine/L-serine Na-dependent exchange (Ala-L in)
1313	1818	ALASm	5-aminolevulinate synthase
1314	299	ALATA_L	L-alanine transaminase
1315	11838	ALATHRNaEx	L-alanine/L-threonine Na-dependent exchange (Ala-L in)
1316	1357	ALAt2r	L-alanine reversible transport via proton symport
1317	11681	ALAt2rL	L-alanine reversible transport via proton symport (lysosome)
1318	1422	ALAt4	Alanine-Sodium symporter
1319	11672	ALAtN1	Alanine transport (Na, H coupled)
1320	220	ALCD1	alcohol dehydrogenase (methanol)
1321	14167	ALCD21_D	alcohol dehydrogenase (D-1,2-propanediol)
1322	14166	ALCD21_L	alcohol dehydrogenase (L-1,2-propanediol)
1323	14169	ALCD22_D	alcohol dehydrogenase (D-lactaldehyde)
1324	14170	ALCD22_L	alcohol dehydrogenase (L-lactaldehyde)
1325	1211	ALCD2if	alcohol dehydrogenase, forward rxn (ethanol -> acetaldehyde)
1326	9528	ALCD2yf	alcohol dehydrogenase (ethanol, NADP), forward reaction
1327	2522	ALDD19x	aldehyde dehydrogenase (phenylacetaldehyde, NAD)
1328	9491	ALDD19x(P)	aldehyde dehydrogenase (phenylacetaldehyde, NADP)
1329	2391	ALDD20x	aldehyde dehydrogenase (indole-3-acetaldehyde, NAD)
1330	2392	ALDD20xm	aldehyde dehydrogenase (indole-3-acetaldehyde, NAD), mitochondrial
1331	14870	ALDD21	aldehyde dehydrogenase (pristanal, NAD)
1332	248	ALDD2x	aldehyde dehydrogenase (acetaldehyde, NAD)
1333	1524	ALDD2xm	aldehyde dehydrogenase (acetylaldehyde, NAD), mitochondrial
1334	249	ALDD2y	aldehyde dehydrogenase (acetaldehyde, NADP)
1335	19776	ALDSTRNte	aldosterone transport
1336	19775	ALDSTRNtm	aldosterone intracellular transport
1337	6820	ALKP	alkaline phosphatase
1338	11422	ALOX12	Arachidonate 12-lipoxygenase
1339	11423	ALOX12R	Arachidonate 12-lipoxygenase R
1340	10213	ALOX15	Arachidonate 15-lipoxygenase
1341	11421	ALOX5	Arachidonate 5-lipoxygenase
1342	19797	ALOX52	Arachidonate 5-lipoxygenase
1343	14752	ALR	Aldose reductase
1344	14160	ALR2	aldose reductase (methylglyoxal)
1345	14161	ALR3	aldose reductase (acetol)
1346	1395	AM6SAD	aminomuconate-semialdehyde dehydrogenase
1347	13927	AMACR2p	alpha-methylacyl-CoA racemase (reductase)
1348	13928	AMACR2r	alpha-methylacyl-CoA racemase (reductase)
1349	9673	AMACRp	alpha-methylacyl-CoA racemase
1350	9675	AMACRr	alpha-methylacyl-CoA racemase
1351	2615	AMANK	N-acetyl-D-mannosamine kinase
1352	2664	AMCOXO	2-aminomuconate reductase
1353	20880	AMETr	S-Adenosyl-L-methionine intracellular diffusion
1354	12111	AMETt2m	S-Adenosyl-L-methionine reversible transport, mitochondrial
1355	2265	AMETtn	S-adenosyl-L-methionine nuclear transport
1356	3569	AMPDA	Adenosine monophosphate deaminase

Column	Reaction #	Abbreviation	Reaction Name
1357	10876	AMPTASECG	alanyl aminopeptidase (cys-gly)
1358	10875	AMPTASECGe	alanyl aminopeptidase (cys-gly) (e)
1359	15149	AMPtp	AMP transporter, peroxisome
1360	13988	AMPtr	AMP transporter, endoplasmic reticulum
1361	10083	AMY1e	alpha-amylase, extracellular (strch1 -> strch2)
1362	10084	AMY2e	alpha-amylase, extracellular (glygn2 -> glygn4)
1363	19765	ANDRSTRNGLCte	glucuronidated compound transport
1364	20020	ANDRSTRNte	androsterone transport
1365	14986	ANDRSTRNtr	androsterone intracellular transport
1366	19702	ANTIPYRENEte	xenobiotic transport
1367	14657	AOBUTDsm	L-2-amino-3-oxobutanoate decarboxylation, mitochondrial
1368	10031	AP4AH1	Ap4A hydrolase, asymmetrically
1369	20181	APAT2rm	3-Aminopropanoate:2-oxoglutarate aminotransferase (m)
1370	20197	APNNOXte	xenobiotic transport
1371	14765	APOC-LYS-BTNP	proteolysis of apoC-Lys-btn
1372	14763	APOC-LYS-BTNPm	proteolysis of apoC-Lys-btn, mitochondrial
1373	14762	APOCF	Apocarboxylase formation
1374	14764	APOCFm	Apocarboxylase formation, mitochondrial
1375	20196	APPNNte	xenobiotic transport
1376	20022	APRGSTRNte	hydroxyprogesterone transport
1377	2980	APRTO2	N-acetylputrescine: oxygen oxireductase (deaminating)
1378	14690	AQCOBALt	Aquacob(III)alamin uptake
1379	2401	ARAB-Lt	L-arabinoase extracellular transport
1380	2051	ARABR	arabinose reductase
1381	19032	ARACHCOAtx	fatty acid intracellular transport
1382	19070	ARACHCPT1	carnitine transferase
1383	19071	ARACHCPT2	carnitine transferase
1384	19069	ARACHCRNt	transport into the mitochondria (carnitine)
1385	19043	ARACHDCOAtx	fatty acid intracellular transport
1386	12455	ARACHDt2	fatty acid transport via diffusion
1387	19800	ARACHDtr	intracellular transport
1388	12456	ARACHt	fatty acid transport via diffusion
1389	11475	ARGDCm	arginine decarboxylase (m)
1390	11878	ARGLYSex	Arginine/Lysine exchanger (Arg in)
1391	373	ARGN	arginase
1392	9719	ARGNm	arginase (m)
1393	2851	ARGSL	argininosuccinate lyase
1394	306	ARGSS	argininosuccinate synthase
1395	11703	ARGt4	L-arginine transport in via sodium symport
1396	11695	ARGtiDF	L-arginine transport via diffusion (extracellular to cytosol)
1397	5289	ARGtm	arginine mitochondrial transport via ornithine carrier
1398	11201	ARSA	Arylsulfatase A
1399	13646	ARTCOAL1	R group coenzyme a ligase
1400	13647	ARTCOAL2	R group coenzyme a ligase
1401	13648	ARTCOAL3	R group coenzyme a ligase
1402	14297	ARTFR11	R group artificial flux
1403	14298	ARTFR12	R group artificial flux (C16:1)
1404	18759	ARTFR13	R group artificial flux
1405	14311	ARTFR202	R group artificial flux (C18:3, n-3)
1406	14314	ARTFR203	R group artificial flux
1407	14313	ARTFR204	R group artificial flux
1408	14315	ARTFR205	R group artificial flux
1409	14316	ARTFR206	R group artificial flux
1410	14317	ARTFR207	R group artificial flux
1411	14318	ARTFR208	R group artificial flux
1412	14319	ARTFR209	R group artificial flux

Column	Reaction #	Abbreviation	Reaction Name
1413	14320	ARTFR210	R group artificial flux
1414	14321	ARTFR211	R group artificial flux
1415	14323	ARTFR212	R group artificial flux
1416	14324	ARTFR213	R group artificial flux
1417	14330	ARTFR31	R group artificial flux
1418	14331	ARTFR32	R group artificial flux
1419	14332	ARTFR33	R group artificial flux
1420	14333	ARTFR34	R group artificial flux
1421	14335	ARTFR41	R group artificial flux
1422	14336	ARTFR42	R group artificial flux
1423	14337	ARTFR43	R group artificial flux
1424	14338	ARTFR44	R group artificial flux
1425	14339	ARTFR45	R group artificial flux
1426	14340	ARTFR46	R group artificial flux
1427	14342	ARTFR51	R group artificial flux
1428	14343	ARTFR52	R group artificial flux
1429	14344	ARTFR53	R group artificial flux
1430	14345	ARTFR54	R group artificial flux
1431	14346	ARTFR55	R group artificial flux
1432	14347	ARTFR56	R group artificial flux
1433	14348	ARTFR57	R group artificial flux
1434	14350	ARTFR61	R group artificial flux
1435	13651	ARTPLM1	R group to palmitate conversion
1436	14736	ARTPLM1m	R group to palmitate conversion
1437	13653	ARTPLM2	R group to palmitate conversion
1438	14737	ARTPLM2m	R group to palmitate conversion
1439	13655	ARTPLM3	R group to palmitate conversion
1440	14738	ARTPLM3m	R group to palmitate conversion
1441	14377	ASAH1	N-acylsphingosine amidohydrolase
1442	10200	ASCBOX	ascorbic acid oxidase
1443	12131	ASCBt	L-ascorbate transport via facilitated diffusion
1444	12130	ASCBt4	L-ascorbate transport via proton symport
1445	11850	ASNALANaEx	L-alanine/L-asparagine Na-dependent exchange (Asn-L in)
1446	11858	ASNCYSNaEx	L-cysteine/L-asparagine Na-dependent exchange (Asn-L in)
1447	11864	ASNGLNNaEx	L-glutamine/L-asparagine Na-dependent exchange (Asn-L in)
1448	9381	ASNNm	L-asparaginase (mitochondrial)
1449	259	ASNS1	asparagine synthase (glutamine-hydrolysing)
1450	11854	ASNSERNaEx	L-serine/L-asparagine Na-dependent exchange (Asn-L in)
1451	11862	ASNTHRNaEx	L-threonine/L-asparagine Na-dependent exchange (Asn-L in)
1452	11691	ASNt4	L-asparagine transport in via sodium symport
1453	11674	ASNtN1	Asparagine transport (Na, H coupled)
1454	11989	ASNtm	L-asparagine transport, mitochondrial
1455	3426	ASP1DC	aspartate 1-decarboxylase
1456	9421	ASPCTr	aspartate carbamoyltransferase (reversible)
1457	11822	ASPDt6	D-aspartate transport via Na, H symport and K antiport
1458	11973	ASPDxt	D-aspartate transport, peroxisomal
1459	5291	ASPGLUm	aspartate-glutamate mitochondrial shuttle
1460	14515	ASPNATm	aspartate N-acetyltransferase, mitochondrial
1461	260	ASPTA	aspartate transaminase
1462	1453	ASPTAm	aspartate transaminase
1463	11821	ASPt6	L-aspartate transport via Na, H symport and K antiport
1464	20199	ATP1ter	ADP/ATP transporter, endoplasmic reticulum
1465	15056	ATP2ter	AMP/ATP transporter, endoplasmic reticulum

Column	Reaction #	Abbreviation	Reaction Name
1466	10439	ATPH1e	ATP diphosphohydrolase
1467	10441	ATPH2e	ATP diphosphohydrolase
1468	4621	ATPS4m	ATP synthase (four protons for one ATP)
1469	18553	ATPasel	V-type ATPase, H+ transporting, lysosomal
1470	2423	ATPtm	ADP/ATP transporter, mitochondrial
1471	14149	ATPtn	ATP diffusion in nucleus
1472	13545	ATPtx	ATP transporter, peroxisomal
1473	11414	AVITE1t	alpha-Tocopherol (Vit. E) transport
1474	11413	AVITE2t	alpha-tocotrienol (Vit. E) transport
1475	8438	A_MANASE	alpha-mannosidase
1476	8533	A_MANASEly	alpha-mannosidase, lysosomal
1477	11078	B3GALT3g	Beta-1,3-galactosyltransferase 3
1478	11132	B3GALT41g	Beta-1,3-galactosyltransferase 4
1479	11133	B3GALT42g	Beta-1,3-galactosyltransferase 4
1480	11134	B3GALT43g	Beta-1,3-galactosyltransferase 4
1481	11135	B3GALT44g	Beta-1,3-galactosyltransferase 4
1482	11081	B3GALT5g	Beta-1,3-galactosyltransferase 5
1483	14594	B3GALTg	Beta galactosyltransferase
1484	14627	B3GNT11g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1
1485	14670	B3GNT12g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1
1486	14621	B3GNT310g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus
1487	14632	B3GNT311g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus
1488	14639	B3GNT312g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus
1489	14644	B3GNT313g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus
1490	14661	B3GNT314g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus
1491	14672	B3GNT315g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus
1492	11061	B3GNT31g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus
1493	11062	B3GNT32g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus
1494	11063	B3GNT33g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus
1495	11117	B3GNT34g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus
1496	11067	B3GNT35g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus
1497	11068	B3GNT36g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus
1498	11116	B3GNT37g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus
1499	11140	B3GNT38g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus
1500	11263	B3GNT39g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus
1501	14592	B3GNT51g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5
1502	13899	BAAT1x	bile acid Coenzyme A: amino acid N-acyltransferase
1503	13900	BAAT2x	bile acid Coenzyme A: amino acid N-acyltransferase

Column	Reaction #	Abbreviation	Reaction Name
1504	13937	BAAT3x	bile acid Coenzyme A: amino acid N-acyltransferase
1505	13965	BAAT4x	bile acid Coenzyme A: amino acid N-acyltransferase
1506	13966	BAAT5x	bile acid Coenzyme A: amino acid N-acyltransferase
1507	5659	BACCL	biotin-[acetyl-CoA-carboxylase] ligase
1508	10498	BACCLm	biotin-[acetyl-CoA-carboxylase] ligase, mitochondrial
1509	11921	BALAVECSEC	B-alanine secretion via secretory vesicle (ATP driven)
1510	20188	BALAtmr	Beta-alanine reversible mitochondrial transport (diffusion)
1511	9767	BAMPPALDOX	beta-Aminopropion aldehyde:NAD+ oxidoreductase
1512	9766	BAMPPALDOXm	beta-Aminopropion aldehyde:NAD+ oxidoreductase (m)
1513	10956	BBHOX	4-Trimethylammoniobutanoate,2-oxoglutarate:oxygen oxidoreductase (3-hydroxylating)
1514	11010	BCDO	beta-Carotene dioxygenase
1515	11053	BDG2HCGHD	beta-D-Glucosyl-2-coumarinate glucohydrolase
1516	5490	BDHm	(R)-3-Hydroxybutanoate:NAD+ oxidoreductase
1517	7333	BDMT_L	GDPmannose:chitobiosyldiphosphodolichol beta-D-mannosyltransferase (liver)
1518	7334	BDMT_U	GDPmannose:chitobiosyldiphosphodolichol beta-D-mannosyltransferase (uterus)
1519	2506	BETALDHx	betaine-aldehyde dehydrogenase
1520	13252	BETALDHxm	betaine-aldehyde dehydrogenase, mitochondrial
1521	5493	BHBt	(R)-3-Hydroxybutanoate transport via H+ symport
1522	5494	BHBtm	(R)-3-Hydroxybutanoate mitochondrial transport via H+ symport
1523	9853	BHMT	betaine-homocysteine S-methyltransferase
1524	12277	BILDGLCURt	bilirubin beta-diglucuronide transport via bicarbonate countertransport
1525	19769	BILDGLCURte	bilirubin beta-diglucuronide transport MDR
1526	19752	BILDGLCURtr	glucuronidated compound transport
1527	12276	BILGLCURt	bilirubin monoglucuronide transport via bicarbonate countertransport
1528	19770	BILGLCURte	bilirubin monoglucuronide transport MDR
1529	19786	BILGLCURtr	glucuronidated compound transport
1530	5596	BILIRED	Nad(p)h biliverdin reductase
1531	12275	BILIRUBt2	bilirubin transport via bicarbonate countertransport
1532	14198	BILIRUBtr	lipid, flip-flop intracellular transport
1533	14767	BIOCYTtn	biocytin transport, nuclear
1534	11304	BMTer_L	B mannosyltransferase, endoplasmic reticulum
1535	11349	BMTer_U	B mannosyltransferase, endoplasmic reticulum
1536	351	BPNT	3',5'-bisphosphate nucleotidase
1537	15235	BPNT2	3',5'-bisphosphate nucleotidase (paps)
1538	10494	BTND1	biotinidase (biotin)
1539	14766	BTND1n	biotinidase (biotin), nuclear
1540	10491	BTNDe	biotinidase (biotin), extracellular
1541	12132	BTNDm	biotinidase (biotin), mitochondrial
1542	14755	BTNPL	holocarboxylase synthestase (biotin protein ligase)
1543	14756	BTNPLm	holocarboxylase synthestase (biotin protein ligase), mitochondrial
1544	1750	BTNt2	Biotin reversible transport via proton symport
1545	14774	BTNt2m	Biotin reversible transport via proton symport, mitochondria
1546	10480	BTNt3i	Biotin transport via sodium symport
1547	14017	BTNt4i	Biotin uptake (antiport)
1548	14768	BTNtn	Biotin transport, nuclear
1549	19604	BUP2	beta-ureidopropionase (D-3-amino-isobutanoate forming)
1550	14990	BUTt2m	Butyrate mitochondrial transport via proton symport, reversible

Column	Reaction #	Abbreviation	Reaction Name
1551	2611	BUTt2r	Butyrate transport via proton symport, reversible
1552	11415	BVITEt	beta-Tocopherol (Vit. E) transport
1553	20878	BZt	benzoate transport (diffusion)
1554	13982	BZtr	Benzene transporter, endoplasmic reticulum
1555	8536	B_MANNASEly	beta-mannosidase, lysosomal
1556	13155	C110CPT2m	C110 transport into the mitochondria
1557	9754	C14STRr	C-14 sterol reductase
1558	4094	C160CPT1	carnitine O-palmitoyltransferase
1559	4093	C160CPT2	C160 transport into the mitochondria
1560	4104	C160CRNt	C160 transport into the mitochondria
1561	12961	C161CPT1	carnitine O-palmitoyltransferase
1562	20156	C161CPT12	carnitine O-palmitoyltransferase
1563	12962	C161CPT2	C161 transport into the mitochondria
1564	20157	C161CPT22	C161 transport into the mitochondria
1565	20158	C161CRN2t	C161 transport into the mitochondria
1566	12963	C161CRNt	C161 transport into the mitochondria
1567	4095	C180CPT1	carnitine O-stearoyl transferase
1568	4101	C180CPT2	carnitine O-stearoyl transferase
1569	4103	C180CRNt	C180 transport into the mitochondria
1570	4100	C181CPT1	carnitine octadecenoyl transferase
1571	4195	C181CPT2	carnitine octadecenoyl transferase
1572	4102	C181CRNt	C181 transport into the mitochondria
1573	4203	C204CPT1	carnitine C20:4 transferase
1574	4204	C204CPT2	arachidonic acid transport into the mitochondria
1575	4201	C204CRNt	arachidonic acid transport into the mitochondria
1576	14282	C226COAtx	fatty acid intracellular transport
1577	4206	C226CPT1	carnitine C22:6 transferase
1578	4207	C226CPT2	C226 transport into the mitochondria
1579	4205	C226CRNt	C226 transport into the mitochondria
1580	11033	C2M26DCOAHLm	cis-2-Methyl-5-isopropylhexa-2,5-dienoyl-CoA hydro-lyase (m)
1581	11044	C2M26DCOAHLx	cis-2-Methyl-5-isopropylhexa-2,5-dienoyl-CoA hydro-lyase (x)
1582	11410	C3STDH1Pr	C-3 sterol dehydrogenase (4-methylzymosterol)
1583	9756	C3STDH1r	C-3 sterol dehydrogenase (4-methylzymosterol)
1584	9762	C3STKR2r	C-3 sterol keto reductase (zymosterol)
1585	9755	C4STMO1r	C-4 sterol methyl oxidase (4,4-dimethylzymosterol)
1586	11411	C4STMO2Pr	C-4 methyl sterol oxidase
1587	9761	C4STMO2r	C-4 methyl sterol oxidase
1588	15219	CAATPS	Ca ATPase
1589	12621	CAMPt	cAMP transport (ATP-dependent)
1590	11002	CAROtr	beta-carotene transport via diffusion
1591	20194	CARVEOLte	xenobiotic transport
1592	19462	CAT2p	catalase A, peroxisomal (ethanol)
1593	4414	CATm	catalase
1594	3223	CATp	catalase A, peroxisomal
1595	12697	CAt7r	calcium / sodium antiporter (1:3), reversible
1596	14693	CBL2OR	NADH:cob(III)alamine oxidoreductase
1597	14694	CBL2tm	Cob(II)alamine transport, mitochondrial
1598	14689	CBLATm	cob(I)alamin adenosyltransferase, mitochondrial
1599	19467	CBPPer	Carbamoyl phosphate phosphotransferase, endoplasmic reticulum
1600	2852	CBPS	carbamoyl-phosphate synthase (glutamine-hydrolysing)
1601	9380	CBPSam	carbamoyl-phosphate synthase (ammonia) (mitochondria
1602	19464	CBPter	carbamoyl phosphate transport, endoplasmic reticulum
1603	11884	CBR1	Carbonyl reductase [NADPH] 1

Column	Reaction #	Abbreviation	Reaction Name
1604	11885	CBR2	Carbonyl reductase [NADPH] 1
1605	11399	CCA_D3t	Calcitroic acid transport from cytosol
1606	11397	CCA_D3tm	Calcitroic acid transport from mitochondria
1607	10937	CDIPTr	phosphatidylinositol synthase (Homo sapiens)
1608	19810	CDPDAGtm	intracellular transport
1609	10564	CDS	phosphatidate cytidylyltransferase
1610	10565	CDSm	phosphatidate cytidylyltransferase
1611	10537	CEPTC	choline phosphotransferase
1612	10538	CEPTE	ethanolamine phosphotransferase
1613	11204	CERK	Ceramide kinase
1614	13387	CERT1gt	ceramide transport protein
1615	13388	CERT1rt	ceramide transport protein
1616	13389	CERT2gt	ceramide transport protein
1617	13390	CERT2rt	ceramide transport protein
1618	11955	CGLYt3(2)	Cys-Gly transport in via proton symport
1619	12622	CGMPt	cGMP transport (ATP-dependent)
1620	9565	CH25H	cholesterol 25-hydroxylase
1621	11892	CHAT	Choline O-acetyltransferase
1622	11893	CHATn	Choline O-acetyltransferase
1623	11899	CHLP	choline phosphate phosphatase
1624	2382	CHLPCTD	choline phosphate cytididyltransferase
1625	13321	CHLtm	choline transport via diffusion (cytosol to mitochondria)
1626	12266	CHOLATEt	cholate transport via bicarbonate countertransport
1627	12616	CHOLATEt2	cholate transport via sodium cotransport
1628	12667	CHOLATEt3	ABC bile acid transporter
1629	9847	CHOLD2m	choline dehydrogenase (FAD acceptor), mitochondrial
1630	2383	CHOLK	Choline kinase
1631	20346	CHOLPtg	choline phosphate intracellular transport
1632	20345	CHOLPtl	choline phosphate intracellular transport
1633	12129	CHOLt4	choline, sodium cotransport
1634	20154	CHOLtg	choline intracellular transport
1635	19524	CHOLtn	Choline transport, nuclear through pores
1636	20155	CHOLtr	choline intracellular transport
1637	12197	CHOLtu	Choline uniport
1638	19773	CHSTEROLSULT	steroid sulfotransferase
1639	12591	CHSTEROLt	cholesterol efflux (ATP depedent)
1640	13535	CHSTEROLt1	cholesterol intracellular transport
1641	13536	CHSTEROLt2	cholesterol intracellular transport
1642	13537	CHSTEROLt3	cholesterol intracellular transport
1643	12601	CHSTEROLtg	cholesterol efflux (ATP depedent), golgi
1644	13713	CHTNASE	chitinase
1645	13712	CHTNASEe	chitinase, extracellular
1646	2302	CITL	Citrate lyase
1647	10811	CITMCOAHm	L-Citramalyl-CoA hydro-lyase, mitochondrial
1648	10812	CITMCOALm	L-Citramalyl-CoA pyruvate-lyase
1649	5288	CITRtm	citrulline mitochondrial transport via proton antiport
1650	12166	CITt4_2	citrate transport via sodium symport
1651	12171	CITt4_4	citrate transport via sodium symport
1652	763	CITtam	citrate transport, mitochondrial
1653	878	CITtbm	citrate transport, mitochondrial
1654	4525	CK	ATP Creatine kinase
1655	9725	CKc	ATP Creatine kinase (c)
1656	12365	CLFORtex	chloride transport via formate countertransport
1657	12367	CLFORtex2	chloride transport via formate countertransport (2:1)
1658	12368	CLHCO3tex2	chloride transport via bicarbonate countertransport (2:1)
1659	12363	CLHCOtex	chloride transport via bicarbonate countertransport

Column	Reaction #	Abbreviation	Reaction Name
1660	12364	CLI2tex	chloride transport via iodide countertransport
1661	12369	CLOHtex2	chloride transport via hydroxide countertransport (2:1)
1662	12366	CLOXAtex2	chloride transport via oxalate countertransport (2:1)
1663	14281	CLPNDCOAtx	fatty acid intracellular transport
1664	19107	CLPNDCPT1	carnitine O-palmitoyltransferase
1665	19126	CLPNDCPT2	carnitine transferase
1666	19088	CLPNDCRNt	transport into the mitochondria (carnitine)
1667	12461	CLPNDt	fatty acid transport via diffusion
1668	10866	CLS_hs	cardiolipin synthase (homo sapiens)
1669	12141	CMPACNAtg	CMP-Sia Golgi transport via CMP antiport
1670	15228	CMPACNAtn	CMP-Sia nuclear export
1671	10638	CMPSAS	CMP sialic acid synthase
1672	10639	CMPSASn	CMP sialic acid synthase, nuclear
1673	1296	CO2t	CO2 transporter via diffusion
1674	2244	CO2ter	CO2 endoplasmic reticular transport via diffusion
1675	2157	CO2tg	CO2 Golgi transport
1676	2756	CO2tm	CO2 transport (diffusion), mitochondrial
1677	1278	CO2tn	CO2 nuclear transport via diffusion
1678	2150	CO2tp	CO2 peroxisomal transport
1679	14655	COAtl	CoA transport in lysosome via diffusion
1680	4074	COAtm	CoA transporter
1681	1535	COAtn	coenzyme A transport, nuclear
1682	1317	COAtp	coenzyme A transport, peroxisomal
1683	13989	COAtr	COA transporter, endoplasmic reticulum
1684	11139	COKECBESr	Carboxylesterase (cocaine) (er)
1685	11131	COQ3m	methyltransferase COQ3
1686	11120	COQ5m	Ubiquinone biosynthesis methyltransferase COQ5
1687	11118	COQ6m	Ubiquinone biosynthesis monooxgenase COQ6
1688	11128	COQ7m	Ubiquinone biosynthesis COQ7
1689	8571	CORE2GTg	Core 2 acetylglucosaminyltransferase, Golgi apparatus
1690	8575	CORE3GTg	Core 3 beta-GlcNAc-transferase, Golgi apparatus
1691	8576	CORE4GTg	Core 4 beta6-GalNAc-transferase, Golgi apparatus
1692	8606	CORE5GTg	Core 5 alpha-GalNAc-transferase, Golgi apparatus
1693	8577	CORE6GTg	Core 6 beta-GlcNAc-transferase A, Golgi apparatus
1694	8607	CORE7GTg	Core 7 alpha-GalNAc-transferase, Golgi apparatus
1695	8608	CORE8GTg	N-acetylgalactosamine 3-alpha-galactosyltransferase, Golgi apparatus
1696	14225	COUCOAFm	p-coumaroyl-CoA formation
1697	19703	COUMARINte	xenobiotic transport
1698	8578	COt	CO transporter via diffusion
1699	9960	CPCTDTX	choline-phosphate cytidylyltransferase
1700	1650	CPPPGO	coproporphyrinogen oxidase (O2 required)
1701	11947	CREATt4(2)r	Creatine transport (sodium symport) (2:1)
1702	14382	CREATtmdiffir	Creatine transport to/from mitochondria via diffusion
1703	20203	CRMPte	crmp_hs transport
1704	15148	CRNCAR3tp	carnitine-propcarnitine carrier, peroxisomal
1705	3221	CRNCARtp	carnitine-acetylcarnitine carrier, peroxisomal
1706	2971	CRNt	L-carnitine reversible transport
1707	12201	CRNtHa	L-carnitine outward transport (H+ antiport)
1708	1518	CRNtim	L-carnitine transport out of mitochondria via diffusion
1709	12199	CRNtuIR	L-carnitine inward uniport
1710	12202	CRNtuNa	L-carnitine inward transport by Na+ symport
1711	13158	CRNtx	carnitine transport peroxisome to mitochondria
1712	14453	CRTNsyn	Creatinine synthase
1713	19792	CRTSLtm	cortisol intracellular transport
1714	19791	CRTSLtr	cortisol intracellular transport

Column	Reaction #	Abbreviation	Reaction Name
1715	19793	CRTSTRNtm	corticosterone intracellular transport
1716	19794	CRTSTRNtr	corticosterone intracellular transport
1717	12462	CRVNCtr	fatty acid transport via diffusion
1718	14403	CSAPASEly	chondroitin sulfate A proteoglycan protease, lysosome (endosome)
1719	14412	CSBPASEly	chondroitin sulfate B proteoglycan protease, lysosome (endosome)
1720	14418	CSCPASEly	chondroitin sulfate C proteoglycan protease, lysosome (endosome)
1721	14428	CSDPASEly	chondroitin sulfate D proteoglycan protease, lysosome (endosome)
1722	14438	CSEPASEly	chondroitin sulfate E proteoglycan protease, lysosome (endosome)
1723	8427	CSNAT2m	carnitine O-aceyltransferase, mitochondrial
1724	13157	CSNAT2x	carnitine dimethyl nonanoyl transferase, revsible, peroxisomal
1725	20844	CSNAT3x	carnitine O-aceyltransferase, peroxisomal
1726	9423	CSNATer	carnitine O-acetyltransferase, endolasmic reticulum
1727	8411	CSNATm	carnitine O-aceyltransferase, mitochondrial
1728	4168	CSNATp	carnitine O-acetyltransferase, reverse direction, peroxisomal
1729	4163	CSNATr	carnitine O-acetyltransferase
1730	3526	CSND	Cytosine deaminase
1731	12552	CSNt	cytosine transport via facilated diffusion
1732	14949	CSPG_At	chondroitin sulfate A transport, golgi to extracellular
1733	14954	CSPG_Atly	chondroitin sulfate A transport, extracellular to lysosome
1734	14950	CSPG_Bt	chondroitin sulfate B transport, golgi to extracellular
1735	14955	CSPG_Btly	chondroitin sulfate B transport, extracellular to lysosome
1736	14951	CSPG_Ct	chondroitin sulfate C transport, golgi to extracellular
1737	14956	CSPG_Ctly	chondroitin sulfate C transport, extracellular to lysosome
1738	14952	CSPG_Dt	chondroitin sulfate D transport, golgi to extracellular
1739	14957	CSPG_Dtly	chondroitin sulfate D transport, extracellular to lysosome
1740	14953	CSPG_Et	chondroitin sulfate E transport, golgi to extracellular
1741	14958	CSPG_Etly	chondroitin sulfate E transport, extracellular to lysosome
1742	12	CSm	citrate synthase
1743	3571	CTPS1	CTP synthase (NH3)
1744	2696	CTPS2	CTP synthase (glutamine)
1745	14148	CTPtn	CTP diffusion in nucleus
1746	11817	CYANSTm	Cyanide sulfurtransferase, mitochondrial
1747	20242	CYANt	Cyanide transport via diffusion (extracellular to cytosol)
1748	20243	CYANtm	Cyanide transport via diffusion (mitochondrial)
1749	4924	CYOOm3	cytochrome c oxidase, mitochondrial Complex IV
1750	4545	CYOR-u10m	ubiquinol-6 cytochrome c reductase, Complex III
1751	11837	CYSALANaEx	L-alanine/L-cysteine Na-dependent exchange (Cys-L in)
1752	14685	CYSAMO	Cysteamine oxygenase
1753	11857	CYSASNNaEx	L-cysteine/L-asparagine Na-dependent exchange (Cys-L in)
1754	11855	CYSGLNNaEx	L-cysteine/L-glutamine Na-dependent exchange (Cys-L in)
1755	11808	CYSGLTH	Glutathione:cystine oxidoreductase
1756	11801	CYSGLUexR	L-cysteine/L-glutamine reversible exchanger
1757	11772	CYSGLYex	L-cysteine/glycine exchanger
1758	11802	CYSGLYexR	L-cysteine/glycine reversible exchanger
1759	11813	CYSLYSL	L-Cystine Lysteine-lyase (deaminating)
1760	5800	CYSO	cysteine oxidase
1761	11841	CYSSERNaEx	L-serine/L-cysteine Na-dependent exchange (Cys-L in)
1762	11815	CYSTA	cysteine transaminase

Column	Reaction #	Abbreviation	Reaction Name
1763	11816	CYSTAm	cysteine transaminase (mitochondrial)
1764	1592	CYSTGL	cystathionine g-lyase
1765	11881	CYSTGLUex	L-cystine/L-glutamate exchanger
1766	11846	CYSTHRNaEx	L-cysteine/L-threonine Na-dependent exchange (Cys-L in)
1767	1588	CYSTS	cystathionine beta-synthase
1768	11880	CYSTSERex	L-cystine/glycine exchanger (cystine in)
1769	11952	CYSt4	L-cysteine reversible transport via sodium symport
1770	11929	CYStec	L-cysteine transport via diffusion (extracellular to cytosol)
1771	3527	CYTD	cytidine deaminase
1772	438	CYTDK1	cytidine kinase (ATP)
1773	20319	CYTDK2m	cytidine kinase (ATP), mitochondrial
1774	10099	CYTDn	cytidine deaminase, nuclear
1775	12544	CYTDt	cytidine facilated transport in cytosol
1776	7882	CYTDt4	cytidine transport in via sodium symport
1777	12144	CYTDt5	cytidine transport (1:2 Na/cytd cotransport)
1778	12574	CYTDtl	Cytidine facilated transport from lysosome
1779	12150	CYTDtm	cytidine facilated transport in mitochondria
1780	19530	CYTDtn	cytidine transport in nucleus
1781	184	CYTK1	cytidylate kinase (CMP)
1782	10261	CYTK10	cytidylate kinase (CMP,dGTP)
1783	10262	CYTK10n	cytidylate kinase (CMP,dGTP),nuclear
1784	10265	CYTK11	cytidylate kinase (dCMP,dGTP)
1785	10266	CYTK11n	cytidylate kinase (dCMP,dGTP),nuclear
1786	10269	CYTK12	cytidylate kinase (dCMP,dCTP)
1787	10270	CYTK12n	cytidylate kinase (dCMP,dCTP),nuclear
1788	10271	CYTK13	cytidylate kinase (dCMP,dATP)
1789	10272	CYTK13n	cytidylate kinase (dCMP,dATP),nuclear
1790	10273	CYTK14	cytidylate kinase (dCMP,UTP)
1791	10274	CYTK14n	cytidylate kinase (dCMP,CTP),nuclear
1792	20318	CYTK1m	cytidylate kinase (CMP),mitochondrial
1793	10230	CYTK1n	cytidylate kinase (CMP),nuclear
1794	185	CYTK2	cytidylate kinase (dCMP)
1795	10231	CYTK2n	cytidylate kinase (dCMP),nuclear
1796	10077	CYTK3	cytidylate kinase (CMP)(GTP)
1797	10236	CYTK3n	cytidylate kinase (dCMP,CTP),nuclear
1798	10078	CYTK4	cytidylate kinase (dCMP)(GTP)
1799	10248	CYTK4n	cytidylate kinase (dCMP,GTP),nuclear
1800	10249	CYTK5	cytidylate kinase (dCMP)
1801	10252	CYTK5n	cytidylate kinase (CMP),nuclear
1802	10254	CYTK6	cytidylate kinase (CMP,CTP)
1803	10253	CYTK6n	cytidylate kinase (CMP,CTP),nuclear
1804	10255	CYTK7	cytidylate kinase (CMP,UTP)
1805	10256	CYTK7n	cytidylate kinase (CMP,UTP),nuclear
1806	10257	CYTK8	cytidylate kinase (CMP,dATP)
1807	10258	CYTK8n	cytidylate kinase (CMP,dATP),nuclear
1808	10259	CYTK9	cytidylate kinase (CMP,dCTP)
1809	10260	CYTK9n	cytidylate kinase (CMP,dCTP),nuclear
1810	19605	D-3AIBt	D-3-amino-isobutyrate transport
1811	2056	D-LACt2	D-lactate transport via proton symport
1812	1078	D-LACtm	D-lactate transport, mitochondrial
1813	19601	D3AIBTm	D-3-Amino-isobutanoate:pyruvate aminotransferase, mitochondrial
1814	3514	DADA	Deoxyadenosine deaminase
1815	9855	DADAe	Deoxyadenosine deaminase, extracellular
1816	160	DADNK	deoxyadenosine kinase
1817	10407	DADNt4	deoxyadenosine transport via diffusion

Column	Reaction #	Abbreviation	Reaction Name
1818	10902	DAGK_hs	Diacylglycerol phosphate kinase (homo sapiens)
1819	10903	DAGKn_hs	Diacylglycerol phosphate kinase (homo sapiens)
1820	20130	DAG_HSter	diacylglycerol ER export
1821	11515	DALAOXx	D-Alanine Oxidase (x)
1822	1322	DALAt2r	D-alanine transport via proton symport
1823	11684	DALAt2rL	D-alanine transport via proton symport (lysosome)
1824	11516	DALAxt	D-Alanine transport to perixosome
1825	10870	DARGOp	D-arginine oxidase, perixosomal
1826	10205	DASCBH	L-Dehydroascorbate lactonohydrolase
1827	10203	DASCBR	dehydroascorbate reductase
1828	11972	DASPO1p	D-aspartate oxidase, peroxisomal
1829	14132	DATPtn	dATP diffusion in nucleus
1830	13239	DCIm	dodecenoyl-Coenzyme A delta isomerase
1831	20249	DCK1m	Deoxycytidine kinase, mitochondrial (ATP)
1832	9845	DCK1n	Deoxycytidine kinase, nuclear (ATP)
1833	9846	DCK2n	Deoxycytidine kinase, nuclear (UTP)
1834	3567	DCMPDA	dCMP deaminase
1835	14280	DCSPTN1COAtx	fatty acid intracellular transport
1836	19106	DCSPTN1CPT1	carnitine O-palmitoyltransferase
1837	19125	DCSPTN1CPT2	carnitine transferase
1838	19087	DCSPTN1CRNt	transport into the mitochondria (carnitine)
1839	12460	DCSPTN1t	fatty acid transport via diffusion
1840	1483	DCT	Dopachrome tautomerase
1841	14135	DCTPtn	dCTP diffusion in nucleus
1842	3528	DCYTD	deoxycytidine deaminase
1843	10098	DCYTDn	deoxycytidine deaminase, nuclear
1844	10409	DCYTt	deoxycytidine transport via diffusion
1845	13838	DDPGAm	2-dehydro-3-deoxy-phosphogluconate aldolase, mitochondrial
1846	12283	DEBRISOQUINEt	debrisoquine uniport
1847	14239	DECDPtm	lipid, flip-flop intracellular transport
1848	7531	DEDOLP1_L	dehydrodolichol diphosphate phosphatase (liver)
1849	7548	DEDOLP1_U	dehydrodolichol diphosphate phosphatase (uterus)
1850	7540	DEDOLP2_L	dehydrodolichol phosphate phosphatase (liver)
1851	7550	DEDOLP2_U	dehydrodolichol phosphate phosphatase (uterus)
1852	7544	DEDOLR_L	dehydrodolichol reductase (liver)
1853	7551	DEDOLR_U	dehydrodolichol reductase (uterus)
1854	10335	DESAT16_2	palmitoyl-CoA desaturase (n-C16:0CoA -> n-C16:1CoA)
1855	10346	DESAT18_10	fatty acyl-CoA desaturase (n-C18:2CoA -> n-C18:3CoA)
1856	10336	DESAT18_3	stearoyl-CoA desaturase (n-C18:0CoA -> n-C18:1CoA)
1857	10337	DESAT18_4	stearoyl-CoA desaturase (n-C18:0CoA -> n-C18:1CoA)
1858	10338	DESAT18_5	stearoyl-CoA desaturase (n-C18:0CoA -> n-C18:1CoA)
1859	10340	DESAT18_6	fatty acyl-CoA desaturase (n-C18:1CoA -> n-C18:2CoA)
1860	10341	DESAT18_7	fatty acyl-CoA desaturase (n-C18:1CoA -> n-C18:2CoA)
1861	10342	DESAT18_8	fatty acyl-CoA desaturase (n-C18:1CoA -> n-C18:2CoA)
1862	10348	DESAT18_9	fatty acyl-CoA desaturase (n-C18:2CoA -> n-C18:3CoA)
1863	10354	DESAT20_1	fatty acyl-CoA desaturase (n-C20:3CoA -> n-C20:4CoA)
1864	10357	DESAT20_2	fatty acyl-CoA desaturase (n-C20:4CoA -> n-C20:5CoA)
1865	10362	DESAT22_1p	fatty acyl-CoA desaturase (n-C22:4CoA -> n-C22:5CoA)
1866	14107	DESAT22_2p	fatty acyl-CoA desaturase (n-C22:5CoA -> n-C22:6CoA)
1867	14278	DESAT24_1	fatty acyl-CoA desaturase (n-C24:5CoA -> n-C24:6CoA)
1868	14782	DGAT	diacylglycerol acyltransferase
1869	19650	DGCHOLte	bile acid intracellular transport
1870	19649	DGCHOLtx	bile acid intracellular transport
1871	2814	DGK1	deoxyguanylate kinase (dGMP:ATP)
1872	20315	DGK2m	deoxyguanylate kinase (dGMP:dATP) (mitochondrial)

Column	Reaction #	Abbreviation	Reaction Name
1873	4500	DGNSKm	deoxyguanosine kinase
1874	10410	DGSNt	deoyguanosine transport via diffusion
1875	20316	DGSNtm	deoyguanosine transport in mitochondria
1876	14133	DGTPtn	dGTP diffusion in nucleus
1877	10154	DGULND	dehydro-L-gulonate decarboxylase
1878	11913	DHAAt1r	dehydroascorbate transport (uniport)
1879	14356	DHAPA	dihydroxyacetone phosphate acyltransferase
1880	14357	DHAPAx	dihydroxyacetone phosphate acyltransferase
1881	14186	DHCHOLESTANATEtm	lipid, flip-flop intracellular transport
1882	9779	DHCR241r	24-dehydrocholesterol reductase [Precursor]
1883	9780	DHCR242r	24-dehydrocholesterol reductase [Precursor]
1884	9781	DHCR243r	24-dehydrocholesterol reductase [Precursor]
1885	9777	DHCR71r	7-dehydrocholesterol reductase
1886	9778	DHCR72r	7-dehydrocholesterol reductase
1887	10891	DHCRD1	dihydroceramide desaturase
1888	10892	DHCRD2	dihydroceramide desaturase
1889	11094	DHDPBMTm	dihydroxydecaprenylbenzoate methyltransferase
1890	12069	DHEASULT	Dehydroepiandrosterone sulfotransferase
1891	12269	DHEASt	dehydroepiandrosterone sulfate transport via bicarbonate countertransport
1892	19777	DHEAStr	dheas intracellular transport
1893	77	DHFR	dihydrofolate reductase
1894	14904	DHFtl	dihydrofolate reversible lysosomal transport
1895	1758	DHFtm	dihydrofolate reversible mitochondrial transport
1896	12084	DHORD9	dihydoorotic acid dehydrogenase (quinone10)
1897	444	DHORTS	dihydroorotase
1898	92	DHPM1	dihydropyrimidinase (5,6-dihydrouracil)
1899	61	DHPM2	dihydropyrimidinase (dihydrothymine)
1900	14579	DHPR	6,7-dihydropteridine reductase
1901	14582	DHPR2	6,7-dihydropteridine reduction
1902	19533	DIDPtn	dIDP nuclear transport
1903	20226	DIGALSGALSIDEte	digalsgalside_hs transport
1904	20210	DIGALSGALSIDEtg	digalsgalside_hs intracellular transport
1905	20137	DIGALSIDEtg	digalside_hs intracellular transport
1906	20136	DIGALSIDEtl	digalside_hs intracellular transport
1907	10412	DINt	deoxyinosine transport via diffusion
1908	19534	DITPtn	dITP nuclear transport
1909	1631	DKMPPD	2,3-diketo-5-methylthio-1-phosphopentane degradation reaction
1910	19100	DLNLCGCPT1	carnitine O-palmitoyltransferase
1911	19119	DLNLCGCPT2	carnitine transferase
1912	19081	DLNLCGCRNt	transport into the mitochondria (carnitine)
1913	12464	DLNLCGt	fatty acid transport via diffusion
1914	19714	DMANTIPYRINEte	xenobiotic transport
1915	108	DMATT	dimethylallyltranstransferase
1916	9743	DMATTx	dimethylallyltranstransferase
1917	11701	DMGDHm	dimethylglycine dehydrogenase, mitochondrial
1918	13323	DMGtm	dimethylglycine transport via diffusion (cytosol to mitochondria)
1919	20832	DMHPTCRNCPT1	carnitine fatty-acyl transferase
1920	20339	DMHPTCRNCPT2	2,6 dimethylheptanoly CoA carnitine transferase
1921	20340	DMHPTCRNt	2,6 dimethylheptanoyl crn transport
1922	20341	DMHPTCRNte	2,6 dimethylheptanoyl carnitine transport
1923	760	DM_nadh	demand NADH
1924	13541	DM_nadh(m)	demand NADH(m)
1925	761	DM_nadph	NADPH demand

Column	Reaction #	Abbreviation	Reaction Name
1926	2796	DNADDP	Deaminido NAD diphosphatase
1927	19528	DNADtn	dNAD transport, nuclear trhough pore
1928	11357	DNAMTSEn	DNA (cytosine-5-)-methyltransferase, nucleus
1929	10183	DNAMTn	DNA (cytosine-5-)-methyltransferase, nucleus
1930	11183	DNDPt10m	dADP transport via dCDP antiport
1931	11184	DNDPt11m	dADP transport via dGDP antiport
1932	11185	DNDPt12m	dADP transport via ADP antiport
1933	11186	DNDPt13m	dADP transport via ATP antiport
1934	11187	DNDPt14m	dUDP transport via dTDP antiport
1935	11188	DNDPt15m	dUDP transport via dGDP antiport
1936	11189	DNDPt16m	dUDP transport via dADP antiport
1937	11190	DNDPt17m	dUDP transport via dCDP antiport
1938	11191	DNDPt18m	dUDP transport via ADP antiport
1939	11193	DNDPt19m	dUDP transport via ATP antiport
1940	11165	DNDPt1m	dATP transport via ADP antiport
1941	11209	DNDPt20m	dTDP transport via ATP antiport
1942	11210	DNDPt21m	dTDP transport via ADP antiport
1943	11211	DNDPt22m	dTDP transport via dUDP antiport
1944	11212	DNDPt23m	dTDP transport via dGTP antiport
1945	11214	DNDPt24m	dTDP transport via dADP antiport
1946	11215	DNDPt25m	dTDP transport via dCDP antiport
1947	11216	DNDPt26m	dCDP transport via dUDP antiport
1948	11217	DNDPt27m	dCDP transport via dTDP antiport
1949	11218	DNDPt28m	dCDP transport via dGDP antiport
1950	11219	DNDPt29m	dCDP transport via dADP antiport
1951	11166	DNDPt2m	dATP transport via ATP antiport
1952	11220	DNDPt30m	dCDP transport via ADP antiport
1953	11221	DNDPt31m	dCDP transport via ATP antiport
1954	11222	DNDPt32m	dGDP transport via ATP antiport
1955	11223	DNDPt33m	dGDP transport via dUDP antiport
1956	11224	DNDPt34m	dGDP transport via dTDP antiport
1957	11225	DNDPt35m	dGDP transport via dADP antiport
1958	11226	DNDPt36m	dGDP transport via dCDP antiport
1959	11227	DNDPt37m	dUTP transport via dTDP antiport
1960	11229	DNDPt38m	dUTP transport via dUDP antiport
1961	11230	DNDPt39m	dUTP transport via dGDP antiport
1962	11176	DNDPt3m	dATP transport via dCDP antiport
1963	11231	DNDPt40m	dUTP transport via dADP antiport
1964	11232	DNDPt41m	dUTP transport via dCDP antiport
1965	11233	DNDPt42m	dUTP transport via ADP antiport
1966	11234	DNDPt43m	dUTP transport via ATP antiport
1967	11235	DNDPt44m	dTTP transport via ATP antiport
1968	11236	DNDPt45m	dTTP transport via ADP antiport
1969	11237	DNDPt46m	dTTP transport via dUDP antiport
1970	11238	DNDPt47m	dTTP transport via dTDP antiport
1971	11239	DNDPt48m	dTTP transport via dGDP antiport
1972	11240	DNDPt49m	dTTP transport via dADP antiport
1973	11175	DNDPt4m	dATP transport via dUDP antiport
1974	11241	DNDPt50m	dTTP transport via dCDP antiport
1975	11242	DNDPt51m	dCTP transport via dCDP antiport
1976	11243	DNDPt52m	dCTP transport via dUDP antiport
1977	11244	DNDPt53m	dCTP transport via dGDP antiport
1978	11245	DNDPt54m	dCTP transport via dADP antiport
1979	11246	DNDPt55m	dCTP transport via ADP antiport
1980	11247	DNDPt56m	dCTP transport via ATP antiport
1981	11248	DNDPt57m	dGTP transport via ATP antiport

Column	Reaction #	Abbreviation	Reaction Name
1982	11249	DNDPt58m	dGTP transport via ADP antiport
1983	11250	DNDPt59m	dGTP transport via dADP antiport
1984	11174	DNDPt5m	dATP transport via dTDP antiport
1985	11251	DNDPt60m	dGTP transport via dUDP antiport
1986	11252	DNDPt61m	dGTP transport via dTDP antiport
1987	11253	DNDPt62m	dGTP transport via dGDP antiport
1988	11254	DNDPt63m	dGTP transport via dCDP antiport
1989	11173	DNDPt6m	dATP transport via dGDP antiport
1990	11177	DNDPt7m	dATP transport via dADP antiport
1991	11181	DNDPt8m	dADP transport via dUDP antiport
1992	11182	DNDPt9m	dADP transport via dTDP antiport
1993	10207	DOGULND1	2,3-dioxo-L-gulonate decarboxylase (L-lyxonate-forming)
1994	10208	DOGULND2	2,3-dioxo-L-gulonate decarboxylase (L-xylonate-forming)
1995	10224	DOGULNO1	2,3-dioxo-L-gulonate:hydrogen peroxide oxireductase
1996	10227	DOGULNO2	2,3-dioxo-L-gulonate:hydrogen peroxide oxireductase
1997	7593	DOLASNT_Ler	Dolichyl-diphosphooligosaccharide:protein-L-asparagine oligopolysaccharidotransferase (liver)
1998	7594	DOLASNT_Uer	Dolichyl-diphosphooligosaccharide:protein-L-asparagine oligopolysaccharidotransferase (uterus)
1999	7304	DOLDPP_Ler	Dolichyl-diphosphate phosphohydrolase, human (liver)
2000	7305	DOLDPP_Uer	Dolichyl-diphosphate phosphohydrolase, human (uterus)
2001	7346	DOLGLCP_Lter	Dolichyl beta-D-glucosyl phosphate flippase (liver)
2002	7347	DOLGLCP_Uter	Dolichyl beta-D-glucosyl phosphate flippase (uterus)
2003	7307	DOLGPP_Ler	Dolichyl-beta-D-glucosyl-phosphate dolichylphosphohydrolase (liver)
2004	7308	DOLGPP_Uer	Dolichyl-beta-D-glucosyl-phosphate dolichylphosphohydrolase (uterus)
2005	7297	DOLICHOL_Lter	dolichol diffusion, human (liver)
2006	7298	DOLICHOL_Uter	dolichol diffusion, human (uterus)
2007	7296	DOLK_L	Dolichol kinase, human (liver)
2008	7299	DOLK_U	Dolichol kinase, human (uterus)
2009	7344	DOLMANP_Lter	dolichol-phosphate mannose flippase (liver)
2010	7345	DOLMANP_Uter	dolichol-phosphate mannose flippase (uterus)
2011	7662	DOLPGT1_Ler	dolichyl-phosphate-glucose-glycolipid alpha-glucosyltransferase (liver)
2012	7660	DOLPGT1_Uer	dolichyl-phosphate-glucose-glycolipid alpha-glucosyltransferase (uterus)
2013	7658	DOLPGT2_Ler	dolichyl-phosphate-glucose-glycolipid alpha-glucosyltransferase (liver)
2014	7655	DOLPGT2_Uer	dolichyl-phosphate-glucose-glycolipid alpha-glucosyltransferase (uterus)
2015	7651	DOLPGT3_Ler	dolichyl-phosphate-glucose-glycolipid alpha-glucosyltransferase (liver)
2016	7650	DOLPGT3_Uer	dolichyl-phosphate-glucose-glycolipid alpha-glucosyltransferase (uterus)
2017	7301	DOLPH_Ler	Dolichol-phosphate phosphohydrolase, human (liver)
2018	7303	DOLPH_Uer	Dolichol-phosphate phosphohydrolase, human (uterus)
2019	7649	DOLPMT1_Ler	dolichyl-phosphate-mannose-glycolipid alpha-mannosyltransferase (liver)
2020	7648	DOLPMT1_Uer	dolichyl-phosphate-mannose-glycolipid alpha-mannosyltransferase (uterus)
2021	7647	DOLPMT2_Ler	dolichyl-phosphate-mannose-glycolipid alpha-mannosyltransferase (liver)
2022	7646	DOLPMT2_Uer	dolichyl-phosphate-mannose-glycolipid alpha-mannosyltransferase (uterus)

Column	Reaction #	Abbreviation	Reaction Name
2023	7645	DOLPMT3_Ler	dolichyl-phosphate-mannose-glycolipid alpha-mannosyltransferase (liver)
2024	7644	DOLPMT3_Uer	dolichyl-phosphate-mannose-glycolipid alpha-mannosyltransferase (uterus)
2025	7643	DOLPMT4_Ler	dolichyl-phosphate-mannose-glycolipid alpha-mannosyltransferase (liver)
2026	7642	DOLPMT4_Uer	dolichyl-phosphate-mannose-glycolipid alpha-mannosyltransferase (uterus)
2027	7313	DOLPMT_L	Dolichyl-phosphate D-mannosyltransferase (liver)
2028	7314	DOLPMT_U	Dolichyl-phosphate D-mannosyltransferase (uterus)
2029	7311	DOLP_Lter	dolichol phosphate flippase (liver)
2030	7312	DOLP_Uter	dolichol phosphate flippase (uterus)
2031	12099	DOPABMO	dopamine beta-monooxygenase
2032	10562	DOPACHRMISO	L-dopachrome isomerase 1
2033	11384	DOPAMT	Dopamine:amet O-methyltransferase
2034	10561	DOPAQNISO1	Dopaquinone isomerase 1
2035	19420	DOPASFt	Dopamine 3-0-sulfate transport (diffusion)
2036	12103	DOPASULT	Dopamine Sulfotransferase
2037	11931	DOPAVESSEC	Dopamine secretion via secretory vesicle (ATP driven)
2038	11938	DOPAt4(2)r	Dopamine reversible transport in via sodium symport (1:2)
2039	12192	DOPAtu	Dopamine uniport
2040	10871	DORNOp	D-ornithine oxidase, perixosomal
2041	2790	DPCOAK	dephospho-CoA kinase
2042	14679	DPCOAPP	pyrophasphatase (dephospho-CoA)
2043	14686	DPCOAtl	dephospho-CoA transport from lysosome via diffusion
2044	3110	DPGM	Diphosphoglyceromutase
2045	755	DPGase	Diphosphoglycerate phosphatase
2046	11095	DPHMBDCm	3-Decaprenyl-4-hydroxy-5-methoxybenzoate decarboxylation
2047	9736	DPMVDx	diphosphomevalonate decarboxylase
2048	14238	DPPS	decaprenyl synthase
2049	10268	DPROOp	D-proline oxidase, perixosomal
2050	2023	DRBK	Deoxyribokinase
2051	20140	DRIBt	deoxyribose transport via diffusion
2052	4640	DRPA	deoxyribose-phosphate aldolase
2053	14373	DSAT	dihydrosphingosine N-acyltransferase
2054	19535	DTDPtn	dTDP nuclear transport
2055	2815	DTMPK	dTMP kinase
2056	14134	DTTPtn	dTTP diffusion in nucleus
2057	19545	DUDPtn	dUDP nuclear transport
2058	2271	DUMPtn	dUMP nuclear transport
2059	9523	DURAD	dihydrouracil dehydrogenase (NADP)
2060	9524	DURAD2	dihydrothymin dehydrogenase (NADP)
2061	2691	DURIK1	deoxyuridine kinase (ATP:Deoxyuridine)
2062	10100	DURIK1m	deoxyuridine kinase (ATP:Deoxyuridine), mitochondrial
2063	1084	DURIPP	deoxyuridine phosphorylase
2064	10413	DURIt	deoxyuridine transport via diffusion
2065	19532	DURItn	deoxyuridine transport in nucleus
2066	4502	DUTPDPm	dUTP diphosphatase
2067	10101	DUTPDPn	dUTP diphosphatase, nuclear
2068	19715	EAFLATOXINte	xenobiotic transport
2069	19724	EBASTINEOHte	xenobiotic transport
2070	19726	EBASTINEOHtr	xenobiotic transport
2071	19723	EBASTINEte	xenobiotic transport
2072	19725	EBASTINEtr	xenobiotic transport
2073	9768	EBP1r	3-beta-hydroxysteroid-delta(8),delta(7)-isomerase

Column	Reaction #	Abbreviation	Reaction Name
2074	9769	EBP2r	3-beta-hydroxysteroid-delta(8),delta(7)-isomerase
2075	11284	ECGISOr	Ecgonine isomerase (ER)
2076	10910	ECOAH12m	3-hydroxyacyl-CoA dehydratase (3-hydroxyisobutyryl-CoA) (mitochondria)
2077	9503	ECOAH1m	3-hydroxyacyl-CoA dehydratase (3-hydroxybutanoyl-CoA) (mitochondria)
2078	9504	ECOAH1x	3-hydroxyacyl-CoA dehydratase (3-hydroxybutanoyl-CoA) (perioxisome)
2079	10917	ECOAH9m	2-Methylprop-2-enoyl-CoA (2-Methylbut-2-enoyl-CoA), mitochondrial
2080	11281	EGMESTr	ecgonine methyl esterase (ER)
2081	1844	EHGLAT	L-erythro-4-Hydroxyglutamate:2-oxoglutarate aminotransferase
2082	13890	EHGLAT2m	L-erythro-4-Hydroxyglutamate:2-oxoglutarate aminotransferase 2, mitochondrial
2083	1842	EHGLATm	L-erythro-4-Hydroxyglutamate:2-oxoglutarate aminotransferase, mitochondrial
2084	19101	EICOSTETCPT1	carnitine O-palmitoyltransferase
2085	19120	EICOSTETCPT2	carnitine transferase
2086	19082	EICOSTETCRNt	transport into the mitochondria (carnitine)
2087	12467	EICOSTETt	fatty acid transport via diffusion
2088	19093	ELAIDCPT1	carnitine O-palmitoyltransferase
2089	19112	ELAIDCPT2	carnitine transferase
2090	19074	ELAIDCRNt	transport into the mitochondria (carnitine)
2091	12450	ELAIDt	fatty acid transport via diffusion
2092	8433	ENGASE	endo-beta-N-acetylglucosaminidase
2093	8450	ENGASE2	endo-beta-N-acetylglucosaminidase
2094	8537	ENGASE2ly	endo-beta-N-acetylglucosaminidase, lysosomal
2095	14457	ENGASE3ly	endo-beta-N-acetylglucosaminidase, lysosomal
2096	8538	ENGASEly	endo-beta-N-acetylglucosaminidase, lysosomal
2097	8099	ENMAN1g	Endomannosidase (glc1man-producing), Golgi apparatus
2098	8095	ENMAN2g	Endomannosidase (glc2man-producing), Golgi apparatus
2099	8093	ENMAN3g	Endomannosidase (glc3man-producing), Golgi apparatus
2100	8120	ENMAN4g	Endomannosidase (m6masnC-producing), Golgi apparatus
2101	8123	ENMAN5g	Endomannosidase (m6masnB2-producing), Golgi apparatus
2102	8124	ENMAN6g	Endomannosidase (m5masnB1-producing), Golgi apparatus
2103	266	ENO	enolase
2104	9952	EPCTX	ethanolamine-phosphate cytidylyltransferase
2105	12270	ESTRADIOLGLCt	estradiol glucuronide transport via bicarbonate countertransport
2106	12623	ESTRADIOLGLCt2	17-beta-D-glucuronide transport (ATP-dependent)
2107	19753	ESTRADIOLGLCtr	glucuronidated compound transport
2108	14982	ESTRADIOLtr	estradiol intracellular transport
2109	19764	ESTRIOLGLCte	glucuronidated compound transport
2110	19754	ESTRIOLGLCtr	glucuronidated compound transport
2111	14987	ESTRIOLtr	estriol intracellular transport
2112	12670	ESTRONEGLCt	ABC transporter
2113	19756	ESTRONEGLCtr	glucuronidated compound transport
2114	12271	ESTRONESt	estrone 3-sulfate transport via bicarbonate countertransport
2115	12620	ESTRONESt2	estrone-3-sulfate transport via sodium cotransport
2116	14983	ESTRONEtr	estrone intracellular transport
2117	12070	ESTSULT	Estrogen sulfotransferase
2118	11580	ETF	electron transfer flavoprotein
2119	11581	ETFQO	Electron transfer flavoprotein-ubiquinone oxidoreductase
2120	2384	ETHAK	Ethanolamine kinase

Column	Reaction #	Abbreviation	Reaction Name
2121	11900	ETHP	ethanolamine phosphate phosphatase
2122	19461	ETOHMO	ethanol monooxygenase
2123	1558	ETOHt	ethanol reversible transport
2124	20151	ETOHtx	ethanol reversible peroxisomal transport
2125	9639	F1PGT	fucose-1-phosphate guanylyltransferase
2126	7758	F6Tg	glycoprotein 6-alpha-L-fucosyltransferase
2127	3282	FA120ACPH	fatty-acyl-ACP hydrolase
2128	3283	FA140ACPH	fatty-acyl-ACP hydrolase
2129	3285	FA141ACPH	fatty-acyl-ACP hydrolase
2130	3286	FA160ACPH	fatty-acyl-ACP hydrolase
2131	3289	FA161ACPH	fatty-acyl-ACP hydrolase
2132	3287	FA180ACPH	fatty-acyl-ACP hydrolase
2133	3290	FA181ACPH	fatty-acyl-ACP hydrolase
2134	13580	FA1821ACPH	fatty-acyl-ACP hydrolase
2135	13581	FA1822ACPH	fatty-acyl-ACP hydrolase
2136	3291	FA182ACPH	fatty-acyl-ACP hydrolase
2137	8130	FACOAL140i	fatty-acid--CoA ligase (tetradecanoate)
2138	14860	FACOAL150	fatty-acid--CoA ligase
2139	4318	FACOAL160i	C160 fatty acid activation
2140	2894	FACOAL161	fatty-acid--CoA ligase (hexadecenoate)
2141	14861	FACOAL170	fatty-acid--CoA ligase
2142	4319	FACOAL180i	C180 fatty acid activation
2143	10279	FACOAL1812	fatty-acid--CoA ligase
2144	10280	FACOAL1813	fatty-acid--CoA ligase
2145	4320	FACOAL181i	C181 fatty acid activation
2146	13577	FACOAL1821	fatty-acid--CoA ligase
2147	10284	FACOAL1822	fatty-acid--CoA ligase
2148	10298	FACOAL1831	fatty-acid--CoA ligase
2149	10299	FACOAL1832	fatty-acid--CoA ligase
2150	10297	FACOAL184	fatty-acid--CoA ligase
2151	14871	FACOAL191	fatty-acid--CoA ligase
2152	10286	FACOAL200	fatty-acid--CoA ligase
2153	10295	FACOAL203	fatty-acid--CoA ligase
2154	10355	FACOAL204	fatty-acid--CoA ligase
2155	10356	FACOAL2042	fatty-acid--CoA ligase
2156	4321	FACOAL204i	arachidonic acid activation
2157	10296	FACOAL205	fatty-acid--CoA ligase
2158	13149	FACOAL206	fatty-acid--CoA ligase
2159	10287	FACOAL224	fatty-acid--CoA ligase
2160	10291	FACOAL2251	fatty-acid--CoA ligase
2161	10292	FACOAL2252	fatty-acid--CoA ligase
2162	14108	FACOAL226	fatty-acid--CoA ligase
2163	4395	FACOAL226i	C226 fatty acid activation
2164	10294	FACOAL240	fatty-acid--CoA ligase
2165	10289	FACOAL241	fatty-acid--CoA ligase
2166	10360	FACOAL244_1	fatty-acid--CoA ligase
2167	10358	FACOAL245_1	fatty-acid--CoA ligase
2168	10359	FACOAL245_2	fatty-acid--CoA ligase
2169	10361	FACOAL246_1	fatty-acid--CoA ligase
2170	10290	FACOAL260	fatty-acid--CoA ligase (n-C26:0)
2171	10777	FACOAL40im	fatty-acid--CoA ligase (butanoate), mitochondrial
2172	8128	FACOAL80i	fatty-acid--CoA ligase (octanoate)
2173	139	FADDP	FAD diphosphatase
2174	13981	FADH2tru	FADH2 transporter, endoplasmic reticulum
2175	13548	FADH2tx	FADH2 transporter, peroxisomal
2176	13976	FADtru	FAD transporter, endoplasmic reticulum

Column	Reaction #	Abbreviation	Reaction Name
2177	13547	FADtx	FAD transporter, peroxisomal
2178	14286	FAEL183	fatty-acyl-CoA elongation (n-C18:3CoA)
2179	14288	FAEL184	fatty-acyl-CoA elongation (n-C20:4CoA)
2180	14287	FAEL204	fatty-acyl-CoA elongation (n-C20:4CoA)
2181	14289	FAEL205	fatty-acyl-CoA elongation (n-C20:5CoA)
2182	11774	FAH1	Fatty acid omega-hydroxylase
2183	11776	FAH2	Fatty acid omega-hydroxylase
2184	11778	FAH3	Fatty acid omega-hydroxylase
2185	2373	FALDH	formaldehyde dehydrogenase
2186	20846	FALDtly	formaldehyde transport via diffusion (lysosomall)
2187	20465	FALDtm	formaldehyde transport via diffusion (mitochondrial)
2188	13160	FAOXC11	Beta oxidation of long chain fatty acid
2189	20831	FAOXC140	Beta oxidation of long chain fatty acid
2190	14353	FAOXC150m	Beta oxidation of long chain fatty acid (odd chain)
2191	4214	FAOXC160	Beta oxidation of long chain fatty acid
2192	18979	FAOXC16080m	Beta oxidation of long chain fatty acid
2193	19002	FAOXC16080x	Beta oxidation of long chain fatty acid
2194	20159	FAOXC161802m	Beta oxidation fatty acid
2195	18978	FAOXC16180m	Beta oxidation fatty acid
2196	14354	FAOXC170m	Beta oxidation of long chain fatty acid (odd chain)
2197	4216	FAOXC180	Beta oxidation of long chain fatty acid
2198	18995	FAOXC180x	Beta oxidation of long chain fatty acid
2199	18988	FAOXC1811601m	Beta oxidation fatty acid
2200	18989	FAOXC1811602m	Beta oxidation fatty acid
2201	18990	FAOXC1811603m	Beta oxidation fatty acid
2202	18986	FAOXC182806m	Beta oxidation of fatty acid
2203	18987	FAOXC18280m	Beta oxidation of fatty acid
2204	18984	FAOXC183803m	Beta oxidation of fatty acid
2205	19011	FAOXC183806m	Beta oxidation of fatty acid
2206	19001	FAOXC183806x	Beta oxidation of long chain fatty acid
2207	19009	FAOXC18480m	Beta oxidation of fatty acid
2208	19000	FAOXC18480x	Beta oxidation of long chain fatty acid
2209	18980	FAOXC200180m	Beta oxidation of long chain fatty acid
2210	18998	FAOXC200180x	Beta oxidation of long chain fatty acid
2211	18983	FAOXC2031836m	Beta oxidation of fatty acid
2212	4285	FAOXC204	Beta oxidation of long chain fatty acid
2213	18981	FAOXC204184m	Beta oxidation fatty acid
2214	19006	FAOXC2051843m	Beta oxidation of fatty acid
2215	18970	FAOXC2051843x	Beta oxidation of long chain fatty acid
2216	19008	FAOXC2242046m	Beta oxidation of long chain fatty acid
2217	18999	FAOXC2242046x	Beta oxidation of long chain fatty acid
2218	19010	FAOXC2251836m	Beta oxidation of fatty acid
2219	18968	FAOXC2251836x	Beta oxidation of long chain fatty acid
2220	19154	FAOXC2252053m	Beta oxidation of long chain fatty acid
2221	18997	FAOXC2252053x	Beta oxidation of long chain fatty acid
2222	4284	FAOXC226	Beta oxidation of long chain fatty acid
2223	19005	FAOXC226205m	Beta oxidation of long chain fatty acid
2224	18967	FAOXC226205x	Beta oxidation of long chain fatty acid
2225	19004	FAOXC240200x	Beta oxidation of long chain fatty acid
2226	19003	FAOXC241181x	Beta oxidation of long chain fatty acid
2227	18991	FAOXC2442246x	Beta oxidation of long chain fatty acid
2228	18993	FAOXC2452253x	Beta oxidation of long chain fatty acid
2229	18992	FAOXC2452256x	Beta oxidation of long chain fatty acid
2230	18994	FAOXC246226x	Beta oxidation of long chain fatty acid
2231	18996	FAOXC260240x	Beta oxidation of long chain fatty acid
2232	8333	FAOXC80	Beta oxidation of med/long chain fatty acid

Column	Reaction #	Abbreviation	Reaction Name
2233	3049	FAS100COA	fatty acyl-CoA synthase (n-C10:0CoA)
2234	3051	FAS120COA	fatty-acyl-CoA synthase (n-C12:0CoA)
2235	3052	FAS140COA	fatty-acyl-CoA synthase (n-C14:0CoA)
2236	3053	FAS160COA	fatty-acyl-CoA synthase (n-C16:0CoA)
2237	3055	FAS180COA	fatty-acyl-CoA synthase (n-C18:0CoA)
2238	3050	FAS80COA_L	fatty acyl-CoA synthase (n-C8:0CoA), lumped reaction
2239	12555	FATP1t	fatty acid electroneutral transport
2240	12556	FATP2t	fatty acid electroneutral transport
2241	12557	FATP3t	fatty acid electroneutral transport
2242	12558	FATP4t	fatty acid electroneutral transport
2243	12559	FATP5t	fatty acid electroneutral transport
2244	12560	FATP6t	fatty acid electroneutral transport
2245	12561	FATP7t	fatty acid electroneutral transport
2246	12562	FATP8t	fatty acid electroneutral transport
2247	12563	FATP9t	fatty acid electroneutral transport
2248	268	FBA	fructose-bisphosphate aldolase
2249	2403	FBA2	D-Fructose 1-phosphate D-glyceraldehyde-3-phosphate-lyase
2250	13867	FBA4	D-Fructose 1-phosphate D-glyceraldehyde-3-phosphate-lyase
2251	19626	FBA5	D-Tagatose 1-phosphate D-glyceraldehyde-3-phosphate-lyase
2252	263	FBP	fructose-bisphosphatase
2253	1040	FBP26	Fructose-2,6-bisphosphate 2-phosphatase
2254	1784	FCLTm	Ferrochelatase, mitochondrial
2255	14878	FCOAH	formyl coa hydrolase
2256	2846	FDH	formate dehydrogenase
2257	13175	FE2t	iron (II) transport
2258	4033	FE2tm	iron (II) transport
2259	13197	FE3R2e	Fe(III) reduction (ascorbate)
2260	9641	FK	Fucokinase
2261	2371	FKYNH	N-Formyl-L-kynurenine amidohydrolase
2262	140	FMNAT	FMN adenylyltransferase
2263	8693	FOLR2	folate reductase
2264	14836	FOLt2	folate transport via anion exchange
2265	14879	FORMCOAtx	formyl coa transport
2266	14916	FORt2m	formate mitochondrial transport
2267	13990	FORtr	FOR transporter, endoplasmic reticulum
2268	19511	FORtrn	Formate transport, nuclear
2269	11740	FPGS	folylpolyglutamate synthetase
2270	11741	FPGS2	folylpolyglutamate synthetase
2271	11744	FPGS2m	folylpolyglutamate synthetase, mitochondrial
2272	11742	FPGS3	folylpolyglutamate synthetase
2273	11745	FPGS3m	folylpolyglutamate synthetase, mitochondrial
2274	11746	FPGS4	folylpolyglutamate synthetase (DHF)
2275	11755	FPGS4m	folylpolyglutamate synthetase (DHF), mitochondrial
2276	11747	FPGS5	folylpolyglutamate synthetase (DHF)
2277	11756	FPGS5m	folylpolyglutamate synthetase (DHF), mitochondrial
2278	11748	FPGS6	folylpolyglutamate synthetase (DHF)
2279	11757	FPGS6m	folylpolyglutamate synthetase (DHF), mitochondrial
2280	11749	FPGS7	folylpolyglutamate synthetase (10fthf)
2281	11752	FPGS7m	folylpolyglutamate synthetase (10fthf), mitochondrial
2282	11750	FPGS8	folylpolyglutamate synthetase (10fthf)
2283	11753	FPGS8m	folylpolyglutamate synthetase (10fthf), mitochondrial
2284	11751	FPGS9	folylpolyglutamate synthetase (10fthf)
2285	11754	FPGS9m	folylpolyglutamate synthetase (10fthf), mitochondrial

Column	Reaction #	Abbreviation	Reaction Name
2286	11743	FPGSm	folylpolyglutamate synthetase, mitochondrial
2287	18424	FRDPtc	lipid, flip-flop intracellular transport
2288	12678	FRDPtr	lipid, flip-flop intracellular transport
2289	110	FRTT	farnesyltranstransferase
2290	11909	FRUt1r	D-fructose transport in via uniport
2291	12126	FRUt4	D-fructose transport via sodium cotransport
2292	6137	FT	farnesyltranstransferase (trans,trans,cis-geranylgeranyl diphosphate-generating)
2293	11759	FTCD	formimidoyltransferase cyclodeaminase
2294	3757	FTHFCL	5-formethyltetrahydrofolate cyclo-ligase
2295	11758	FTHFDH	formyltetrahydrofolate dehydrogenase
2296	4043	FTHFL	formate-tetrahydrofolate ligase
2297	4042	FTHFLm	formate-tetrahydrofolate ligase, mitochondrial
2298	19667	FUC13GALACGLCGAL14ACGLCGALGLUSIDEte	blood group intracellular transport
2299	20166	FUC13GALACGLCGAL14ACGLCGALGLUSIDEtg	blood group intracellular transport
2300	19669	FUC14GALACGLCGALGLUSIDEte	blood group intracellular transport
2301	20167	FUC14GALACGLCGALGLUSIDEtg	blood group intracellular transport
2302	19671	FUCACGALFUCGALACGLCGALGLUSIDEte	blood group intracellular transport
2303	20168	FUCACGALFUCGALACGLCGALGLUSIDEtg	blood group intracellular transport
2304	19673	FUCACNGAL14ACGLCGALGLUSIDEte	blood group intracellular transport
2305	20169	FUCACNGAL14ACGLCGALGLUSIDEtg	blood group intracellular transport
2306	19675	FUCACNGALACGLCGALGLUSIDEte	blood group intracellular transport
2307	20170	FUCACNGALACGLCGALGLUSIDEtg	blood group intracellular transport
2308	14588	FUCASE2e	alpha-fucosidase, extracellular
2309	14455	FUCASE2ly	alpha-fucosidase, lysosomal
2310	8452	FUCASEe	alpha-fucosidase, extracellular
2311	8539	FUCASEly	alpha-fucosidase, lysosomal
2312	19677	FUCFUC12GAL14ACGLCGALGLUSIDEte	blood group intracellular transport
2313	20171	FUCFUC12GAL14ACGLCGALGLUSIDEtg	blood group intracellular transport
2314	19679	FUCFUC132GALACGLCGAL14ACGLCGALGLUSIDEte	blood group intracellular transport
2315	20172	FUCFUC132GALACGLCGAL14ACGLCGALGLUSIDEtg	blood group intracellular transport
2316	19681	FUCFUCFUCGALACGLC13GALACGLCGAL14ACGLCGALGLUSIDEte	blood group intracellular transport
2317	20173	FUCFUCFUCGALACGLC13GALACGLCGAL14ACGLCGALGLUSIDEtg	blood group intracellular transport
2318	19686	FUCFUCFUCGALACGLCGAL14ACGLCGALGLUSIDEte	blood group intracellular transport

Column	Reaction #	Abbreviation	Reaction Name
2319	20174	FUCFUCFUCGALACGLCGAL14ACGLCGALGLUSIDEtg	blood group intracellular transport
2320	19688	FUCFUCGALACGLCGALGLUSIDEte	blood group intracellular transport
2321	20175	FUCFUCGALACGLCGALGLUSIDEtg	blood group intracellular transport
2322	19690	FUCGAL14ACGLCGALGLUSIDEte	blood group intracellular transport
2323	20176	FUCGAL14ACGLCGALGLUSIDEtg	blood group intracellular transport
2324	19692	FUCGALFUCGALACGLCGALGLUSIDEte	blood group intracellular transport
2325	20177	FUCGALFUCGALACGLCGALGLUSIDEtg	blood group intracellular transport
2326	20227	FUCGALGBSIDEte	fucgalgbside_hs transport
2327	20211	FUCGALGBSIDEtg	fucgalgbside_hs intracellular transport
2328	14921	FUCtly	L-fucose efflux from lysosome
2329	542	FUM	fumarase
2330	2670	FUMAC	fumarylacetoacetase
2331	20297	FUMSO3tm	Fumarate:sulfite antiport, mitochondrial
2332	20298	FUMSO4tm	Fumarate:sulfate antiport, mitochondrial
2333	20247	FUMTSULtm	Fumarate:thiosulfate antiport, mitochondrial
2334	544	FUMm	fumarase, mitochondrial
2335	8364	FUMtm	fumarate transport, mitochondrial
2336	11070	FUT11g	Galactoside 2-alpha-L-fucosyltransferase 1
2337	14599	FUT12g	Galactoside 2-alpha-L-fucosyltransferase 1
2338	14622	FUT14g	Galactoside 2-alpha-L-fucosyltransferase 1
2339	14635	FUT15g	Galactoside 2-alpha-L-fucosyltransferase 1
2340	14642	FUT16g	Galactoside 2-alpha-L-fucosyltransferase 1
2341	14645	FUT17g	Galactoside 2-alpha-L-fucosyltransferase 1
2342	14663	FUT18g	Galactoside 2-alpha-L-fucosyltransferase 1
2343	14595	FUT31g	fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood group included) 1
2344	14598	FUT32g	fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood group included) 1
2345	14604	FUT33g	fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood group included) 1
2346	14605	FUT34g	fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood group included) 1
2347	14606	FUT35g	fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood group included) 1
2348	14674	FUT910g	Alpha-(1,3)-fucosyltransferase
2349	14675	FUT911g	Alpha-(1,3)-fucosyltransferase
2350	14623	FUT91g	Alpha-(1,3)-fucosyltransferase
2351	14626	FUT92g	Alpha-(1,3)-fucosyltransferase
2352	14633	FUT93g	Alpha-(1,3)-fucosyltransferase
2353	14651	FUT94g	Alpha-(1,3)-fucosyltransferase
2354	14653	FUT95g	Alpha-(1,3)-fucosyltransferase
2355	14665	FUT96g	Alpha-(1,3)-fucosyltransferase
2356	14668	FUT97g	Alpha-(1,3)-fucosyltransferase
2357	14669	FUT98g	Alpha-(1,3)-fucosyltransferase
2358	14673	FUT99g	Alpha-(1,3)-fucosyltransferase
2359	7336	G12MT1_L	Glycolipid 1,2-alpha-D-mannosyltransferase (liver)
2360	7337	G12MT1_U	Glycolipid 1,2-alpha-D-mannosyltransferase (uterus)
2361	7338	G12MT2_L	Glycolipid 1,2-alpha-D-mannosyltransferase (liver)

Column	Reaction #	Abbreviation	Reaction Name
2362	7339	G12MT2_U	Glycolipid 1,2-alpha-D-mannosyltransferase (uterus)
2363	7340	G13MT_L	Glycolipid 1,3-alpha-D-mannosyltransferase (liver)
2364	7341	G13MT_U	Glycolipid 1,3-alpha-D-mannosyltransferase (uterus)
2365	11452	G14T10g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi
2366	11453	G14T11g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi
2367	11454	G14T12g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi
2368	11455	G14T13g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi
2369	11456	G14T14g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi
2370	11457	G14T15g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi
2371	11458	G14T16g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi
2372	11460	G14T17g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi
2373	11519	G14T18g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi
2374	11523	G14T19g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi
2375	11526	G14T20g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi
2376	11530	G14T21g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi
2377	11395	G14T2g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi
2378	11425	G14T3g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi
2379	11429	G14T4g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi
2380	11432	G14T5g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi
2381	11436	G14T6g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi
2382	11439	G14T7g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi
2383	11450	G14T8g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi
2384	11451	G14T9g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi
2385	7760	G14Tg	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase
2386	7342	G16MT_L	Glycolipid 1,6-alpha-D-mannosyltransferase (liver)
2387	7343	G16MT_U	Glycolipid 1,6-alpha-D-mannosyltransferase (uterus)
2388	8152	G1M6MASNB1terg	g1m6masnB1 endoplasmic reticulum to Golgi transport
2389	8119	G1M7MASNBterg	g1m7masnC endoplasmic reticulum to Golgi transport
2390	8118	G1M7MASNCterg	g1m7masnC endoplasmic reticulum to Golgi transport
2391	7753	G1M8MASNterg	g1m8masn transport from endoplasmic reticulum to Golgi apparatus
2392	2487	G1PTT	glucose-1-phosphate thymidylyltransferase
2393	8090	G2M8MASNterg	g2m8masn transport from endoplasmic reticulum to Golgi apparatus

Column	Reaction #	Abbreviation	Reaction Name
2394	8091	G3M8MASNterg	g3m8masn transport from endoplasmic reticulum to Golgi apparatus
2395	257	G3PD1	glycerol-3-phosphate dehydrogenase (NAD)
2396	13392	G3PD2m	glycerol-3-phosphate dehydrogenase (FAD), mitochondrial
2397	3649	G5SADrm	L-glutamate 5-semialdehyde dehydratase, reversible, mitochondrial
2398	3635	G5SADs	L-glutamate 5-semialdehyde dehydratase (spontaneous)
2399	9628	G5SDym	glutamate-5-semialdehyde dehydrogenase (m)
2400	246	G6PDA	glucosamine-6-phosphate deaminase
2401	9551	G6PDH1er	glucose-6-phosphate dehydrogenase, endoplasmic reticulum
2402	10043	G6PDH1rer	glucose-6-phosphate dehydrogenase, endoplasmic reticulum
2403	2941	G6PDH2r	glucose 6-phosphate dehydrogenase
2404	10042	G6PDH2rer	glucose 6-phosphate dehydrogenase, endoplasmic reticulum
2405	6036	G6PPer	glucose-6-phosphate phosphatase, edoplasmic reticular
2406	2341	G6Pter	glucose 6-phosphate endoplasmic reticular transport via diffusion
2407	11922	GABAVESSEC	GABA secretion via secretory vesicle (ATP driven)
2408	9723	GACMTRc	guanidinoacetate N-methyltransferase (c)
2409	11292	GACPAILter	glucosaminyl-acylphosphatidylinositol ER flippase
2410	11198	GAL3ST11	Galactosylceramide sulfotransferase
2411	11199	GAL3ST12	Galactosylceramide sulfotransferase
2412	20228	GALACGLCGALGBSIDEte	galacglcgalgbside_hs transport
2413	20212	GALACGLCGALGBSIDEtg	galacglcgalgbside_hs intracellular transport
2414	14473	GALASE10ly	beta-galactosidase, lysosomal
2415	14474	GALASE11ly	beta-galactosidase, lysosomal
2416	14475	GALASE12ly	beta-galactosidase, lysosomal
2417	14476	GALASE13ly	beta-galactosidase, lysosomal
2418	14495	GALASE14ly	beta-galactosidase, lysosomal
2419	14497	GALASE15ly	beta-galactosidase, lysosomal
2420	14526	GALASE16ly	beta-galactosidase, lysosomal
2421	14527	GALASE17ly	beta-galactosidase, lysosomal
2422	14528	GALASE18ly	beta-galactosidase, lysosomal
2423	14529	GALASE19ly	beta-galactosidase, lysosomal
2424	8540	GALASE1ly	beta-galactosidase, lysosomal
2425	14530	GALASE20ly	beta-galactosidase, lysosomal
2426	14460	GALASE3ly	beta-galactosidase, lysosomal
2427	14464	GALASE4ly	beta-galactosidase, lysosomal
2428	14468	GALASE5ly	beta-galactosidase, lysosomal
2429	14469	GALASE6ly	beta-galactosidase, lysosomal
2430	14470	GALASE7ly	beta-galactosidase, lysosomal
2431	14471	GALASE8ly	beta-galactosidase, lysosomal
2432	14472	GALASE9ly	beta-galactosidase, lysosomal
2433	11262	GALC	Galactocerebrosidase
2434	19694	GALFUC12GAL14ACGLCGALGLUSIDEte	blood group intracellular transport
2435	20178	GALFUC12GAL14ACGLCGALGLUSIDEtg	blood group intracellular transport
2436	19696	GALFUCGALACGLCGAL14ACGLCGALGLUSIDEte	blood group intracellular transport
2437	20179	GALFUCGALACGLCGAL14ACGLCGALGLUSIDEtg	blood group intracellular transport

Column	Reaction #	Abbreviation	Reaction Name
2438	19698	GALGALFUCFUCGALAC GLCGALACGLCGAL14AC GLCGALGLUSIDEte	blood group intracellular transport
2439	20180	GALGALFUCFUCGALAC GLCGALACGLCGAL14AC GLCGALGLUSIDEtg	blood group intracellular transport
2440	20229	GALGALGALTHCRMte	galgalgalthcrm_hs transport
2441	20213	GALGALGALTHCRMtg	galgalgalthcrm_hs intracellular transport
2442	20138	GALGLUSIDEtg	galgluside_hs intracellular transport
2443	20135	GALGLUSIDEtl	galgluside_hs intracellular transport
2444	11098	GALGT1	Beta-1,4 N-acetylgalactosaminyltransferase
2445	11099	GALGT2	Beta-1,4 N-acetylgalactosaminyltransferase
2446	11100	GALGT3	Beta-1,4 N-acetylgalactosaminyltransferase
2447	11101	GALGT4	Beta-1,4 N-acetylgalactosaminyltransferase
2448	2818	GALK	galactokinase
2449	11559	GALNACT1g	UDPGal-chondroitin acetylgalactosaminyltransferase I, Golgi
2450	11566	GALNACT2g	uridine diphosphoacetylgalactosamine-chondroitin acetylgalactosaminyltransferase II, Golgi
2451	11571	GALNACT3g	uridine diphosphoacetylgalactosamine-chondroitin acetylgalactosaminyltransferase II, Golgi
2452	11575	GALNACT4g	uridine diphosphoacetylgalactosamine-chondroitin acetylgalactosaminyltransferase II, Golgi
2453	11595	GALNACT5g	uridine diphosphoacetylgalactosamine-chondroitin acetylgalactosaminyltransferase II, Golgi
2454	8565	GALNTg	GalNAc transferase, Golgi apparatus
2455	9927	GALOR	D-Galactose:NADP+ 1-oxidoreductase
2456	20331	GALSIDEtg	galactocerebroside intracellular transport
2457	20877	GALSIDEtl	galactocerebroside intracellular transport
2458	199	GALT	galactose-1-phosphate uridylyltransferase
2459	11556	GALT2g	UDP-D-galactose:galactosylxylose galactosyltransferase, Golgi apparatus
2460	11552	GALTg	UDP-D-galactose:D-xylose galactosyltransferase, Golgi apparatus
2461	201	GALU	UTP-glucose-1-phosphate uridylyltransferase
2462	11908	GALt1r	galactose transport (uniport)
2463	11964	GALt2_2	D-galactose transport via proton symport
2464	12124	GALt4	galactose transport via sodium symport
2465	11962	GALt4_2	galactose transport via sodium symport
2466	14923	GALtly	galactose efflux from lysosome
2467	10095	GAMYe	glucoamylase, extracellular (glygn5 -> malt)
2468	11907	GAMt1r	glucosamine transport (uniport)
2469	11359	GAO1	Ganglioside O-acetylation
2470	12547	GAO1g	Ganglioside O-acetylation
2471	11361	GAO2	Ganglioside O-acetylation
2472	12550	GAO2g	Ganglioside O-acetylation
2473	2841	GAPD	glyceraldehyde-3-phosphate dehydrogenase
2474	3637	GARFT	phosphoribosylglycinamide formyltransferase
2475	8541	GASNASE2ly	glycosylasparaginase, lysosomal
2476	14456	GASNASE3ly	glycosylasparaginase, lysosomal
2477	8542	GASNASEly	glycosylasparaginase, lysosomal
2478	11394	GBA	Glucosylceramidase
2479	11261	GBAl	Glucosylceramidase
2480	11076	GBGT1	globoside alpha-1,3-N-acetylgalactosaminyltransferase 1
2481	20328	GBSIDEte	globoside transport
2482	20327	GBSIDEtl	globoside intracellular transport

Column	Reaction #	Abbreviation	Reaction Name
2483	1967	GCALDD	Glycolaldehyde dehydrogenase
2484	10519	GCALDDm	Glycolaldehyde dehydrogenase, mitochondrial
2485	3714	GCC2am	glycine-cleavage complex (lipoamide), mitochondrial
2486	3713	GCC2bim	glycine-cleavage system (lipoamide) irreversible, mitochondrial
2487	2283	GCC2cm	glycine-cleavage complex (lipoamide), mitochondrial
2488	3715	GCCam	glycine-cleavage complex (lipoylprotein), mitochondrial
2489	3716	GCCbim	glycine-cleavage complex (lipoylprotein) irreversible, mitochondrial
2490	2282	GCCcm	glycine-cleavage complex (lipoylprotein), mitochondrial
2491	12267	GCHOLAt	glycocholate transport via bicarbonate countertransport
2492	12618	GCHOLAt2	glycocholate transport via sodium cotransport
2493	12669	GCHOLAt3	ABC bile acid transporter
2494	19651	GCHOLAte	bile acid intracellular transport
2495	19652	GCHOLAtx	bile acid intracellular transport
2496	14660	GCNTg	N-acetyllactosaminide beta-1,6-N-acetylglucosaminyl-transferase
2497	20230	GD1B2te	gd1b2_hs transport
2498	20214	GD1B2tg	gd1b2_hs intracellular transport
2499	20231	GD1Cte	gd1c_hs transport
2500	20215	GD1Ctg	gd1c_hs intracellular transport
2501	19653	GDCHOLAte	bile acid intracellular transport
2502	19654	GDCHOLAtx	bile acid intracellular transport
2503	12156	GDPFUCtg	GDPFuc Golgi transport via CMP antiport
2504	20334	GDPtg	GDP intracellular transport
2505	3537	GF6PTA	glutamine-fructose-6-phosphate transaminase
2506	5638	GFUCS	GDP-L-fucose synthase
2507	14854	GGH-10FTHF5GLUe	Gamma-glutamyl hydrolase (10FTHF5GLU), extracellular
2508	14855	GGH-10FTHF5GLUl	Gamma-glutamyl hydrolase (10FTHF5GLU), lysosomal
2509	14856	GGH-10FTHF6GLUe	Gamma-glutamyl hydrolase (10FTHF6GLU), extracellular
2510	14857	GGH-10FTHF6GLUl	Gamma-glutamyl hydrolase (10FTHF6GLU), lysosomal
2511	14859	GGH-10FTHF7GLUe	Gamma-glutamyl hydrolase (10FTHF7GLU), extracellular
2512	14858	GGH-10FTHF7GLUl	Gamma-glutamyl hydrolase (10FTHF7GLU), lysosomal
2513	14848	GGH-5DHFe	Gamma-glutamyl hydrolase (5DHF), extracellular
2514	14849	GGH-5DHFl	Gamma-glutamyl hydrolase (5DHF), lysosomal
2515	14847	GGH-5THFe	Gamma-glutamyl hydrolase (5THF), extracellular
2516	14846	GGH-5THFl	Gamma-glutamyl hydrolase (5THF), lysosomal
2517	14850	GGH-6DHFe	Gamma-glutamyl hydrolase (6DHF), extracellular
2518	14851	GGH-6DHFl	Gamma-glutamyl hydrolase (6DHF), lysosomal
2519	14845	GGH-6THFe	Gamma-glutamyl hydrolase (6THF), extracellular
2520	14844	GGH-6THFl	Gamma-glutamyl hydrolase (6THF), lysosomal
2521	14852	GGH-7DHFe	Gamma-glutamyl hydrolase (7DHF), extracellular
2522	14853	GGH-7DHFl	Gamma-glutamyl hydrolase (7DHF), lysosomal
2523	14843	GGH-7THFe	Gamma-glutamyl hydrolase (7THF), extracellular
2524	14842	GGH-7THFl	Gamma-glutamyl hydrolase (7THF), lysosomal
2525	11537	GGLUCT	gamma-glutamylcyclotransferase
2526	10093	GGNG	glycogenin self-glucosylation
2527	10002	GGT5r	Gamma-glutamyltransferase 5
2528	19812	GGT6	Gamma-glutamyltransferase
2529	7410	GGT_L	geranylgeranyltransferase (liver)
2530	7546	GGT_U	geranylgeranyltransferase (uterus)
2531	1584	GHMT2r	glycine hydroxymethyltransferase, reversible
2532	1583	GHMT2rm	glycine hydroxymethyltransferase, reversible, mitochondrial
2533	11404	GHMT3	glycine hydroxymethyltransferase
2534	11405	GHMT3m	glycine hydroxymethyltransferase, mitochondrial

Column	Reaction #	Abbreviation	Reaction Name
2535	186	GK1	guanylate kinase (GMP:ATP)
2536	20323	GK1m	guanylate kinase (GMP:ATP), mitochondrial
2537	10177	GLACO	D-Glucuronolactone:NAD+ oxidoreductase
2538	10178	GLACOm	D-Glucuronolactone:NAD+ oxidoreductase, mitochondrial
2539	13768	GLACter	D-glucurono-6,3-lactone transport, endoplasmic reticulum
2540	11275	GLAl	galactosidase, alpha
2541	11264	GLB1	Beta-galactosidase
2542	10067	GLBRAN	1,4-alpha-glucan branching enzyme (glygn1 -> glygn2)
2543	11722	GLCAASE1ly	beta-glucuronidase, lysosomal
2544	14406	GLCAASE4ly	beta-glucuronidase, lysosomal
2545	14422	GLCAASE5ly	beta-glucuronidase, lysosomal
2546	14436	GLCAASE6ly	beta-glucuronidase, lysosomal
2547	14448	GLCAASE7ly	beta-glucuronidase, lysosomal
2548	14549	GLCAASE8ly	beta-glucuronidase, lysosomal
2549	14552	GLCAASE9ly	beta-glucuronidase, lysosomal
2550	11626	GLCAE1g	chondroitin-glucuronate 5-epimerase
2551	11627	GLCAE2g	heparosan-N-sulfate-glucuronate 5-epimerase
2552	11565	GLCAT2g	chondroitin glucuronyltransferase II, Golgi apparatus
2553	11570	GLCAT3g	chondroitin glucuronyltransferase II, Golgi apparatus
2554	11574	GLCAT4g	chondroitin glucuronyltransferase II, Golgi apparatus
2555	11594	GLCAT5g	chondroitin glucuronyltransferase II, Golgi apparatus
2556	11612	GLCAT6g	heparan glucuronyltransferase II
2557	11617	GLCAT7g	heparan glucuronyltransferase II
2558	11618	GLCAT8g	heparan glucuronyltransferase II
2559	11619	GLCAT9g	heparan glucuronyltransferase II
2560	11557	GLCATg	UDP-D-glucuronate:galactosylgalactosylxylose glucuronosyltransferase, Golgi apparatus
2561	11812	GLCMter	glucose transport via membrane vesicle
2562	11715	GLCNACASE1ly	alpha-N-acetylglucosaminidase, lysosomal
2563	11720	GLCNACASE2ly	alpha-N-acetylglucosaminidase, lysosomal
2564	11730	GLCNACASE3ly	alpha-N-acetylglucosaminidase, lysosomal
2565	11731	GLCNACASE4ly	alpha-N-acetylglucosaminidase, lysosomal
2566	11766	GLCNACASE5ly	alpha-N-acetylglucosaminidase, lysosomal
2567	11624	GLCNACDASg	GlcNAc N-deacetylase / N-sulfotransferase
2568	7329	GLCNACPT_L	UDP-GlcNAc:dolichol-phosphate GlcNAc phosphotransferase (liver)
2569	7330	GLCNACPT_U	UDP-GlcNAc:dolichol-phosphate GlcNAc phosphotransferase (uterus)
2570	14968	GLCNACT1g	alpha-N-acetylglucosaminyltransferase I, Golgi apparatus
2571	11613	GLCNACT2g	alpha-N-acetylglucosaminyltransferase II
2572	11614	GLCNACT3g	alpha-N-acetylglucosaminyltransferase II
2573	11615	GLCNACT4g	alpha-N-acetylglucosaminyltransferase II
2574	11616	GLCNACT5g	alpha-N-acetylglucosaminyltransferase II
2575	7331	GLCNACT_L	UDP-GlcNAc:N-acetyl-D-glucosaminyl diphosphodolichol N-acetyl-D-glucosaminyltransferase (liver)
2576	7332	GLCNACT_U	UDP-GlcNAc:N-acetyl-D-glucosaminyl diphosphodolichol N-acetyl-D-glucosaminyltransferase (uterus)
2577	13435	GLCURter	glucuronate endoplasmic reticular transport
2578	13784	GLCURtly	glucuronate transport into lysososme
2579	11809	GLCt1r	glucose transport (uniport)
2580	11963	GLCt2_2	D-glucose transport in via proton symport
2581	11967	GLCt2r	D-glucose transport in via proton symport
2582	12112	GLCt4	glucose transport via sodium symport
2583	11961	GLCt4_2	glucose transport via sodium symport
2584	10014	GLCter	glucose transport, endoplasmic reticulum
2585	13532	GLCtg	glucose transport, Golgi apparatus

Column	Reaction #	Abbreviation	Reaction Name
2586	14920	GLCtly	glucose efflux from lysosome
2587	10070	GLDBRAN	glycogen debranching enzyme
2588	10066	GLGNS1	glycogen synthase (ggn -> glygn1)
2589	11848	GLNALANaEx	L-alanine/L-glutamine Na-dependent exchange (Gln-L in)
2590	11863	GLNASNNaEx	L-glutamine/L-asparagine Na-dependent exchange (Gln-L in)
2591	11856	GLNCYSNaEx	L-cysteine/L-glutamine Na-dependent exchange (Gln-L in)
2592	10194	GLNLASEer	gluconolactonase, endoplasmic reticulum
2593	3539	GLNS	glutamine synthetase
2594	11852	GLNSERNaEx	L-serine/L-glutamine Na-dependent exchange (Gln-L in)
2595	11860	GLNTHRNaEx	L-threonine/L-glutamine Na-dependent exchange (Gln-L in)
2596	11698	GLNt4	L-glutamine reversible transport via sodium symport
2597	11673	GLNtN1	Glutamine transport (Na, H coupled)
2598	11980	GLNtm	L-glutamine transport via electroneutral transporter
2599	10068	GLPASE1	glycogen phosphorylase (glygn2 -> dxtrn)
2600	10094	GLPASE2	glycogen phosphorylase (amyls -> glc-D)
2601	10276	GLRASE	glucuronolactone reductase
2602	9630	GLU5Km	glutamate 5-kinase (m)
2603	3540	GLUCYS	gamma-glutamylcysteine synthetase
2604	2960	GLUDC	Glutamate Decarboxylase
2605	9365	GLUDxm	glutamate dehydrogenase (NAD) (mitochondrial)
2606	9366	GLUDym	glutamate dehydrogenase (NADP), mitochondrial
2607	9368	GLUNm	glutaminase (mitochondrial)
2608	3542	GLUPRT	glutamine phosphoribosyldiphosphate amidotransferase
2609	9501	GLUTCOADHm	glutaryl-CoA dehydrogenase (mitochondria)
2610	11910	GLUVESSEC	L-glutamate secretion via secretory vesicle (ATP driven)
2611	1509	GLUt2m	L-glutamate reversible transport via proton symport, mitochondrial
2612	11820	GLUt6	Glutamate transport via Na, H symport and K antiport
2613	14915	GLUt7l	Glutamate transport, lysosomal
2614	19801	GLUtr	intracellular transport
2615	10459	GLXO1	glyoxylate oxidase
2616	13862	GLXO2p	glyoxylate oxidase, peroxisomal
2617	13858	GLXtm	glyoxylate transport, mitochondrial
2618	1526	GLXtp	glyoxylate transport, peroxisomal
2619	9722	GLYAMDTRc	glycine amidinotransferase (c)
2620	9642	GLYATm	glycine C-acetyltransferase
2621	11948	GLYBt4(2)r	Betaine transport (sodium symport) (2:1)
2622	13322	GLYBtm	Glycine betaine transport via diffusion (mitochondria to cytosol)
2623	20239	GLYC-St	L-glycerate export
2624	1930	GLYC3Ptm	glycerol-3-phosphate shuttle
2625	6159	GLYCK2	glycerate kinase
2626	2128	GLYCLTDy	Glycolate dehydrogenase (NADP)
2627	13863	GLYCLTDym	Glycolate dehydrogenase (NADP), mitochondrial
2628	19517	GLYCLTtp	glycolate transport into peroxisome
2629	10489	GLYCTO1p	Glycolate oxidase, peroxisome
2630	1551	GLYCt	glycerol transport via channel
2631	4023	GLYCtm	glycerol transport
2632	256	GLYK	glycerol kinase
2633	4419	GLYKm	glycerol kinase
2634	455	GLYOX	hydroxyacylglutathione hydrolase
2635	456	GLYOXm	hydroxyacylglutathione hydrolase, mitochondrial
2636	10251	GLYOp	glycine oxidase, perixosomal
2637	11920	GLYVESSEC	Glycine secretion via secretory vesicle (ATP driven)
2638	1362	GLYt2r	glycine reversible transport via proton symport

Column	Reaction #	Abbreviation	Reaction Name
2639	11683	GLYt2rL	glycine reversible transport via proton symport (lysosome)
2640	11690	GLYt4	glycine transport via sodium symport
2641	11943	GLYt7(211)r	glycine reversible transport via sodium and chloride symport (2:1:1)
2642	11944	GLYt7(311)r	glycine reversible transport via sodium and chloride symport (3:1:1)
2643	4037	GLYtm	glycine passive transport to mitochondria
2644	14021	GLYtp	glycine passive transport to peroxisome
2645	2304	GMAND	GDP-D-mannose dehydratase
2646	3543	GMPR	GMP reductase
2647	2926	GMPS2	GMP synthase
2648	19549	GMPtn	GMP nuclear transport
2649	2843	GND	phosphogluconate dehydrogenase
2650	20143	GNDer	phosphogluconate dehydrogenase, endoplasmic reticulum
2651	9862	GNMT	glycine N-methyltransferase
2652	20233	GP1CALPHAte	gp1calpha_hs transport
2653	20217	GP1CALPHAtg	gp1calpha_hs intracellular transport
2654	20232	GP1Cte	gp1c_hs transport
2655	20216	GP1Ctg	gp1c_hs intracellular transport
2656	14777	GPAM_hs	glycerol-3-phosphate acyltransferase
2657	14780	GPAMm_hs	glycerol-3-phosphate acyltransferase
2658	2531	GPDDA1	Glycerophosphodiester phosphodiesterase (Glycerophosphocholine)
2659	11280	GPIAT	glucosaminylphosphatidyl inositol acetyltransferase
2660	11341	GPIDA2er	glycophosphatidylinositol (GPI) deacylase, endoplasmic reticulum
2661	11340	GPIDAer	glycophosphatidylinositol (GPI) deacylase, endoplasmic reticulum
2662	11283	GPIMTer_L	GlcN-acylPI mannosyltransferase, endoplasmic reticulum
2663	11350	GPIMTer_U	GlcN-acylPI mannosyltransferase, endoplasmic reticulum
2664	20235	GQ1BALPHAte	gq1balpha_hs transport
2665	20219	GQ1BALPHAtg	gq1balpha_hs intracellular transport
2666	20234	GQ1Bte	gq1b_hs transport
2667	20218	GQ1Btg	gq1b_hs intracellular transport
2668	109	GRTT	geranyltranstransferase
2669	9742	GRTTx	geranyltranstransferase
2670	20317	GSNKm	guanosine kinase (mitochondrial)
2671	12542	GSNt	guanosine facilated transport in cytosol
2672	12095	GSNt4	guanosine transport in via sodium symport
2673	12096	GSNt5	guanosine transport in via sodium (1:2) symport
2674	12578	GSNtl	guanosine facilated transport from lysosome
2675	12147	GSNtm	guanosine facilated transport in mitochondria
2676	20236	GT1Ate	gt1a_hs transport
2677	20220	GT1Atg	gt1a_hs intracellular transport
2678	10201	GTHDH	Glutathione dehydrogenase (dehydroascorbate reductase)
2679	1411	GTHO	glutathione oxidoreductase
2680	4913	GTHOm	glutathione oxidoreductase
2681	1410	GTHP	glutathione peridoxase
2682	10878	GTHPe	glutathione peroxidase (e)
2683	4914	GTHPm	glutathione peroxidase, mitochondria
2684	4912	GTHRDt	Glutathione transport into mitochondria
2685	19804	GTHRDtr	glutathione transport via diffusion
2686	3545	GTHS	glutathione synthetase
2687	11539	GTMLTe	g-glutamyltransferase (e)
2688	7819	GTPCI	GTP cyclohydrolase I
2689	11635	GTPCIn	GTP cyclohydrolase I, nuclear

Column	Reaction #	Abbreviation	Reaction Name
2690	14147	GTPtn	GTP diffusion in nucleus
2691	10076	GUACYC	guanylate cyclase
2692	3312	GUAD	guanine deaminase
2693	2808	GUAPRT	guanine phosphoribosyltransferase
2694	2102	GUAt	Guanine transport
2695	13433	GULLACter	gulonolactone endoplasmic reticular transport
2696	10152	GULN3D	L-gulonate 3-dehydrogenase
2697	10189	GULNDer	gulonate dehydrogenase, endoplasmic reticulum
2698	13439	GULNter	L-gulonate endoplasmic reticular export
2699	13430	GUR1PP	Glucuronate 1-phosphate phosphatase
2700	9367	GluForTx	Glutamate formimidoyltransferase
2701	4415	H2CO3D	carboxylic acid dissociation
2702	6253	H2CO3D2	carboxylic acid dissociation
2703	20852	H2CO3D2m	carboxylic acid dissociation, mitochondrial
2704	4417	H2CO3Dm	carboxylic acid dissociation
2705	11302	H2ETer	H2 phosphoethanolaminyl transferase, endoplasmic reticulum
2706	11285	H2MTer_L	H2 mannosyltransferase, endoplasmic reticulum
2707	11351	H2MTer_U	H2 mannosyltransferase, endoplasmic reticulum
2708	13679	H2O2syn	Hydrogen peroxide synthesis (NADPH dependent)
2709	20854	H2O2t	hydrogen peroxide transport via diffusion
2710	13514	H2O2tly	hydrogen peroxide lysosomal transport via diffusion
2711	20853	H2O2tm	hydrogen peroxide mitochondrial transport
2712	19550	H2O2tn	hydrogen peroxide nuclear transport
2713	1282	H2O2tp	hydrogen peroxide peroxisomal transport via diffusion
2714	868	H2Ot	H2O transport via diffusion
2715	2159	H2Oter	H2O endoplasmic reticulum transport
2716	13512	H2Otg	H2O transport, Golgi apparatus
2717	13513	H2Otly	H2O transport, lysosomal
2718	875	H2Otm	H2O transport, mitochondrial
2719	777	H2Otn	H2O transport, nuclear
2720	2153	H2Otp	H2O transport, peroxisomal
2721	11306	H3ETer	H3 phosphoethanolaminyl transferase, endoplasmic reticulum
2722	11305	H3MTer_L	H3 mannosyltransferase, endoplasmic reticulum
2723	11352	H3MTer_U	H3 mannosyltransferase, endoplasmic reticulum
2724	11308	H4ET3er	H4 phosphoethanolaminyl transferase, endoplasmic reticulum
2725	11307	H4ETer	H4 phosphoethanolaminyl transferase, endoplasmic reticulum
2726	11303	H5MTer_L	H5 mannosyltransferase, endoplasmic reticulum
2727	11353	H5MTer_U	H5 mannosyltransferase, endoplasmic reticulum
2728	11309	H6'ET2er	H6' phosphoethanolaminyl transferase, endoplasmic reticulum
2729	11310	H6'ETer	H6' phosphoethanolaminyl transferase, endoplasmic reticulum
2730	11313	H6ET3er	H6 phosphoethanolaminyl transferase, endoplasmic reticulum
2731	11344	H6MTer_L	H6 mannosyltransferase, endoplasmic reticulum
2732	11354	H6MTer_U	H6 mannosyltransferase, endoplasmic reticulum
2733	11315	H7'ETer	H7' phosphoethanolaminyl transferase, endoplasmic reticulum
2734	11338	H7'TAer	H7' transamidase, endoplasmic reticulum
2735	11314	H7ET2er	H7 phosphoethanolaminyl transferase, endoplasmic reticulum
2736	11345	H7MTer_L	H7 mannosyltransferase, endoplasmic reticulum

Column	Reaction #	Abbreviation	Reaction Name
2737	11355	H7MTer_U	H7 mannosyltransferase, endoplasmic reticulum
2738	11346	H8MTer_L	H8 mannosyltransferase, endoplasmic reticulum
2739	11356	H8MTer_U	H8 mannosyltransferase, endoplasmic reticulum
2740	11337	H8TAer	H8 transamidase, endoplasmic reticulum
2741	9505	HACD1m	3-hydroxyacyl-CoA dehydrogenase (acetoacetyl-CoA) (mitochondria)
2742	9506	HACD1x	3-hydroxyacyl-CoA dehydrogenase (acetoacetyl-CoA) (peroxisome)
2743	10918	HACD9m	3-hydroxyacyl-CoA dehydrogenase (2-Methylacetoacetyl-CoA), mitochondrial
2744	14547	HAS1	hyaluronan synthase
2745	14546	HAS2	hyaluronan synthase
2746	14967	HAtly	hyaluronan transport, extracellular to lysosome
2747	11090	HBZOPT10m	Hydroxybenzoate Decaprenyltransferase
2748	2911	HCO3Em	HCO3 equilibration reaction
2749	12045	HCO3_CLt	bicarbonate transport (Cl-/HCO3- exchange)
2750	12049	HCO3_NAt	bicarbonate transport (Na/HCO3 cotransport)
2751	19716	HCOUMARINte	xenobiotic transport
2752	20131	HDCAter	palmitate ER export
2753	12444	HDCAtr	fatty acid transport via diffusion
2754	12445	HDCEAtr	fatty acid transport via diffusion
2755	20160	HDD2COAtx	hdd2coa intracellular transport
2756	19758	HESTRATRIOLte	hydroxylated estrogen derivative transport
2757	19757	HESTRATRIOLtr	hydroxylated estrogen derivative transport
2758	2842	HEX1	hexokinase (D-glucose:ATP)
2759	671	HEX10	hexokinase (D-glucosamine:ATP)
2760	666	HEX4	hexokinase (D-mannose:ATP)
2761	669	HEX7	hexokinase (D-fructose:ATP)
2762	19030	HEXCCOAtx	fatty acid intracellular transport
2763	19092	HEXCCPT1	carnitine O-palmitoyltransferase
2764	19111	HEXCCPT2	carnitine transferase
2765	19073	HEXCCRNt	transport into the mitochondria (carnitine)
2766	12459	HEXCt	fatty acid transport via diffusion
2767	2672	HGNTOR	Homogentisate:oxygen 1,2-oxidoreductase (decyclizing)
2768	10418	HIBDm	3-hydroxyisobutyrate dehydrogenase, mitochondrial
2769	380	HISD	histidase
2770	7384	HISDC	histidine decarboxylase
2771	10535	HISTASE	Histaminase
2772	11934	HISTAVESSEC	Histamine secretion via secretory vesicle (ATP driven)
2773	12193	HISTAtu	Histamine uniport
2774	11700	HISt4	L-histidine transport in via sodium symport
2775	11671	HIStN1	Histidine transport (Na, H coupled)
2776	11696	HIStiDF	L-histidine transport via diffusion (extracellular to cytosol)
2777	2668	HKYNH	3-Hydroxy-L-kynurenine hydrolase
2778	7098	HKt	H+/K+ gastric/non-gastric P-ATPase and ABC ATPase
2779	4	HMBS	hydroxymethylbilane synthase
2780	9732	HMGCOARr	Hydroxymethylglutaryl CoA reductase (ir)
2781	9733	HMGCOARx	Hydroxymethylglutaryl CoA reductase (ir)
2782	6785	HMGCOASi	Hydroxymethylglutaryl CoA synthase (ir)
2783	9720	HMGCOASim	Hydroxymethylglutaryl CoA synthase (ir)
2784	1933	HMGCOAtm	Hydroxymethylglutaryl-CoA reversible mitochondrial transport
2785	14000	HMGCOAtx	Hydroxymethylglutaryl-CoA reversible peroxisomal transport
2786	4424	HMGLm	hydroxymethylglutaryl-CoA lyase
2787	9731	HMGLx	hydroxymethylglutaryl-CoA lyase

Column	Reaction #	Abbreviation	Reaction Name
2788	11705	HOMt4	L-homoserine via sodium symport
2789	11915	HOXG	Heme oxygenase 1
2790	14451	HPACtr	hydroxyphenylacetate transport via diffusion
2791	14103	HPCLx	2-hydroxyphytanoyl-CoA lyase
2792	14865	HPDCACRNCPT1	carnitine fatty-acyl transferase
2793	14866	HPDCACRNCPT2	heptadecanoate transport into the mitochondria
2794	14868	HPDCACRNt	heptadecanoate transport into the mitochondria
2795	19805	HPDCAt	fatty acid transport via diffusion
2796	3560	HPROxm	L-hydroxyproline dehydrogenase (NAD), mitochondrial
2797	10518	HPYRDC	hydroxypyruvate decarboxylase
2798	13864	HPYRDCm	hydroxypyruvate decarboxylase, mitochondria
2799	10505	HPYRR2x	hydroxypyruvate reductase (NADH)
2800	2130	HPYRRy	Hydroxypyruvate reductase (NADPH)
2801	14022	HPYRtp	hydroxypyruate transport, peroxisomal
2802	15088	HRETNtn	4-hydroxyretinoic acid transport, Nuclear
2803	14390	HS1ly	heparan-N-sulfatase, lysosomal
2804	14395	HS2ly	heparan-N-sulfatase, lysosomal
2805	14396	HS3ly	heparan-N-sulfatase, lysosomal
2806	14397	HS4ly	heparan-N-sulfatase, lysosomal
2807	14575	HSAT1ly	heparan-glucosaminide N-acetyltransferase, lysosomal
2808	14574	HSAT2ly	heparan-glucosaminide N-acetyltransferase, lysosomal
2809	14572	HSAT3ly	heparan-glucosaminide N-acetyltransferase, lysosomal
2810	14571	HSAT4ly	heparan-glucosaminide N-acetyltransferase, lysosomal
2811	11435	HSD11B1r	11-beta-hydroxysteroid dehydrogenase type 1
2812	11434	HSD11B2r	11-beta-hydroxysteroid dehydrogenase type 2
2813	9943	HSD17B1	testicular 17-beta-hydroxysteroid dehydrogenase
2814	14989	HSD17B2r	17-beta-hydroxysteroid dehydrogenase
2815	9966	HSD17B3r	testicular 17-beta-hydroxysteroid dehydrogenase
2816	13934	HSD17B42x	hydroxysteroid (17-beta) dehydrogenase 4
2817	9679	HSD17B4x	hydroxysteroid (17-beta) dehydrogenase 4
2818	9971	HSD17B7r	testicular 17-beta-hydroxysteroid dehydrogenase
2819	14991	HSD17B8r	17-beta-hydroxysteroid dehydrogenase
2820	20867	HSD17B9r	17-beta-hydroxysteroid dehydrogenase (type 7)
2821	20864	HSD3A1r	3 alpha-hydroxysteroid dehydrogenase (type 3)
2822	20865	HSD3A2r	3 alpha-hydroxysteroid dehydrogenase (type 3)
2823	9874	HSD3B11	3 beta-hydroxysteroid dehydrogenase/delta 5-->4-isomerase type I
2824	9967	HSD3B11r	3 beta-hydroxysteroid dehydrogenase/delta 5-->4-isomerase type I
2825	9968	HSD3B12r	3 beta-hydroxysteroid dehydrogenase/delta 5-->4-isomerase type I
2826	9878	HSD3B13	3 beta-hydroxysteroid dehydrogenase/delta 5-->4-isomerase type I
2827	9969	HSD3B13r	3 beta-hydroxysteroid dehydrogenase/delta 5-->4-isomerase type I
2828	20869	HSD3B2r	3 beta-hydroxysteroid dehydrogenase type 1
2829	20870	HSD3B3r	3 beta-hydroxysteroid dehydrogenase type 1
2830	9648	HSD3B7	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7
2831	9649	HSD3B7P	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7
2832	11770	HSPASEly	heparan sulfate proteoglycan protease, lysosome (endosome)
2833	14965	HSPGt	heparan sulfate transport, golgi to extracellular
2834	14966	HSPGtly	heparan sulfate transport, extracellular to lysosome
2835	19718	HTAXOLte	xenobiotic transport

Column	Reaction #	Abbreviation	Reaction Name
2836	12576	HXANtl	hypoxanthine facilated transport from lysosome
2837	14088	HXANtx	hypoxanthine diffusion in peroxisome
2838	441	HXPRT	hypoxanthine phosphoribosyltransferase (Hypoxanthine)
2839	1732	HYPOE	hypothetical enyme
2840	11001	HYPTROX	Hypotaurine oxidase
2841	1155	HYXNt	Hypoxanthine transport
2842	5333	Htm	Uncoupling protein
2843	13967	Htr	H transporter, endoplasmic reticulum
2844	13997	Htx	H transporter, peroxisome
2845	486	ICDHxm	Isocitrate dehydrogenase (NAD+)
2846	3109	ICDHy	isocitrate dehydrogenase (NADP)
2847	489	ICDHyp	Isocitrate dehydrogenase (NADP+)
2848	10041	ICDHyrm	Isocitrate dehydrogenase (NADP+)
2849	13661	IDHPOXOX2b	Iodide:hydrogen-peroxide oxidoreductase 2
2850	9459	IDHPOXOX3	Iodide:hydrogen-peroxide oxidoreductase 3
2851	9461	IDHPOXOX4	Iodide:hydrogen-peroxide oxidoreductase 4
2852	13660	IDHPOXOXb	Iodide:hydrogen-peroxide oxidoreductase
2853	11716	IDOAASE1ly	alpha-L-iduronidase, lysosomal
2854	11735	IDOAASE2ly	alpha-L-iduronidase, lysosomal
2855	11736	IDOAASE3ly	alpha-L-iduronidase, lysosomal
2856	14416	IDOAASE4ly	alpha-L-iduronidase, lysosomal
2857	14925	IDOURtly	iduronate transport into lysososme
2858	19546	IDPtn	IDP nuclear transport
2859	319	ILETA	isoleucine transaminase
2860	1326	ILETAm	isoleucine transaminase, mitochondrial
2861	11949	ILEt4	L-isoleucine transport in via sodium symport
2862	12595	ILEt5m	Isoleucine mitochondrial transport
2863	11925	ILEtec	L-isoleucine transport via diffusion (extracellular to cytosol)
2864	9351	IMACTD	Imidazole acetaldeyde dehydrogenase
2865	9352	IMACTD_m	Imidazole acetaldeyde dehydrogenase (mito)
2866	399	IMPC	IMP cyclohydrolase
2867	400	IMPD	IMP dehydrogenase
2868	10921	INOSTO	inositol oxygenase
2869	20321	INSKm	insosine kinase, mitochondrial
2870	11960	INSTt2r	inositol transport in via proton symport
2871	12113	INSTt4	inositol transport via sodium symport
2872	12128	INSTt4_2	inositol transport via sodium symport
2873	2574	INSt	Inosine transport (diffusion)
2874	12093	INSt4	inosine transport in via sodium symport
2875	12094	INSt5	inosine transport in via sodium (1:2) symport
2876	12573	INStl	inosine facilated transport from lysosome
2877	12538	INStm	inosine facilated transport in mitochondria
2878	9737	IPDDIx	isopentenyl-diphosphate D-isomerase
2879	6236	ITCOAL1m	Itaconate--CoA ligase (GDP-forming), mitochondrial
2880	3271	ITCOALm	Itaconate--CoA ligase (ADP-forming), mitochondrial
2881	19547	ITPtn	ITP nuclear transport
2882	7861	IZPN	imidazolonepropionase
2883	12127	It	Iodide uniport
2884	6648	KAS8	b-ketoacyl synthetase (palmitate, n-C16:0)
2885	13052	KCC2t	K+-Cl- cotransporter (NH4+)
2886	13051	KCCt	K+-Cl- cotransport
2887	10646	KDNH	2-keto-3deoxy-D-glycero-D-galactononic acid phosphohydrolase
2888	9644	KHK	ketohexokinase
2889	13865	KHK2	ketohexokinase (D-xylulose)

Column	Reaction #	Abbreviation	Reaction Name
2890	19624	KHK3	ketohexokinase (D-tagatose)
2891	14960	KSII_CORE2t	keratan sulfate II (core2) transport, golgi to extracellular
2892	14963	KSII_CORE2tly	keratan sulfate II (core 2) transport, extracellular to lysosome
2893	14961	KSII_CORE4t	keratan sulfate II (core4) transport, golgi to extracellular
2894	14964	KSII_CORE4tly	keratan sulfate II (core 4) transport, extracellular to lysosome
2895	14959	KSIt	keratan sulfate I transport, golgi to extracellular
2896	14962	KSItly	keratan sulfate I transport, extracellular to lysosome
2897	2675	KYN	kynureninase
2898	3489	KYN3OX	kynurenine 3-monooxygenase
2899	9507	KYNAKGAT	L-Kynurenine:2-oxoglutarate aminotransferase
2900	11610	KYNATESYN	4-(2-Aminophenyl)-2,4-dioxobutanoate dehydratase
2901	12674	Kt3g	potassium transport via proton antiport
2902	18718	L-LACDcm	L-Lactate dehydrogenase, cytosolic/mitochondrial
2903	1552	L-LACt2r	L-lactate reversible transport via proton symport
2904	12474	L-LACt4r	L-lactate reversible transport via sodium symport
2905	14450	L-LACtcm	L-lactate transport via diffusion (cytosol to mitochondria)
2906	1295	L-LACtm	L-lactate transport, mitochondrial
2907	9889	LACZe	b-galactosidase, extracellular
2908	9883	LACZly	b-galactosidase,lysosomal
2909	9623	LALDD	D-lactaldehyde dehydrogenase
2910	9624	LALDO	D-Lactaldehyde:NAD+ oxidoreductase (glutathione-formylating)
2911	9625	LALDO2	D-Lactaldehyde:NADP+ 1-oxidoreductase
2912	20016	LALDO2x	D-Lactaldehyde:NAD+ 1-oxidoreductase
2913	14654	LAPCOAl	lysosomal acid phosphorylase (CoA)
2914	2949	LCADi	lactaldehyde dehydrogenase
2915	14171	LCADi_D	lactaldehyde dehydrogenase
2916	14176	LCADi_Dm	lactaldehyde dehydrogenase, mitochondrial
2917	14174	LCADim	lactaldehyde dehydrogenase, mitochondrial
2918	14712	LCAT1e	Lecithin-cholesterol acyltransferase
2919	19513	LCTStg	lactose transport from Golgi to extracellular (via vesicle)
2920	19514	LCTStl	lactose transport from cytosol to lysosome (via autophagocytosis)
2921	14564	LCYSTAT	L-Cysteate:2-oxoglutarate aminotransferase
2922	14565	LCYSTATm	L-Cysteate:2-oxoglutarate aminotransferase, mitochondrial
2923	9860	LCYSTCBOXL	3-Sulfoalanine carboxy-lyase
2924	293	LDH_D	D-lactate dehydrogenase
2925	2847	LDH_L	L-lactate dehydrogenase
2926	4416	LDH_Lm	L-lactate dehydrogenase
2927	19798	LEUKTRA4tr	leukotriene intracellular transport
2928	19799	LEUKTRB4tr	leukotriene intracellular transport
2929	12274	LEUKTRC4t	leukotriene C4 transport via bicarbonate countertransport
2930	19809	LEUKTRD4tr	leukotriene intracellular transport
2931	82	LEUTA	leucine transaminase
2932	705	LEUTAm	leucine transaminase, mitochondrial
2933	11693	LEUt4	L-leucine transport in via sodium symport
2934	12594	LEUt5m	leucine mitochondrial transport
2935	11924	LEUtec	L-leucine transport via diffusion (extracellular to cytosol)
2936	10872	LFORKYNHYD	L-Formylkynurenine hydrolase
2937	19031	LGNCCOAtx	fatty acid intracellular transport
2938	19091	LGNCCPT1	carnitine O-palmitoyltransferase
2939	19110	LGNCCPT2	transport into the mitochondria (carnitine)
2940	19072	LGNCCRNt	transport into the mitochondria (carnitine)
2941	12463	LGNCt	fatty acid transport via diffusion

Column	Reaction #	Abbreviation	Reaction Name
2942	457	LGTHL	lactoylglutathione lyase
2943	20193	LIMNENte	xenobiotic transport
2944	14387	LINKDEG1ly	degradation of proteoglycan linkage region, lysosomal
2945	14417	LINKDEG2ly	degradation of proteoglycan linkage region, lysosomal
2946	14427	LINKDEG3ly	degradation of proteoglycan linkage region, lysosomal
2947	14449	LINKDEG4ly	degradation of proteoglycan linkage region, lysosomal
2948	10481	LIPOti	Lipoate transport via sodium symport
2949	19096	LNELDCCPT1	carnitine O-palmitoyltransferase
2950	19115	LNELDCCPT2	carnitine transferase
2951	19077	LNELDCCRNt	transport into the mitochondria (carnitine)
2952	12454	LNELDCt	fatty acid transport via diffusion
2953	19097	LNLCCPT1	carnitine O-palmitoyltransferase
2954	19116	LNLCCPT2	carnitine transferase
2955	19078	LNLCCRNt	transport into the mitochondria (carnitine)
2956	13579	LNLCt	Linoleic acid (n-C18:2) transport in via diffusion
2957	19099	LNLNCACPT1	carnitine O-palmitoyltransferase
2958	19118	LNLNCACPT2	carnitine transferase
2959	19080	LNLNCACRNt	transport into the mitochondria (carnitine)
2960	12452	LNLNCAt	fatty acid transport via diffusion
2961	19098	LNLNCGCPT1	carnitine O-palmitoyltransferase
2962	19117	LNLNCGCPT2	carnitine transferase
2963	19079	LNLNCGCRNt	transport into the mitochondria (carnitine)
2964	12451	LNLNCGt	fatty acid transport via diffusion
2965	3410	LNS14DM	cytochrome P450 lanosterol 14-alpha-demethylase (NADP)
2966	9753	LNS14DMr	cytochrome P450 lanosterol 14-alpha-demethylase
2967	9748	LNSTLSr	lanosterol synthase
2968	10860	LPASE	lysophospholipase
2969	9936	LPCOXp	L-pipecolate oxidase, peroxisomal
2970	14378	LPS	lipase
2971	14366	LPS2	lipase
2972	14367	LPS2e	lipase, extracellular
2973	14368	LPS3	lipase
2974	14369	LPS3e	lipase, extracellular
2975	14374	LPS4e	phospholipase
2976	14379	LPSe	lipase
2977	15060	LRAT	Lecithin retinol acyltransferase
2978	15108	LRAT1	Lecithin retinol acyltransferase (11-cis)
2979	15107	LRAT2	Lecithin retinol acyltransferase (9-cis)
2980	11320	LS3	Lumisterol 3 formation
2981	9771	LSTO1r	Lathosterol oxidase
2982	9772	LSTO2r	Lathosterol oxidase
2983	9998	LTA4H	Leukotriene A-4 hydrolase
2984	19811	LTC4CP	Leukotriene C4 carboxypeptidase
2985	19803	LTC4Sr	Leukotriene C4 synthase
2986	19808	LTD4DP	Leukotriene D4 dipeptidase
2987	9580	LTDCL	L-Tryptophan decarboxy-lyase
2988	11026	LYSMTF1n	histone-lysine N-methyltransferase, nuclear
2989	11027	LYSMTF2n	histone-lysine N-methyltransferase, nuclear
2990	11028	LYSMTF3n	histone-lysine N-methyltransferase, nuclear
2991	12661	LYSOXp	L-lysine oxidase, peroxisomal
2992	11953	LYSt4	L-lysine transport in via sodium symport
2993	11697	LYStiDF	L-lysine transport via diffusion (extracellular to cytosol)
2994	12950	LYStip	L-lysine transport, peroxisomal (irreversible)
2995	5290	LYStm	Lysine mitochondrial transport via ornithine carrier
2996	14827	LYStn	L-lysine transport, nuclear
2997	7754	M1316Mg	mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase

Column	Reaction #	Abbreviation	Reaction Name
2998	7711	M13N2Tg	alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase
2999	7770	M13N4Tg	alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase
3000	7769	M14NTg	beta-1,4-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase
3001	7772	M16N4Tg	alpha-1,6-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase
3002	7771	M16N6Tg	alpha-1,6-mannosyl-glycoprotein 6-beta-N-acetylglucosaminyltransferase
3003	7756	M16NTg	alpha-1,6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase
3004	11348	M4ATAer	M4A transamidase, endoplasmic reticulum
3005	11343	M4BET2er	M4B phosphoethanolaminyl transferase, endoplasmic reticulum
3006	11347	M4BTAer	M4B transamidase, endoplasmic reticulum
3007	11342	M4CET3er	M4C phosphoethanolaminyl transferase, endoplasmic reticulum
3008	8051	M4MPDOL_Lter	m4mpdol flippase
3009	8052	M4MPDOL_Uter	m4mpdol flippase
3010	7718	M7MASNBterg	m7masnB transport from endoplasmic reticulum to Golgi apparatus
3011	8054	M8MASNterg	m8masn transport from ER to Golgi apparatus
3012	2669	MACACI	maleylacetoacetate isomerase
3013	9358	MACOXO	3-Methylimidazole acetaldehyde:NAD+ oxidoreductase
3014	20296	MALSO3tm	Malate:sulfite antiport, mitochondrial
3015	20299	MALSO4tm	Malate:sulfate antiport, mitochondrial
3016	690	MALT	alpha-glucosidase
3017	20248	MALTSULtm	Malate:thiosulfate antiport, mitochondrial
3018	9993	MALTe	alpha-glucosidase, extracellular
3019	9992	MALTly	alpha-glucosidase, lysosomal
3020	11912	MALTt1r	maltose transport (uniport)
3021	985	MALtm	malate transport, mitochondrial
3022	2536	MAN1PT2	mannose-1-phosphate guanylyltransferase (GDP)
3023	8116	MAN1_6B1er	mannosidase I, endoplasmic reticulum (g1m6masnB1-producing)
3024	8114	MAN1_7Ber	mannosidase I, endoplasmic reticulum (g1m7masnB-producing)
3025	8117	MAN2_6B1er	mannosidase II, endoplasmic reticulum (g1m6masnB1-producing)
3026	8115	MAN2_7Cer	mannosidase II, endoplasmic reticulum (g1m7masnC-producing)
3027	244	MAN6PI	mannose-6-phosphate isomerase
3028	11905	MANt1r	mannose transport (uniport)
3029	12125	MANt4	D-mannose transport via sodium cotransport
3030	15052	MANter	mannose efflux from endoplasmic reticulum
3031	15051	MANtg	mannose efflux from Golgi apparatus
3032	14924	MANtly	mannose efflux from lysosome
3033	9399	MAOLNOR	monoamine oxidase (L-Normetanephrine)
3034	13484	MAOX	Methylamine oxidase
3035	10429	MCCCrm	methylcrotonoyl-CoA carboxylase, mitochondrial
3036	9550	MCD	Malonyl-CoA Decarboxylase cytoplasmic
3037	8386	MCDm	Malonyl-CoA Decarboxylase, mitochondrial
3038	9549	MCDp	Malonyl-CoA Decarboxylase peroxisomal
3039	2250	MCITS	2-methylcitrate synthase
3040	20240	MCLACCYSR	3-mercaptolactate:cysteine reductase

Column	Reaction #	Abbreviation	Reaction Name
3041	10179	MCLOR	3-Mercaptolactate:NAD+ oxidoreductase
3042	3441	MCOATA	Malonyl-CoA-ACP transacylase
3043	3337	MCOATAm	Malonyl-CoA-ACP transacylase, mitochondrial
3044	13722	MCPST	3-mercaptopyruvate sulfurtransferase
3045	541	MDH	malate dehydrogenase
3046	543	MDHm	malate dehydrogenase, mitochondrial
3047	1630	MDRPD	5-Methylthio-5-deoxy-D-ribulose 1-phosphate dehydratase
3048	2942	ME1m	malic enzyme (NAD), mitochondrial
3049	2848	ME2	malic enzyme (NADP)
3050	540	ME2m	malic enzyme (NADP), mitochondrial
3051	10809	MECOALm	mesaconate--CoA ligase (ADP-forming), mitochondrial
3052	10810	MECOAS1m	mesaconate--CoA ligase (GDP-forming)
3053	9609	MELATN23DOX	Melatonin:oxygen 2,3-dioxygenase (indole-decyclizing)
3054	9608	MELATNOX	Melatonin:NADP oxidoreductase
3055	7721	MEOHt2	Methanol diffusion
3056	20845	MEOHtly	Methanol transporter, lysosome
3057	13985	MEOHtr	Methanol transporter, endoplasmic reticulum
3058	20192	MEPIVESSte	metanephrine secretion via secretory vesicle (ATP driven)
3059	20241	MERCPLACCYSt	3-mercaptolactate-cysteine disulfide transport, extracellular
3060	10816	MESCOALm	Mesaconyl-CoA pyruvate-lyase
3061	369	METAT	methionine adenosyltransferase
3062	11871	METLEUex	Methionine/Leucine exchange (Met in)
3063	7846	METS	methionine synthase
3064	11699	METt4	L-methionine transport in via sodium symport
3065	11927	METtec	L-methionine transport via diffusion (extracellular to cytosol)
3066	9734	MEVK1x	mevalonate kinase (atp)
3067	7633	MG1er	mannosyl-oligosaccharide glucosidase, endoplasmic reticulum
3068	7634	MG2er	mannosyl-oligosaccharide glucosidase, endoplasmic reticulum
3069	7636	MG3er	mannosyl-oligosaccharide glucosidase, endoplasmic reticulum
3070	10814	MGACONm	methylglutaconase, mitochondrial
3071	10907	MGCHrm	methylglutaconyl-CoA hydratase (reversible), mitochondrial
3072	269	MGSA	methylglyoxal synthase
3073	14084	MGSA2	methyglyoxylate synthase 2 (from g3p)
3074	9356	MHISOR	N-Methylhistamine:oxygen oxidoreductase (deaminating)
3075	10936	MI13456PK	inositol-1,3,4,5,6-pentakisphosphate 2-kinase
3076	19594	MI13456Ptn	inositol 1,3,4,5,6-pentakisphosphate nuclear transport (diffusion)
3077	10980	MI1345PKn	inositol-1,3,4,5-triphosphate 6-kinase, nucleus
3078	10930	MI1345PP	inositol-1,3,4,5-trisphosphate 5-phosphatase
3079	10977	MI1346PKn	inositol-1,3,4,6-tetrakisphosphate 5-kinase, nucleus
3080	19572	MI1346Ptn	1D-myo-Inositol 1,3,4,6-tetrakisphosphate nuclear transport (diffusion)
3081	11035	MI134P4P	inositol-1,3,4-trisphosphate 4-phosphatase
3082	10933	MI134PK	inositol-1,3,4-trisphosphate 6-kinase
3083	10928	MI134PP	inositol-1,3,4-trisphosphate 1-phosphatase
3084	10927	MI13PP	inositol-1,3-bisphosphate 3-phosphatase
3085	10981	MI1456PKn	inositol-1,4,5,6- tetrakisphosphate 3-kinase, nucleus
3086	10978	MI145P6Kn	inositol-1,4,5-triphosphate 6-kinase, nucleus
3087	10932	MI145PK	inositol-1,4,5-trisphosphate 3-kinase
3088	10979	MI145PKn	inositol-1,4,5-trisphosphate 3-kinase, nucleus
3089	10929	MI145PP	inositol-1,4,5-trisphosphate 5-phosphatase

Column	Reaction #	Abbreviation	Reaction Name
3090	11036	MI14P4P	inositol-1,4-bisphosphate 4-phosphatase
3091	10925	MI14PP	inositol-1,4-bisphosphate 1-phosphatase
3092	19573	MI14Ptn	inositol 1,4-bisphosphate nuclear transport (diffusion)
3093	19575	MI1P-Dtn	inositol 1-phosphate nuclear transport (diffusion)
3094	2540	MI1PP	myo-inositol 1-phosphatase
3095	2656	MI1PS	myo-Inositol-1-phosphate synthase
3096	10935	MI3456PK	inositol-3,4,5,6-tetrakisphosphate 1-kinase
3097	10926	MI34PP	inositol-3,4-bisphosphate 4-phosphatase
3098	10923	MI3PP	myo-inositol 3-phosphatase
3099	10924	MI4PP	myo-inositol 4-phosphatase
3100	20161	MICITDr	2-methylisocitrate dehydratase
3101	19592	MINOHPtn	inositol hexakisphosphate nuclear transport (diffusion)
3102	2513	MLTG1	Maltodextrin glucosidase (maltotriose)
3103	9995	MLTG1e	Maltodextrin glucosidase (maltotriose), extracellular
3104	9994	MLTG1ly	Maltodextrin glucosidase (maltotriose), lysosome
3105	7704	MM5ag	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus
3106	7697	MM5bg	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus
3107	7698	MM5cg	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus
3108	7694	MM6B1ag	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus
3109	7695	MM6B1bg	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus
3110	7696	MM6B2g	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus
3111	7702	MM6ag	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus
3112	7703	MM6bg	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus
3113	7701	MM7Ag	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus
3114	7692	MM7B1g	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus
3115	7693	MM7B2g	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus
3116	7700	MM7Cag	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus
3117	7699	MM7Cbg	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus
3118	7689	MM8Ag	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus
3119	7686	MM8Ber	mannosyl-oligosaccharide 1,2-alpha-mannosidase, endoplasmic reticulum
3120	7690	MM8Cg	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus
3121	3201	MMCD	Methylmalonyl-CoA decarboxylase
3122	14199	MMCDm	Methylmalonyl-CoA decarboxylase, mitochondrial
3123	14200	MMCDp	Methylmalonyl-CoA decarboxylase, peroxisomal
3124	8367	MMEm	methylmalonyl-CoA epimerase/racemase
3125	12775	MMMm	methylmalonyl-CoA mutase
3126	4509	MMSAD1m	methylmalonate-semialdehyde dehydrogenase
3127	10821	MMSAD3m	methylmalonate-semialdehyde dehydrogenase (malonic semialdehyde), mitochondrial

Column	Reaction #	Abbreviation	Reaction Name
3128	14096	MMTSADm	malonate-semialdehyde dehydrogenase (acetylating), mitochondrial
3129	14781	MOGAT	monoacylglycerol acyltransferase
3130	7109	MTAP	5'-methylthioadenosine phosphorylase
3131	7850	MTHFC	methenyltetrahydrofolate cyclohydrolase
3132	7852	MTHFCm	methenyltetrahydrifikate cyclohydrolase, mitochondrial
3133	7853	MTHFD	methylenetetrahydrofolate dehydrogenase (NADP)
3134	10526	MTHFD2	methylenetetrahydrofolate dehydrogenase (NAD)
3135	10524	MTHFD2m	methylenetetrahydrofolate dehydrogenase (NAD), mitochondrial
3136	7855	MTHFDm	methylenetetrahydrofolate dehydrogenase (NADP), mitochondrial
3137	7858	MTHFR3	5,10-methylenetetrahydrofolatereductase (NADPH)
3138	14750	MTHGXLt	Methylglyoxal transport (cytosol to extracellular)
3139	301	MTRI	5-methylthioribose-1-phosphate isomerase
3140	20461	N2M2NMASNt	n2m2nmasn transport, Golgi to extracellular
3141	20462	N2M2NMASNtly	n2m2nmasn transport, extracellular to lysosome
3142	8569	N3Tg	N-acetylgalactosamine 3-beta-galactosyltransferase, Golgi apparatus
3143	8609	N4Tg	N-acetylgalactosamine 4-beta-galactosyltransferase, Golgi apparatus
3144	1414	NABTNO	N4-Acetylaminobutanal:NAD+ oxidoreductase
3145	10640	NABTNOm	N4-Acetylaminobutanal:NAD+ oxidoreductase (m)
3146	9353	NACASPAH	N-Acetyl-L-aspartate amidohydrolase
3147	14516	NACASPtm	N-acetyl-L-aspartate transport (mitochondria to cytosol)
3148	20046	NACHEX10ly	beta-N-acetylhexosaminidase, lysosomal
3149	20045	NACHEX11ly	beta-N-acetylhexosaminidase, lysosomal
3150	20048	NACHEX12ly	beta-N-acetylhexosaminidase, lysosomal
3151	20049	NACHEX13ly	beta-N-acetylhexosaminidase, lysosomal
3152	20051	NACHEX14ly	beta-N-acetylhexosaminidase, lysosomal
3153	20052	NACHEX15ly	beta-N-acetylhexosaminidase, lysosomal
3154	20054	NACHEX16ly	beta-N-acetylhexosaminidase, lysosomal
3155	20055	NACHEX17ly	beta-N-acetylhexosaminidase, lysosomal
3156	20057	NACHEX18ly	beta-N-acetylhexosaminidase, lysosomal
3157	20058	NACHEX19ly	beta-N-acetylhexosaminidase, lysosomal
3158	14405	NACHEX1ly	beta-N-acetylhexosaminidase, lysosomal
3159	20060	NACHEX20ly	beta-N-acetylhexosaminidase, lysosomal
3160	20061	NACHEX21ly	beta-N-acetylhexosaminidase, lysosomal
3161	20063	NACHEX22ly	beta-N-acetylhexosaminidase, lysosomal
3162	20024	NACHEX23ly	beta-N-acetylhexosaminidase, lysosomal
3163	20025	NACHEX24ly	beta-N-acetylhexosaminidase, lysosomal
3164	20026	NACHEX25ly	beta-N-acetylhexosaminidase, lysosomal
3165	20027	NACHEX26ly	beta-N-acetylhexosaminidase, lysosomal
3166	14930	NACHEX27ly	beta-N-acetylhexosaminidase, lysosomal
3167	14408	NACHEX2ly	beta-N-acetylhexosaminidase, lysosomal
3168	14413	NACHEX3ly	beta-N-acetylhexosaminidase, lysosomal
3169	14420	NACHEX4ly	beta-N-acetylhexosaminidase, lysosomal
3170	14425	NACHEX5ly	beta-N-acetylhexosaminidase, lysosomal
3171	14430	NACHEX6ly	beta-N-acetylhexosaminidase, lysosomal
3172	14437	NACHEX7ly	beta-N-acetylhexosaminidase, lysosomal
3173	14443	NACHEX8ly	beta-N-acetylhexosaminidase, lysosomal
3174	14444	NACHEX9ly	beta-N-acetylhexosaminidase, lysosomal
3175	14502	NACHEXA10ly	beta-N-acetylhexosaminidase A, lysosomal
3176	14503	NACHEXA11ly	beta-N-acetylhexosaminidase A, lysosomal
3177	14504	NACHEXA12ly	beta-N-acetylhexosaminidase A, lysosomal
3178	14505	NACHEXA13ly	beta-N-acetylhexosaminidase A, lysosomal

Column	Reaction #	Abbreviation	Reaction Name
3179	14506	NACHEXA14ly	beta-N-acetylhexosaminidase A, lysosomal
3180	14507	NACHEXA15ly	beta-N-acetylhexosaminidase A, lysosomal
3181	14508	NACHEXA16ly	beta-N-acetylhexosaminidase A, lysosomal
3182	14509	NACHEXA17ly	beta-N-acetylhexosaminidase A, lysosomal
3183	14510	NACHEXA18ly	beta-N-acetylhexosaminidase A, lysosomal
3184	14511	NACHEXA19ly	beta-N-acetylhexosaminidase A, lysosomal
3185	14410	NACHEXA1ly	beta-N-acetylhexosaminidase A, lysosomal
3186	14536	NACHEXA20ly	beta-N-acetylhexosaminidase A, lysosomal
3187	14537	NACHEXA21ly	beta-N-acetylhexosaminidase A, lysosomal
3188	14540	NACHEXA22ly	beta-N-acetylhexosaminidase A, lysosomal
3189	14414	NACHEXA2ly	beta-N-acetylhexosaminidase A, lysosomal
3190	14421	NACHEXA3ly	beta-N-acetylhexosaminidase A, lysosomal
3191	14426	NACHEXA4ly	beta-N-acetylhexosaminidase A, lysosomal
3192	14431	NACHEXA5ly	beta-N-acetylhexosaminidase A, lysosomal
3193	14432	NACHEXA6ly	beta-N-acetylhexosaminidase A, lysosomal
3194	14446	NACHEXA7ly	beta-N-acetylhexosaminidase A, lysosomal
3195	14447	NACHEXA8ly	beta-N-acetylhexosaminidase A, lysosomal
3196	14501	NACHEXA9ly	beta-N-acetylhexosaminidase A, lysosomal
3197	1796	NACUP	Nicotinic acid uptake
3198	4313	NADH2-u10m	NADH dehydrogenase, mitochondrial
3199	15145	NADHtpu	NADH transporter, peroxisome
3200	13977	NADHtru	NADH transporter, endoplasmic reticulum
3201	33	NADK	NAD kinase
3202	171	NADN	NAD nucleosidase
3203	10515	NADNe	NAD nucleosidase,extracellular
3204	13979	NADPHtru	NADPH transporter, endoplasmic reticulum
3205	13998	NADPHtxu	NADPH transporter, peroxisome
3206	2811	NADPN	NADP nucleosidase
3207	10514	NADPNe	NADP nucleosidase,extracellular
3208	13980	NADPtru	NADP transporter, endoplasmic reticulum
3209	13999	NADPtxu	NADP transporter, peroxisome
3210	37	NADS2	NAD synthase (glutamine-hydrolysing)
3211	19526	NADtn	NAD transport, nuclear through pores
3212	15146	NADtpu	NAD transporter, peroxisome
3213	13974	NADtru	NAD transporter, endoplasmic reticulum
3214	14541	NAGA2ly	N-acetylgalactosaminidase, alpha-
3215	20859	NAGAlby	N-acetylgalactosaminidase, beta-
3216	11074	NAGAly	N-acetylgalactosaminidase, alpha-
3217	14542	NAGLCAly	N-acetylglucosaminidase, lysosomal
3218	12050	NAHCO3_HCLt	bicarbonate transport (HCl/NaHCO3 exchange)
3219	12115	NAIt	Na+ / iodide cotransport
3220	11965	NAt	sodium transport (uniport)
3221	1085	NAt3_1	sodium proton antiporter (H:NA is 1:1)
3222	12672	NAt3_1g	sodium proton antiporter (H:NA is 1:1)
3223	12617	NAt5	sodium/ammonium proton antiporter
3224	19419	NAtx	sodium transport via diffusion (perioxisome)
3225	9763	NBAHH_ir	Nalpha-(beta-alanyl)-L-histidine hydrolase IR
3226	8202	NCAMUP	Nicotinamide acid uptake
3227	13050	NCCt	Na+-Cl- cotransport
3228	12695	NCKt	Na+/Ca2+-K+ exchange
3229	12696	NCNt	Na+/Ca2+-NH4+ exchange
3230	11147	NDP10ex	nucleoside-diphosphatase (IDP), extracellular
3231	11143	NDP3ex	nucleoside-diphosphatase (GDP), extracellular
3232	801	NDP6	nucleoside-diphosphatase (dCDP)
3233	15237	NDP7er	nucleoside-diphosphatase (UDP), endoplasmic reticulum
3234	11144	NDP7ex	nucleoside-diphosphatase (UDP), extracellular

Column	Reaction #	Abbreviation	Reaction Name
3235	13534	NDP7g	nucleoside-diphosphatase (UDP), Golgi apparatus
3236	803	NDP8	nucleoside-diphosphatase (dUDP)
3237	11149	NDP8ex	nucleoside-diphosphatase (UTP), extracellular
3238	2816	NDPK1	nucleoside-diphosphate kinase (ATP:GDP)
3239	9819	NDPK10	nucleoside-diphosphate kinase (ATP:dIDP)
3240	9827	NDPK10m	nucleoside-diphosphate kinase (ATP:dIDP), mitochondrial
3241	9826	NDPK10n	nucleoside-diphosphate kinase (ATP:dIDP), nuclear
3242	9825	NDPK1m	nucleoside-diphosphate kinase (ATP:GDP), mitochondrial
3243	9820	NDPK1n	nucleoside-diphosphate kinase (ATP:GDP), nuclear
3244	190	NDPK2	nucleoside-diphosphate kinase (ATP:UDP)
3245	9824	NDPK2m	nucleoside-diphosphate kinase (ATP:UDP), mitochondrial
3246	9821	NDPK2n	nucleoside-diphosphate kinase (ATP:UDP), nuclear
3247	191	NDPK3	nucleoside-diphosphate kinase (ATP:CDP)
3248	9828	NDPK3m	nucleoside-diphosphate kinase (ATP:CDP), mitochondrial
3249	9822	NDPK3n	nucleoside-diphosphate kinase (ATP:CDP),nuclear
3250	192	NDPK4	nucleoside-diphosphate kinase (ATP:dTDP)
3251	9830	NDPK4m	nucleoside-diphosphate kinase (ATP:dTDP), mitochondrial
3252	9829	NDPK4n	nucleoside-diphosphate kinase (ATP:dTDP), nuclear
3253	443	NDPK5	nucleoside-diphosphate kinase (ATP:dGDP)
3254	9832	NDPK5m	nucleoside-diphosphate kinase (ATP:dGDP), mitochondrial
3255	9831	NDPK5n	nucleoside-diphosphate kinase (ATP:dGDP), nuclear
3256	132	NDPK6	nucleoside-diphosphate kinase (ATP:dUDP)
3257	9834	NDPK6m	nucleoside-diphosphate kinase (ATP:dUDP), mitochondrial
3258	9833	NDPK6n	nucleoside-diphosphate kinase (ATP:dUDP), nuclear
3259	2801	NDPK7	nucleoside-diphosphate kinase (ATP:dCDP)
3260	9836	NDPK7m	nucleoside-diphosphate kinase (ATP:dCDP), mitochondrial
3261	9835	NDPK7n	nucleoside-diphosphate kinase (ATP:dCDP), nuclear
3262	133	NDPK8	nucleoside-diphosphate kinase (ATP:dADP)
3263	9838	NDPK8m	nucleoside-diphosphate kinase (ATP:dADP), mitochondrial
3264	9837	NDPK8n	nucleoside-diphosphate kinase (ATP:dADP), nuclear
3265	1438	NDPK9	nucleoside-diphosphate kinase (ATP:IDP)
3266	9840	NDPK9m	nucleoside-diphosphate kinase (ATP:IDP), mitochondrial
3267	9839	NDPK9n	nucleoside-diphosphate kinase (ATP:IDP), nuclear
3268	12611	NH4t3r	ammonia transport via proton antiport
3269	19374	NH4tn	ammonia nuclear transport
3270	2280	NH4tp	ammonia peroxisomal transport
3271	13187	NICRNS	NICRNS
3272	19529	NICRNTtn	NICRNT transport, nuclear trhough pore
3273	19704	NIFEDIPINEte	xenobiotic transport
3274	13053	NKCC2t	Na+-K+-Cl- cotransport (NH4+)
3275	12745	NKCCt	Na+-K+-Cl- cotransport
3276	1811	NMNATm	nicotinamide-nucleotide adenylyltransferase, mitochondrial
3277	9544	NMNATn	nicotinamide-nucleotide adenylyltransferase
3278	10516	NMNATr	nicotinamide-nucleotide adenylyltransferase
3279	143	NMNS	NMN synthetase
3280	19527	NMNtn	NMN transport, nuclear trhough pore
3281	11089	NMPTRCOX	N-Methylputrescine:oxygen oxidoreductase (deaminating)
3282	173	NNAT	nicotinate-nucleotide adenylyltransferase
3283	1810	NNATm	nicotinate-nucleotide adenylyltransferase, mitochondrial
3284	9543	NNATn	nicotinate-nucleotide adenylyltransferase
3285	6171	NNATr	nicotinate-nucleotide adenylyltransferase
3286	2769	NNDPR	nicotinate-nucleotide diphosphorylase (carboxylating)
3287	10512	NNMT	Nicotinamide N-methyltransferase
3288	12097	NORANMT	noradrenaline N-methyltransferase

Column	Reaction #	Abbreviation	Reaction Name
3289	10159	NOS1	Nitric Oxide Synthase (intermediate forming)
3290	10166	NOS2	Nitric Oxide Synthase (NO forming)
3291	6008	NOt	NO transport (diffusion)
3292	13200	NP1	nucleotide phosphatase
3293	19705	NPTHLte	xenobiotic transport
3294	19421	NRPPHRSFt	norepinephrine sulfate transport (diffusion)
3295	12106	NRPPHRSULT	Norepinephrine Sulfotransferase
3296	11933	NRPPHRVESSEC	Noradrenaline secretion via secretory vesicle (ATP driven)
3297	11937	NRPPHRt4(2)r	Norepinephrine reversible transport in via sodium symport (1:2)
3298	12196	NRPPHRtu	Norepinephrine uniport
3299	19035	NRVNCCOAtx	fatty acid intracellular transport
3300	19095	NRVNCCPT1	carnitine O-palmitoyltransferase
3301	19114	NRVNCCPT2	carnitine transferase
3302	19076	NRVNCCRNt	transport into the mitochondria (carnitine)
3303	12458	NRVNCt	fatty acid transport via diffusion
3304	8574	NS26T2g	alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase
3305	8567	NS26Tg	alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase
3306	13188	NT5C	5'-nucleotidase
3307	2697	NTD1	5'-nucleotidase (dUMP)
3308	175	NTD10	5'-nucleotidase (XMP)
3309	176	NTD11	5'-nucleotidase (IMP)
3310	10419	NTD12	5'-nucleotidase (dIMP)
3311	10414	NTD1m	5'-nucleotidase (dUMP),mitochondrial
3312	448	NTD2	5'-nucleotidase (UMP)
3313	10430	NTD2e	5'-nucleotidase (UMP), extracellular
3314	12650	NTD2l	5'-nucleotidase (UMP), lysosome
3315	10416	NTD2m	5'-nucleotidase (UMP), mitochondrial
3316	449	NTD3	5'-nucleotidase (dCMP)
3317	12654	NTD3l	5'-nucleotidase (dCMP), lysosomal
3318	450	NTD4	5'-nucleotidase (CMP)
3319	10431	NTD4e	5'-nucleotidase (CMP), extracellular
3320	12649	NTD4l	5'-nucleotidase (CMP), lysosome
3321	451	NTD5	5'-nucleotidase (dTMP)
3322	12653	NTD5l	5'-nucleotidase (dTMP), lysosomal
3323	10415	NTD5m	5'-nucleotidase (dTMP), mitochondrial
3324	452	NTD6	5'-nucleotidase (dAMP)
3325	12651	NTD6l	5'-nucleotidase (dAMP), lysosome
3326	2698	NTD7	5'-nucleotidase (AMP)
3327	10433	NTD7e	5'-nucleotidase (AMP), extracellular
3328	12646	NTD7l	5'-nucleotidase (AMP), lysosome
3329	453	NTD8	5'-nucleotidase (dGMP)
3330	12652	NTD8l	5'-nucleotidase (dGMP), lysosomal
3331	174	NTD9	5'-nucleotidase (GMP)
3332	10432	NTD9e	5'-nucleotidase (GMP), extracellular
3333	12648	NTD9l	5'-nucleotidase (GMP), lysosome
3334	14816	NTMELYStner	protein trimethyl lysine transport (nucleus to ER)
3335	6225	NTP3e	nucleoside-triphosphatase (GTP)
3336	9745	NTPP10	Nucleoside triphosphate pyrophosphorylase (ditp)
3337	9747	NTPP11	Nucleoside triphosphate pyrophosphorylase (xtp)
3338	9738	NTPP9	Nucleoside triphosphate pyrophosphorylase (itp)
3339	13752	NaKt	Na+/K+ exchanging ATPase
3340	10086	O16G1e	oligo-1,6-glucosidase (glygn4 -> glygn5), extracellular
3341	10090	O16G2e	oligo-1,6-glucosidase (strch2 ->strch3), extracellular
3342	20850	O2St	superoxide anion transport via diffusion (extracellular)
3343	20851	O2Stm	superoxide anion transport via diffusion (mitochondria)

Column	Reaction #	Abbreviation	Reaction Name
3344	20849	O2Stn	superoxide anion transport via diffusion (nucleus)
3345	20848	O2Stx	superoxide anion transport via diffusion (peroxisome)
3346	1298	O2t	o2 transport (diffusion)
3347	2158	O2ter	O2 transport, endoplasmic reticulum
3348	762	O2tm	O2 transport (diffusion)
3349	15238	O2tn	O2 nuclear transport
3350	13516	O2tp	O2 transport, peroxisomal
3351	20237	OAGD3te	oagd3_hs transport
3352	20221	OAGD3tg	oagd3_hs intracellular transport
3353	20238	OAGT3te	oagt3_hs transport
3354	20222	OAGT3tg	oagt3_hs intracellular transport
3355	10993	OBDHc	2-Oxobutanoate dehydrogenase, cytosolic
3356	3992	OCBTm	ornithine carbamoyltransferase, irreversible
3357	8359	OCCOAtm	Octanoyl-CoA transport, diffusion
3358	19037	OCCOAtx	fatty acid intracellular transport
3359	12448	OCDCAtr	fatty acid transport via diffusion
3360	12447	OCDCEAtr	fatty acid transport via diffusion
3361	3986	OCOAT1m	3-oxoacid CoA-transferase
3362	8146	OCTAt	Octanoate transport via diffusion
3363	19038	ODECOAtx	fatty acid intracellular transport
3364	10904	OIVD1m	2-oxoisovalerate dehydrogenase (acylating; 4-methyl-2-oxopentaoate), mitochondrial
3365	10905	OIVD2m	2-oxoisovalerate dehydrogenase (acylating; 3-methyl-2-oxobutanoate), mitochondrial
3366	10906	OIVD3m	2-oxoisovalerate dehydrogenase (acylating; 3-methyl-2-oxopentanoate), mitochondrial
3367	19706	OMEPRAZOLEte	xenobiotic transport
3368	446	OMPDC	orotidine-5'-phosphate decarboxylase
3369	19719	ONPTHLte	xenobiotic transport
3370	10877	OPAHir	5-Oxoproline amidohydrolase (ATP-hydrolysing) (ir)
3371	15089	ORETNF	4-oxo-retinoic acid formation (oxidation)
3372	15117	ORETNF2	13-cis-4-oxo-retinoic acid formation (oxidation)
3373	15090	ORETNtn	4-oxo-retinoic acid transport, Nuclear
3374	15121	ORETNtn2	13-cis-4-oxo-retinoic acid transport, Nuclear
3375	1218	ORNDC	Ornithine Decarboxylase
3376	9721	ORNTArm	ornithine transaminase reversible (m)
3377	2435	ORNt3m	ornithine mitochondrial transport via proton antiport
3378	5287	ORNt4m	ornithine mitochondrial transport exchange with citruline
3379	11704	ORNtiDF	ornithine transport via diffusion (extracellular to cytosol)
3380	447	ORPT	orotate phosphoribosyltransferase
3381	12362	OXAHCOtex	oxalate transport via bicarbonate countertransport
3382	19516	OXAtp	oxalate transport out of peroxisome
3383	19772	P45011A1m	Cytochrome P450 11A1, mitochondrial [Precursor]
3384	9909	P45011B11m	Steroid 11-beta-hydroxylase
3385	9910	P45011B12m	Steroid 11-beta-hydroxylase
3386	9949	P45011B21m	Steroid 11-beta-hydroxylase
3387	9870	P45017A1r	Cytochrome P450 17A1
3388	9869	P45017A2r	Cytochrome P450 17A1
3389	9937	P45017A3r	Cytochrome P450 17A1
3390	9941	P45017A4r	Cytochrome P450 17A1
3391	9963	P45019A1r	aromatase
3392	9964	P45019A2r	aromatase
3393	11670	P4501B1r	cytochrome P450 1B1
3394	9916	P45021A1r	Steroid 21-hydroxylase
3395	9914	P45021A2r	Steroid 21-hydroxylase

Column	Reaction #	Abbreviation	Reaction Name
3396	9660	P45027A11m	5-beta-cholestane-3-alpha,7-alpha,12-alpha-triol 27-hydroxylase
3397	9665	P45027A12m	5-beta-cholestane-3-alpha,7-alpha,12-alpha-triol 27-hydroxylase
3398	13902	P45027A13m	5-beta-cholestane-3-alpha,7-alpha,12-alpha-triol 27-hydroxylase
3399	13891	P45027A14m	5-beta-cytochrome P450, family 27, subfamily A, polypeptide 1
3400	13907	P45027A15m	5-beta-cytochrome P450, family 27, subfamily A, polypeptide 1
3401	13909	P45027A16m	Cytochrome P450 27
3402	9567	P45027A1m	Cytochrome P450 27
3403	11669	P4502A6	cytochrome P450 2A6
3404	11666	P4502C18	cytochrome P450 2C18
3405	11663	P4502C19	cytochrome P450 2C19
3406	11668	P4502C8	cytochrome P450 2C8
3407	11667	P4502C9	cytochrome P450 2C9
3408	11901	P4502C92	cytochrome P450 2C9
3409	11902	P4502C93	cytochrome P450 2C9
3410	11903	P4502C94	cytochrome P450 2C9
3411	11662	P4502D6	cytochrome P450 2D6
3412	11661	P4502E1	cytochrome P450 2E1
3413	11660	P4502F1	cytochrome P450 2F1
3414	9569	P45039A1r	oxysterol 7-alpha-hydroxylase
3415	11659	P4503A4	cytochrome P450 3A4
3416	11656	P4503A43r	cytochrome p450 P450 3A43
3417	11657	P4503A5	cytochrome P450 3A5
3418	11655	P4503A7r	cytochrome p450 P450 3A7
3419	9563	P45046A1r	cytochrome P450, family 46, subfamily A, polypeptide 1
3420	11609	P4504B1r	cytochrome P450 4B1
3421	11588	P4504F121r	cytochrome p450 4F12/4F2
3422	11589	P4504F122r	cytochrome p450 4F12/4F2
3423	11590	P4504F123r	cytochrome p450 4F12/4F2
3424	11591	P4504F81r	cytochrome p450 4F8
3425	9562	P4507A1r	cytochrome P450, family 7, subfamily A, polypeptide 1
3426	9570	P4507B11r	oxysterol 7alpha-hydroxylase
3427	9571	P4507B12r	oxysterol 7alpha-hydroxylase
3428	9710	P4508B11r	sterol 12-alpha-hydroxylase
3429	9712	P4508B13r	sterol 12-alpha-hydroxylase (nadh)
3430	19866	P450LTB4r	cytochrome p450 leukotriene B4
3431	1470	P450SCC1m	cholesterol monooxygenase
3432	3319	P5CDm	1-pyrroline-5-carboxylate dehydrogenase, mitochondrial
3433	3629	P5CR	pyrroline-5-carboxylate reductase
3434	11289	P5CRm	pyrroline-5-carboxylate reductase (m)
3435	7185	P5CRx	pyrroline-5-carboxylate reductase
3436	11290	P5CRxm	pyrroline-5-carboxylate reductase (m)
3437	3239	PACCOAL	phenylacetate-CoA ligase
3438	12075	PAFH	Platelet-activating factor acetylhydrolase
3439	14980	PAFHe	Platelet-activating factor acetylhydrolase
3440	10807	PAFS	alkyl glycerol phosphocholine acetyl transferase
3441	19571	PAIL45P_HStn	phosphatidylinositol 4,5-bisphosphate nuclear transport (diffusion)
3442	19574	PAIL4P_HStn	phosphatidylinositol 4-phosphate nuclear transport (diffusion)
3443	19591	PAIL_HStn	phosphatidylinositol nuclear transport (diffusion)
3444	14681	PAN4PP	phosphatase (pan4p)

Column	Reaction #	Abbreviation	Reaction Name
3445	12155	PAPStg	3'-Phosphoadenylyl sufate Golgi transport
3446	15236	PAPtg	adenosine 3',5'-bisphosphate Golgi transport
3447	14999	PA_HSter	phosphatidate scramblase
3448	15000	PA_HStg	phosphatidate scramblase
3449	19525	PA_HStn	phosphatidate transport, nuclear
3450	15010	PCFLOPm	phosphatidylcholine flippase
3451	11889	PCHOLP_hs	choline phosphatase
3452	11888	PCHOLPg_hs	choline phosphatase
3453	11886	PCHOLPm_hs	choline phosphatase
3454	11887	PCHOLPr_hs	choline phosphatase
3455	14997	PCHOL_HSter	phosphatidylcholine scramblase
3456	14998	PCHOL_HStg	phosphatidylcholine scramblase
3457	2973	PCLAD	picolinic acid decarboxylase
3458	11406	PCLYSOX	Procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase
3459	14383	PCREATtmdiffir	Phosphocreatine transport to/from mitochondria via diffusion
3460	19738	PCRNtc	transport into the cytosol from peroxisome (carnitine)
3461	19739	PCRNtm	transport into the mitochondria from cytosol (carnitine)
3462	5206	PCm	pyruvate carboxylase
3463	12666	PCt	phosphatidylcholine transporter
3464	2655	PDE1	3',5'-cyclic-nucleotide phosphodiesterase
3465	9958	PDE1g	3',5'-cyclic-nucleotide phosphodiesterase,Golgi
3466	4690	PDE4	3',5'-cyclic-nucleotide phosphodiesterase
3467	9959	PDE4g	3',5'-cyclic-nucleotide phosphodiesterase, Golgi
3468	11276	PDE4n	3',5'-cyclic-nucleotide phosphodiesterase, Nucleus
3469	11	PDHm	pyruvate dehydrogenase
3470	1729	PDX5PO	pyridoxine 5'-phosphate oxidase
3471	1821	PDXPP	Pyridoxine 5-phosphate phosphatase
3472	2521	PEAMNO	Phenethylamine oxidase
3473	11288	PECGONCOATr	Pseudoecgonine CoA transferase (ER)
3474	15005	PEFLIP	phosphatidylethanolamine flippase
3475	15007	PEFLIPm	phosphatidylethanolamine flippase
3476	3084	PEPCK	Phosphoenolpyruvate carboxykinase (GTP)
3477	4418	PEPCKm	Phosphoenolpyruvate carboxykinase (GTP)
3478	14775	PEPLYStn	peptide (lysine) nuclear transport via diffusion
3479	20195	PERILLYLte	xenobiotic transport
3480	18982	PEROXx	peroxisomal lumped long chain fatty acid oxidation
3481	2385	PETHCT	phosphoethanolamine cytidyltransferase
3482	19599	PETOHMm_hs	phosphatidylethanolamine N-methyltransferase
3483	19600	PETOHMr_hs	phosphatidylethanolamine N-methyltransferase
3484	14995	PE_HSter	phosphatidylethanolamine scramblase
3485	14996	PE_HStg	phosphatidylethanolamine scramblase
3486	20872	PE_HStm	phosphatidylethanolamine scramblase
3487	267	PFK	phosphofructokinase
3488	698	PFK26	6-phosphofructo-2-kinase
3489	2865	PGCD	phosphoglycerate dehydrogenase
3490	9973	PGDI	Prostaglandin-H2 D-isomerase [Precursor]
3491	9972	PGDIr	Prostaglandin-H2 D-isomerase [Precursor]
3492	9991	PGESr	Prostaglandin E synthase
3493	271	PGI	glucose-6-phosphate isomerase
3494	9997	PGISr	Prostaglandin I2 synthase
3495	273	PGK	phosphoglycerate kinase
3496	278	PGL	6-phosphogluconolactonase
3497	2286	PGLYCP	Phosphoglycolate phosphatase
3498	9555	PGLer	6-phosphogluconolactonase, endoplasmic reticulum
3499	272	PGM	phosphoglycerate mutase

Column	Reaction #	Abbreviation	Reaction Name
3500	2819	PGMT	phosphoglucomutase
3501	10862	PGPPT	phosphatidyl-CMP: glycerophosphate phosphatidyltransferase
3502	10863	PGPP_hs	Phosphatidylglycerol phosphate phosphatase (homo sapiens)
3503	15226	PGS	Prostaglandin G/H synthase
3504	15227	PGSr	Prostaglandin G/H synthase
3505	11634	PHACCOAGLNAC	Phenylacetyl-CoA:L-glutamine alpha-N-phenylacetyltransferase
3506	3492	PHCDm	L-1-pyrroline-3-hydroxy-5-carboxylate dehydrogenase
3507	3565	PHCHGSm	L-1-Pyrroline-3-hydroxy-5-carboxylate spontaneous conversion to L-4-Hydroxyglutamate semialdehyde, mitochondrial
3508	14513	PHEACGLNt	PHEACGLN extracellular transport via diffusion
3509	14687	PHEMEt	heme transport
3510	8500	PHEMEtm	Heme transport to cytosol
3511	2860	PHETA1	phenylalanine transaminase
3512	9484	PHETA1m	phenylalanine transaminase (m)
3513	14585	PHETHPTOX2	L-Phenylalanine,tetrahydrobiopterin:oxygen oxidoreductase (4-hydroxylating)
3514	11694	PHEt4	L-phenylalanine transport in via sodium symport
3515	11928	PHEtec	L-phenylalanine transport via diffusion (extracellular to cytosol)
3516	9490	PHYCBOXL	L-Phenylalanine carboxy-lyase
3517	14100	PHYHx	Phytanoyl-CoA dioxygenase, peroxisomal
3518	10501	PHYQt	Phylloquinone transport
3519	19806	PHYTt	fatty acid transport via diffusion
3520	10889	PI345P3P	phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase
3521	19612	PI345P3Pn	phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase, nuclear
3522	11040	PI345P5P	phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase
3523	19611	PI345P5Pn	phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase, nuclear
3524	19617	PI34P3Pn	phosphatidylinositol-3,4-bisphosphate 3-phosphatase, nuclear
3525	19609	PI34P4Pn	phosphatidylinositol-3,4-bisphosphate 4-phosphatase, nuclear
3526	11039	PI34P5K	phosphatidylinositol 3,4-bisphosphate 5-kinase
3527	19610	PI34P5Kn	phosphatidylinositol 3,4-bisphosphate 5-kinase, nuclear
3528	19602	PI35P3P	phosphatidylinositol-3,5-bisphosphate 3-phosphatase
3529	19607	PI3P3Pn	phosphatidylinositol-3-phosphate 3-phosphatase, nuclear
3530	11037	PI3P4K	phosphatidylinositol 3-phosphate 4-kinase
3531	19608	PI3P4Kn	phosphatidylinositol 3-phosphate 4-kinase, nuclear
3532	11043	PI3P5K	phosphatidylinositol 3-phosphate 5-kinase
3533	19603	PI3PP	phosphatidylinositol-3-phosphate 3-phosphatase
3534	10879	PI45P3K	phosphatidylinositol 4,5-bisphosphate 3-kinase
3535	19613	PI45P3Kn	phosphatidylinositol 4,5-bisphosphate 3-kinase, nuclear
3536	11047	PI45P4P	phosphatidylinositol-4,5-bisphosphate 4-phosphatase
3537	10868	PI45P5P	phosphatidylinositol-4,5-bisphosphate 5-phosphatase
3538	19614	PI45P5Pn	phosphatidylinositol-4,5-bisphosphate 5-phosphatase, nuclear
3539	10995	PI45PLC	phosphatidylinositol 4,5-bisphosphate phospholipase C
3540	11023	PI45PLCn	phosphatidylinositol 4,5-bisphosphate phospholipase C, nucleus
3541	10988	PI4P3K	phosphatidylinositol 4-phosphate 3-kinase

Column	Reaction #	Abbreviation	Reaction Name
3542	10989	PI4P3Ker	phosphatidylinositol 4-phosphate 3-kinase, endoplasmic reticulum
3543	19616	PI4P3Kn	phosphatidylinositol 4-phosphate 3-kinase, nuclear
3544	19619	PI4P4Pn	phosphatidylinositol-4-phosphate 4-phosphatase, nuclear
3545	10764	PI4P5K	phosphatidylinositol 4-phosphate 5-kinase
3546	19615	PI4P5Kn	phosphatidylinositol 4-phosphate 5-kinase, nuclear
3547	11020	PI4PLC	phosphatidylinositol 4-phosphate phospholipase C
3548	11022	PI4PLCn	phosphatidylinositol 4-phosphate phospholipase C, nucleus
3549	10922	PI4PP	phosphatidylinositol-4-phosphate 4-phosphatase
3550	11042	PI5P3K	phosphatidylinositol-5-phosphate 3-kinase
3551	11046	PI5P3Ker	phosphatidylinositol-5-phosphate 3-kinase, endoplasmic reticulum
3552	10890	PI5P4K	phosphatidylinositol-5-phosphate 4-kinase
3553	19621	PI5P4Kn	phosphatidylinositol-5-phosphate 4-kinase, nuclear
3554	11051	PIACGT	phosphatidylinositol N-acetylglucosaminyltransferase
3555	10987	PIK3	phosphatidylinositol 3-kinase
3556	10990	PIK3er	phosphatidylinositol 3-kinase, endoplasmic reticulum
3557	19606	PIK3n	phosphatidylinositol 3-kinase, nuclear
3558	10770	PIK4	phosphatidylinositol 4-kinase
3559	19618	PIK4n	phosphatidylinositol 4-kinase, nuclear
3560	11041	PIK5	phosphatidylinositol 5-kinase
3561	19620	PIK5n	phosphatidylinositol 5-kinase, nuclear
3562	10998	PIPLC	phosphatidylinositol phospholipase C
3563	11021	PIPLCn	phosphatidylinositol phospholipase C, nucleus
3564	2757	PIt2m	phosphate transporter, mitochondrial
3565	6677	PIt7	phosphate transport in/out via three Na+ symporter
3566	11904	PIt7ir	phosphate transport in/out via three Na+ symporter (irreversible)
3567	12351	PIt8	phosphate transport in/out via Na+ symporter
3568	12352	PIt9	phosphate transport in/out via two Na+ symporter
3569	10015	PIter	phosphate transport, endoplasmic reticulum
3570	15037	PItg	phosphate transport, Golgi apparatus
3571	19522	PItn	phosphate transport, nuclear
3572	13996	PItx	Phosphate transporter, peroxisome
3573	10805	PLA2	phospholipase A2
3574	10858	PLA2_2	phospholipase A2
3575	12086	PLA2_2e	phospholipase A2
3576	14553	PLYSPSer	protein lysine peptidase (endoplasmic reticulum)
3577	243	PMANM	phosphomannomutase
3578	9735	PMEVKx	phosphomevalonate kinase
3579	10983	PMI12346PH	5-diphosphoinositol-1,2,3,4,6-pentakisphosphate diphosphohydrolase
3580	10986	PMI12346PHn	5-diphosphoinositol-1,2,3,4,6-pentakisphosphate diphosphohydrolase, nuclear
3581	10984	PMI1346PH	diphosphoinositol-1,3,4,6-tetrakisphosphate diphosphohydrolase
3582	10985	PMI1346PHn	diphosphoinositol-1,3,4,6-tetrakisphosphate diphosphohydrolase, nucleus
3583	19036	PMTCOAtx	fatty acid intracellular transport
3584	15045	PNP	purine-nucleoside phosphorylase
3585	7471	PNTEH	Hydrolase Class (RXN R02973)
3586	2788	PNTK	pantothenate kinase
3587	9471	PNTKm	pantothenate kinase (mitochondrial)
3588	10482	PNTOt5	Pantothenate sodium symporter II
3589	295	PPA	inorganic diphosphatase

Column	Reaction #	Abbreviation	Reaction Name
3590	12355	PPA2	inorganic triphosphatase
3591	19518	PPA2m	inorganic triphosphatase, mitochondrial
3592	10451	PPAP	phosphatidic acid phosphatase
3593	10034	PPAer	inorganic diphosphatase, endoplasmic reticulum
3594	458	PPAm	inorganic diphosphatase
3595	15047	PPAn	inorganic diphosphatase, nuclear
3596	8421	PPAt	Propionate transport, diffusion
3597	8422	PPAtm	Propionate transport, diffusion
3598	3553	PPBNGS	porphobilinogen synthase
3599	87	PPCDC	phosphopantothenoylcysteine decarboxylase
3600	4425	PPCOACm	Propionyl-CoA carboxylase, mitochondrial
3601	10750	PPCOAOm	Propanoyl-CoA:FAD 2,3-oxidoreductase, mitochondrial
3602	12665	PPD2CSPp	PPD2CSPp
3603	20257	PPDOx	Propane-1,2-diol:NAD+ 1-oxidoreductase
3604	9633	PPDOy	Propane-1,2-diol:NADP+ 1-oxidoreductase
3605	13983	PPItr	Diphosphate transporter, endoplasmic reticulum
3606	13995	PPItx	Diphosphate transporter, peroxisome
3607	258	PPM	phosphopentomutase
3608	19593	PPMI12346Ptn	5-diphosphatidylinositol pentakisphosphate nuclear transport (diffusion)
3609	19595	PPMI1346Ptn	diphosphatidylinositol tetrakisphosphate nuclear transport (diffusion)
3610	9465	PPNCL3	phosphopantothenate-cysteine ligase
3611	11409	PPOR	Phenylpyruvate:oxygen oxidoreductase (hydroxylating,decarboxylating)
3612	1761	PPPG9tm	protoporphyrinogen IX mitochondrial transport
3613	3296	PPPGOm	protoporphyrinogen oxidase, mitochondrial
3614	19512	PPPItn	Inorganic triphosphate transport through nuclear pore
3615	3556	PRAGSr	phosphoribosylglycinamide synthase
3616	3640	PRAIS	phosphoribosylaminoimidazole synthase
3617	3641	PRASCS	phosphoribosylaminoimidazolesuccinocarboxamide synthase
3618	11975	PRDX	Peroxidase (multiple substrates)
3619	11976	PRDXl	Peroxidase (multiple substrates)
3620	3558	PRFGS	phosphoribosylformylglycinamidine synthase
3621	19774	PRGNLONESULT	steroid sulfotransferase
3622	19795	PRGNLONEtm	pregnenolone intracellular transport
3623	19796	PRGNLONEtr	pregnenolone intracellular transport
3624	14873	PRISTANALtx	pristanal peroxisomal transport
3625	14874	PRISTCOAtx	pristcoa peroxisomal transport
3626	15132	PRISTtx	prist peroxisomal transport
3627	3650	PRO1x	proline oxidase (L-proline, NAD)
3628	3652	PRO1xm	proline oxidase (NAD), mitochondrial
3629	10172	PROAKGOX1r	L-Proline,2-oxoglutarate:oxygen oxidoreductase (4-hydroxylating) (ER)
3630	3642	PROD2	Proline dehydrogenase
3631	10169	PROD2m	Proline dehydrogenase (m)
3632	11685	PRODt2r	D-proline reversible transport via proton symport
3633	11686	PRODt2rL	D-proline reversible transport via proton symport (lysosome)
3634	12263	PROSTGD2t	prostaglandin transport via bicarbonate countertransport
3635	12264	PROSTGE1t	prostaglandin transport via bicarbonate countertransport
3636	12625	PROSTGE1t3	prostaglandine E1 transport (ATP-dependent)
3637	12265	PROSTGE2t	prostaglandin transport via bicarbonate countertransport
3638	12279	PROSTGE2t2	prostaglandin uniport
3639	12626	PROSTGE2t3	prostaglandine E2 transport (ATP-dependent)

Column	Reaction #	Abbreviation	Reaction Name
3640	12280	PROSTGF2t	prostaglandin uniport
3641	1368	PROt2r	L-proline reversible transport via proton symport
3642	11682	PROt2rL	L-proline reversible transport via proton symport (lysosome)
3643	1802	PROt4	Na+/Proline-L symporter
3644	11946	PROt4(2)r	Proline transport (sodium symport) (2:1)
3645	1502	PROtm	L-proline transport, mitochondrial
3646	9818	PRPNCOAHYDm	Propenoyl-CoA hydrolase (m)
3647	9817	PRPNCOAHYDx	Propenoyl-CoA hydrolase (x)
3648	343	PRPPS	phosphoribosylpyrophosphate synthetase
3649	11823	PSDm_hs	Phosphatidylserine decarboxylase
3650	913	PSERT	phosphoserine transaminase
3651	15006	PSFLIP	phosphatidylserine flippase
3652	15008	PSFLIPm	phosphatidylserine flippase
3653	4642	PSP_L	phosphoserine phosphatase (L-serine)
3654	10545	PSSA1_hs	Phosphatidylserine synthase homo sapiens
3655	10544	PSSA2_hs	Phosphatidylserine synthase homo sapiens
3656	15001	PS_HSter	phosphatidylserine scramblase
3657	15002	PS_HStg	phosphatidylserine scramblase
3658	14862	PTDCACRNCPT1	carnitine fatty-acyl transferase
3659	14863	PTDCACRNCPT2	pentadecanoate transport into the mitochondria
3660	14867	PTDCACRNt	pentadecanoate transport into the mitochondria
3661	19807	PTDCAt	fatty acid transport via diffusion
3662	13833	PTE2x	peroxisomal acyl-CoA thioesterase
3663	14143	PTE3x	peroxisomal acyl-CoA thioesterase
3664	14144	PTE4x	peroxisomal acyl-CoA thioesterase
3665	14145	PTE5x	peroxisomal acyl-CoA thioesterase
3666	7821	PTHPS	6-pyruvoyltetrahydropterin synthase
3667	11636	PTHPSn	6-pyruvoyltetrahydropterin synthase, nuclear
3668	89	PTPAT	pantetheine-phosphate adenylyltransferase
3669	10641	PTRCAT1	Putrescine acetyltransferase
3670	10635	PTRCOX1	Putrescine:oxygen oxidoreductase (deaminating)
3671	134	PUNP1	purine-nucleoside phosphorylase (Adenosine)
3672	135	PUNP2	purine-nucleoside phosphorylase (Deoxyadenosine)
3673	136	PUNP3	purine-nucleoside phosphorylase (Guanosine)
3674	137	PUNP4	purine-nucleoside phosphorylase (Deoxyguanosine)
3675	420	PUNP5	purine-nucleoside phosphorylase (Inosine)
3676	421	PUNP6	purine-nucleoside phosphorylase (Deoxyinosine)
3677	422	PUNP7	purine-nucleoside phosphorylase (Xanthosine)
3678	11316	PVD3	Previtamin D3 formation
3679	11024	PYAM5POr	pyridoxamine 5'-phosphate oxidase
3680	14578	PYAM5Ptm	Pyridoxamine 5'-phosphate transport via diffusion, mitochondrial
3681	1727	PYDAMK	pyridoxamine kinase
3682	10952	PYDAMtr	pyridoxamine transport via diffusion
3683	14577	PYDX5Ptm	Pyridoxal 5'-phosphate transport via diffusion, mitochondrial
3684	10953	PYDXDH	pyridoxal dehydrogenase
3685	3019	PYDXK	pyridoxal kinase
3686	1726	PYDXNK	pyridoxine kinase
3687	10951	PYDXNtr	pyridoxine transport via diffusion
3688	1820	PYDXPP	Pyridoxal 5-phosphate phosphatase
3689	10950	PYDXtr	pyridoxal transport via diffusion
3690	265	PYK	pyruvate kinase
3691	11031	PYLALDOX	Perillyl aldehyde:NAD+ oxidoreductase
3692	11032	PYLALDOXm	Perillyl aldehyde:NAD+ oxidoreductase (m)

Column	Reaction #	Abbreviation	Reaction Name
3693	1083	PYNP2r	pyrimidine-nucleoside phosphorylase (uracil)
3694	876	PYRt2m	pyruvate mitochondrial transport via proton symport
3695	2279	PYRt2p	pyruvate peroxisomal transport via proton symport
3696	1828	PYRt2r	pyruvate reversible transport via proton symport
3697	9495	QUILSYN	Quinolinate Synthase (Eukaryotic)
3698	15074	RADH	retinal dehydrogenase
3699	15076	RADH2	retinal dehydrogenase (NADPH)
3700	19520	RADH3	retinal dehydrogenase
3701	19521	RADH4	retinal dehydrogenase (NADPH)
3702	15084	RAHY	retinoic acid hydroxylation (P450)
3703	15097	RAI1	retinal isomerase (11-cis)
3704	15096	RAI2	retinal isomerase (9-cis)
3705	15116	RAI3	13-cis-retinoic acid isomerase
3706	15119	RAI4	13-cis-4-oxo-retinoic acid isomerase
3707	15078	RAtn	Retinoate transport, nuclear
3708	15120	RAtn3	13-cis-retinoic acid transport, nuclear
3709	119	RBFK	riboflavin kinase
3710	255	RBK	ribokinase
3711	54	RBK_D	D-ribulokinase
3712	19568	RBTt	ribitol transport via passive diffusion
3713	11011	RDH1	retinol dehydrogenase (all-trans)
3714	11015	RDH1a	retinol dehydrogenase (all-trans,NADPH)
3715	11013	RDH2	retinol dehydrogenase (9-cis,NADH)
3716	11016	RDH2a	retinol dehydrogenase (9-cis,NADPH)
3717	11014	RDH3	retinol dehydrogenase (11-cis,NADH)
3718	11017	RDH3a	retinol dehydrogenase (11-cis,NADPH)
3719	15154	RDH4	retinol dehydrogenase (13-cis,NADH)
3720	15062	RETFA	retinol acyltransferase
3721	15091	RETFAt	fatty acid retinol efflux
3722	15112	RETFAt1	fatty acid retinol efflux (9-cis)
3723	15111	RETFAt2	fatty acid retinol efflux (11-cis)
3724	15071	RETH	retinyl ester hydrolase
3725	15102	RETH1	retinyl ester hydrolase (9-cis)
3726	15104	RETH1e	retinyl ester hydrolase (9-cis), extracellular
3727	15109	RETH2	retinyl ester hydrolase (11-cis)
3728	15110	RETH2e	retinyl ester hydrolase (11-cis), extracellular
3729	15069	RETHe	retinyl ester hydrolase, extracellular
3730	15100	RETI1	retinol isomerase (11-cis)
3731	15101	RETI2	retinol isomerase (9-cis)
3732	19519	RETI3	retinol isomerase (13-cis)
3733	15087	RETNCOA	Retinoyl CoA formation
3734	15092	RETNGLCt	retinoyl glucuronide efflux
3735	20310	RETNGLCt2	retinoyl glucuronide efflux (13-cis)
3736	20312	RETNGLCt2r	retinoyl glucuronide efflux (13-cis) from ER
3737	20311	RETNGLCtr	retinoyl glucuronide efflux from ER
3738	15113	RETNt	retinoic acid transport
3739	20313	RETNtr	retinoic acid transport in ER
3740	20314	RETNtr2	retinoic acid transport in ER (13-cis)
3741	10968	RETt	Retinol transport via faciliated diffusion
3742	9512	RIBFLVt3	riboflavin transport (ATP dependent)
3743	19566	RIBt	ribose transport via diffusion
3744	1554	RIBt2	ribose transport in via proton symporter
3745	423	RNDR1	ribonucleoside-diphosphate reductase (ADP)
3746	424	RNDR2	ribonucleoside-diphosphate reductase (GDP)
3747	425	RNDR3	ribonucleoside-diphosphate reductase (CDP)
3748	426	RNDR4	ribonucleoside-diphosphate reductase (UDP)

Column	Reaction #	Abbreviation	Reaction Name
3749	144	RNMK	ribosylnicotinamide kinase
3750	281	RPE	ribulose 5-phosphate 3-epimerase
3751	280	RPI	ribose-5-phosphate isomerase
3752	14299	RTOT1	R total flux
3753	14325	RTOT2	R total flux
3754	14334	RTOT3	R total flux
3755	14341	RTOT4	R total flux
3756	14349	RTOT5	R total flux
3757	14351	RTOT6	R total flux
3758	14269	RTOTAL2CRNCPT1	carnitine fatty-acyl transferase
3759	14272	RTOTAL2CRNCPT2	R group transport into the mitochondria
3760	14275	RTOTAL2CRNt	R group transport into the mitochondria
3761	14270	RTOTAL3CRNCPT1	carnitine fatty-acyl transferase
3762	14273	RTOTAL3CRNCPT2	R group transport into the mitochondria
3763	14276	RTOTAL3CRNt	R group transport into the mitochondria
3764	14267	RTOTALCRNCPT1	carnitine fatty-acyl transferase
3765	14271	RTOTALCRNCPT2	R group transport into the mitochondria
3766	14274	RTOTALCRNt	R group transport into the mitochondria
3767	14326	RTOT_2	R total flux 2 position
3768	14327	RTOT_3	R total flux 3 position
3769	20325	Rtotaltl	fatty acid intracellular transport
3770	20326	Rtotaltp	fatty acid intracellular transport
3771	11393	S23T2g	beta-galactoside alpha-2,3-sialyltransferase (core 2)
3772	11407	S23T3g	beta-galactoside alpha-2,3-sialyltransferase (complex N-glycan)
3773	11520	S23T4g	beta-galactoside alpha-2,3-sialyltransferase
3774	8573	S23Tg	beta-galactoside alpha-2,3-sialyltransferase (T antigen)
3775	7767	S26Tg	beta-galactoside alpha-2,6-sialyltransferase
3776	15053	S2L2FN2M2MASNt	s2l2fn2m2masn transport, Golgi to extracellular
3777	15049	S2L2FN2M2MASNtly	s2l2fn2m2masn transport, extracellular to lysosome
3778	15050	S2L2N2M2MASNtly	s2l2n2m2masn transport, extracellular to lysosome
3779	11573	S2T1g	chondroitin 2-sulfotransferase, Golgi
3780	11578	S2T2g	chondroitin 2-sulfotransferase, Golgi
3781	11607	S2T3g	uronyl 2-sulfotransferase, Golgi
3782	11629	S2T4g	uronyl 2-sulfotransferase, Golgi
3783	11733	S2TASE1ly	iduronate-2-sulfatase, lysosomal
3784	11734	S2TASE2ly	iduronate-2-sulfatase, lysosomal
3785	14415	S2TASE3ly	iduronate-2-sulfatase, lysosomal
3786	14433	S2TASE4ly	glucuronate-2-sulfatase, lysosomal
3787	14434	S2TASE5ly	glucuronate-2-sulfatase, lysosomal
3788	11678	S3T1g	heparin-glucosamine 3-O-sulfotransferase
3789	11679	S3T2g	heparin-glucosamine 3-O-sulfotransferase
3790	11680	S3T3g	heparin-glucosamine 3-O-sulfotransferase
3791	14402	S3TASE1ly	N-acetylglucosamine-3-sulfatase, lysosomal
3792	14401	S3TASE2ly	N-acetylglucosamine-3-sulfatase, lysosomal
3793	11768	S3TASE3ly	N-acetylglucosamine-3-sulfatase, lysosomal
3794	11564	S4T1g	chondroitin 4-sulfotransferase, Golgi apparatus
3795	11567	S4T2g	chondroitin 4-sulfotransferase, Golgi apparatus
3796	11596	S4T3g	chondroitin 4-sulfotransferase, Golgi apparatus
3797	11600	S4T4g	chondroitin 4-sulfotransferase, Golgi apparatus
3798	11601	S4T5g	chondroitin 4-sulfotransferase, Golgi apparatus
3799	11606	S4T6g	chondroitin 4-sulfotransferase, Golgi apparatus
3800	14404	S4TASE1ly	N-acetylgalactosamine-4-sulfatase, lysosomal
3801	14407	S4TASE2ly	N-acetylgalactosamine-4-sulfatase, lysosomal
3802	14411	S4TASE3ly	N-acetylgalactosamine-4-sulfatase, lysosomal
3803	14439	S4TASE4ly	N-acetylgalactosamine-4-sulfatase, lysosomal

Column	Reaction #	Abbreviation	Reaction Name
3804	14440	S4TASE5ly	N-acetylgalactosamine-4-sulfatase, lysosomal
3805	11466	S6T10g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus
3806	11467	S6T11g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus
3807	11468	S6T12g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus
3808	11469	S6T13g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus
3809	11470	S6T14g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus
3810	11471	S6T15g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus
3811	11525	S6T16g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus
3812	11529	S6T17g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus
3813	11531	S6T18g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus
3814	11569	S6T19g	chondroitin 6-sulfotransferase, Golgi apparatus
3815	11428	S6T1g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus
3816	11572	S6T20g	chondroitin 6-sulfotransferase, Golgi apparatus
3817	11577	S6T21g	chondroitin 6-sulfotransferase, Golgi apparatus
3818	11593	S6T22g	chondroitin 6-sulfotransferase, Golgi apparatus
3819	11597	S6T23g	chondroitin 6-sulfotransferase, Golgi apparatus
3820	11602	S6T24g	chondroitin 6-sulfotransferase, Golgi apparatus
3821	11630	S6T25g	heparan sulfate 6-sulfotransferase, Golgi apparatus
3822	11431	S6T2g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus
3823	11433	S6T3g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus
3824	11438	S6T4g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus
3825	11461	S6T5g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus
3826	11462	S6T6g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus
3827	11463	S6T7g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus
3828	11464	S6T8g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus
3829	11465	S6T9g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus
3830	14459	S6TASE10ly	galactose-6-sulfate sulfatase, lysosomal
3831	14461	S6TASE11ly	N-acetylglucosamine-6-sulfatase, lysosomal
3832	14465	S6TASE12ly	N-acetylglucosamine-6-sulfatase, lysosomal
3833	14477	S6TASE13ly	N-acetylglucosamine-6-sulfatase, lysosomal
3834	14478	S6TASE14ly	N-acetylglucosamine-6-sulfatase, lysosomal
3835	14479	S6TASE15ly	N-acetylglucosamine-6-sulfatase, lysosomal
3836	14480	S6TASE16ly	N-acetylglucosamine-6-sulfatase, lysosomal
3837	14481	S6TASE17ly	N-acetylglucosamine-6-sulfatase, lysosomal
3838	14482	S6TASE18ly	N-acetylglucosamine-6-sulfatase, lysosomal
3839	14483	S6TASE19ly	N-acetylglucosamine-6-sulfatase, lysosomal
3840	14389	S6TASE1ly	N-acetylglucosamine-6-sulfatase, lysosomal
3841	14484	S6TASE20ly	N-acetylglucosamine-6-sulfatase, lysosomal

Column	Reaction #	Abbreviation	Reaction Name
3842	14485	S6TASE21ly	N-acetylglucosamine-6-sulfatase, lysosomal
3843	14519	S6TASE22ly	galactose-6-sulfate sulfatase, lysosomal
3844	14521	S6TASE23ly	N-acetylglucosamine-6-sulfatase, lysosomal
3845	14522	S6TASE24ly	N-acetylglucosamine-6-sulfatase, lysosomal
3846	14523	S6TASE25ly	galactose-6-sulfate sulfatase, lysosomal
3847	14524	S6TASE26ly	N-acetylglucosamine-6-sulfatase, lysosomal
3848	14393	S6TASE2ly	N-acetylglucosamine-6-sulfatase, lysosomal
3849	14394	S6TASE3ly	N-acetylglucosamine-6-sulfatase, lysosomal
3850	14419	S6TASE4ly	N-acetylgalactosamine-6-sulfatase, lysosomal
3851	14423	S6TASE5ly	N-acetylgalactosamine-6-sulfatase, lysosomal
3852	14429	S6TASE6ly	N-acetylgalactosamine-6-sulfatase, lysosomal
3853	14435	S6TASE7ly	N-acetylgalactosamine-6-sulfatase, lysosomal
3854	14441	S6TASE8ly	N-acetylgalactosamine-6-sulfatase, lysosomal
3855	14442	S6TASE9ly	N-acetylgalactosamine-6-sulfatase, lysosomal
3856	10882	SACCD3m	saccharopine dehydrogenase (NADP, L-lysine forming), mitochondrial
3857	10883	SACCD4m	saccharopine dehydrogenase (NAD, L-glutamate forming), mitochondrial
3858	2866	SADT	sulfate adenylyltransferase
3859	12100	SALMCOM	S-Adenosyl-L-methionine:catechol O-methyltransferase
3860	11919	SALMCOM2	S-Adenosyl-L-methionine:catechol O-methyltransferase
3861	9355	SAMHISTA	S-Adenosyl-L-methionine:histamine N-tele-methyltransferase
3862	9935	SARCOXp	sarcosine oxidase, peroxisomal
3863	14628	SARCStex	Sarcosine transport (extracellular to cytosol)
3864	14646	SARCStm	Sarcosine transport (mitochondrial)
3865	14638	SARCStp	Sarcosine transport (peroxisomal)
3866	9728	SARDHm	Sarcosine dehydrogenase (m)
3867	5555	SBPP1er	sphingoid base-phosphate phosphatase (sphinganine 1-phosphatase), endoplasmic reticulum
3868	11192	SBPP3er	sphingoid base-phosphate phosphatase (sphinganine 1-phosphatase), endoplasmic reticulum
3869	2050	SBTD_D2	D-sorbitol dehydrogenase (D-fructose producing)
3870	3355	SBTR	D-sorbitol reductase
3871	13147	SCP21x	Sterol carrier protein 2
3872	13148	SCP22x	Sterol carrier protein 2
3873	13935	SCP2x	peroxisomal thiolase 2
3874	13964	SCP3x	peroxisomal thiolase 2
3875	9702	SCPx	peroxisomal thiolase 2
3876	10019	SEAHCYSHYD	Se-Adenosylselenohomocysteine hydrolase
3877	11513	SEAHCYStn	Se-adenosyl-seleno-L-homocysteine nuclear transport
3878	11512	SEASMETtn	Se-adenosyl-seleno-L-methionine nuclear transport
3879	10023	SELADT	selenate adenylyltransferase
3880	10025	SELCYSLY	selenocysteine lyase
3881	20665	SELCYSLY2	selenocysteine lyase
3882	10017	SELCYSTGL	selanocystathionine g-lyase
3883	10018	SELCYSTS	selanocystathionine beta-synthase
3884	10022	SELMETAT	selenomethionine adenosyltransferase
3885	2456	SELNPS	Selenophosphate synthase
3886	12164	SELt4_3	selenate transport via sodium symport
3887	11835	SERALANaEx	L-alanine/L-serine Na-dependent exchange (Ser-L in)
3888	11853	SERASNNaEx	L-serine/L-asparagine Na-dependent exchange (Ser-L in)
3889	11840	SERCYSNaEx	L-serine/L-cysteine Na-dependent exchange (Ser-L in)
3890	11794	SERDGLNexR	D-Serine/Glutamine reversible exchange
3891	11793	SERDGLYexR	D-Serine/Glycine reversible exchange
3892	11851	SERGLNNaEx	L-serine/L-glutamine Na-dependent exchange (Ser-L in)

Column	Reaction #	Abbreviation	Reaction Name
3893	11792	SERGLNexR	L-Serine/Glutamine reversible exchange
3894	11791	SERGLYexR	L-Serine/Glycine reversible exchange
3895	13491	SERHL	L-Serine hydro-lyase
3896	20496	SERLYSNaex	Serine/Lysine Na-dependent exchange (Ser in)
3897	1878	SERPT	serine C-palmitoyltransferase
3898	11842	SERTHRNaEx	L-serine/L-threonine Na-dependent exchange (Ser-L in)
3899	3430	SERt4	L-serine via sodium symport
3900	11923	SERtN1	Serine transport (Na, H coupled)
3901	14769	SERtp	L-serine transport, peroxisomal
3902	2374	SFGTH	S-Formylglutathione hydralase
3903	20134	SGALSIDEtg	sgalside_hs intracellular transport
3904	20133	SGALSIDEtl	sgalside_hs intracellular transport
3905	11268	SGPL11r	Sphingosine-1-phosphate lyase 1
3906	19742	SGPL12r	Sphingosine-1-phosphate lyase
3907	8434	SIAASE	sialidase
3908	14458	SIAASE2ly	sialidase, lysosomal
3909	14517	SIAASE3ly	sialidase, lysosomal
3910	14518	SIAASE4ly	sialidase, lysosomal
3911	8543	SIAASEly	sialidase, lysosomal
3912	11083	SIAT4Bg	Beta-galactoside alpha-2,3-sialyltransferase, Golgi apparatus
3913	11096	SIAT9g	Lactosylceramide alpha-2,3-sialyltransferase, Golgi apparatus
3914	2395	SLCBK1	sphingolipid long chain base kinase (sphinganine)
3915	14569	SLDt	L-sulfolactate transport (cytosol to extracellular)
3916	8555	SLDx	L-sulfolactate dehydrogenase (NAD+)
3917	14568	SLDxm	L-sulfolactate dehydrogenase (NAD+), mitochondrial
3918	11279	SMPD3g	sphingomyelin phosphodiesterase 3, neutral membrane (neutral sphingomyelinase II)
3919	11159	SMPD3l	sphingomyelin phosphodiesterase 3, neutral membrane (neutral sphingomyelinase II)
3920	20875	SMPD4	sphingomyelinase
3921	11396	SMS	Sphingomyelin synthase (homo sapiens)
3922	12373	SO4CLtex2	sulfate transport via chloride countertransport (2:1)
3923	12361	SO4HCOtex	sulfate transport via bicarbonate countertransport
3924	12370	SO4OXAtex2	sulfate transport via oxalate countertransport (2:1)
3925	12165	SO4t4_2	sulfate transport via sodium symport
3926	12162	SO4t4_3	sulfate transport via sodium symport
3927	14309	SOAT11	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1
3928	14310	SOAT11r	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1
3929	14328	SOAT12	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1
3930	14329	SOAT12r	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1
3931	20876	SPC_HSt	sphingosylphosphorylcholine transport (diffusion)
3932	20204	SPH1Pte	sph1p transport
3933	20205	SPH1Ptr	sph1p intracellular transport
3934	19743	SPHGNtr	sphinganine intracellular transport
3935	19728	SPHINGStl	sphingosine intracellular transport
3936	19727	SPHINGStr	sphingosine intracellular transport
3937	11162	SPHK21c	sphingosine kinase 2
3938	19741	SPHMDAc	sphingomyelin deacylase
3939	20125	SPHMYLNtg	sphingomyelin intracellular transport
3940	20124	SPHMYLNtl	sphingomyelin intracellular transport

Column	Reaction #	Abbreviation	Reaction Name
3941	19729	SPHS1Pte	sphingosine-1-phosphate transport
3942	20206	SPHS1Ptr	sphingosine-1-phosphate transport
3943	11295	SPMDOX	Spermidine:(acceptor) oxidoreductase
3944	312	SPMS	spermidine synthase
3945	2518	SPODM	superoxide dismutase
3946	13662	SPODMe	superoxide dismutase, extracellular
3947	4915	SPODMm	superoxide dismutase
3948	13671	SPODMn	superoxide dismutase, nuclear
3949	13669	SPODMx	superoxide dismutase, peroxisome
3950	11638	SPR	sepiapterin reductase
3951	1342	SPRMS	spermine synthase
3952	14586	SPRn	sepiapterin reductase, nuclear
3953	14005	SPTix	serine-pyruvate aminotransferase (irreversible), peroxisomal
3954	2011	SQLEr	Squalene epoxidase, endoplasmic reticular (NADP)
3955	9744	SQLSr	Squalene synthase
3956	20866	SR5AR2r	3-oxo-5-alpha-steroid 4-dehydrogenase
3957	9965	SR5ARr	3-oxo-5-alpha-steroid 4-dehydrogenase
3958	9611	SRTN23OX	5-Hydroxytryptamine:oxygen 2,3-dioxygenase (indole-decyclizing)
3959	9607	SRTNACT	Acetyl-CoA:aralkylamine N-acetyltransferase
3960	9613	SRTNMTX	S-Adenosyl-L-methionine:amine N-methyltransferase (srtn)
3961	12189	SRTNt6(2)r	Seratonin reversible transport in via sodium symport/potassium antiport (1:2)
3962	12191	SRTNtu	Serotonin uniport
3963	10873	SSALxm	succinate-semialdehyde dehydrogenase (NAD) reversible (mitochondrial)
3964	11126	ST3GAL21g	CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransferase, Golgi apparatus
3965	11129	ST3GAL22g	CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransferase, Golgi apparatus
3966	11130	ST3GAL23g	CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransferase, Golgi apparatus
3967	14597	ST3GAL31g	ST3 beta-galactoside alpha-2,3-sialyltransferase 3
3968	14624	ST3GAL61g	Type 2 lactosamine alpha-2,3-sialyltransferase
3969	14641	ST3GAL62g	Type 2 lactosamine alpha-2,3-sialyltransferase
3970	11104	ST6GALNAC21	Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2
3971	11105	ST6GALNAC22	Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2
3972	11107	ST6GALNAC23	Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2
3973	11108	ST6GALNAC24	Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2
3974	11109	ST6GALNAC25	Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2
3975	11110	ST6GALNAC26	Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2
3976	11111	ST6GALNAC27	Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2
3977	11112	ST6GALNAC28	Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2
3978	11119	ST6GALNAC31	Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 3

Column	Reaction #	Abbreviation	Reaction Name
3979	11400	ST6GALNAC61	sialytransferase 7 ((alpha-N-acetylneuraminyl 2,3-betagalactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialytransferase) F
3980	11125	ST6GALNAC62	sialytransferase 7 ((alpha-N-acetylneuraminyl 2,3-betagalactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialytransferase) F
3981	11085	ST8SIA11	Beta-galactoside alpha-2,3-sialyltransferase
3982	11086	ST8SIA12	Beta-galactoside alpha-2,3-sialyltransferase
3983	11087	ST8SIA51g	Beta-galactoside alpha-2,3-sialyltransferase
3984	11113	ST8SIA52g	Beta-galactoside alpha-2,3-sialyltransferase
3985	11114	ST8SIA53g	Beta-galactoside alpha-2,3-sialyltransferase
3986	11115	ST8SIA54g	Beta-galactoside alpha-2,3-sialyltransferase
3987	11291	ST8SIA55g	Beta-galactoside alpha-2,3-sialyltransferase
3988	14625	ST8SIA56g	Alpha-2,8-sialyltransferase 8E
3989	19033	STCOAtx	fatty acid intracellular transport
3990	19103	STRDNCCPT1	carnitine O-palmitoyltransferase
3991	19122	STRDNCCPT2	carnitine transferase
3992	19084	STRDNCCRNt	transport into the mitochondria (carnitine)
3993	12466	STRDNCt	fatty acid transport via diffusion
3994	19779	STS1	Steryl-sulfatase
3995	12072	STS1r	Steryl-sulfatase
3996	19780	STS2	Steryl-sulfatase
3997	12073	STS2r	Steryl-sulfatase
3998	19782	STS3	Steryl-sulfatase
3999	19781	STS3r	Steryl-sulfatase
4000	19783	STS4	Steryl-sulfatase
4001	19784	STS4r	Steryl-sulfatase
4002	5321	SUCCt2m	succinate transport, mitochondrial
4003	12167	SUCCt4_2	succinate transport via sodium symport
4004	12173	SUCCt4_3	succinate transport via sodium symport
4005	15152	SUCCtp	succinate transporter, peroxisome
4006	1176	SUCD1m	succinate dehydrogenase
4007	510	SUCOAS1m	Succinate--CoA ligase (GDP-forming)
4008	2761	SUCOASm	Succinate--CoA ligase (ADP-forming)
4009	1547	SUCRe	sucrose hydrolyzing enxyme, extracellular
4010	18717	SULFOX	sulfite oxidase
4011	11034	T2M26DCOAHLm	trans-2-Methyl-5-isopropylhexa-2,5-dienoyl-CoA hydro-lyase (m)
4012	11045	T2M26DCOAHLx	trans-2-Methyl-5-isopropylhexa-2,5-dienoyl-CoA hydro-lyase (x)
4013	14224	T4HCINNMFM	4-hydroxycinnamate formation
4014	11049	T4HCINNOX	4-Coumarate:oxygen oxidoreductase
4015	19625	TAGAT-Dt	D-tagatose uptake via diffusion
4016	282	TALA	transaldolase
4017	11945	TAURt4(2)r	taurine transport (sodium symport) (2:1)
4018	11517	TAURtcx	taurine transport (sodium symport) (cytosol to peroxisome)
4019	19707	TAXOLte	xenobiotic transport
4020	12268	TCHOLAt	taurocholate transport via bicarbonate countertransport
4021	12619	TCHOLAt2	taurocholate transport via sodium cotransport
4022	12668	TCHOLAt3	ABC bile acid transporter
4023	19655	TCHOLAte	bile acid intracellular transport
4024	19656	TCHOLAtx	bile acid intracellular transport
4025	20244	TCYNTt	Thiocyanate transport via diffusion (cytosol to extracellular)
4026	20245	TCYNTtm	Thiocyanate transport via diffusion (mitochondrial)
4027	19657	TDCHOLAte	bile acid intracellular transport

Column	Reaction #	Abbreviation	Reaction Name
4028	19658	TDCHOLAtx	bile acid intracellular transport
4029	9482	TDP	thiamine triphosphatase
4030	2492	TDPDRE	dTDP-4-dehydrorhamnose 3,5-epimerase
4031	2493	TDPDRR	dTDP-4-dehydrorhamnose reductase
4032	2490	TDPGDH	dTDPglucose 4,6-dehydratase
4033	14062	TDPm	thiamine triphosphatase, mitochondrial
4034	19039	TETHEX3COAtx	fatty acid intracellular transport
4035	12472	TETHEX3t	fatty acid transport via diffusion
4036	19046	TETPENT3COAtx	fatty acid intracellular transport
4037	19108	TETPENT3CPT1	carnitine O-palmitoyltransferase
4038	19127	TETPENT3CPT2	carnitine transferase
4039	19090	TETPENT3CRNt	transport into the mitochondria (carnitine)
4040	12471	TETPENT3t	fatty acid transport via diffusion
4041	19044	TETPENT6COAtx	fatty acid intracellular transport
4042	19109	TETPENT6CPT1	carnitine O-palmitoyltransferase
4043	19128	TETPENT6CPT2	carnitine transferase
4044	19089	TETPENT6CRNt	transport into the mitochondria (carnitine)
4045	12468	TETPENT6t	fatty acid transport via diffusion
4046	19042	TETTET6COAtx	fatty acid intracellular transport
4047	19104	TETTET6CPT1	carnitine O-palmitoyltransferase
4048	19123	TETTET6CPT2	carnitine transferase
4049	19085	TETTET6CRNt	transport into the mitochondria (carnitine)
4050	12469	TETTET6t	fatty acid transport via diffusion
4051	14584	THBPT4ACAMDASE	Tetrahydrobiopterin-4a-carbinolamine dehydratase
4052	14183	THCHOLSTOICtm	lipid, flip-flop intracellular transport
4053	5323	THD1m	NAD(P) transhydrogenase
4054	14837	THFt2	tetrahydrofolate transport via anion exchange
4055	14903	THFtl	5,6,7,8-Tetrahydrofolate transport, diffusion, lysosomal
4056	1418	THFtm	5,6,7,8-Tetrahydrofolate transport, diffusion, mitochondrial
4057	7883	THMDt4	thymidine transport in via sodium symport
4058	12145	THMDt5	thymidine transport (1:2 Na/Thymd cotransport)
4059	14011	THMMPt4	Thiamine monophosphate transport in via anion antiport
4060	14065	THMMPtm	Thiamine monophosphate transport, mitochondrial
4061	3625	THMP	thiamin phosphatase
4062	14069	THMPPtm	Thiamine diphosphate transport in via anion antiport, mitochondria
4063	9481	THMTP	thiamine-triphosphatase
4064	14070	THMTPt	Thiamine triphosphate transport in via anion antiport
4065	14009	THMt2m	Thiamine transport in via proton symport, mitochondrial
4066	14016	THMt3	Thiamine transport in via proton antiport
4067	12939	THP2Ctp	2,3,4,5-Tetrahydropyridine-2-carboxylate transport, peroxisomal
4068	11839	THRALANaEx	L-alanine/L-threonine Na-dependent exchange (Thr-L in)
4069	11861	THRASNNaEx	L-threonine/L-asparagine Na-dependent exchange (Thr-L in)
4070	11845	THRCYSNaEx	L-cysteine/L-threonine Na-dependent exchange (Thr-L in)
4071	324	THRD_L	L-threonine deaminase
4072	11859	THRGLNNaEx	L-threonine/L-glutamine Na-dependent exchange (Thr-L in)
4073	11800	THRGLNexR	L-threonine/glycine reversible exchange
4074	11799	THRGLYexR	L-threonine/glycine reversible exchange
4075	365	THRS	threonine synthase
4076	11843	THRSERNaEx	L-serine/L-threonine Na-dependent exchange (Thr-L in)
4077	2476	THRt4	L-threonine via sodium symport
4078	4021	THYMDt1	thymd transport
4079	12577	THYMDtl	thymidine facilated transport from lysosome
4080	4011	THYMDtm	thymd transport

Column	Reaction #	Abbreviation	Reaction Name
4081	12551	THYMt	thymine reversible transport via facilated diffusion
4082	12272	THYOXt	T4 transport via bicarbonate countertransport
4083	12489	THYOXt2	T4 transport via facilitated diffusion
4084	12123	THYPX	thyroid peroxidase
4085	283	TKT1	transketolase
4086	4641	TKT2	transketolase
4087	10964	TMABADH	4-trimethylaminobutyraldehyde dehydrogenase
4088	432	TMDK1	thymidine kinase (ATP:thymidine)
4089	4532	TMDK1m	thymidine kinase (ATP:thymidine)
4090	3871	TMDPK	thiamine diphosphokinase
4091	435	TMDPP	thymidine phosphorylase
4092	3352	TMDPPK	thiamine-diphosphate kinase
4093	431	TMDS	thymidylate synthase
4094	10959	TMLYSOX	trimethyllysine dioxygenase
4095	14817	TMLYSter	trimethyl-L-lysine transport (ER to cytosol)
4096	19040	TMNDNCCOAtx	fatty acid intracellular transport
4097	19105	TMNDNCCPT1	carnitine O-palmitoyltransferase
4098	19124	TMNDNCCPT2	carnitine transferase
4099	19086	TMNDNCCRNt	transport into the mitochondria (carnitine)
4100	12465	TMNDNCt	fatty acid transport via diffusion
4101	19708	TOLBUTAMIDEte	xenobiotic transport
4102	276	TPI	triose-phosphate isomerase
4103	2817	TRDR	thioredoxin reductase (NADPH)
4104	10104	TRDR2	Thioredoxin (ubiquinone 10) reductase (NADPH)
4105	10105	TRDR3	Thioredoxin (ubiquinone 10) reductase (NADH)
4106	1436	TRDRm	thioredoxin reductase (NADPH)
4107	695	TREH	alpha,alpha-trehalase
4108	2462	TREHe	alpha,alpha-trehalase
4109	19422	TRIODTHYSUFt	Triiodothyronine sulfate transport (diffusion)
4110	12107	TRIODTHYSULT	Triiodothyronine Sulfotransferase
4111	12273	TRIODTHYt	T3 transport via bicarbonate countertransport
4112	12490	TRIODTHYt2	T3 transport via facilitated diffusion
4113	11870	TRIOK	triokinase
4114	14583	TRPHYDRO2	L-Tryptophan,tetrahydrobiopterin:oxygen oxidoreductase (5-hydroxylating)
4115	1389	TRPO2	L-Tryptophan:oxygen 2,3-oxidoreductase (decyclizing)
4116	12567	TRPt	L-tryptophan transport
4117	11951	TRPt4	L-tryptophan transport in via sodium symport
4118	9585	TRYPTAOX	Tryptamine:oxygen oxidoreductase(deaminating)(flavin-containing)
4119	11319	TS3	Tachysterol 3 formation
4120	19768	TSTSTERONEGLCte	glucuronidated compound transport
4121	19759	TSTSTERONEGLCtr	glucuronidated compound transport
4122	20335	TSTSTERONESULT	testosterone sulfotransferase
4123	20337	TSTSTERONESte	sulfonated testosterone transport
4124	14984	TSTSTERONEtr	testosterone intracellular transport
4125	12163	TSULt4_3	thiosulfate transport via sodium symport
4126	1924	TTDCAt	Tetradecanoate (n-C14:0) transport in via uniport
4127	20625	TTDCPT1	carnitine O-palmitoyltransferase
4128	20626	TTDCPT2	carnitine transferase
4129	20624	TTDCRNt	transport into the mitochondria (carnitine)
4130	20860	TXA2te	thromboxane A2 transport
4131	20332	TXA2tr	thromboxane A2 intracellular transport
4132	10004	TXASr	Thromboxane-A synthase
4133	19423	TYMSFt	Tyramine O-sulfate transport (diffusion)
4134	12104	TYMSULT	Tyramine Sulfotransferase

Column	Reaction #	Abbreviation	Reaction Name
4135	14587	TYR3MO2	tyrosine 3-monooxygenase
4136	9390	TYRASE	Tyrosinase
4137	11604	TYRCBOX	L-Tyrosine carboxy-lyase
4138	10557	TYRDOPO	Tyrosine:dopa oxidase
4139	10559	TYRDOPO3	Tyrosine:dopa oxidase (dopaquinone producing 2)
4140	11608	TYROXDAc	Tyramine:oxygen oxidoreductase(deaminating)(flavin-containing) (cytosol)
4141	331	TYRTA	tyrosine transaminase
4142	1402	TYRTAm	tyrosine transaminase, mitochondrial
4143	12566	TYRt	L-tyrosine transport
4144	11950	TYRt4	L-tyrosine transport in via sodium symport
4145	10594	UAG2EMAi	UDP-N-acetyl-D-glucosamine 2-epimerase (Hydrolysis)
4146	9866	UAG4E	UDP-N-acetylglucosamine 4-epimerase
4147	10650	UAGALDP	UDP-N-acetylgalactosamine diphosphorylase
4148	476	UAGDP	UDP-N-acetylglucosamine diphosphorylase
4149	20329	UDPACGALtl	udpacgal intracellular transport
4150	7309	UDPDOLPT_L	UDPglucose:dolichyl-phosphate beta-D-glucosyltransferase (liver)
4151	7310	UDPDOLPT_U	UDPglucose:dolichyl-phosphate beta-D-glucosyltransferase (uterus)
4152	13426	UDPG1P	UDPglucuronate uridine-monophosphohydrolase
4153	200	UDPG4E	UDPglucose 4-epimerase
4154	12142	UDPGALtg	UDP-Gal Golgi transport via CMP antiport
4155	3196	UDPGD	UDPglucose 6-dehydrogenase
4156	12158	UDPGLCAter	UDPGlcA endoplasmic reticulum transport via UMP antiport
4157	15034	UDPGLCAtg	UDPGlcA Golgi transport via UMP antiport
4158	15035	UDPGLCter	UDP-Glc endoplasmic reticulum transport via CMP antiport
4159	12143	UDPGLCtg	UDP-Glc Golgi transport via CMP antiport
4160	13743	UDPGLDCg	UDP-D-glucuronate decarboxylase, Golgi apparatus
4161	10141	UDPGNP	UDPglucuronate uridine-diphosphohydrolase
4162	10072	UDPGP	UDPglucose pyrophosphohydrolase
4163	15036	UDPXYLter	UDP-Xyl endoplasmic reticular transport via CMP antiport
4164	13272	UDPXYLtg	UDP-Xyl Golgi transport via CMP antiport
4165	20330	UDPtl	udp intracellular transport
4166	9892	UGALGTg	UDPgalactose:D-glucose 4-beta-D-galactosyltransferase, Golgi apparatus
4167	12161	UGALNACter	UDP-GalNAc endoplasmic reticulum transport via CMP antiport
4168	12154	UGALNACtg	UDP-GalNAc Golgi transport via CMP antiport
4169	11260	UGCG	Ceramide glucosyltransferase
4170	12157	UGLCNACtg	UDP-GlcNAc Golgi transport via CMP antiport
4171	1171	UGLT	UDPglucose--hexose-1-phosphate uridylyltransferase
4172	19785	UGT1A10r	UDP-glucuronosyltransferase 1-10 precursor, microsomal
4173	11781	UGT1A1r	UDP-glucuronosyltransferase 1-10 precursor, microsomal
4174	11784	UGT1A2r	UDP-glucuronosyltransferase 1-10 precursor, microsomal
4175	11782	UGT1A3r	UDP-glucuronosyltransferase 1-10 precursor, microsomal
4176	11785	UGT1A4r	UDP-glucuronosyltransferase 1-10 precursor, microsomal
4177	11786	UGT1A5r	UDP-glucuronosyltransferase 1-10 precursor, microsomal
4178	15118	UGT1A5r2	UDP-glucuronosyltransferase 1-10 precursor, microsomal (13-cis)
4179	11788	UGT1A6r	UDP-glucuronosyltransferase 1-10 precursor, microsomal
4180	11789	UGT1A7r	UDP-glucuronosyltransferase 1-10 precursor, microsomal
4181	11790	UGT1A8r	UDP-glucuronosyltransferase 1-10 precursor, microsomal
4182	14981	UGT1A9r	UDP-glucuronosyltransferase 1-10 precursor, microsomal
4183	2813	UMPK	UMP kinase

Column	Reaction #	Abbreviation	Reaction Name
4184	10235	UMPK2	UMP kinase (CTP)
4185	10234	UMPK2n	UMP kinase (CTP),nuclear
4186	10238	UMPK3	UMP kinase (UTP)
4187	10237	UMPK3n	UMP kinase (UTP),nuclear
4188	10239	UMPK4	UMP kinase (GTP)
4189	10240	UMPK4n	UMP kinase (GTP),nuclear
4190	10242	UMPK5	UMP kinase (dATP)
4191	10241	UMPK5n	UMP kinase (dATP),nuclear
4192	10245	UMPK6	UMP kinase (dCTP)
4193	10244	UMPK6n	UMP kinase (dCTP),nuclear
4194	10246	UMPK7	UMP kinase (dGTP)
4195	10247	UMPK7n	UMP kinase (dGTP),nuclear
4196	20307	UMPKm	UMP kinase (mitochondrial, ATP)
4197	1446	UMPKn	UMP kinase, nuclear
4198	2921	UNK2	2-keto-4-methylthiobutyrate transamination
4199	3645	UNK3	2-keto-4-methylthiobutyrate transamination
4200	5	UPP3S	uroporphyrinogen-III synthase
4201	6	UPPDC1	uroporphyrinogen decarboxylase (uroporphyrinogen III)
4202	9786	UPPN	b-ureidopropionase
4203	19376	URATEt	urate export from cytosol
4204	19375	URATEtx	urate export from peroxisome
4205	12549	URAt	uracil transport via facilated diffusion
4206	2874	URCN	urocanase
4207	2092	UREAt	Urea transport via facilitate diffusion
4208	11966	UREAt5	urea, water cotransport
4209	14363	UREAtm	Urea transport via diffusion
4210	20322	URIDK2m	uridylate kinase (dUMP), mitochondrial
4211	436	URIK1	uridine kinase (ATP:Uridine)
4212	12553	URIt	uridine facilated transport in cytosol
4213	7884	URIt4	uridine transport in via sodium symport
4214	12089	URIt5	uridine transport in via sodium symport (1:2)
4215	10282	UROLACer	uronolactonase, endoplasmic reticulum
4216	14150	UTPtn	UTP diffusion in nucleus
4217	12570	Uritl	uridine facilated transport from lysosome
4218	12149	Uritm	uridine facilated transport in mitochondria
4219	19531	Uritn	uridine transport in nucleus
4220	19094	VACCCPT1	carnitine O-palmitoyltransferase
4221	19113	VACCCPT2	carnitine transferase
4222	19075	VACCCRNt	transport into the mitochondria (carnitine)
4223	12449	VACCt	fatty acid transport via diffusion
4224	320	VALTA	valine transaminase
4225	3805	VALTAm	valine transaminase, mitochondiral
4226	11954	VALt4	L-valine transport in via sodium symport
4227	12593	VALt5m	Valine reversible mitochondrial transport
4228	11926	VALtec	L-valine transport via diffusion (extracellular to cytosol)
4229	11317	VD3	Vitamin D3 formation
4230	11326	VITD2Hm	Vitamin D-25-hydroxylase (D2)
4231	11332	VITD2t	Vitamin D2 release
4232	11335	VITD2tm	Vitamin D2 transport from mitochondria
4233	11323	VITD3Hm	Vitamin D-25-hydroxylase (D3)
4234	11321	VITD3t	Vitamin D3 release
4235	20308	VITD3t2	Vitamin D3 uptake
4236	11336	VITD3tm	Vitamin D3 transport from mitochondria
4237	20309	VITD3tm3	Vitamin D3 transport in mitochondria
4238	13910	VLCS2p	Very-long-chain-fatty-acid-CoA ligase
4239	13911	VLCS2r	Very-long-chain-fatty-acid-CoA ligase

Column	Reaction #	Abbreviation	Reaction Name
4240	13901	VLCSp	Very-long-chain-fatty-acid-CoA ligase
4241	13903	VLCSr	Very-long-chain-fatty-acid-CoA ligase
4242	19720	WHDDCAte	xenobiotic transport
4243	19721	WHHDCAte	xenobiotic transport
4244	20132	WHTSTSTERONEte	omega hydroxy testosterone transport
4245	19722	WHTTDCAte	xenobiotic transport
4246	9843	XANDp	xanthine dehydrogenase, peroxisomal
4247	14089	XANtx	xanthine diffusion in peroxisome
4248	12077	XAO2x	xanthine oxidase
4249	12080	XAOx	xanthine oxidase,peroxisomal
4250	19642	XOL27OHtm	27 hydroxy cholesterol transport
4251	14181	XOL7AH2tm	lipid, flip-flop intracellular transport
4252	14182	XOL7AH2tr	lipid, flip-flop intracellular transport
4253	14180	XOL7AONEtr	lipid, flip-flop intracellular transport
4254	12681	XOLDIOLONEt	lipid, flip-flop intracellular transport
4255	14177	XOLDIOLONEtm	lipid, flip-flop intracellular transport
4256	14714	XOLEST2te	cholesterol ester transporter
4257	14713	XOLESTte	cholesterol ester transporter
4258	19643	XOLTRI24tc	24 trihydroxy cholesterol transport
4259	19644	XOLTRI24te	24 trihydroxy cholesterol transport
4260	19645	XOLTRI25tc	25 trihydroxy cholesterol transport
4261	19646	XOLTRI25te	25 trihydroxy cholesterol transport
4262	19647	XOLTRI27tc	27 trihydroxy cholesterol transport
4263	19648	XOLTRI27te	27 trihydroxy cholesterol transport
4264	14179	XOLTRIOLtm	lipid, flip-flop intracellular transport
4265	14178	XOLTRIOLtr	lipid, flip-flop intracellular transport
4266	14927	XSERtg	Xyl-L-Ser (protein) transport from endoplasmic reticulum to Golgi apparatus
4267	254	XYLK	xylulokinase
4268	10156	XYLTD_Dr	xylitol dehydrogenase (D-xyulose-forming)
4269	11551	XYLTer	UDP-xylose:protein xylosyltransferase, endoplasmic reticulum
4270	2052	XYLTt	Xylitol transport via passive diffusion
4271	10155	XYLUR	xylulose reductase
4272	1556	XYLt	D-xylose reversible transport
4273	14922	XYLtly	Xylose efflux from lysosome
4274	11412	YVITEt	gamma-Tocopherol (Vit. E) transport
4275	14773	biomass_mm_1_no_glygln	Mouse Biomass 1 (no glycogen)

Table 5: *H. sapiens* Recon 1 intrasystem reactions. Metabolic and intrasystem transport reactions are listed alphabetically by reaction abbreviation. Compartmentalization is denoted by the following abbreviations. Reactions that occur entirely within one compartment have abbreviations at the beginning of the equation; otherwise, abbreviations follow each metabolite.

Compartment Abbreviations

[c], cytoplasm	[m], mitochondrion
[e], extracellular	[n], nucleus
[g], Golgi appratus	[r], endoplasmic reticulum
[l], lysosome	[x], peroxisome

E.C. #, Enzyme Commission numbers; Gene association, Boolean logic statement describing relationship between loci and reactions.

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
10FTHF5GLUtl	5-glutamyl-10FTHF transport, lysosomal	10fthf5glu[c] --> 10fthf5glu[l]		Transport, Lysosomal	
10FTHF5GLUtm	5-glutamyl-10FTHF transport, mitochondrial	10fthf5glu[m] --> 10fthf5glu[c]		Transport, Mitochondrial	
10FTHF6GLUtl	6-glutamyl-10FTHF transport, lysosomal	10fthf6glu[c] --> 10fthf6glu[l]		Transport, Lysosomal	
10FTHF6GLUtm	6-glutamyl-10FTHF transport, mitochondrial	10fthf6glu[m] --> 10fthf6glu[c]		Transport, Mitochondrial	
10FTHF7GLUtl	7-glutamyl-10FTHF transport, lysosomal	10fthf7glu[c] --> 10fthf7glu[l]		Transport, Lysosomal	
10FTHF7GLUtm	7-glutamyl-10FTHF transport, mitochondrial	10fthf7glu[m] --> 10fthf7glu[c]		Transport, Mitochondrial	
10FTHFtl	10-Formyltetrahydrofolate lysosomal transport via diffusion	10fthf[c] <==> 10fthf[l]		Transport, Lysosomal	
10FTHFtm	10-Formyltetrahydrofolate mitochondrial transport via diffusion	10fthf[c] <==> 10fthf[m]		Transport, Mitochondrial	
11DOCRTSLtm	11-deoxycortisol intracellular transport	11docrtsl[c] <==> 11docrtsl[m]		Transport, Mitochondrial	
11DOCRTSLtr	11-deoxycortisol intracellular transport	11docrtsl[c] <==> 11docrtsl[r]		Transport, Endoplasmic Reticular	
11DOCRTSTRNtm	11-deoxycorticosterone intracellular transport	11docrtstrn[c] <==> 11docrtstrn[m]		Transport, Mitochondrial	
11DOCRTSTRNtr	11-deoxycorticosterone intracellular transport	11docrtstrn[c] <==> 11docrtstrn[r]		Transport, Endoplasmic Reticular	
13DAMPPOX	1,3-Diaminopropane:oxygen oxidoreductase (deaminating)	[c] : 13dampp + h2o + o2 --> bamppald + h2o2 + nh4	1.4.3.6	beta-Alanine metabolism	(26.1 or 314.1 or 314.2 or 8639.1)
1a,24,25VITD2Hm	1-alpha-Vitamin D-24,25-hydroxylase (D2)	[m] : 2425dhvitd2 + h + nadph + o2 --> 1a2425thvitd2 + h2o + nadp		Vitamin D	
1a,24,25VITD3Hm	1-alpha-Vitamin D-24,25-hydroxylase (D3)	[m] : 2425dhvitd3 + h + nadph + o2 --> 1a2425thvitd3 + h2o + nadp		Vitamin D	
1a,25VITD2Hm	1-alpha,24R,25-Vitamin D-hydroxylase (D2)	[m] : 1a25dhvitd2 + h + nadph + o2 --> 1a2425thvitd2 + h2o + nadp		Vitamin D	
1a,25VITD3Hm	1-alpha,24R,25-Vitamin D-hydroxylase (D3)	[m] : 1a25dhvitd3 + h + nadph + o2 --> 1a2425thvitd3 + h2o + nadp		Vitamin D	
1MNCAMti	N1-Methylnicotinamide transport	1mncam[c] + atp[c] + h2o[c] --> 1mncam[e] + adp[c] + h[c] + pi[c]		Transport, Extracellular	
1PPDCRp	delta1-piperideine-2-carboxylate reductase, perixosomal	[x] : 1pipdn2c + h + nadh --> Lpipecol + nad		Lysine Metabolism	
24,25DHVITD2t	24,25-Dihydroxyvitamin D2 transport from cytoplasm	2425dhvitd2[c] --> 2425dhvitd2[e]		Transport, Extracellular	
24,25DHVITD2tm	24,25-Dihydroxyvitamin D2 transport from mitochondria	2425dhvitd2[m] --> 2425dhvitd2[c]		Transport, Mitochondrial	
24,25DHVITD3t	24,25-Dihydroxyvitamin D3 transport from cytoplasm	2425dhvitd3[c] --> 2425dhvitd3[e]		Transport, Extracellular	
24,25DHVITD3tm	24,25-Dihydroxyvitamin D3 transport from mitochondria	2425dhvitd3[m] --> 2425dhvitd3[c]		Transport, Mitochondrial	
24,25VITD2Hm	24R-Vitamin D-25-hydroxylase (D2)	[m] : 25hvitd2 + h + nadph + o2 --> 2425dhvitd2 + h2o + nadp		Vitamin D	1591.1
24,25VITD3Hm	24R-Vitamin D-25-hydroxylase (D3)	[m] : 25hvitd3 + h + nadph + o2 --> 2425dhvitd3 + h2o + nadp		Vitamin D	1591.1
24NPHte	xenobiotic transport	24nph[e] <==> 24nph[c]		Transport, Extracellular	
25HVITD2t	25-hydroxyvitamin D2 transport from cytoplasm	25hvitd2[c] --> 25hvitd2[e]		Transport, Extracellular	
25HVITD2tin	25-hydroxyvitamin D2 transport in cytoplasm	25hvitd2[e] --> 25hvitd2[c]		Transport, Extracellular	
25HVITD2tin-m	25-hydroxyvitamin D2 transport in mitochondria	25hvitd2[c] --> 25hvitd2[m]		Transport, Mitochondrial	
25HVITD2tm	25-hydroxyvitamin D2 transport from mitochondria	25hvitd2[m] --> 25hvitd2[c]		Transport, Mitochondrial	
25HVITD3t	25-hydroxyvitamin D3 transport from cytoplasm	25hvitd3[c] --> 25hvitd3[e]		Transport, Extracellular	
25HVITD3tin	25-hydroxyvitamin D3 transport in cytoplasm	25hvitd3[e] --> 25hvitd3[c]		Transport, Extracellular	
25HVITD3tin-m	25-hydroxyvitamin D3 transport in mitochondria	25hvitd3[c] --> 25hvitd3[m]		Transport, Mitochondrial	
25HVITD3tm	25-hydroxyvitamin D3 transport from mitochondria	25hvitd3[m] --> 25hvitd3[c]		Transport, Mitochondrial	
25VITD2Hm	1-alpha-Vitamin D-25-hydroxylase (D2)	[m] : 25hvitd2 + h + nadph + o2 --> 1a25dhvitd2 + h2o + nadp		Vitamin D	1594.1
25VITD3Hm	1-alpha-Vitamin D-25-hydroxylase (D3)	[m] : 25hvitd3 + h + nadph + o2 --> 1a25dhvitd3 + h2o + nadp		Vitamin D	1594.1
2AMACHYD	2-Aminoacrylate hydrolysis	[c] : 2amac + h2o --> nh4 + pyr		Glycine, Serine, and Threonine Metabolism	
2AMACSULT	2-Aminoacrylate sulfotransferase	[c] : 2amac + nadph + paps --> Lcyst + nadp + pap		Cysteine Metabolism	
2AMADPTm	L-2-aminoadipate shuttle (cytosol/mitochondria)	L2aadp[c] + akg[m] <==> L2aadp[m] + akg[c]		Lysine Metabolism	89874.1
2DR1PP	2-deoxy-D-ribose 1-phosphate phosphorylase	[c] : 2dr1p + h2o --> drib + pi	3.1.3.10	Pyrimidine Catabolism	
2HBO	2-Hydroxybutyrate:NAD+ oxidoreductase	[c] : 2hb + nad <==> 2obut + h + nadh	1.1.1.27	Propanoate Metabolism	((3945.1 and 3939.1) or 3945.1 or 3939.1 or 55293.1 or 3948.1 or 3948.2 or 160287.1 or 92483.1)
2HBt2	2-hydroxybutyrate cotransport with proton	2hb[e] + h[e] <==> 2hb[c] + h[c]		Transport, Extracellular	(6566.1 or 9194.1 or 9123.1)
2HCO3_NAt	bicarbonate transport (Na/HCO3 1:2 cotransport)	(2) hco3[e] + na1[e] <==> (2) hco3[c] + na1[c]		Transport, Extracellular	(8671.1 or 57835.1 or 57835.2 or 57835.3 or 57835.4)
2MCITt	2-methylcitrate transport via diffusion	2mcit[c] <==> 2mcit[e]		Transport, Extracellular	
2OXOADOXm	2-Oxoadipate:lipoamde 2-oxidoreductase(decarboxylating and acceptor-succinylating) (mitochondria)	[m] : 2oxoadp + coa + nad --> co2 + glutcoa + nadh	1.2.4.2	Lysine Metabolism	((4967.1 and (8050.1 and 1738.1) and 1743.1) or (1743.1 and 4967.2 and (8050.1 and 1738.1)))
2OXOADPTm	2-oxoadipate shuttle (cytosol/mitochondria)	2oxoadp[c] + akg[m] <==> 2oxoadp[m] + akg[c]		Tryptophan metabolism	89874.1
34DHOXPEGOX	3,4-Dihydroxyphenylethyleneglycol:NAD+ oxidoreductase	[c] : 34dhmald + h + nadh <==> 34dhoxpeg + nad	1.1.1.1	Tyrosine metabolism	(131.1 or 137872.1 or (124.1 and 126.1) or (124.1 and 125.1) or (126.1 and 125.1) or 127.1 or 128.1 or 130.1)
34DHOXPEGt	3,4-Dihydroxyphenylethyleneglycol transport (diffusion)	34dhoxpeg[c] <==> 34dhoxpeg[e]		Transport, Extracellular	
34DHPHAMT	3,4-Dihydroxyphenylacetate:amet O-methyltransferase	[c] : 34dhpha + amet --> ahcys + h + homoval	2.1.1.6	Tyrosine metabolism	(1312.1 or 1312.2)

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
34DHPHEt	3,4-Dihydroxy-L-phenylalanine transport	34dhphe[e] <==> 34dhphe[c]		Transport, Extracellular	117247.1
34DHPLACOX	3,4-Dihydroxyphenylacetaldehyde:NAD+ oxidoreductase	[c] : 34dhpac + h2o + nad --> 34dhpha + (2) h + nadh	1.2.1.5	Tyrosine metabolism	(222.1 or 221.1 or 220.1 or 218.1)
34DHPLACOX(NADP)	3,4-Dihydroxyphenylacetaldehyde:NADP+ oxidoreductase	[c] : 34dhpac + h2o + nadp <==> 34dhpha + (2) h + nadph	1.2.1.5	Tyrosine metabolism	(222.1 or 218.1 or 221.1)
34DHXMANDACOX	3,4-Dihydroxymandelaldehyde:NAD+ oxidoreductase	[c] : 34dhmald + h2o + nad --> 34dhoxmand + (2) h + nadh	1.2.1.5	Tyrosine metabolism	(221.1 or 220.1 or 218.1)
34DHXMANDACOX(NADP)	3,4-Dihydroxymandelaldehyde:NADP+ oxidoreductase	[c] : 34dhmald + h2o + nadp <==> 34dhoxmand + (2) h + nadph	1.2.1.5	Tyrosine metabolism	(221.1 or 222.1)
34HPLFM	3-(4-hydroxyphenyl-)lactate formation	[m] : 34hpp + h + nadh --> 34hpl + nad		Ubiquinone Biosynthesis	
34HPPOR	4-Hydroxyphenylpyruvate:oxygen oxidoreductase	[c] : 34hpp + o2 --> co2 + hgentis	1.13.11.27	Tyrosine metabolism	3242.1
35cGMPtn	35cGMP nuclear transport	35cgmp[c] <==> 35cgmp[n]		Transport, Nuclear	
3AIBt	3-amino-isobutyrate transport	3aib[c] --> 3aib[e]		Transport, Extracellular	
3AIBTm	L-3-aminoisobutyrate transaminase, mitochondrial	[m] : 2mop + glu-L <==> 3aib + akg	2.6.1.22	Valine, Leucine, and Isoleucine Metabolism	(18.1 or 18.2)
3AIBtm	3-amino-isobutyrate transport, mitochondrial	3aib[m] --> 3aib[c]		Transport, Mitochondrial	(18.1 or 18.2)
3DPHBH1	Hydroxylation of 3-Decaprenyl-4-hydroxybenzoate (NADH)	[m] : 3dphb + h + nadh + o2 --> 3dpdhb + h2o + nad		Ubiquinone Biosynthesis	
3DPHBH2	Hydroxylation of 3-Decaprenyl-4-hydroxybenzoate (NADPH)	[m] : 3dphb + h + nadph + o2 --> 3dpdhb + h2o + nadp		Ubiquinone Biosynthesis	
3DSPHR	3-Dehydrosphinganine reductase	[c] : 3dsphgn + h + nadph --> nadp + sphgn	1.1.1.102	Sphingolipid Metabolism	2531.1
3HAO	3-hydroxyanthranilate 3,4-dioxygenase	[c] : 3hanthrn + o2 --> cmusa + h	1.13.11.6	Tryptophan metabolism	23498.1
3HBCDm	3-hydroxybutyryl-CoA dehydratase, mitochondrial	[m] : b2coa + h2o <==> 3hbcoa-R	4.2.1.55	Butanoate Metabolism	55268.1
3HBCOAHLm	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	[m] : 3hibutcoa + h2o --> 3hmp + coa + h	3.1.2.4	Valine, Leucine, and Isoleucine Metabolism	
3HCO3_NAt	bicarbonate transport (Na/HCO3 1:3 cotransport)	(3) hco3[e] + na1[e] <==> (3) hco3[c] + na1[c]		Transport, Extracellular	(8671.1 or 57835.1 or 57835.2 or 57835.3 or 57835.4)
3HKYNAKGAT	3-Hydroxy-L-kynurenine:2-oxoglutarate aminotransferase	[c] : akg + hLkynr --> 42A3HP24DB + glu-L	2.6.1.7	Tryptophan metabolism	(51166.1 or 51166.2 or 883.1)
3HLYTCL	3-Hydroxy-L-tyrosine carboxy-lyase	[c] : 34dhphe + h --> co2 + dopa	4.1.1.28	Tyrosine metabolism	1644.1
3HPCOAHYD	3-hydroxyisobutyryl-Coenzyme A hydrolase	[c] : 3hpcoa + h2o --> 3hpp + coa + h	3.1.2.4	beta-Alanine metabolism	(26275.1 or 26275.2)
3HPPD	3-hydroxypropionate dehydrogenase	[c] : 3hpp + nad <==> h + msa + nadh	1.1.1.59	Propanoate Metabolism	
3HXKYNDCL	3-Hydroxykynurenamine decarboxy-lyase	[c] : h + hLkynr --> 3hxkynam + co2	4.1.1	Tryptophan metabolism	1644.1
3HXKYNOXDA	3-Hydroxykynurenamine:oxygen oxidoreductase(deaminating)(flavin-containing)	[c] : 3hxkynam + o2 --> 48dhoxquin + h2o2 + nh4	1.4.3.4	Tryptophan metabolism	(4128.1 or 4129.1)
3M4HDXPAC	3-Methoxy-4-hydroxyphenylacetaldehyde:NAD+ oxidoreductase	[c] : 3mox4hpac + h2o + nad <==> (2) h + homoval + nadh	1.2.1.5	Tyrosine metabolism	(221.1 or 220.1 or 222.1 or 218.1)
3MLDAt	3MLDA extracellular transport via diffusion	3mlda[c] <==> 3mlda[e]		Transport, Extracellular	
3MOBt2im	3-methyl-2-oxobutanoate mitochondrial transport via proton symport	3mob[c] + h[c] --> 3mob[m] + h[m]		Transport, Mitochondrial	
3MOPt2im	3-Methyl-2-oxopentanoate mitochondrial transport via proton symport	3mop[c] + h[c] --> 3mop[m] + h[m]		Transport, Mitochondrial	
3MOX4HOXPGALDOX	3-Methoxy-4-hydroxyphenylglycolaldehyde:NAD+ oxidoreductase	[c] : 3m4hpga + h2o + nad --> 3mox4hoxm + (2) h + nadh	1.2.1.5	Tyrosine metabolism	(220.1 or 218.1 or 221.1 or 222.1)
3MOX4HOXPGALDOX(NADP)	3-Methoxy-4-hydroxyphenylglycolaldehyde:NADP+ oxidoreductase	[c] : 3m4hpga + h2o + nadp <==> 3mox4hoxm + (2) h + nadph	1.2.1.5	Tyrosine metabolism	(220.1 or 218.1 or 221.1 or 222.1)
3MOXTYROX	3-Methoxytyramine:oxygen oxidoreductase (deaminating)	[c] : 3moxtyr + h2o + o2 --> 3mox4hpac + h2o2 + nh4	1.4.3.4	Tyrosine metabolism	(4128.1 or 4129.1)
3NTD7l	3'-nucleotidase (AMP), lysosome	[l] : 3amp + h2o --> adn + pi		Nucleic acid degradation	53.1
3SALAASPm	cysteinesulfinate-aspartate mitochondrial shuttle	3sala[m] + asp-L[c] <==> 3sala[c] + asp-L[m]		Transport, Mitochondrial	(10165.1 or 8604.1)
3SALACBOXL	3-Sulfino-L-alanine carboxy-lyase	[c] : 3sala + h --> co2 + hyptaur	4.1.1.15	Taurine and hypotaurine metabolism	(2571.1 or 2571.2 or 2572.1 or 51380.1)
3SALAOX	cysteinesulfinic acid oxidase	[c] : (2) 3sala + (2) h + o2 --> (2) Lcyst		Taurine and hypotaurine metabolism	
3SALATAi	3-sulfino-alanine transaminase (irreversible)	[c] : 3sala + akg + h --> 3snpyr + glu-L		Cysteine Metabolism	2805.1
3SALATAim	3-sulfino-alanine transaminase (irreversible), mitochondrial	[m] : 3sala + akg + h --> 3snpyr + glu-L		Cysteine Metabolism	2806.1
3SPYRSP	3-sulfinopyruvate hydrolase (spotaneous reaction)	[c] : 3snpyr + h2o --> h + pyr + so3		Cysteine Metabolism	
3SPYRSPm	3-sulfinopyruvate hydrolase (spotaneous reaction), mitochondrial	[m] : 3snpyr + h2o --> h + pyr + so3		Cysteine Metabolism	
41R1H2MAE12BOOX	4-[(1R)-1-Hydroxy-2-(methylamino)ethyl]-1,2-benzenediol:oxygen oxidoreductase(deaminating)(flavin-containing)	[c] : adrml + h2o + o2 --> 34dhmald + h2o2 + mma	1.4.3.4	Tyrosine metabolism	(4128.1 or 4129.1)
41R2A1H12BOOX	4-[(1R)-2-Amino-1-hydroxyethyl]-1,2-benzenediol:oxygen oxidoreductase(deaminating)(flavin-containing)	[c] : h2o + nrpphr + o2 --> 34dhmald + h2o2 + nh4	1.4.3.4	Tyrosine metabolism	(4128.1 or 4129.1)
42A12BOOX	4-(2-Aminoethyl)-1,2-benzenediol:oxygen oxidoreductase(deaminating)(flavin-containing)	[c] : dopa + h2o + o2 --> 34dhpac + h2o2 + nh4	1.4.3.6	Tyrosine metabolism	(26.1 or 314.1 or 314.2 or 8639.1 or 4128.1 or 4129.1)
4ABUTtm	4-aminobutanoate mitochondrial transport via diffusion	4abut[c] <==> 4abut[m]		Transport, Mitochondrial	
4HBZCOAFm	4-hydroxybenzoyl-CoA formation	[m] : coa + coucoa + h2o + nad --> 4hbzcoa + accoa + h + nadh		Ubiquinone Biosynthesis	
4HBZFm	4-hydroxybenzoate formation	[m] : 4hbzcoa + h2o --> 4hbz + coa + h		Ubiquinone Biosynthesis	
4HDEBRISOQUINEte	xenobiotic transport	4hdebrisoquine[e] <==> 4hdebrisoquine[c]		Transport, Extracellular	
4HGLSDm	L-4-hydroxyglutamate semialdehyde dehydrogenase, mitochondrial	[m] : 4hglusa + h2o + nad <==> e4hglu + (2) h + nadh	1.5.1.12	Arginine and Proline Metabolism	(8659.1 or 8659.2)
4HOXPACDOX(NADP)	4-Hydroxyphenylacetaldehyde:NADP+ oxidoreductase	[c] : 4hoxpacd + h2o + nadp <==> 4hphac + (2) h + nadph	1.2.1.5	Tyrosine metabolism	(220.1 or 218.1 or 221.1 or 222.1)
4MOPt2im	4-methyl-2-oxopentanoate mitochondrial transport via proton symport	4mop[c] + h[c] --> 4mop[m] + h[m]		Transport, Mitochondrial	
4MTOLBUTAMIDEte	xenobiotic transport	4mtolbutamide[e] <==> 4mtolbutamide[c]		Transport, Extracellular	
4NPHSFte	xenobiotic transport	4nphsf[e] <==> 4nphsf[c]		Transport, Extracellular	

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
4NPHSULT	4-Nitrophenol Sulfotransferase	[c] : 4nph + paps --> 4nphsf + h + pap	2.8.2.1	CYP Metabolism	(6817.1 or 6817.2 or 6817.3 or 6817.4 or 6817.5 or 6799.1 or 6799.2 or 6818.1 or 6818.2 or 6818.3)
4NPHte	xenobiotic transport	4nph[e] <==> 4nph[c]		Transport, Extracellular	
4PYRDX	4-Pyridoxal secretion	4pyrdx[c] + atp[c] + h2o[c] --> 4pyrdx[e] + adp[c] + h[c] + pi[c]		Transport, Extracellular	
5ADTSTSTERONEGLCte	glucuronidated compound transport	5adtststeroneglc[c] + atp[c] + h2o[c] --> 5adtststeroneglc[e] + adp[c] + h[c] + pi[c]		Transport, Extracellular	4363.1
5ADTSTSTERONEGLCtr	glucuronidated compound transport	5adtststeroneglc[c] <==> 5adtststeroneglc[r]		Transport, Endoplasmic Reticular	
5ADTSTSTERONESte	sulfonated testosterone transport	5adtststerones[c] <==> 5adtststerones[e]		Transport, Extracellular	
5ADTSTSTERONESULT	5alpha-Dihydrotestosterone sulfotransferase	[c] : 5adtststerone + paps --> 5adtststerones + h + pap	2.8.2.2	Steroid Metabolism	6822.1
5ADTSTSTERONEte	5 alpha dihydrotesterone transport	5adtststerone[e] <==> 5adtststerone[c]		Transport, Extracellular	
5ADTSTSTERONEtr	5 alpha dihydrotesterone intracellular transport	5adtststerone[r] <==> 5adtststerone[c]		Transport, Endoplasmic Reticular	
5AOPtm	5-Aminolevulinate mitochondrial transport	5aop[c] <==> 5aop[m]		Heme Biosynthesis	
5DHFtl	5-glutamyl-DHF transport, lysosomal	5dhf[c] --> 5dhf[l]		Transport, Lysosomal	
5FTHFt2	5-formyltetrahydrofolate transport via anion exchange	5fthf[e] + oh1[c] <==> 5fthf[c] + oh1[e]		Transport, Extracellular	(6573.1 or 6573.2)
5HLTDL	5-Hydroxy-L-tryptophan decarboxy-lyase	[c] : 5htrp + h --> co2 + srtn	4.1.1.28	Tryptophan metabolism	1644.1
5HOMEPRAZOLEte	xenobiotic transport	5homeprazole[e] <==> 5homeprazole[c]		Transport, Extracellular	
5HOXINDACTO2OX	5-Hydroxyindoleacetaldehyde:oxygen oxidoreductase	[c] : 5hoxindact + h2o + o2 --> 5hoxindoa + h + h2o2	1.2.3.1	Tryptophan metabolism	316.1
5HOXINDACTOX	5-Hydroxyindoleacetaldehyde:NAD+ oxidoreductase	[c] : 5hoxindact + h2o + nad --> 5hoxindoa + (2) h + nadh	1.2.1.3	Tryptophan metabolism	(216.1 or 8854.1 or 8854.2 or 8854.3 or 224.1 or 501.1 or 223.1)
5HOXINDACTOXm	5-Hydroxyindoleacetaldehyde:NAD+ oxidoreductase (mito)	[m] : 5hoxindact + h2o + nad --> 5hoxindoa + (2) h + nadh	1.2.1.3	Tryptophan metabolism	(219.1 or 217.1 or 8659.1 or 8659.2)
5HOXINOXDA	5-Hydroxytryptamine:oxygen oxidoreductase(deaminating)(flavin-containing)	[c] : h2o + o2 + srtn --> 5hoxindact + h2o2 + nh4	1.4.3.4	Tryptophan metabolism	(4128.1 or 4129.1)
5HTRPDOX	5-Hydroxy-L-tryptophan:oxygen 2,3-dioxygenase (indole-decyclizing)	[c] : 5htrp + o2 --> 5hoxnfkyn	1.13.11.42	Tryptophan metabolism	3620.1
5HTRPVESSEC	5-hydroxy-L-tryptophan secretion via secretory vesicle (ATP driven)	(3) 5htrp[c] + (2) atp[c] + (2) h2o[c] --> (3) 5htrp[e] + (2) adp[c] + (2) h[c] + (2) pi[c]		Transport, Extracellular	(6570.1 or 6571.1)
5HXKYNDCL	5-Hydroxykynurenamine decarboxy-lyase	[c] : 5hxkyn + h --> 5hxkynam + co2	4.1.1.28	Tryptophan metabolism	1644.1
5HXKYNOXDA	5-Hydroxykynurenamine:oxygen oxidoreductase(deaminating)(flavin-containing)	[c] : 5hxkynam + o2 --> 46dhoxquin + h2o2 + nh4	1.4.3.4	Tryptophan metabolism	(4128.1 or 4129.1)
5MTHFt	5-Methyltetrahydrofolate transport via receptor binding and protolysis	5mthf[e] <==> 5mthf[c]		Transport, Extracellular	(2348.1 or 2348.2 or 2348.3 or 2348.4 or 2348.5 or 2348.6 or 2351.1 or 2352.1)
5MTHFt2	5-methyltetrahydrofolate transport via anion exchange	5mthf[e] + oh1[c] <==> 5mthf[c] + oh1[e]		Transport, Extracellular	(6573.1 or 6573.2)
5THFtl	5-glutamyl-THF transport, lysosomal	5thf[c] --> 5thf[l]		Transport, Lysosomal	
5THFtm	5-glutamyl-THF transport,m mitochondrial	5thf[m] --> 5thf[c]		Transport, Mitochondrial	
6DHFtl	6-glutamyl-DHF transport, lysosomal	6dhf[c] --> 6dhf[l]		Transport, Lysosomal	
6DHFtm	6-glutamyl-DHF transport,m mitochondrial	6dhf[m] --> 6dhf[c]		Transport, Mitochondrial	
6HTSTSTERONEte	hydroxylated testosterone transport	6htststerone[c] <==> 6htststerone[e]		Transport, Extracellular	
6HTSTSTERONEtr	hydroxylated testosterone transport	6htststerone[c] <==> 6htststerone[r]		Transport, Endoplasmic Reticular	
6THFtl	6-glutamyl-THF transport, lysosomal	6thf[c] --> 6thf[l]		Transport, Lysosomal	
6THFtm	6-glutamyl-THF transport,m mitochondrial	6thf[m] --> 6thf[c]		Transport, Mitochondrial	
7DHCHSTEROLtr	cholesterol precursor intracellular transport	7dhchsterol[r] <==> 7dhchsterol[c]		Transport, Endoplasmic Reticular	
7DHFtl	7-glutamyl-DHF transport, lysosomal	7dhf[c] --> 7dhf[l]		Transport, Lysosomal	
7DHFtm	7-glutamyl-DHF transport,m mitochondrial	7dhf[m] --> 7dhf[c]		Transport, Mitochondrial	
7THFtl	7-glutamyl-THF transport, lysosomal	7thf[c] --> 7thf[l]		Transport, Lysosomal	
7THFtm	7-glutamyl-THF transport,m mitochondrial	7thf[m] --> 7thf[c]		Transport, Mitochondrial	
A_MANASE	alpha-mannosidase	[c] : (2) h2o + m2mn --> (2) man + mn	3.2.1.24	N-Glycan Degradation	4123.1
A_MANASEly	alpha-mannosidase, lysosomal	[l] : (2) h2o + m2mn --> (2) man + mn	3.2.1.24	N-Glycan Degradation	4125.1
A4GALTc	Lactosylceramide 4-alpha-galactosyltransferase	[c] : galgluside_hs + udpgal --> h + thcrm_hs + udp		Sphingolipid Metabolism	53947.1
A4GALTg	Lactosylceramide 4-alpha-galactosyltransferase	[g] : galgluside_hs + udpgal --> h + thcrm_hs + udp		Sphingolipid Metabolism	53947.1
A4GNT1g	alpha 1,4-N-acetylglucosaminyltransferase, Golgi apparatus	[g] : T_antigen + uacgam --> gncore1 + h + udp		O-Glycan Biosynthesis	51146.1
A4GNT2g	alpha 1,4-N-acetylglucosaminyltransferase, Golgi apparatus	[g] : core2 + uacgam --> gncore2 + h + udp		O-Glycan Biosynthesis	51146.1
AACOAT	Acetoacetyl-CoA:acetate CoA-transferase	[c] : acac + atp + coa <==> aacoa + amp + ppi	6.2.1.16	Propanoate Metabolism	65985.1
AACTOOR	Aminoacetone:oxygen oxidoreductase(deaminating)(flavin-containing)	[c] : aact + h2o + o2 --> h2o2 + mthgxl + nh4		Glycine, Serine, and Threonine Metabolism	8639.1
AACTtm	Aminoacetone transport (mitochondrial)	aact[m] --> aact[c]		Transport, Mitochondrial	
AAPSAS	AAPSAS	[c] : h + h2o + thp2c --> L2aadp6sa		Lysine Metabolism	
AASAD3	L-aminoadipate-semialdehyde dehydrogenase (NADH)	[c] : L2aadp6sa + h2o + nad --> L2aadp + (2) h + nadh	1.2.1.31	Lysine Metabolism	
AASAD3m	L-aminoadipate-semialdehyde dehydrogenase (NADH), mitochondrial	[m] : L2aadp6sa + h2o + nad --> L2aadp + (2) h + nadh	1.2.1.31	Lysine Metabolism	
AATAi	2-aminoadipate transaminase, irreversible	[c] : L2aadp + akg --> 2oxoadp + glu-L	2.6.1.39	Lysine Metabolism	(51166.1 or 51166.2)
ABO1g	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase)	[g] : fucgalacglcgalgluside_hs + udpacgal --> acgalfucgalacglcgalgluside_hs + h + udp		Blood Group Biosynthesis	28.1
ABO2g	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase)	[g] : fucgalacglcgalgluside_hs + udpgal --> galfucgalacglcgalgluside_hs + h + udp		Blood Group Biosynthesis	28.1
ABO3g	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase)	[g] : fuc12gal14acglcgalgluside_hs + udpgal --> galfuc12gal14acglcgalgluside_hs + h + udp		Blood Group Biosynthesis	28.1

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
ABO4g	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase)	[g] : fuc12gal14acglcgalgluside_hs + udpacgal --> acgalfuc12gal14acglcgalgluside_hs + h + udp		Blood Group Biosynthesis	28.1
ABO5g	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase)	[g] : fucgalacgalfuc12gal14acglcgalgluside_hs + udpacgal --> acgalfucgalacgalfuc12gal14acglcgalgluside_hs + h + udp		Blood Group Biosynthesis	28.1
ABO6g	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase)	[g] : fucgalacglcgal14acglcgalgluside_hs + udpacgal --> acgalfucgalacglcgal14acglcgalgluside_hs + h + udp		Blood Group Biosynthesis	28.1
ABO7g	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase)	[g] : fucgalacgalfucgalacglcgal14acglcgalgluside_hs + udpacgal --> acgalfucgalacgalfucgalacglcgal14acglcgalgluside_hs + h + udp		Blood Group Biosynthesis	28.1
ABO8g	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase)	[g] : fucgalacglcgal14acglcgalgluside_hs + udpgal --> galfucgalacglcgal14acglcgalgluside_hs + h + udp		Blood Group Biosynthesis	28.1
ABO9g	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase)	[g] : fucfucgalacglcgalacglcgal14acglcgalgluside_hs + (2) udpgal --> galgalfucfucgalacglcgalacglcgal14acglcgalgluside_hs + (2) h + (2) udp		Blood Group Biosynthesis	28.1
ABTArm	4-aminobutyrate transaminase, reversible (mitochondrial)	[m] : 4abut + akg <==> glu-L + sucsal	2.6.1.19	Glutamate metabolism	(18.1 or 18.2)
ABTD	L-arabinitol 4-dehydrogenase	[c] : abt + nad <==> h + nadh + xylu-L	1.1.1.12	Pentose and Glucuronate Interconversions	
ABTti	L-arabinitol transport via passive diffusion	abt[c] --> abt[e]		Transport, Extracellular	
ABUTD	Aminobutyraldehyde dehydrogenase	[c] : 4abutn + h2o + nad --> 4abut + (2) h + nadh	1.2.1.19	beta-Alanine metabolism	223.1
ABUTt2r	4-aminobutyrate reversible transport in via proton symport	4abut[e] + h[e] <==> 4abut[c] + h[c]		Transport, Extracellular	206358.1
ABUTt2rL	4-aminobutyrate reversible transport in via proton symport (lysosome)	4abut[l] + h[l] <==> 4abut[c] + h[c]		Transport, Lysosomal	206358.1
ABUTt4(2)r	4-aminobutyrate reversible transport in via sodium symport (1:2)	4abut[e] + (2) na1[e] <==> 4abut[c] + (2) na1[c]		Transport, Extracellular	(6538.1 or 6539.1 or 6540.1 or 6529.1)
ACACT1	acetyl-CoA C-acetyltransferase	[c] : (2) accoa --> aacoa + coa	2.3.1.9	Cholesterol Metabolism	39.1
ACACT10m	acetyl-CoA C-acetyltransferase, mitochondrial	[m] : 2maacoa + coa <==> accoa + ppcoa	2.3.1.9	Valine, Leucine, and Isoleucine Metabolism	38.1
ACACT1r	acetyl-CoA C-acetyltransferase	[c] : (2) accoa <==> aacoa + coa	2.3.1.9	Tryptophan metabolism	39.1
ACACT1rm	acetyl-CoA C-acetyltransferase, mitochondrial	[m] : (2) accoa <==> aacoa + coa	2.3.1.9	Tryptophan metabolism	((3032.1 and 3030.1) or 38.1)
ACACT1x	acetyl-CoA C-acetyltransferase, mitochondrial	[x] : (2) accoa --> aacoa + coa	2.3.1.9	Cholesterol Metabolism	39.1
ACACt2	acetoacetate transport via proton symport	acac[e] + h[e] <==> acac[c] + h[c]		Transport, Extracellular	(6566.1 or 9194.1)
ACACt2m	Acetoacetate mitochondrial transport via H+ symport	acac[c] + h[c] <==> acac[m] + h[m]		Transport, Mitochondrial	6566.1
ACACT4p	acetyl-CoA C-acetyltransferase (octanoyl-CoA), peroxisomal	[x] : 3odcoa + coa --> accoa + occoa	2.3.1.16	Fatty Acid Metabolism	30.1
ACACT5p	acetyl-CoA C-acyltransferase (decanoyl-CoA), peroxisomal	[x] : 3oddcoa + coa --> accoa + dcacoa	2.3.1.16	Fatty Acid Metabolism	30.1
ACACT6p	acetyl-CoA C-acetyltransferase (dodecanoyl), peroxisomal	[x] : 3otdcoa + coa --> accoa + ddcacoa	2.3.1.16	Fatty Acid Metabolism	30.1
ACACT7p	acetyl-CoA acyltransferase (tetradecanoyl-CoA), peroxisomal	[x] : 3ohdcoa + coa --> accoa + tdcoa	2.3.1.16	Fatty Acid Metabolism	30.1
ACACT8p	acetyl-CoA acyltransferase (hexadecanoyl-CoA), peroxisomal	[x] : 3ohodcoa + coa --> accoa + pmtcoa	2.3.1.16	Fatty Acid Metabolism	30.1
ACACT9p	acetyl-CoA acyltransferase (tetracosanoyl-CoA), peroxisomal	[x] : 3ohxccoa + coa --> accoa + ttccoa	2.3.1.16	Fatty Acid Metabolism	30.1
ACACtx	acetoacetate intracellular transport unknown mechanism	acac[c] <==> acac[x]		Transport, Peroxisomal	
ACALDt	acetaldehyde reversible transport	acald[e] <==> acald[c]		Transport, Extracellular	
ACALDtm	acetaldehyde mitochondrial diffusion	acald[m] <==> acald[c]		Transport, Mitochondrial	
ACALDtx	acetaldehyde peroxisomal diffusion	acald[x] <==> acald[c]		Transport, Peroxisomal	
ACCOAC	acetyl-CoA carboxylase	[c] : accoa + atp + hco3 --> adp + h + malcoa + pi	6.4.1.2	Fatty Acid Metabolism	(31.2 or 31.4 or 31.1 or 31.3 or 31.5 or (31.2 and 32.1) or (31.3 and 32.1) or (31.4 and 32.1) or (31.5 and 32.1) or (31.1 and 32.1))
ACCOACm	Acetyl-Coa carboxylase, beta isoform	[m] : accoa + atp + hco3 --> adp + h + malcoa + pi	6.4.1.2	Fatty Acid Metabolism	32.1
ACCOAgt	acetyl-coa transport	accoa[c] <==> accoa[g]		Transport, Extracellular	9197.1
ACCOAL	acetate-CoA ligase (ADP-forming)	[c] : atp + coa + ppa --> adp + pi + ppcoa	6.2.1.13	Propanoate Metabolism	(55902.1 or 55902.2)
ACCOALm	acetate-CoA ligase (AMP-forming)	[m] : atp + coa + ppa --> amp + ppcoa + ppi	6.2.1.17	Propanoate Metabolism	84532.1
ACCOAtn	acetyl-CoA transport, nuclear	accoa[c] <==> accoa[n]		Transport, Nuclear	
ACCOAtr	acetyl-coa transport	accoa[c] <==> accoa[r]		Transport, Endoplasmic Reticular	9197.1
ACETONEt2	acetone transport via proton symport	acetone[e] + h[e] <==> acetone[c] + h[c]		Transport, Extracellular	(6566.1 or 9194.1 or 9123.1)
ACETONEt2m	acetone mitochondrial transport via proton symport	acetone[c] + h[c] <==> acetone[m] + h[m]		Transport, Mitochondrial	6566.1
ACGAGBSIDEtg	acgagbside_hs intracellular transport	acgagbside_hs[c] <==> acgagbside_hs[g]		Transport, Golgi Apparatus	
ACGAGBSIDEtl	acgagbside_hs intracellular transport	acgagbside_hs[c] <==> acgagbside_hs[l]		Transport, Lysosomal	
ACGALFUCGALACGALFUC12GAL14ACGLCGALGLUSIDEte	blood group intracellular transport	acgalfucgalacgalfuc12gal14acglcgalgluside_hs[e] <==> acgalfucgalacgalfuc12gal14acglcgalgluside_hs[c]		Transport, Extracellular	
ACGALFUCGALACGALFUC12GAL14ACGLCGALGLUSIDEtg	blood group intracellular transport	acgalfucgalacgalfuc12gal14acglcgalgluside_hs[g] <==> acgalfucgalacgalfuc12gal14acglcgalgluside_hs[c]		Transport, Golgi Apparatus	
ACGALFUCGALACGALFUCGALACGLCGAL14ACGLCGALGLUSIDEte	blood group intracellular transport	acgalfucgalacgalfucgalacglcgal14acglcgalgluside_hs[e] <==> acgalfucgalacgalfucgalacglcgal14acglcgalgluside_hs[c]		Transport, Extracellular	
ACGALFUCGALACGALFUCGALACGLCGAL14ACGLCGALGLUSIDEtg	blood group intracellular transport	acgalfucgalacgalfucgalacglcgal14acglcgalgluside_hs[g] <==> acgalfucgalacgalfucgalacglcgal14acglcgalgluside_hs[c]		Transport, Golgi Apparatus	
ACGALK	N-acetylgalactosamine kinase	[c] : acgal + atp --> acgal1p + adp + h		Aminosugar Metabolism	
ACGALK2	N-acetylgalactosamine kinase (ITP)	[c] : acgal + itp --> acgal1p + h + idp		Aminosugar Metabolism	

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
ACGALtlg	N-acetyl-galactosamine intracellular transport	acgal[g] <==> acgal[c]		Transport, Golgi Apparatus	
ACGALtly	N-acetyl-galactosamine lysosomal efflux	acgal[l] --> acgal[c]		Transport, Lysosomal	
ACGAM2E	N-acetylglucosamine 2-epimerase	[c] : acgam <==> acmana	5.1.3.8	Aminosugar Metabolism	5973.1
ACGAM6PSi	N-acetylglucosamine-6-phosphate synthase	[c] : accoa + gam6p --> acgam6p + coa + h	2.3.1.4	Aminosugar Metabolism	64841.1
ACGAMK	N-acetylglucosamine kinase	[c] : acgam + atp --> acgam6p + adp + h	2.7.1.59	Aminosugar Metabolism	55577.1
ACGAMPM	phosphoacetylglucosamine mutase	[c] : acgam6p <==> acgam1p	5.4.2.3	Aminosugar Metabolism	5238.1
ACGAMtly	N-acetyl-glucosamine lysosomal efflux	acgam[l] --> acgam[c]		Transport, Lysosomal	
ACGBGBSIDEtg	acgbgbside_hs intracellular transport	acgbgbside_hs[c] <==> acgbgbside_hs[g]		Transport, Golgi Apparatus	
ACGBGBSIDEtl	acgbgbside_hs intracellular transport	acgbgbside_hs[c] <==> acgbgbside_hs[l]		Transport, Lysosomal	
ACGPID	N-acetylglucosaminylphosphatidylinositol deacetylase	[c] : acgpail_hs + h2o --> ac + gpail_hs	3.5.1.89	Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	9487.1
ACGSm	N-acteylglutamate synthase, mitochondrial	[m] : accoa + glu-L --> acglu + coa + h	2.3.1.1	Urea cycle/amino group metabolism	162417.1
ACHEe	Acetylcholinesterase	[e] : ach + h2o --> ac + chol + h	3.1.1.7	Glycerophospholipid Metabolism	(43.1 or 43.2)
ACHtn	Acetylcholin transport, nuclear trhough pores	ach[n] <==> ach[c]		Transport, Nuclear	
ACHVESSEC	Acetylcholine secretion via secretory vesicle (ATP driven)	(3) ach[c] + (2) atp[c] + (2) h2o[c] --> (3) ach[e] + (2) adp[c] + (2) h[c] + (2) pi[c]		Transport, Extracellular	6572.1
ACITL	ATP-Citrate lyase	[c] : atp + cit + coa --> accoa + adp + oaa + pi		Citric Acid Cycle	(47.1 or 47.2)
ACN13ACNGALGBSIDEte	acn13acngalgbside_hs transport	acn13acngalgbside_hs[c] <==> acn13acngalgbside_hs[e]		Transport, Extracellular	
ACN13ACNGALGBSIDEtg	acn13acngalgbside_hs intracellular transport	acn13acngalgbside_hs[c] <==> acn13acngalgbside_hs[g]		Transport, Golgi Apparatus	
ACN23ACNGALGBSIDEte	acn23acngalgbside transport	acn23acngalgbside_hs[c] <==> acn23acngalgbside_hs[e]		Transport, Extracellular	
ACN23ACNGALGBSIDEtg	acn23acngalgbside intracellular transport	acn23acngalgbside_hs[c] <==> acn23acngalgbside_hs[g]		Transport, Golgi Apparatus	
ACNACNGAL14ACGLCGALGLUSIDEte	blood group intracellular transport	acnacngal14acglcgalgluside_hs[e] <==> acnacngal14acglcgalgluside_hs[c]		Transport, Extracellular	
ACNACNGAL14ACGLCGALGLUSIDEtg	blood group intracellular transport	acnacngal14acglcgalgluside_hs[g] <==> acnacngal14acglcgalgluside_hs[c]		Transport, Golgi Apparatus	
ACNACNGALGBSIDEte	acnacngalgbside_hs transport	acnacngalgbside_hs[c] <==> acnacngalgbside_hs[e]		Transport, Extracellular	
ACNACNGALGBSIDEtg	acnacngalgbside_hs intracellular transport	acnacngalgbside_hs[c] <==> acnacngalgbside_hs[g]		Transport, Golgi Apparatus	
ACNAM9PL	N-Acetylneuraminate 9-phosphate pyruvate-lyase (pyruvate-phosphorylating)	[c] : acmanap + h2o + pep --> acnamp + pi		Aminosugar Metabolism	54187.1
ACNAM9PL2	N-Acetylneuraminate 9-phosphate pyruvate-lyase (pyruvate-phosphorylating)	[c] : h2o + man6p + pep --> kdnp + pi		Aminosugar Metabolism	54187.1
ACNAMlt	N-acetylneuraminate transport into lysososme	acnam[c] + h[c] <==> acnam[l] + h[l]		Transport, Lysosomal	26503.1
ACNAMPH	N-Acetylneuraminate 9-phosphate phosphohydrolase	[c] : acnamp + h2o --> acnam + pi	3.1.3.29	Aminosugar Metabolism	
ACNAMtn	N-acetylneuraminate nuclear import	acnam[c] --> acnam[n]		Transport, Nuclear	
ACNGALACGLCGAL14ACGLCGALGLUSIDEte	blood group intracellular transport	acngalacglcgal14acglcgalgluside_hs[e] <==> acngalacglcgal14acglcgalgluside_hs[c]		Transport, Extracellular	
ACNGALACGLCGAL14ACGLCGALGLUSIDEtg	blood group intracellular transport	acngalacglcgal14acglcgalgluside_hs[g] <==> acngalacglcgal14acglcgalgluside_hs[c]		Transport, Golgi Apparatus	
ACNMLr	N-Acetylneuraminate lyase (reversible)	[c] : acnam <==> acmana + pyr	4.1.3.3	Aminosugar Metabolism	
ACOAD10m	acyl-CoA dehydrogenase (2-methylbutanoyl-CoA), mitochondrial	[m] : 2mbcoa + fad --> 2mb2coa + fadh2	1.3.99.12	Valine, Leucine, and Isoleucine Metabolism	(36.1 or 34.1)
ACOAD1fm	acyl-CoA dehydrogenase (butanoyl-CoA), mitochondrial	[m] : btcoa + fad --> b2coa + fadh2	1.3.99.2	Butanoate Metabolism	(27034.1 or 34.1 or 36.1 or 28976.1 or 80724.1 or 84129.1 or 35.1)
ACOAD8m	acyl-CoA dehydrogenase (isovaleryl-CoA), mitochondrial	[m] : fad + ivcoa --> 3mb2coa + fadh2	1.3.99.10	Valine, Leucine, and Isoleucine Metabolism	3712.1
ACOAD9m	acyl-CoA dehydrogenase (isobutyryl-CoA), mitochondrial	[m] : fad + ibcoa --> 2mp2coa + fadh2	1.3.99.12	Valine, Leucine, and Isoleucine Metabolism	(34.1 or 27034.1)
ACOAHi	acetyl-CoA hydrolase	[c] : accoa + h2o --> ac + coa + h	3.1.2.1	Pyruvate Metabolism	134526.1
ACOAO7p	acyl-CoA oxidase (hexadecanoyl-CoA), peroxisomal	[x] : o2 + pmtcoa --> h2o2 + hdd2coa	1.3.3.6	Fatty Acid Metabolism	(51.1 or 51.2)
ACOATA	Acetyl-CoA ACP transacylase	[c] : ACP + accoa <==> acACP + coa	2.3.1.38	Fatty Acid Metabolism	2194.1
ACODA	acetylornithine deacetylase	[c] : acorn + h2o --> ac + orn	3.5.1.16	Urea cycle/amino group metabolism	95.1
ACONT	aconitase	[c] : cit <==> icit	4.2.1.3	Citric Acid Cycle	(3658.1 or 48.1)
ACONTm	Aconitate hydratase	[m] : cit <==> icit	4.2.1.3	Citric Acid Cycle	50.1
ACOX22x	acyl-Coenzyme A oxidase 2, branched chain	[x] : dhcholoylcoa + fadh2 + (0.5) o2 --> fad + thcholoylcoa	1.3.3.6	Bile Acid Biosynthesis	8309.1
ACOX2x	acyl-Coenzyme A oxidase 2, branched chain	[x] : cholcoas + fadh2 + o2 --> cholcoads + fad + (2) h2o	1.3.3.6	Bile Acid Biosynthesis	8309.1
ACP1(FMN)	acid phosphatase (FMN)	[c] : fmn + h2o --> pi + ribflv	3.1.3.2	Riboflavin Metabolism	(52.1 or 52.2 or 52.3)
ACRNtm	O-acetylcarnintine transport into mitochondria via diffusion	acrn[c] --> acrn[m]		Transport, Mitochondrial	788.1
ACS	acetyl-CoA synthetase	[c] : ac + atp + coa --> accoa + amp + ppi	6.2.1.1	Glycolysis/Gluconeogenesis	(65985.1 or 55902.1 or 55902.2)
ACS2	acetyl-CoA synthase (propionate)	[c] : atp + coa + ppa --> amp + ppcoa + ppi	6.2.1.1	Propanoate Metabolism	(55902.1 or 55902.2 or 65985.1)
ACSm	acetyl-CoA synthetase	[m] : ac + atp + coa --> accoa + amp + ppi	6.2.1.1	Glycolysis/Gluconeogenesis	84532.1
ACSOMT	S-Adenosyl-L-methionine:N-acetylserotonin O-methyltransferase	[c] : 5hoxindoa + amet --> 5moxact + ahcys + h	2.1.1.4	Tryptophan metabolism	438.1
ACSRTNMT	S-Adenosyl-L-homocysteine:N-acetylserotonin O-methyltransferase	[c] : Nacsertn + amet --> ahcys + h + melatn	2.1.1.4	Tryptophan metabolism	438.1
ACt2m	acetate mitochondrial transport via proton symport	ac[c] + h[c] <==> ac[m] + h[m]		Transport, Mitochondrial	
ACt2r	acetate reversible transport via proton symport	ac[e] + h[e] <==> ac[c] + h[c]		Transport, Extracellular	
ACtg	acetate transport, Golgi apparatus	ac[c] <==> ac[g]		Transport, Golgi Apparatus	
ACTLMO	acetol monooxygenase	[c] : acetol + h + nadph + o2 --> (2) h2o + mthgxl + nadp		Pyruvate Metabolism	1571.1
ACTNMO	acetone monooxygenase	[c] : acetone + h + nadph + o2 --> acetol + h2o + nadp		Pyruvate Metabolism	1571.1
ACYP	acylphosphatase	[c] : 13dpg + h2o --> 3pg + h + pi	3.6.1.7	Glycolysis/Gluconeogenesis	(98.1 or 97.1 or 97.2 or 112611.1)
ADA	Adenosine deaminase	[c] : adn + h + h2o --> ins + nh4	3.5.4.4	Purine Catabolism	100.1
ADAe	Adenosine deaminase, extracellular	[e] : adn + h + h2o --> ins + nh4	3.5.4.4	Nucleotides	100.1
ADCim	Acetoacetate decarboxylation (irreversible), mitochondrial	[m] : acac + h --> acetone + co2	4.1.1.4	Propanoate Metabolism	
ADEt	adenine reversible transport, cytosol	ade[e] <==> ade[c]		Transport, Extracellular	3177.1

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
ADEtl	adenine facilated transport from lysosome	ade[l] <==> ade[c]		Transport, Lysosomal	55315.1
ADHAPtx	intracellular transport (peroxisome)	adhap_hs[c] <==> adhap_hs[x]		Transport, Peroxisomal	
ADK1	adenylate kinase	[c] : amp + atp <==> (2) adp	2.7.4.3	Nucleotides	(203.1 or 26289.2 or 26289.1 or 122481.1)
ADK1m	adenylate kinase, mitochondrial	[m] : amp + atp <==> (2) adp	2.7.4.3	Nucleotides	(205.1 or 205.2 or 205.3 or 204.1 or 204.2 or 204.3)
ADK3	adentylate kinase (GTP)	[c] : amp + gtp <==> adp + gdp		Nucleotides	(26289.1 or 26289.2)
ADK3m	adentylate kinase (GTP)	[m] : amp + gtp <==> adp + gdp		Nucleotides	50808.1
ADKd	adenylate kinase (d form)	[c] : damp + datp <==> (2) dadp	2.7.4.3	Nucleotides	(26289.2 or 26289.1)
ADMDC	adenosylmethionine decarboxylase	[c] : amet + h --> ametam + co2	4.1.1.50	Arginine and Proline Metabolism	262.1
ADNCYC	adenylate cyclase	[c] : atp --> camp + ppi	4.6.1.1	Nucleotides	(107.1 or 108.1 or 109.1 or 196883.1 or 111.1 or 112.1 or 112.2 or 113.1 or 114.1 or 115.1 or 55811.1)
ADNK1	adenosine kinase	[c] : adn + atp --> adp + amp + h	2.7.1.20	Nucleotides	(132.1 or 132.2)
ADNK1m	adenosine kinase, mitochondrial	[m] : adn + atp --> adp + amp + h	2.7.1.20	Nucleotides	
ADNt	adenosine facilated transport in cytosol	adn[e] <==> adn[c]		Transport, Extracellular	(3177.1 or 2030.1)
ADNt4	adenosine transport (Na/Adn cotransport)	adn[e] + na1[e] --> adn[c] + na1[c]		Transport, Extracellular	(9154.1 or 9153.1 or 64078.1 or 9154.2)
ADNt5	adenosine transport (1:2 Na/Adn cotransport)	adn[e] + (2) na1[e] --> adn[c] + (2) na1[c]		Transport, Extracellular	64078.1
ADNtl	adenosine facilated transport from lysosome	adn[l] <==> adn[c]		Transport, Lysosomal	55315.1
ADNtm	adenosine facilated transport in mitochondria	adn[c] <==> adn[m]		Transport, Mitochondrial	2030.1
ADPGLC	ADPglucose diphosphatase	[c] : adpglc + h2o --> amp + g1p + (2) h	3.6.1.21	Nucleotides	11164.1
ADPMAN	ADPmannose diphosphatase	[c] : adpman + h2o --> amp + (2) h + man1p	3.6.1.21	Nucleotides	11164.1
ADPRDP	ADPribose diphosphatase	[c] : adprib + h2o --> amp + (2) h + r5p	3.6.1.13	Nucleotides	11164.1
ADPRDPm	ADPribose diphosphatase (mitochondrial)	[m] : adprib + h2o --> amp + (2) h + r5p	3.6.1.13	Nucleotides	(53343.1 or 53343.2 or 53343.3)
ADPRIBt	ADPribose transport	adprib[e] --> adprib[c]		Transport, Extracellular	952.1
ADPT	adenine phosphoribosyltransferase	[c] : ade + prpp --> amp + ppi	2.4.2.7	Salvage Pathway	353.1
ADPtx	ADP transporter, peroxisomal	adp[c] <==> adp[x]		Transport, Peroxisomal	
ADRNCOAtx	fatty acid intracellular transport	adrncoa[c] <==> adrncoa[x]		Transport, Peroxisomal	
ADRNCPT1	carnitine O-palmitoyltransferase	[c] : adrncoa + crn --> adrncrn + coa	2.3.1.21	Carnitine shuttle	(1375.4 or 1374.1 or 126129.1 or 1375.3 or 1375.2 or 1375.1)
ADRNCPT2	carnitine transferase	[m] : adrncrn + coa --> adrncoa + crn		Carnitine shuttle	1376.1
ADRNCRNt	transport into the mitochondria (carnitine)	adrncrn[c] --> adrncrn[m]		Carnitine shuttle	(788.1 or 788.1)
ADRNLPVESSEC	Adrenaline secretion via secretory vesicle (ATP driven)	(3) adrnl[c] + (2) atp[c] + (2) h2o[c] --> (2) adp[c] + (3) adrnl[e] + (2) h[c] + (2) pi[c]		Transport, Extracellular	(6570.1 or 6571.1)
ADRNt	fatty acid transport via diffusion	adrn[e] <==> adrn[c]		Transport, Extracellular	
ADSELK	adenylyl-selenate kinase	[c] : adsel + atp --> 3padsel + adp + h	2.7.1.25	Selenoamino acid metabolism	(9061.1 or 9060.1)
ADSK	adenylyl-sulfate kinase	[c] : aps + atp --> adp + h + paps	2.7.1.25	Nucleotides	(9060.1 or 9061.1)
ADSL1	adenylosuccinate lyase	[c] : dcamp --> amp + fum	4.3.2.2	Nucleotides	(158.1 or 158.2)
ADSL2	adenylosuccinate lyase	[c] : 25aics --> aicar + fum	4.3.2.2	IMP Biosynthesis	(158.1 or 158.2)
ADSS	adenylosuccinate synthase	[c] : asp-L + gtp + imp --> dcamp + gdp + (2) h + pi	6.3.4.4	Nucleotides	(159.1 or 122622.2 or 122622.1)
AFLATOXINte	xenobiotic transport	aflatoxin[e] <==> aflatoxin[c]		Transport, Extracellular	
AG13T10g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	[g] : ksi_pre18 + uacgam --> h + ksi_pre19 + udp	2.4.1.149	Keratan sulfate biosynthesis	(374907.2 or 374907.1 or 10678.1 or 10678.2 or 79369.1 or 11041.1 or 93010.1 or 284208.1 or 10331.1)
AG13T11g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	[g] : ksi_pre21 + uacgam --> h + ksi_pre22 + udp	2.4.1.149	Keratan sulfate biosynthesis	(374907.2 or 374907.1 or 10678.1 or 10678.2 or 79369.1 or 11041.1 or 93010.1 or 284208.1 or 10331.1)
AG13T12g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	[g] : ksi_pre24 + uacgam --> h + ksi_pre25 + udp	2.4.1.149	Keratan sulfate biosynthesis	(374907.2 or 374907.1 or 10678.1 or 10678.2 or 79369.1 or 11041.1 or 93010.1 or 284208.1 or 10331.1)
AG13T13g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	[g] : ksi_pre27 + uacgam --> h + ksi_pre28 + udp	2.4.1.149	Keratan sulfate biosynthesis	(374907.2 or 374907.1 or 10678.1 or 10678.2 or 79369.1 or 11041.1 or 93010.1 or 284208.1 or 10331.1)
AG13T14g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	[g] : ksi_pre30 + uacgam --> h + ksi_pre31 + udp	2.4.1.149	Keratan sulfate biosynthesis	(374907.2 or 374907.1 or 10678.1 or 10678.2 or 79369.1 or 11041.1 or 93010.1 or 284208.1 or 10331.1)
AG13T15g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	[g] : ksi_pre33 + uacgam --> h + ksi_pre34 + udp	2.4.1.149	Keratan sulfate biosynthesis	(374907.2 or 374907.1 or 10678.1 or 10678.2 or 79369.1 or 11041.1 or 93010.1 or 284208.1 or 10331.1)

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
AG13T16g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	[g] : ksii_core4_pre2 + uacgam --> h + ksii_core4_pre3 + udp	2.4.1.149	Keratan sulfate biosynthesis	(374907.2 or 374907.1 or 10678.1 or 10678.2 or 10331.1 or 79369.1 or 11041.1 or 93010.1 or 284208.1)
AG13T17g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	[g] : ksii_core4_pre4 + uacgam --> h + ksii_core4_pre5 + udp	2.4.1.149	Keratan sulfate biosynthesis	(284208.1 or 93010.1 or 11041.1 or 79369.1 or 10331.1 or 10678.2 or 10678.1 or 374907.1 or 374907.2)
AG13T18g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	[g] : ksii_core4_pre7 + uacgam --> h + ksii_core4_pre8 + udp	2.4.1.149	Keratan sulfate biosynthesis	(284208.1 or 93010.1 or 11041.1 or 79369.1 or 10331.1 or 10678.2 or 10678.1 or 374907.1 or 374907.2)
AG13T1g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	[g] : ksii_core2_pre2 + uacgam --> h + ksii_core2_pre3 + udp	2.4.1.149	Keratan sulfate biosynthesis	(10331.1 or 374907.2 or 374907.1 or 10678.1 or 10678.2 or 79369.1 or 11041.1 or 93010.1 or 284208.1)
AG13T2g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	[g] : ksii_core2_pre4 + uacgam --> h + ksii_core2_pre5 + udp	2.4.1.149	Keratan sulfate biosynthesis	(10331.1 or 374907.2 or 374907.1 or 10678.1 or 10678.2 or 79369.1 or 11041.1 or 93010.1 or 284208.1)
AG13T3g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	[g] : ksii_core2_pre7 + uacgam --> h + ksii_core2_pre8 + udp	2.4.1.149	Keratan sulfate biosynthesis	(10678.2 or 79369.1 or 11041.1 or 93010.1 or 284208.1 or 10331.1 or 374907.2 or 374907.1 or 10678.1)
AG13T4g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	[g] : ksi_pre1 + uacgam --> h + ksi_pre2 + udp	2.4.1.149	Keratan sulfate biosynthesis	(374907.2 or 374907.1 or 10678.1 or 10678.2 or 79369.1 or 11041.1 or 93010.1 or 284208.1 or 10331.1)
AG13T5g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	[g] : ksi_pre3 + uacgam --> h + ksi_pre4 + udp	2.4.1.149	Keratan sulfate biosynthesis	(374907.2 or 374907.1 or 10678.1 or 10678.2 or 79369.1 or 11041.1 or 93010.1 or 284208.1 or 10331.1)
AG13T6g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	[g] : ksi_pre6 + uacgam --> h + ksi_pre7 + udp	2.4.1.149	Keratan sulfate biosynthesis	(374907.2 or 374907.1 or 10678.1 or 10678.2 or 79369.1 or 11041.1 or 93010.1 or 284208.1 or 10331.1)
AG13T7g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	[g] : ksi_pre9 + uacgam --> h + ksi_pre10 + udp	2.4.1.149	Keratan sulfate biosynthesis	(374907.2 or 374907.1 or 10678.1 or 10678.2 or 79369.1 or 11041.1 or 93010.1 or 284208.1 or 10331.1)
AG13T8g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	[g] : ksi_pre12 + uacgam --> h + ksi_pre13 + udp	2.4.1.149	Keratan sulfate biosynthesis	(374907.2 or 374907.1 or 10678.1 or 10678.2 or 79369.1 or 11041.1 or 93010.1 or 284208.1 or 10331.1)
AG13T9g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	[g] : ksi_pre15 + uacgam --> h + ksi_pre16 + udp	2.4.1.149	Keratan sulfate biosynthesis	(374907.2 or 374907.1 or 10678.1 or 10678.2 or 79369.1 or 11041.1 or 93010.1 or 284208.1 or 10331.1)
AGDC	N-acetylglucosamine-6-phosphate deacetylase	[c] : acgam6p + h2o --> ac + gam6p	3.5.1.25	Aminosugar Metabolism	51005.1
AGLPC	alkyl acylglycerol phosphocholine transferase	[c] : ak2g_hs + cdpchol --> ak2gchol_hs + cmp + h + h2o		Glycerophospholipid Metabolism	
AGLPED	alkyl acyl glycerophosphoethanolamine desaturase	[c] : ak2gpe_hs + h + nadph + o2 --> dak2gpe_hs + (2) h2o + nadp		Glycerophospholipid Metabolism	
AGLPET	alkyl acylglycerol phosphoethanolamine transferase	[c] : ak2g_hs + cdpea + h --> ak2gpe_hs + cmp + h2o		Glycerophospholipid Metabolism	
AGLPH	alkyl glycerol phosphate hydrolase	[c] : ak2gp_hs + h2o --> ak2g_hs + pi		Glycerophospholipid Metabolism	
AGLPR	alkyl glycerol phosphate reductase	[c] : akdhap_hs + h + nadph --> akgp_hs + nadp		Glycerophospholipid Metabolism	
AGLPT	alkyl glycerol phosphate acyltransferase	[c] : Rtotal2 + akgp_hs + h --> ak2gp_hs + h2o		Glycerophospholipid Metabolism	
AGMTm	agmatinase (m)	[m] : agm + h2o --> ptrc + urea	3.5.3.11	Arginine and Proline Metabolism	79814.1
AGPAT1	1-acylglycerol-3-phosphate O-acyltransferase 1	[c] : Rtotal2coa + alpa_hs --> coa + pa_hs	2.3.1.51	Triacylglycerol Synthesis	(56895.1 or 55326.1 or 56894.2 or 137964.1 or 10554.1 or 10555.1 or 56894.1)
AGPex	alkyl glycerol phosphate transport	akdhap_hs[c] <==> akdhap_hs[x]		Transport, Peroxisomal	

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
AGPRim	N-acetyl-g-glutamyl-phosphate reductase, irreversible, mitochondrial	[m] : acg5p + h + nadph --> acg5sa + nadp + pi	1.2.1.38	Urea cycle/amino group metabolism	5832.1
AGPSx	alkylglycerone phosphate synthase	[x] : adhap_hs + alkylR1oh --> Rtotal + akdhap_hs + h	2.5.1.26	Glycerophospholipid Metabolism	8540.1
AGTim	alanine-glyoxylate transaminase (irreversible), mitochondrial	[m] : ala-L + glx --> gly + pyr	2.6.1.44	Alanine and Aspartate Metabolism	(64902.1 or 64850.1)
AGTix	alanine-glyoxylate transaminase (irreversible), (peroxisomal)	[x] : ala-L + glx --> gly + pyr	2.6.1.44	Alanine and Aspartate Metabolism	189.1
AHANDROSTANGLCte	glucuronidated compound transport	ahandrostanglc[c] + atp[c] + h2o[c] --> adp[c] + ahandrostanglc[e] + h[c] + pi[c]		Transport, Extracellular	4363.1
AHANDROSTANGLCtr	glucuronidated compound transport	ahandrostanglc[c] <==> ahandrostanglc[r]		Transport, Endoplasmic Reticular	
AHC	adenosylhomocysteinase	[c] : ahcys + h2o <==> adn + hcys-L	3.3.1.1	Methionine Metabolism	(191.1 or 10768.1 or 10768.2)
AHCYStn	S-adenosyl-L-homocysteine nuclear transport	ahcys[c] <==> ahcys[n]		Transport, Nuclear	
AHCYStr	S-Adenosyl-L-homocysteine intracellular diffusion	ahcys[c] <==> ahcys[r]		Transport, Endoplasmic Reticular	
AHEXASE2ly	beta-N-acetylhexosaminidase, lysosomal	[l] : (3) h2o + n2m2nmn --> (3) acgam + m2mn	3.2.1.52	N-Glycan Degradation	(3074.1 or (3074.1 and 3073.1) or 3073.1)
AHEXASEly	beta-N-acetylhexosaminidase, lysosomal	[l] : (2) h2o + n2m2mn --> (2) acgam + m2mn	3.2.1.52	N-Glycan Degradation	(3073.1 or (3074.1 and 3073.1) or 3074.1)
AICART	phosphoribosylaminoimidazolecarboxamide formyltransferase	[c] : 10fthf + aicar <==> fprica + thf	2.1.2.3	IMP Biosynthesis	471.1
AIRCr	phosphoribosylaminoimidazole carboxylase	[c] : air + co2 <==> 5aizc + h	4.1.1.21	IMP Biosynthesis	10606.1
AKGDm	2-oxoglutarate dehydrogenase	[m] : akg + coa + nad --> co2 + nadh + succoa	1.2.4.2	Citric Acid Cycle	((4967.1 and (8050.1 and 1738.1) and 1743.1) or ((8050.1 and 1738.1) and 1743.1 and 4967.2))
AKGMALtm	alpha-ketoglutarate/malate transporter	akg[m] + mal-L[c] <==> akg[c] + mal-L[m]		Transport, Mitochondrial	8402.1
AKGt4_3	AKG transport via sodium symport	akg[e] + (3) na1[e] <==> akg[c] + (3) na1[c]		Transport, Extracellular	(64849.1 or 64849.2)
AKGtp	AKG transporter, peroxisome	akg[c] <==> akg[x]		Transport, Peroxisomal	
AKR1C1	aldo-keto reductase family 1, member C1 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihydrodiol dehydrogenase 4)	[c] : h + nadph + prgstrn --> aprgstrn + nadp		Steroid Metabolism	1645.1
AKR1C41	aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihydrodiol dehydrogenase 4)	[c] : h + nadh + xol7ah --> nad + xol7ah2	1.1.1.50	Bile Acid Biosynthesis	1109.1
AKR1C42	aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihydrodiol dehydrogenase 4)	[c] : h + nadh + xoldioloneh --> nad + xoltriol	1.1.1.50	Bile Acid Biosynthesis	1109.1
AKR1D	aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase)	[c] : h + nadph + xol7aone --> nadp + xol7ah		Bile Acid Biosynthesis	6718.1
AKR1D2	aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase)	[c] : h + nadph + xoldiolone --> nadp + xoldioloneh		Bile Acid Biosynthesis	6718.1
ALAASNNaEx	L-alanine/L-asparagine Na-dependent exchange (Ala-L in)	ala-L[e] + asn-L[c] + na1[e] --> ala-L[c] + asn-L[e] + na1[c]		Transport, Extracellular	6510.1
ALACYSNaEx	L-alanine/L-cysteine Na-dependent exchange (Ala-L in)	ala-L[e] + cys-L[c] + na1[e] --> ala-L[c] + cys-L[e] + na1[c]		Transport, Extracellular	(6509.1 or 6510.1)
ALADGLNexR	L-alanine/glutamine reversible exchange	ala-D[e] + gln-L[c] <==> ala-D[c] + gln-L[e]		Transport, Extracellular	(6520.1 and 56301.1)
ALADGLYexR	D-alanine/glycine reversible exchange	ala-D[e] + gly[c] <==> ala-D[c] + gly[e]		Transport, Extracellular	(6520.1 and 56301.1)
ALAGLNexR	L-alanine/glutamine reversible exchange	ala-L[e] + gln-L[c] <==> ala-L[c] + gln-L[e]		Transport, Extracellular	(56301.1 and 6520.1)
ALAGLNNaEx	L-alanine/L-glutamine Na-dependent exchange (Ala-L in)	ala-L[e] + gln-L[c] + na1[e] --> ala-L[c] + gln-L[e] + na1[c]		Transport, Extracellular	6510.1
ALAGLYexR	L-alanine/glycine reversible exchange	ala-L[e] + gly[c] <==> ala-L[c] + gly[e]		Transport, Extracellular	(6520.1 and 56301.1)
ALAR	alanine racemase	[c] : ala-L <==> ala-D	5.1.1.1	Alanine and Aspartate Metabolism	11212.1
ALASERNaEx	L-alanine/L-serine Na-dependent exchange (Ala-L in)	ala-L[e] + na1[e] + ser-L[c] --> ala-L[c] + na1[c] + ser-L[e]		Transport, Extracellular	(6509.1 or 6510.1)
ALASm	5-aminolevulinate synthase	[m] : gly + h + succoa --> 5aop + co2 + coa	2.3.1.37	Glycine, Serine, and Threonine Metabolism	(23464.1 or 211.1 or 211.2 or 212.1)
ALAt2r	L-alanine reversible transport via proton symport	ala-L[e] + h[e] <==> ala-L[c] + h[c]		Transport, Extracellular	206358.1
ALAt2rL	L-alanine reversible transport via proton symport (lysosome)	ala-L[l] + h[l] <==> ala-L[c] + h[c]		Transport, Lysosomal	206358.1
ALAt4	Alanine-Sodium symporter	ala-L[e] + na1[e] --> ala-L[c] + na1[c]		Transport, Extracellular	(11254.1 or 55089.1 or 54407.1 or 81539.1 or 6541.1 or 6542.1 or 84889.1)
ALATA_L	L-alanine transaminase	[c] : akg + ala-L <==> glu-L + pyr	2.6.1.2	Glutamate metabolism	(2875.1 or 84706.1)
ALATHRNaEx	L-alanine/L-threonine Na-dependent exchange (Ala-L in)	ala-L[e] + na1[e] + thr-L[c] --> ala-L[c] + na1[c] + thr-L[e]		Transport, Extracellular	(6509.1 or 6510.1)
ALAtN1	Alanine transport (Na, H coupled)	ala-L[e] + h[c] + (2) na1[e] <==> ala-L[c] + h[e] + (2) na1[c]		Transport, Extracellular	(92745.1 or 10991.1)
ALCD1	alcohol dehydrogenase (methanol)	[c] : meoh + nad <==> fald + h + nadh		Miscellaneous	(124.1 or (124.1 and 125.1) or (124.1 and 126.1) or (126.1 and 125.1) or 126.1 or 131.1 or 128.1 or 284273.1 or 125.1 or 127.1 or 130.1 or 137872.1 or 284273.2)
ALCD21_D	alcohol dehydrogenase (D-1,2-propanediol)	[c] : 12ppd-R + nad --> h + lald-D + nadh		Pyruvate Metabolism	(125.1 or (126.1 and 125.1) or 126.1 or 127.1 or 128.1 or 130.1 or 131.1 or 137872.1 or 124.1 or 284273.1 or 284273.2 or (124.1 and 125.1) or (124.1 and 126.1))

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
ALCD21_L	alcohol dehydrogenase (L-1,2-propanediol)	[c] : 12ppd-S + nad --> h + lald-L + nadh		Pyruvate Metabolism	((124.1 and 125.1) or (124.1 and 126.1) or 124.1 or 137872.1 or 131.1 or 130.1 or 128.1 or 127.1 or 126.1 or (126.1 and 125.1) or 125.1 or 284273.2 or 284273.1)
ALCD22_D	alcohol dehydrogenase (D-lactaldehyde)	[c] : lald-D + nad --> h + mthgxl + nadh		Pyruvate Metabolism	(124.1 or (124.1 and 125.1) or (124.1 and 126.1) or 125.1 or (126.1 and 125.1) or 126.1 or 127.1 or 128.1 or 130.1 or 131.1 or 137872.1 or 284273.1 or 284273.2)
ALCD22_L	alcohol dehydrogenase (L-lactaldehyde)	[c] : lald-L + nad --> h + mthgxl + nadh		Pyruvate Metabolism	(124.1 or (124.1 and 125.1) or (124.1 and 126.1) or 125.1 or (126.1 and 125.1) or 126.1 or 127.1 or 128.1 or 130.1 or 131.1 or 137872.1 or 284273.1 or 284273.2)
ALCD2if	alcohol dehydrogenase, forward rxn (ethanol -> acetaldehyde)	[c] : etoh + nad --> acald + h + nadh	1.1.1.1	Glycolysis/Gluconeogenesis	(124.1 or 125.1 or 126.1 or (124.1 and 125.1) or 126.1 or (124.1 and 126.1) or (126.1 and 125.1) or 127.1 or 128.1 or 130.1 or 131.1 or 137872.1 or 284273.1 or 284273.2)
ALCD2yf	alcohol dehydrogenase (ethanol, NADP), forward reaction	[c] : etoh + nadp --> acald + h + nadph	1.1.1.2	Glycolysis/Gluconeogenesis	(10327.1 or 10327.2)
ALDD19x	aldehyde dehydrogenase (phenylacetaldehyde, NAD)	[c] : h2o + nad + pacald --> (2) h + nadh + pac	1.2.1.39	Phenylalanine metabolism	(218.1 or 220.1 or 221.1 or 222.1)
ALDD19x(P)	aldehyde dehydrogenase (phenylacetaldehyde, NADP)	[c] : h2o + nadp + pacald --> (2) h + nadph + pac	1.2.1.39	Phenylalanine metabolism	(218.1 or 220.1 or 221.1 or 222.1)
ALDD20x	aldehyde dehydrogenase (indole-3-acetaldehyde, NAD)	[c] : h2o + id3acald + nad --> (2) h + ind3ac + nadh		Tryptophan metabolism	(223.1 or 501.1 or 224.1 or 8854.1 or 8854.2 or 8854.3 or 216.1)
ALDD20xm	aldehyde dehydrogenase (indole-3-acetaldehyde, NAD), mitochondrial	[m] : h2o + id3acald + nad --> (2) h + ind3ac + nadh		Tryptophan metabolism	(8659.1 or 8659.2 or 217.1 or 219.1)
ALDD21	aldehyde dehydrogenase (pristanal, NAD)	[c] : h2o + nad + pristanal --> (2) h + nadh + prist		Fatty Acid Metabolism	224.1
ALDD2x	aldehyde dehydrogenase (acetaldehyde, NAD)	[c] : acald + h2o + nad --> ac + (2) h + nadh	1.2.1.3	Glycolysis/Gluconeogenesis	(216.1 or 8854.1 or 8854.2 or 8854.3 or 220.1 or 218.1 or 224.1 or 221.1 or 222.1 or 223.1 or 501.1)
ALDD2xm	aldehyde dehydrogenase (acetylaldehyde, NAD), mitochondrial	[m] : acald + h2o + nad --> ac + (2) h + nadh	1.2.1.3	Glycolysis/Gluconeogenesis	(219.1 or 217.1)
ALDD2y	aldehyde dehydrogenase (acetaldehyde, NADP)	[c] : acald + h2o + nadp --> ac + (2) h + nadph	1.2.1.4	Glycolysis/Gluconeogenesis	(8854.1 or 8854.2 or 8854.3 or 218.1 or 224.1 or 221.1 or 222.1 or 223.1)
ALDSTRNte	aldosterone transport	aldstrn[c] <==> aldstrn[e]		Transport, Extracellular	
ALDSTRNtm	aldosterone intracellular transport	aldstrn[c] <==> aldstrn[m]		Transport, Mitochondrial	
ALKP	alkaline phosphatase	[c] : dhap + h2o --> dha + pi	3.1.3.1	Glycerophospholipid Metabolism	(251.1 or 250.1 or 249.1 or 248.1)
ALOX12	Arachidonate 12-lipoxygenase	[c] : arachd + o2 --> 12HPET	1.13.11.31	Eicosanoid Metabolism	239.1
ALOX12R	Arachidonate 12-lipoxygenase R	[c] : arachd + o2 --> 12RHPET	1.13.11.31	Eicosanoid Metabolism	242.1
ALOX15	Arachidonate 15-lipoxygenase	[c] : arachd + o2 --> 15HPET	1.13.11.33	Eicosanoid Metabolism	(247.1 or 246.1)
ALOX5	Arachidonate 5-lipoxygenase	[c] : arachd + o2 --> 5HPET	1.13.11.34	Eicosanoid Metabolism	240.1
ALOX52	Arachidonate 5-lipoxygenase	[c] : 5HPET --> h2o + leuktrA4		Eicosanoid Metabolism	240.1
ALR	Aldose reductase	[c] : h2o + mthgxl + nadp --> (2) h + nadph + pyr	1.1.1.2	Glycine, Serine, and Threonine Metabolism	231.1
ALR2	aldose reductase (methylglyoxal)	[c] : h + mthgxl + nadph --> acetol + nadp		Pyruvate Metabolism	(8574.1 or 231.1 or 10327.1 or 10327.2)
ALR3	aldose reductase (acetol)	[c] : acetol + h + nadph --> 12ppd-S + nadp		Pyruvate Metabolism	(8574.1 or 231.1 or 10327.1 or 10327.2)
AM6SAD	aminomuconate-semialdehyde dehydrogenase	[c] : am6sa + h2o + nad --> amuco + (2) h + nadh	1.2.1.32	Tryptophan metabolism	
AMACR2p	alpha-methylacyl-CoA racemase (reductase)	[x] : dhcholestancoa + (0.5) o2 --> dhcholoylcoa + h2o	5.1.99.4	Bile Acid Biosynthesis	(23600.1 or 23600.2)
AMACR2r	alpha-methylacyl-CoA racemase (reductase)	[r] : dhcholestancoa + (0.5) o2 --> dhcholoylcoa + h2o	5.1.99.4	Bile Acid Biosynthesis	(23600.1 or 23600.2)
AMACRp	alpha-methylacyl-CoA racemase	[x] : cholcoar --> cholcoas	5.1.99.4	Bile Acid Biosynthesis	(23600.1 or 23600.2)
AMACRr	alpha-methylacyl-CoA racemase	[r] : cholcoar --> cholcoas	5.1.99.4	Bile Acid Biosynthesis	(23600.1 or 23600.2)
AMANK	N-acetyl-D-mannosamine kinase	[c] : acmana + atp --> acmanap + adp + h	2.7.1.60	Aminosugar Metabolism	(10020.1 or 55577.1)
AMCOXO	2-aminomuconate reductase	[c] : amuco + h + h2o + nadph --> 2oxoadp + nadp + nh4		Tryptophan metabolism	
AMETr	S-Adenosyl-L-methionine intracellular diffusion	amet[c] <==> amet[r]		Transport, Endoplasmic Reticular	
AMETt2m	S-Adenosyl-L-methionine reversible transport, mitochondrial	ahcys[m] + amet[c] <==> ahcys[c] + amet[m]		Transport, Mitochondrial	(115286.3 or 115286.1 or 115286.2)

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
AMETtn	S-adenosyl-L-methionine nuclear transport	amet[c] <==> amet[n]		Transport, Nuclear	
AMPDA	Adenosine monophosphate deaminase	[c] : amp + h + h2o --> imp + nh4		Nucleotides	(270.1 or 272.1 or 271.1 or 271.2 or 271.3)
AMPTASECG	alanyl aminopeptidase (cys-gly)	[c] : cgly + h2o --> cys-L + gly	3.4.11.2	Glutathione Metabolism	290.1
AMPTASECGe	alanyl aminopeptidase (cys-gly) (e)	[e] : cgly + h2o --> cys-L + gly	3.4.11.2	Glutathione Metabolism	290.1
AMPtp	AMP transporter, peroxisome	amp[c] <==> amp[x]		Transport, Peroxisomal	
AMPtr	AMP transporter, endoplasmic reticulum	amp[c] <==> amp[r]		Transport, Endoplasmic Reticular	
AMY1e	alpha-amylase, extracellular (strch1 -> strch2)	[e] : (8) h2o + strch1 --> (8) glc-D + strch2	3.2.1.1	Starch and Sucrose Metabolism	(276.1 or 276.2 or 277.1 or 278.1 or 279.1 or 280.1 or (6519.1 and 11136.1) or 6520.1)
AMY2e	alpha-amylase, extracellular (glygn2 -> glygn4)	[e] : glygn2 + (8) h2o --> (8) glc-D + glygn4	3.2.1.1	Starch and Sucrose Metabolism	(276.1 or 276.2 or 277.1 or 278.1 or 279.1 or 280.1 or (6519.1 and 11136.1) or 6520.1)
ANDRSTRNGLCte	glucuronidated compound transport	andrstrnglc[c] + atp[c] + h2o[c] --> adp[c] + andrstrnglc[e] + h[c] + pi[c]		Transport, Extracellular	4363.1
ANDRSTRNte	androsterone transport	andrstrn[e] <==> andrstrn[c]		Transport, Extracellular	
ANDRSTRNtr	androsterone intracellular transport	andrstrn[r] <==> andrstrn[c]		Transport, Endoplasmic Reticular	
ANTIPYRENEte	xenobiotic transport	antipyrene[e] <==> antipyrene[c]		Transport, Extracellular	
AOBUTDsm	L-2-amino-3-oxobutanoate decarboxylation, mitochondrial	[m] : 2aobut + h --> aact + co2		Glycine, Serine, and Threonine Metabolism	
AP4AH1	Ap4A hydrolase, asymmetrically	[c] : ap4a + h2o --> amp + atp + (2) h	3.6.1.17	Nucleotides	(318.1 or 318.2 or 318.3)
APAT2rm	3-Aminopropanoate:2-oxoglutarate aminotransferase (m)	[m] : akg + ala-B <==> glu-L + msa	2.6.1.19	beta-Alanine metabolism	(18.1 or 18.2)
APNNOXte	xenobiotic transport	apnnox[e] <==> apnnox[c]		Transport, Extracellular	
APOCF	Apocarboxylase formation	[c] : apoC + lys-L --> apoC-Lys + h + h2o		Biotin Metabolism	
APOCFm	Apocarboxylase formation, mitochondrial	[m] : apoC + lys-L --> apoC-Lys + h + h2o		Biotin Metabolism	
APOC-LYS-BTNP	proteolysis of apoC-Lys-btn	[c] : apoC-Lys_btn + h2o --> apoC + biocyt		Biotin Metabolism	
APOC-LYS-BTNPm	proteolysis of apoC-Lys-btn, mitochondrial	[m] : apoC-Lys_btn + h2o --> apoC + biocyt		Biotin Metabolism	
APPNNte	xenobiotic transport	appnn[e] <==> appnn[c]		Transport, Extracellular	
APRGSTRNte	hydroxyprogesterone transport	aprgstrn[e] <==> aprgstrn[c]		Transport, Extracellular	
APRTO2	N-acetylputrescine: oxygen oxireductase (deaminating)	[c] : aprut + h2o + o2 --> h2o2 + n4abutn + nh4	1.4.3.4	Arginine and Proline Metabolism	(4128.1 or 4129.1)
AQCOBALt	Aquacob(III)alamin uptake	aqcobal[e] --> aqcobal[c]		Transport, Extracellular	
ARAB-Lt	L-arabinoase extracellular transport	arab-L[e] <==> arab-L[c]		Transport, Extracellular	
ARABR	arabinose reductase	[c] : arab-L + h + nadph --> abt + nadp	1.1.1.21	Pentose and Glucuronate Interconversions	(231.1 or 10327.1 or 10327.2 or 8574.1)
ARACHCOAtx	fatty acid intracellular transport	arachcoa[c] <==> arachcoa[x]		Transport, Peroxisomal	
ARACHCPT1	carnitine transferase	[c] : arachcoa + crn --> arachcrn + coa	2.3.1.21	Carnitine shuttle	(1375.4 or 1374.1 or 126129.1 or 1375.3 or 1375.2 or 1375.1)
ARACHCPT2	carnitine transferase	[m] : arachcrn + coa --> arachcoa + crn		Carnitine shuttle	1376.1
ARACHCRNt	transport into the mitochondria (carnitine)	arachcrn[c] --> arachcrn[m]		Carnitine shuttle	788.1
ARACHDCOAtx	fatty acid intracellular transport	arachdcoa[c] <==> arachdcoa[x]		Transport, Peroxisomal	
ARACHDt2	fatty acid transport via diffusion	arachd[e] <==> arachd[c]		Transport, Extracellular	
ARACHDtr	intracellular transport	arachd[c] <==> arachd[r]		Transport, Endoplasmic Reticular	
ARACHt	fatty acid transport via diffusion	arach[e] <==> arach[c]		Transport, Extracellular	
ARGDCm	arginine decarboxylase (m)	[m] : arg-L + h --> agm + co2	4.1.1.19	Arginine and Proline Metabolism	113451.1
ARGLYSex	Arginine/Lysine exchanger (Arg in)	arg-L[e] + lys-L[c] --> arg-L[c] + lys-L[e]		Transport, Extracellular	(6520.1 and 9057.1)
ARGN	arginase	[c] : arg-L + h2o --> orn + urea	3.5.3.1	Urea cycle/amino group metabolism	383.1
ARGNm	arginase (m)	[m] : arg-L + h2o --> orn + urea	3.5.3.1	Urea cycle/amino group metabolism	384.1
ARGSL	argininosuccinate lyase	[c] : argsuc <==> arg-L + fum	4.3.2.1	Alanine and Aspartate Metabolism	435.1
ARGSS	argininosuccinate synthase	[c] : asp-L + atp + citr-L --> amp + argsuc + h + ppi	6.3.4.5	Alanine and Aspartate Metabolism	(445.1 or 445.2)
ARGt4	L-arginine transport in via sodium symport	arg-L[e] + na1[e] --> arg-L[c] + na1[c]		Transport, Extracellular	11254.1
ARGtiDF	L-arginine transport via diffusion (extracellular to cytosol)	arg-L[e] --> arg-L[c]		Transport, Extracellular	(55089.1 or 6541.1 or 6542.1 or 84889.1)
ARGtm	arginine mitochondrial transport via ornithine carrier	arg-L[c] + h[m] <==> arg-L[m] + h[c]		Transport, Mitochondrial	(83884.1 or 10166.1)
ARSA	Arylsulfatase A	[l] : h2o + sgalside_hs --> galside_hs + h + so4	3.1.6.8	Sphingolipid Metabolism	410.1
ARTCOAL1	R group coenzyme a ligase	[c] : Rtotal + coa <==> Rtotalcoa		R Group Synthesis	
ARTCOAL2	R group coenzyme a ligase	[c] : Rtotal2 + coa <==> Rtotal2coa		R Group Synthesis	
ARTCOAL3	R group coenzyme a ligase	[c] : Rtotal3 + coa <==> Rtotal3coa		R Group Synthesis	
ARTFR11	R group artificial flux	[c] : pmtcoa --> R1coa_hs		R Group Synthesis	
ARTFR12	R group artificial flux (C16:1)	fadh2[m] + hdcoa[c] --> R1coa_hs[c] + fad[m]		R Group Synthesis	
ARTFR13	R group artificial flux	[c] : tdcoa --> (0.875) R1coa_hs		R Group Synthesis	
ARTFR202	R group artificial flux (C18:3, n-3)	(2) fadh2[m] + h[m] + lnlncacoa[c] + nadph[m] --> (1.125) R2coa_hs[c] + (2) fad[m] + nadp[m]		R Group Synthesis	
ARTFR203	R group artificial flux	(2) fadh2[m] + h[m] + lnlncgcoa[c] + nadph[m] --> (1.125) R2coa_hs[c] + (2) fad[m] + nadp[m]		R Group Synthesis	
ARTFR204	R group artificial flux	(2) fadh2[m] + (2) h[m] + (2) nadph[m] + strdnccoa[c] --> (1.125) R2coa_hs[c] + (2) fad[m] + (2) nadp[m]		R Group Synthesis	
ARTFR205	R group artificial flux	dlnlcgcoa[c] + (2) fadh2[m] + h[m] + nadph[m] --> (1.25) R2coa_hs[c] + (2) fad[m] + nadp[m]		R Group Synthesis	
ARTFR206	R group artificial flux	arachdcoa[c] + (2) fadh2[m] + (2) h[m] + (2) nadph[m] --> (1.25) R2coa_hs[c] + (2) fad[m] + (2) nadp[m]		R Group Synthesis	
ARTFR207	R group artificial flux	[c] : arachcoa --> (1.25) R2coa_hs		R Group Synthesis	
ARTFR208	R group artificial flux	(3) fadh2[m] + (2) h[m] + (2) nadph[m] + tmndnccoa[c] --> (1.25) R2coa_hs[c] + (3) fad[m] + (2) nadp[m]		R Group Synthesis	
ARTFR209	R group artificial flux	adrncoa[c] + (2) fadh2[m] + (2) h[m] + (2) nadph[m] --> (1.375) R2coa_hs[c] + (2) fad[m] + (2) nadp[m]		R Group Synthesis	
ARTFR210	R group artificial flux	fadh2[m] + h[m] + lnlccoa[c] + nadph[m] --> (1.125) R2coa_hs[c] + fad[m] + nadp[m]		R Group Synthesis	
ARTFR211	R group artificial flux	clpndcoa[c] + (3) fadh2[m] + (2) h[m] + (2) nadph[m] --> (1.375) R2coa_hs[c] + (3) fad[m] + (2) nadp[m]		R Group Synthesis	
ARTFR212	R group artificial flux	dcsptn1coa[c] + (3) fadh2[m] + (2) h[m] + (2) nadph[m] --> (1.375) R2coa_hs[c] + (3) fad[m] + (2) nadp[m]		R Group Synthesis	
ARTFR213	R group artificial flux	c226coa[c] + (3) fadh2[m] + (3) h[m] + (3) nadph[m] --> (1.375) R2coa_hs[c] + (3) fad[m] + (3) nadp[m]		R Group Synthesis	
ARTFR31	R group artificial flux	[c] : stcoa --> (1.125) R3coa_hs		R Group Synthesis	

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
ARTFR32	R group artificial flux	fadh2[m] + odecoa[c] --> (1.125) R3coa_hs[c] + fad[m]		R Group Synthesis	
ARTFR33	R group artificial flux	fadh2[m] + vacccoa[c] --> (1.125) R3coa_hs[c] + fad[m]		R Group Synthesis	
ARTFR34	R group artificial flux	(2) fadh2[m] + lneldccoa[c] --> (1.125) R3coa_hs[c] + (2) fad[m]		R Group Synthesis	
ARTFR41	R group artificial flux	fadh2[m] + hdcoa[c] --> R4coa_hs[c] + fad[m]		R Group Synthesis	
ARTFR42	R group artificial flux	fadh2[m] + odecoa[c] --> (1.125) R4coa_hs[c] + fad[m]		R Group Synthesis	
ARTFR43	R group artificial flux	fadh2[m] + vacccoa[c] --> (1.125) R4coa_hs[c] + fad[m]		R Group Synthesis	
ARTFR44	R group artificial flux	(2) fadh2[m] + lneldccoa[c] --> (1.125) R4coa_hs[c] + (2) fad[m]		R Group Synthesis	
ARTFR45	R group artificial flux	fadh2[m] + nrvnccoa[c] --> (1.5) R4coa_hs[c] + fad[m]		R Group Synthesis	
ARTFR46	R group artificial flux	fadh2[m] + od2coa[c] --> (1.125) R4coa_hs[c] + fad[m]		R Group Synthesis	
ARTFR51	R group artificial flux	[c] : lgnccoa --> (1.5) R5coa_hs		R Group Synthesis	
ARTFR52	R group artificial flux	[c] : hexccoa --> (1.625) R5coa_hs		R Group Synthesis	
ARTFR53	R group artificial flux	eicostetcoa[c] + (2) fadh2[m] + (2) h[m] + (2) nadph[m] --> (1.25) R5coa_hs[c] + (2) fad[m] + (2) nadp[m]		R Group Synthesis	
ARTFR54	R group artificial flux	(3) fadh2[m] + (2) h[m] + (2) nadph[m] + tetpent6coa[c] --> (1.5) R5coa_hs[c] + (3) fad[m] + (2) nadp[m]		R Group Synthesis	
ARTFR55	R group artificial flux	(3) fadh2[m] + (2) h[m] + (2) nadph[m] + tetpent3coa[c] --> (1.5) R5coa_hs[c] + (3) fad[m] + (2) nadp[m]		R Group Synthesis	
ARTFR56	R group artificial flux	(2) fadh2[m] + (2) h[m] + (2) nadph[m] + tettet6coa[c] --> (1.5) R5coa_hs[c] + (2) fad[m] + (2) nadp[m]		R Group Synthesis	
ARTFR57	R group artificial flux	(3) fadh2[m] + (3) h[m] + (3) nadph[m] + tethex3coa[c] --> (1.5) R5coa_hs[c] + (3) fad[m] + (3) nadp[m]		R Group Synthesis	
ARTFR61	R group artificial flux	fadh2[m] + hdd2coa[c] --> R6coa_hs[c] + fad[m]		R Group Synthesis	
ARTPLM1	R group to palmitate conversion	[c] : Rtotalcoa <==> pmtcoa		R Group Synthesis	
ARTPLM1m	R group to palmitate conversion	[m] : Rtotalcoa <==> pmtcoa		R Group Synthesis	
ARTPLM2	R group to palmitate conversion	[c] : Rtotal2coa <==> pmtcoa		R Group Synthesis	
ARTPLM2m	R group to palmitate conversion	[m] : Rtotal2coa <==> pmtcoa		R Group Synthesis	
ARTPLM3	R group to palmitate conversion	[c] : Rtotal3coa <==> pmtcoa		R Group Synthesis	
ARTPLM3m	R group to palmitate conversion	[m] : Rtotal3coa <==> pmtcoa		R Group Synthesis	
ASAH1	N-acylsphingosine amidohydrolase	[l] : crm_hs + h2o --> Rtotal + sphings	3.5.1.23	Sphingolipid Metabolism	(427.1 or 427.2)
ASCBOX	ascorbic acid oxidase	[c] : ascb-L + (2) h + (2) o2s --> dhdascb + (2) h2o2		Ascorbate and Aldarate Metabolism	
ASCBt	L-ascorbate transport via facilitated diffusion	ascb-L[e] <==> ascb-L[c]		Transport, Extracellular	
ASCBt4	L-ascorbate transport via proton symport	ascb-L[e] + na1[e] <==> ascb-L[c] + na1[c]		Transport, Extracellular	(9963.1 or 9963.2 or 9962.1 or 9962.2)
ASNALANaEx	L-alanine/L-asparagine Na-dependent exchange (Asn-L in)	ala-L[c] + asn-L[e] + na1[e] --> ala-L[e] + asn-L[c] + na1[c]		Transport, Extracellular	6510.1
ASNCYSNaEx	L-cysteine/L-asparagine Na-dependent exchange (Asn-L in)	asn-L[e] + cys-L[c] + na1[e] --> asn-L[c] + cys-L[e] + na1[c]		Transport, Extracellular	6510.1
ASNGLNNaEx	L-glutamine/L-asparagine Na-dependent exchange (Asn-L in)	asn-L[e] + gln-L[c] + na1[e] --> asn-L[c] + gln-L[e] + na1[c]		Transport, Extracellular	6510.1
ASNNm	L-asparaginase (mitochondrial)	[m] : asn-L + h2o --> asp-L + nh4	3.5.1.1	Alanine and Aspartate Metabolism	80150.1
ASNS1	asparagine synthase (glutamine-hydrolysing)	[c] : asp-L + atp + gln-L + h2o --> amp + asn-L + glu-L + h + ppi	6.3.5.4	Alanine and Aspartate Metabolism	(440.1 or 440.2 or 440.3)
ASNSERNaEx	L-serine/L-asparagine Na-dependent exchange (Asn-L in)	asn-L[e] + na1[e] + ser-L[c] --> asn-L[c] + na1[c] + ser-L[e]		Transport, Extracellular	6510.1
ASNt4	L-asparagine transport in via sodium symport	asn-L[e] + na1[e] --> asn-L[c] + na1[c]		Transport, Extracellular	(11254.1 or 55089.1 or 54407.1 or 81539.1)
ASNTHRNaEx	L-threonine/L-asparagine Na-dependent exchange (Asn-L in)	asn-L[e] + na1[e] + thr-L[c] --> asn-L[c] + na1[c] + thr-L[e]		Transport, Extracellular	6510.1
ASNtm	L-asparagine transport, mitochondrial	asn-L[c] --> asn-L[m]		Transport, Mitochondrial	
ASNtN1	Asparagine transport (Na, H coupled)	asn-L[e] + h[c] + (2) na1[e] <==> asn-L[c] + h[e] + (2) na1[c]		Transport, Extracellular	(92745.1 or 10991.1)
ASP1DC	aspartate 1-decarboxylase	[c] : asp-L + h --> ala-B + co2	4.1.1.11	beta-Alanine metabolism	(2571.1 or 2571.2)
ASPCTr	aspartate carbamoyltransferase (reversible)	[c] : asp-L + cbp <==> cbasp + h + pi	2.1.3.2	Pyrimidine Biosynthesis	790.1
ASPDt6	D-aspartate transport via Na, H symport and K antiport	asp-D[e] + h[e] + k[c] + (3) na1[e] --> asp-D[c] + h[c] + k[e] + (3) na1[c]		Transport, Extracellular	(6505.1 or 6506.1 or 6507.1 or 6511.1 or 6512.1)
ASPDxt	D-aspartate transport, peroxisomal	asp-D[x] <==> asp-D[c]		Transport, Peroxisomal	
ASPGLUm	aspartate-glutamate mitochondrial shuttle	asp-L[m] + glu-L[c] + h[c] <==> asp-L[c] + glu-L[m] + h[m]		Transport, Mitochondrial	(8604.1 or 10165.1)
ASPNATm	aspartate N-acetyltransferase, mitochondrial	[m] : accoa + asp-L --> Nacasp + coa + h	2.3.1.17	Alanine and Aspartate Metabolism	
ASPt6	L-aspartate transport via Na, H symport and K antiport	asp-L[e] + h[e] + k[c] + (3) na1[e] --> asp-L[c] + h[c] + k[e] + (3) na1[c]		Transport, Extracellular	(6505.1 or 6506.1 or 6507.1 or 6511.1 or 6512.1)
ASPTA	aspartate transaminase	[c] : akg + asp-L <==> glu-L + oaa	2.6.1.1	Alanine and Aspartate Metabolism	2805.1
ASPTAm	aspartate transaminase	[m] : akg + asp-L <==> glu-L + oaa	2.6.1.1	Alanine and Aspartate Metabolism	2806.1
ATP1ter	ADP/ATP transporter, endoplasmic reticulum	adp[r] + atp[c] <==> adp[c] + atp[r]		Transport, Endoplasmic Reticular	
ATP2ter	AMP/ATP transporter, endoplasmic reticulum	amp[r] + atp[c] <==> amp[c] + atp[r]		Transport, Endoplasmic Reticular	
ATPasel	V-type ATPase, H+ transporting, lysosomal	atp[c] + (3) h[c] + h2o[c] --> adp[c] + (4) h[l] + pi[c]	3.6.3.14	Transport, Lysosomal	
ATPH1e	ATP diphosphohydrolase	[e] : atp + (2) h2o --> amp + (2) h + (2) pi	3.6.1.5	Nucleotides	(953.1 or 955.1 or 956.1 or 954.2 or 957.1 or 954.1)
ATPH2e	ATP diphosphohydrolase	[e] : adp + h2o --> amp + h + pi	3.6.1.5	Nucleotides	(953.1 or 955.1 or 956.1 or 954.1 or 957.1 or 954.2)
ATPS4m	ATP synthase (four protons for one ATP)	adp[m] + (4) h[c] + pi[m] --> atp[m] + (3) h[m] + h2o[m]	3.6.3.14	Oxidative Phosphorylation	
ATPtm	ADP/ATP transporter, mitochondrial	adp[c] + atp[m] --> adp[m] + atp[c]		Transport, Mitochondrial	(291.1 or 292.1 or 293.1)
ATPtn	ATP diffusion in nucleus	atp[c] <==> atp[n]		Transport, Nuclear	
ATPtx	ATP transporter, peroxisomal	atp[c] <==> atp[x]		Transport, Peroxisomal	
AVITE1t	alpha-Tocopherol (Vit. E) transport	avite1[e] --> avite1[c]		Transport, Extracellular	
AVITE2t	alpha-tocotrienol (Vit. E) transport	avite2[e] --> avite2[c]		Transport, Extracellular	
B_MANNASEly	beta-mannosidase, lysosomal	[l] : h2o + mn --> acgam + man	3.2.1.25	N-Glycan Degradation	4126.1

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
B3GALT3g	Beta-1,3-galactosyltransferase 3	[g] : thcrm_hs + udpacgal --> gbside_hs + h + udp	2.4.1.79	Sphingolipid Metabolism	(8706.1 or 8706.2 or 8706.3 or 8706.4)
B3GALT41g	Beta-1,3-galactosyltransferase 4	[g] : ga2_hs + udpgal --> ga1_hs + h + udp	2.4.1.62	Sphingolipid Metabolism	8705.1
B3GALT42g	Beta-1,3-galactosyltransferase 4	[g] : gm2_hs + udpgal --> gm1_hs + h + udp	2.4.1.62	Sphingolipid Metabolism	8705.1
B3GALT43g	Beta-1,3-galactosyltransferase 4	[g] : gd2_hs + udpgal --> gd1b_hs + h + udp	2.4.1.62	Sphingolipid Metabolism	8705.1
B3GALT44g	Beta-1,3-galactosyltransferase 4	[g] : gt2_hs + udpgal --> gt1c_hs + h + udp	2.4.1.62	Sphingolipid Metabolism	8705.1
B3GALT5g	Beta-1,3-galactosyltransferase 5	[g] : gbside_hs + udpgal --> galgbside_hs + h + udp		Sphingolipid Metabolism	(10317.1 or 10317.2 or 10317.3 or 10317.4 or 10317.5)
B3GALTg	Beta galactosyltransferase	[g] : acglcgalgluside_hs + udpgal --> galacglcgalgluside_hs + h + udp	2.4.1.86	Blood Group Biosynthesis	
B3GNT11g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1	[g] : gal14acglcgalgluside_hs + uacgam --> acglcgal14acglcgalgluside_hs + h + udp		Blood Group Biosynthesis	10678.1
B3GNT12g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1	[g] : galacglcgal14acglcgalgluside_hs + uacgam --> acglc13galacglcgal14acglcgalgluside_hs + h + udp		Blood Group Biosynthesis	(10678.1 or 10678.2)
B3GNT310g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus	[g] : acglcgalgluside_hs + udpgal --> gal14acglcgalgluside_hs + h + udp		Blood Group Biosynthesis	10331.1
B3GNT311g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus	[g] : acgalfuc12gal14acglcgalgluside_hs + udpgal --> galacgalfuc12gal14acglcgalgluside_hs + h + udp		Blood Group Biosynthesis	10331.1
B3GNT312g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus	[g] : acglcgal14acglcgalgluside_hs + udpgal --> galacglcgal14acglcgalgluside_hs + h + udp		Blood Group Biosynthesis	10331.1
B3GNT313g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus	[g] : acgalfucgalacglcgal14acglcgalgluside_hs + udpgal --> galacgalfucgalacglcgal14acglcgalgluside_hs + h + udp		Blood Group Biosynthesis	10331.1
B3GNT314g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus	[g] : acglcgalacglcgal14acglcgalgluside_hs + udpgal --> galacglcgalacglcgal14acglcgalgluside_hs + h + udp		Blood Group Biosynthesis	10331.1
B3GNT315g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus	[g] : acglc13galacglcgal14acglcgalgluside_hs + udpgal --> galacglc13galacglcgal14acglcgalgluside_hs + h + udp		Blood Group Biosynthesis	10331.1
B3GNT31g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus	[g] : thcrm_hs + udpgal --> galthcrm_hs + h + udp		Sphingolipid Metabolism	10331.1
B3GNT32g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus	[g] : galthcrm_hs + udpgal --> galgalthcrm_hs + h + udp		Sphingolipid Metabolism	10331.1
B3GNT33g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus	[g] : galgalthcrm_hs + udpgal --> galgalgalthcrm_hs + h + udp		Sphingolipid Metabolism	10331.1
B3GNT34g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus	[g] : galgbside_hs + uacgam --> acglcgalgbside_hs + h + udp		Sphingolipid Metabolism	10331.1
B3GNT35g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus	[g] : acglcgalgbside_hs + udpgal --> galacglcgalgbside_hs + h + udp		Sphingolipid Metabolism	10331.1
B3GNT36g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus	[g] : acgal + gbside_hs --> acgbgbside_hs + h2o		Sphingolipid Metabolism	10331.1
B3GNT37g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus	[g] : gm2a_hs + udpgal --> gm1a_hs + h + udp		Sphingolipid Metabolism	10331.1
B3GNT38g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus	[g] : galside_hs + udpgal --> digalside_hs + h + udp		Sphingolipid Metabolism	10331.1
B3GNT39g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus	[g] : gluside_hs + udpgal --> galgluside_hs + h + udp		Sphingolipid Metabolism	10331.1
B3GNT51g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5	[g] : galgluside_hs + uacgam --> acglcgalgluside_hs + h + udp		Blood Group Biosynthesis	84002.1
BAAT1x	bile acid Coenzyme A: amino acid N-acyltransferase	[x] : cholcoa + gly --> coa + gchola	2.3.1.65	Bile Acid Biosynthesis	570.1
BAAT2x	bile acid Coenzyme A: amino acid N-acyltransferase	[x] : cholcoa + taur --> coa + tchola	2.3.1.65	Bile Acid Biosynthesis	570.1
BAAT3x	bile acid Coenzyme A: amino acid N-acyltransferase	[x] : dgcholcoa + gly --> coa + dgchol	2.3.1.65	Bile Acid Biosynthesis	570.1
BAAT4x	bile acid Coenzyme A: amino acid N-acyltransferase	[x] : dcholcoa + gly --> coa + gdchola	2.3.1.65	Bile Acid Biosynthesis	570.1
BAAT5x	bile acid Coenzyme A: amino acid N-acyltransferase	[x] : dcholcoa + taur --> coa + tdchola	2.3.1.65	Bile Acid Biosynthesis	570.1
BACCL	biotin-[acetyl-CoA-carboxylase] ligase	[c] : atp + btn + h --> btamp + ppi	6.3.4.15	Biotin Metabolism	3141.1
BACCLm	biotin-[acetyl-CoA-carboxylase] ligase, mitochondria	[m] : atp + btn + h --> btamp + ppi	6.3.4.15	Biotin Metabolism	3141.1
BALAtmr	Beta-alanine reversible mitochondrial transport (diffusion)	ala-B[c] <==> ala-B[m]		Transport, Mitochondrial	
BALAVECSEC	B-alanine secretion via secretory vesicle (ATP driven	(3) ala-B[c] + atp[c] + h2o[c] --> adp[c] + (3) ala-B[e] + h[c] + pi[c]		Transport, Extracellular	140679.1
BAMPPALDOX	beta-Aminopropion aldehyde:NAD+ oxidoreductase	[c] : bamppald + h2o + nad --> ala-B + (2) h + nadh	1.2.1.3	beta-Alanine metabolism	(216.1 or 223.1 or 224.1 or 501.1 or 8854.1 or 8854.2 or 8854.3)
BAMPPALDOXm	beta-Aminopropion aldehyde:NAD+ oxidoreductase (m)	[m] : bamppald + h2o + nad --> ala-B + (2) h + nadh	1.2.1.3	beta-Alanine metabolism	(217.1 or 219.1 or 8659.1 or 8659.2)
BBHOX	4-Trimethylammoniobutanoate,2-oxoglutarate:oxygen oxidoreductase (3-hydroxylating)	[c] : 4tmeabutn + akg + o2 --> co2 + crn + succ		Lysine Metabolism	8424.1
BCDO	beta-Carotene dioxygenase	[c] : caro + o2 --> (2) retinal	1.14.99.36	Vitamin A Metabolism	53630.1
BDG2HCGHD	beta-D-Glucosyl-2-coumarinate glucohydrolase	[c] : bdg2hc + h2o --> 2coum + glc-D + h	3.2.1.21	Stilbene, coumarine and lignin biosynthesis	57733.1
BDHm	(R)-3-Hydroxybutanoate:NAD+ oxidoreductase	[m] : bhb + nad <==> acac + h + nadh	1.1.1.30	Butanoate Metabolism	(622.2 or 622.1 or 622.3)
BDMT_L	GDPmannose:chitobiosyldiphosphodolichol beta-D-mannosyltransferase (liver)	[c] : (0.1) chito2pdol_L + gdpmann --> gdp + h + (0.1) mpdol_L	2.4.1.142	N-Glycan Biosynthesis	56052.1
BDMT_U	GDPmannose:chitobiosyldiphosphodolichol beta-D-mannosyltransferase (uterus)	[c] : (0.1) chito2pdol_U + gdpmann --> gdp + h + (0.1) mpdol_U	2.4.1.142	N-Glycan Biosynthesis	56052.1
BETALDHx	betaine-aldehyde dehydrogenase	[c] : betald + h2o + nad --> glyb + (2) h + nadh	1.2.1.8	Glycine, Serine, and Threonine Metabolism	223.1
BETALDHxm	betaine-aldehyde dehydrogenase, mitochondrial	[m] : betald + h2o + nad --> glyb + (2) h + nadh	1.2.1.8	Glycine, Serine, and Threonine Metabolism	

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
BHBt	(R)-3-Hydroxybutanoate transport via H+ symport	bhb[e] + h[e] <==> bhb[c] + h[c]		Transport, Extracellular	
BHBtm	(R)-3-Hydroxybutanoate mitochondrial transport via H+ symport	bhb[c] + h[c] <==> bhb[m] + h[m]		Transport, Mitochondrial	
BHMT	betaine-homocysteine S-methyltransferase	[c] : glyb + hcys-L --> dmgly + met-L	2.1.1.5	Glycine, Serine, and Threonine Metabolism	(23743.1 or 635.1)
BILDGLCURt	bilirubin beta-diglucuronide transport via bicarbonate countertransport	bildglcur[e] + hco3[c] <==> bildglcur[c] + hco3[e]		Transport, Extracellular	10599.1
BILDGLCURte	bilirubin beta-diglucuronide transport MDR	atp[c] + bildglcur[c] + h2o[c] <==> adp[c] + bildglcur[e] + h[c] + pi[c]		Transport, Extracellular	4363.1
BILDGLCURtr	glucuronidated compound transport	bildglcur[c] <==> bildglcur[r]		Transport, Endoplasmic Reticular	
BILGLCURt	bilirubin monoglucuronide transport via bicarbonate countertransport	bilglcur[e] + hco3[c] <==> bilglcur[c] + hco3[e]		Transport, Extracellular	(10599.1 or 28234.1)
BILGLCURte	bilirubin monoglucuronide transport MDR	atp[c] + bilglcur[c] + h2o[c] <==> adp[c] + bilglcur[e] + h[c] + pi[c]		Transport, Extracellular	4363.1
BILGLCURtr	glucuronidated compound transport	bilglcur[c] <==> bilglcur[r]		Transport, Endoplasmic Reticular	
BILIRED	Nad(p)h biliverdin reductase	[c] : biliverd + h + nadph --> bilirub + nadp	1.3.1.24	Heme Degradation	(645.1 or 644.1)
BILIRUBt2	bilirubin transport via bicarbonate countertransport	bilirub[e] + hco3[c] <==> bilirub[c] + hco3[e]		Transport, Extracellular	10599.1
BILIRUBtr	lipid, flip-flop intracellular transport	bilirub[c] <==> bilirub[r]		Transport, Endoplasmic Reticular	
BIOCYTtn	biocytin transport, nuclear	biocyt[c] <==> biocyt[n]		Transport, Nuclear	
BMTer_L	B mannosyltransferase, endoplasmic reticulum	[r] : (0.1) dolmanp_L + memgacpail_hs --> (0.1) dolp_L + h + m2emgacpail_hs		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	9488.1
BMTer_U	B mannosyltransferase, endoplasmic reticulum	[r] : (0.1) dolmanp_U + memgacpail_hs --> (0.1) dolp_U + h + m2emgacpail_hs		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	9488.1
BPNT	3',5'-bisphosphate nucleotidase	[c] : h2o + pap --> amp + pi	3.1.3.7	Nucleotides	10380.1
BPNT2	3',5'-bisphosphate nucleotidase (paps)	[c] : h2o + paps --> aps + pi	3.1.3.7	Nucleotides	10380.1
BTND1	biotinidase (biotin)	[c] : biocyt + h2o --> btn + lys-L	3.5.1.12	Biotin Metabolism	686.1
BTND1n	biotinidase (biotin), nuclear	[n] : biocyt + h2o --> btn + lys-L	3.5.1.12	Biotin Metabolism	686.1
BTNDe	biotinidase (biotin), extracellular	[e] : biocyt + h2o --> btn + lys-L	3.5.1.12	Biotin Metabolism	686.1
BTNDm	biotinidase (biotin), mitochondrial	[m] : biocyt + h2o --> btn + lys-L	3.5.1.12	Biotin Metabolism	686.1
BTNPL	holocarboxylase synthestase (biotin protein ligase)	[c] : apoC-Lys + btamp --> amp + apoC-Lys_btn + h		Biotin Metabolism	3141.1
BTNPLm	holocarboxylase synthestase (biotin protein ligase), mitochondrial	[m] : apoC-Lys + btamp --> amp + apoC-Lys_btn + h		Biotin Metabolism	3141.1
BTNt2	Biotin reversible transport via proton symport	btn[e] + h[e] <==> btn[c] + h[c]		Transport, Extracellular	6566.1
BTNt2m	Biotin reversible transport via proton symport, mitochondria	btn[c] + h[c] <==> btn[m] + h[m]		Transport, Mitochondrial	6566.1
BTNt3i	Biotin transport via sodium symport	atp[c] + btn[e] + h2o[c] + (2) na1[e] --> adp[c] + btn[c] + h[c] + (2) na1[c] + pi[c]		Transport, Extracellular	8884.1
BTNt4i	Biotin uptake (antiport)	btn[e] + h[c] --> btn[c] + h[e]		Transport, Extracellular	80704.1
BTNtn	Biotin transport, nuclear	btn[c] <==> btn[n]		Transport, Nuclear	
BUP2	beta-ureidopropionase (D-3-amino-isobutanoate forming)	[c] : 3uib + (2) h + h2o --> 3aib-D + co2 + nh4	3.5.1.6	Pyrimidine Catabolism	51733.1
BUTt2m	Butyrate mitochondrial transport via proton symport, reversible	but[c] + h[c] <==> but[m] + h[m]		Transport, Mitochondrial	6566.1
BUTt2r	Butyrate transport via proton symport, reversible	but[e] + h[e] <==> but[c] + h[c]		Transport, Extracellular	6566.1
BVITEt	beta-Tocopherol (Vit. E) transport	bvite[e] --> bvite[c]		Transport, Extracellular	
BZt	benzoate transport (diffusion)	bz[e] <==> bz[c]		Transport, Extracellular	
BZtr	Benzene transporter, endoplasmic reticulum	bz[c] <==> bz[r]		Transport, Endoplasmic Reticular	
C110CPT2m	C110 transport into the mitochondria	[m] : coa + dmnoncrn --> crn + dmnoncoa		Fatty Acid Metabolism	
C14STRr	C-14 sterol reductase	[r] : 44mctr + h + nadph --> 44mzym + nadp	1.3.1.70	Cholesterol Metabolism	7108.1
C160CPT1	carnitine O-palmitoyltransferase	[c] : crn + pmtcoa --> coa + pmtcrn	2.3.1.21	Carnitine shuttle	(1375.1 or 1374.1 or 1375.2 or 1375.3 or 1375.4 or 126129.1)
C160CPT2	C160 transport into the mitochondria	[m] : coa + pmtcrn --> crn + pmtcoa		Carnitine shuttle	1376.1
C160CRNt	C160 transport into the mitochondria	pmtcrn[c] --> pmtcrn[m]		Carnitine shuttle	788.1
C161CPT1	carnitine O-palmitoyltransferase	[c] : crn + hdcoa --> coa + hdcecrn	2.3.1.21	Carnitine shuttle	(1375.4 or 1374.1 or 126129.1 or 1375.3 or 1375.2 or 1375.1)
C161CPT12	carnitine O-palmitoyltransferase	[c] : crn + hdd2coa --> coa + hdd2crn	2.3.1.21	Carnitine shuttle	(1375.1 or 1374.1 or 1375.2 or 1375.3 or 1375.4 or 126129.1)
C161CPT2	C161 transport into the mitochondria	[m] : coa + hdcecrn --> crn + hdcoa		Carnitine shuttle	1376.1
C161CPT22	C161 transport into the mitochondria	[m] : coa + hdd2crn --> crn + hdd2coa		Carnitine shuttle	1376.1
C161CRN2t	C161 transport into the mitochondria	hdd2crn[c] --> hdd2crn[m]		Carnitine shuttle	788.1
C161CRNt	C161 transport into the mitochondria	hdcecrn[c] --> hdcecrn[m]		Carnitine shuttle	788.1
C180CPT1	carnitine O-stearoyl transferase	[c] : crn + stcoa --> coa + stcrn	2.3.1.21	Carnitine shuttle	(126129.1 or 1374.1 or 1375.1 or 1375.2 or 1375.3 or 1375.4)
C180CPT2	carnitine O-stearoyl transferase	[m] : coa + stcrn --> crn + stcoa		Carnitine shuttle	1376.1
C180CRNt	C180 transport into the mitochondria	stcrn[c] --> stcrn[m]		Carnitine shuttle	788.1
C181CPT1	carnitine octadecenoyl transferase	[c] : crn + odecoa --> coa + odecrn	2.3.1.21	Carnitine shuttle	(1374.1 or 1375.1 or 1375.2 or 1375.3 or 1375.4 or 126129.1)
C181CPT2	carnitine octadecenoyl transferase	[m] : coa + odecrn --> crn + odecoa		Carnitine shuttle	1376.1
C181CRNt	C181 transport into the mitochondria	odecrn[c] --> odecrn[m]		Carnitine shuttle	788.1
C204CPT1	carnitine C20:4 transferase	[c] : arachdcoa + crn --> arachdcrn + coa	2.3.1.21	Carnitine shuttle	(1374.1 or 1375.1 or 1375.2 or 1375.3 or 1375.4 or 126129.1)
C204CPT2	arachidonic acid transport into the mitochondria	[m] : arachdcrn + coa --> arachdcoa + crn		Carnitine shuttle	1376.1
C204CRNt	arachidonic acid transport into the mitochondria	arachdcrn[c] --> arachdcrn[m]		Carnitine shuttle	
C226COAtx	fatty acid intracellular transport	c226coa[c] <==> c226coa[x]		Transport, Peroxisomal	
C226CPT1	carnitine C22:6 transferase	[c] : c226coa + crn --> c226crn + coa	2.3.1.21	Carnitine shuttle	(1374.1 or 1375.1 or 1375.2 or 1375.3 or 1375.4 or 126129.1)
C226CPT2	C226 transport into the mitochondria	[m] : c226crn + coa --> c226coa + crn		Carnitine shuttle	1376.1
C226CRNt	C226 transport into the mitochondria	c226crn[c] --> c226crn[m]		Carnitine shuttle	
C2M26DCOAHLm	cis-2-Methyl-5-isopropylhexa-2,5-dienoyl-CoA hydro lyase (m)	[m] : c2m26dcoa + h2o <==> 3h26dm5coa	4.2.1.17	Limonene and pinene degradation	((3030.1 and 3032.1) or 549.1)
C2M26DCOAHLx	cis-2-Methyl-5-isopropylhexa-2,5-dienoyl-CoA hydro lyase (x)	[x] : c2m26dcoa + h2o <==> 3h26dm5coa	4.2.1.17	Limonene and pinene degradation	(1891.1 or 1962.1)
C3STDH1Pr	C-3 sterol dehydrogenase (4-methylzymosterol)	[r] : 4mzym_int1 + nadp --> 4mzym_int2 + co2 + h + nadph	5.3.3.1	Cholesterol Metabolism	50814.1

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
C3STDH1r	C-3 sterol dehydrogenase (4-methylzymosterol)	[r] : 4mzym_int1 + nad --> 4mzym_int2 + co2 + h + nadh	5.3.3.1	Cholesterol Metabolism	50814.1
C3STKR2r	C-3 sterol keto reductase (zymosterol)	[r] : h + nadph + zym_int2 --> nadp + zymst		Cholesterol Metabolism	3295.1
C4STMO1r	C-4 sterol methyl oxidase (4,4-dimethylzymosterol)	[r] : 44mzym + (3) h + (3) nadph + (3) o2 --> 4mzym_int1 + (4) h2o + (3) nadp		Cholesterol Metabolism	6307.1
C4STMO2Pr	C-4 methyl sterol oxidase	[r] : 4mzym_int2 + nadp + o2 --> co2 + h + nadph + zym_int2		Cholesterol Metabolism	50814.1
C4STMO2r	C-4 methyl sterol oxidase	[r] : 4mzym_int2 + nad + o2 --> co2 + h + nadh + zym_int2		Cholesterol Metabolism	(6307.1 or 50814.1)
CAATPS	Ca ATPase	atp[c] + (2) ca2[c] + h2o[c] --> adp[c] + (2) ca2[e] + h[e] + pi[c]	3.6.3.6	Transport, Extracellular	(491.1 or 493.1 or 490.1 or 492.1)
CAMPt	cAMP transport (ATP-dependent)	atp[c] + camp[c] + h2o[c] --> adp[c] + camp[e] + h[c] + pi[c]		Transport, Extracellular	(10257.1 or 10057.1 or 10057.2)
CAROtr	beta-carotene transport via diffusion	caro[e] <==> caro[c]		Transport, Extracellular	
CARVEOLte	xenobiotic transport	carveol[e] <==> carveol[c]		Transport, Extracellular	
CAT2p	catalase A, peroxisomal (ethanol)	[x] : etoh + h2o2 --> acald + (2) h2o	1.11.1.6	Glycolysis/Gluconeogenesis	847.1
CAt7r	calcium / sodium antiporter (1:3), reversible	ca2[c] + (3) na1[e] <==> ca2[e] + (3) na1[c]		Transport, Extracellular	(6546.1 or 6543.1 or 6547.1 or 6547.2 or 6547.3 or 6547.4 or 6547.5 or 6547.6)
CATm	catalase	[m] : (2) h2o2 --> (2) h2o + o2	1.11.1.6	ROS Detoxification	847.1
CATp	catalase A, peroxisomal	[x] : (2) h2o2 --> (2) h2o + o2	1.11.1.6	Miscellaneous	847.1
CBL2OR	NADH:cob(III)alamine oxidoreductase	[c] : (2) aqcobal + h + nadh --> (2) cbl2 + (2) h2o + nad		Vitamin B12 Metabolism	
CBL2tm	Cob(II)alamine transport, mitochondrial	cbl2[c] --> cbl2[m]		Transport, Mitochondrial	166785.1
CBLATm	cob(I)alamin adenosyltransferase, mitochondrial	[m] : atp + cbl1 + h <==> adocbl + pppi	2.5.1.17	Vitamin B12 Metabolism	166785.1
CBPPer	Carbamoyl phosphate phosphotransferase, endoplasmic reticulum	[r] : cbp + glc-D + h --> co2 + g6p + nh4		Glycolysis/Gluconeogenesis	(2538.1 or 92579.1 or 57818.1)
CBPS	carbamoyl-phosphate synthase (glutamine-hydrolysing)	[c] : (2) atp + gln-L + h2o + hco3 --> (2) adp + cbp + glu-L + (2) h + pi	6.3.5.5	Pyrimidine Biosynthesis	790.1
CBPSam	carbamoyl-phosphate synthase (ammonia) (mitochondria	[m] : (2) atp + hco3 + nh4 --> (2) adp + cbp + (2) h + pi	6.3.4.16	Glutamate metabolism	(1373.1 or 1373.2)
CBPter	carbamoyl phosphate transport, endoplasmic reticulum	cbp[c] + pi[c] + ppi[c] <==> cbp[r] + pi[r] + ppi[r]		Transport, Endoplasmic Reticular	
CBR1	Carbonyl reductase [NADPH] 1	[c] : h + nadph + prostg1 --> nadp + prostge1		Eicosanoid Metabolism	873.1
CBR2	Carbonyl reductase [NADPH] 1	[c] : h + nadph + prostge2 --> nadp + prostgf2		Eicosanoid Metabolism	873.1
CCA_D3t	Calcitroic acid transport from cytosol	cca_d3[c] --> cca_d3[e]		Transport, Extracellular	
CCA_D3tm	Calcitroic acid transport from mitochondria	cca_d3[m] --> cca_d3[c]		Transport, Mitochondrial	
CDIPTr	phosphatidylinositol synthase (Homo sapiens)	[c] : cdpdag_hs + inost <==> cmp + h + pail_hs	2.7.8.11	Glycerophospholipid Metabolism	(10423.2 or 10423.1)
CDPDAGtm	intracellular transport	cdpdag_hs[c] <==> cdpdag_hs[m]		Transport, Mitochondrial	
CDS	phosphatidate cytidylyltransferase	[c] : ctp + h + pa_hs --> cdpdag_hs + ppi	2.7.7.41	Glycerophospholipid Metabolism	1040.1
CDSm	phosphatidate cytidylyltransferase	[m] : ctp + h + pa_hs --> cdpdag_hs + ppi	2.7.7.41	Glycerophospholipid Metabolism	8760.1
CEPTC	choline phosphotransferase	[c] : cdpchol + dag_hs --> cmp + h + pchol_hs		Glycerophospholipid Metabolism	(10390.1 or 56994.1)
CEPTE	ethanolamine phosphotransferase	[c] : cdpea + dag_hs --> cmp + h + pe_hs		Glycerophospholipid Metabolism	10390.1
CERK	Ceramide kinase	[c] : atp + crm_hs --> adp + crmp_hs + h	2.7.1.138	Sphingolipid Metabolism	(64781.1 or 64781.2)
CERT1gt	ceramide transport protein	crm_hs[c] <==> crm_hs[g]		Transport, Golgi Apparatus	10087.1
CERT1rt	ceramide transport protein	crm_hs[c] <==> crm_hs[r]		Transport, Endoplasmic Reticular	10087.1
CERT2gt	ceramide transport protein	gluside_hs[c] <==> gluside_hs[g]		Transport, Golgi Apparatus	10087.1
CERT2rt	ceramide transport protein	gluside_hs[c] <==> gluside_hs[r]		Transport, Endoplasmic Reticular	10087.1
CGLYt3(2)	Cys-Gly transport in via proton symport	cgly[e] + (2) h[e] --> cgly[c] + (2) h[c]		Transport, Extracellular	6565.1
CGMPt	cGMP transport (ATP-dependent)	35cgmp[c] + atp[c] + h2o[c] --> 35cgmp[e] + adp[c] + h[c] + pi[c]		Transport, Extracellular	(10257.1 or 10057.1 or 10057.2)
CH25H	cholesterol 25-hydroxylase	[r] : chsterol + h + nadph + o2 --> h2o + nadp + xol25oh		Bile Acid Biosynthesis	9023.1
CHAT	Choline O-acetyltransferase	[c] : accoa + chol <==> ach + coa		Glycerophospholipid Metabolism	(1103.2 or 1103.1 or 1103.3 or 1103.4)
CHATn	Choline O-acetyltransferase	[n] : accoa + chol <==> ach + coa		Glycerophospholipid Metabolism	(1103.1 or 1103.2 or 1103.3 or 1103.4)
CHLP	choline phosphate phosphatase	[c] : cholp + h2o --> chol + pi	2.7.7.15	Glycerophospholipid Metabolism	162466.1
CHLPCTD	choline phosphate cytididyltransferase	[c] : cholp + ctp + h --> cdpchol + ppi	2.7.7.15	Glycerophospholipid Metabolism	(5130.1 or 9468.1)
CHLtm	choline transport via diffusion (cytosol to mitochondria)	chol[c] <==> chol[m]		Transport, Mitochondrial	
CHOLATEt	cholate transport via bicarbonate countertransport	cholate[e] + hco3[c] <==> cholate[c] + hco3[e]		Transport, Extracellular	(6579.1 or 10599.1)
CHOLATEt2	cholate transport via sodium cotransport	cholate[e] + (2) na1[e] --> cholate[c] + (2) na1[c]		Transport, Extracellular	(6554.1 or 6555.1)
CHOLATEt3	ABC bile acid transporter	atp[c] + cholate[c] + h2o[c] --> adp[c] + cholate[e] + h[c] + pi[c]		Transport, Extracellular	(8647.1 or 8714.1 or 8714.2 or 8714.3)
CHOLD2m	choline dehydrogenase (FAD acceptor), mitochondria	[m] : chol + fad --> betald + fadh2		Glycine, Serine, and Threonine Metabolism	55349.1
CHOLK	Choline kinase	[c] : atp + chol --> adp + cholp + h	2.7.1.32	Glycerophospholipid Metabolism	(1119.1 or 1119.2 or 1120.1 or 1120.2)
CHOLPtg	choline phosphate intracellular transport	cholp[c] <==> cholp[g]		Transport, Golgi Apparatus	
CHOLPtl	choline phosphate intracellular transport	cholp[c] <==> cholp[l]		Transport, Lysosomal	
CHOLt4	choline, sodium cotransport	chol[e] + na1[e] <==> chol[c] + na1[c]		Transport, Extracellular	60482.1
CHOLtg	choline intracellular transport	chol[g] <==> chol[c]		Transport, Golgi Apparatus	
CHOLtn	Choline transport, nuclear through pores	chol[c] <==> chol[n]		Transport, Nuclear	
CHOLtr	choline intracellular transport	chol[r] <==> chol[c]		Transport, Endoplasmic Reticular	
CHOLtu	Choline uniport	chol[e] <==> chol[c]		Transport, Extracellular	(6582.1 or 6582.2 or 6584.1)
CHSTEROLSULT	steroid sulfotransferase	[c] : chsterol + paps --> chsterols + h + pap	2.8.2.2	Steroid Metabolism	6820.1
CHSTEROLt	cholesterol efflux (ATP depedent)	atp[c] + chsterol[c] + h2o[c] --> adp[c] + chsterol[e] + h[c] + pi[c]		Transport, Extracellular	19.1
CHSTEROLt1	cholesterol intracellular transport	chsterol[l] <==> chsterol[m]		Transport, Mitochondrial	10948.1
CHSTEROLt2	cholesterol intracellular transport	chsterol[r] <==> chsterol[m]		Transport, Mitochondrial	
CHSTEROLt3	cholesterol intracellular transport	chsterol[c] <==> chsterol[m]		Transport, Mitochondrial	
CHSTEROLtg	cholesterol efflux (ATP depedent), golgi	atp[c] + chsterol[g] + h2o[c] --> adp[c] + chsterol[c] + h[c] + pi[c]		Transport, Golgi Apparatus	19.1
CHTNASE	chitinase	[c] : chtn + (2) h2o --> (3) acgam	3.2.1.14	Aminosugar Metabolism	(27159.1 or 1118.1 or 54682.1)
CHTNASEe	chitinase, extracellular	[e] : chtn + (2) h2o --> (3) acgam	3.2.1.14	Aminosugar Metabolism	27159.2
CITL	Citrate lyase	[c] : cit --> ac + oaa	4.1.3.6	Citric Acid Cycle	(171425.1 or 171425.2)
CITMCOAHm	L-Citramalyl-CoA hydro-lyase, mitochondrial	[m] : h2o + itaccoa <==> citmcoa-L	4.2.1.56	C5-Branched dibasic acid metabolism	

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
CITMCOALm	L-Citramalyl-CoA pyruvate-lyase	[m] : citmcoa-L --> accoa + pyr	4.1.3.25	C5-Branched dibasic acid metabolism	
CITRtm	citrulline mitochondrial transport via proton antiport	citr-L[m] <==> citr-L[c]		Transport, Mitochondrial	(83884.1 or 10166.1)
CITt4_2	citrate transport via sodium symport	cit[e] + (2) na1[e] <==> cit[c] + (2) na1[c]		Transport, Extracellular	9058.1
CITt4_4	citrate transport via sodium symport	cit[e] + (4) na1[e] <==> cit[c] + (4) na1[c]		Transport, Extracellular	284111.1
CITtam	citrate transport, mitochondrial	cit[c] + mal-L[m] <==> cit[m] + mal-L[c]		Transport, Mitochondrial	6576.1
CITtbm	citrate transport, mitochondrial	cit[c] + pep[m] <==> cit[m] + pep[c]		Transport, Mitochondrial	6576.1
CK	ATP Creatine kinase	[m] : atp + creat <==> adp + pcreat	2.7.3.2	Urea cycle/amino group metabolism	(1159.1 or 1160.1)
CKc	ATP Creatine kinase (c)	[c] : atp + creat <==> adp + pcreat	2.7.3.2	Urea cycle/amino group metabolism	(1152.1 or 1158.1 or (1158.1 and 1152.1))
CLFORtex	chloride transport via formate countertransport	cl[e] + (2) for[c] --> cl[c] + (2) for[e]		Transport, Extracellular	5172.1
CLFORtex2	chloride transport via formate countertransport (2:1)	(2) cl[e] + for[c] --> (2) cl[c] + for[e]		Transport, Extracellular	(65010.1 or 65010.2 or 65010.3)
CLHCO3tex2	chloride transport via bicarbonate countertransport (2:1)	(2) cl[e] + hco3[c] --> (2) cl[c] + hco3[e]		Transport, Extracellular	(65010.1 or 65010.2 or 65010.3)
CLHCOtex	chloride transport via bicarbonate countertransport	cl[e] + (2) hco3[c] --> cl[c] + (2) hco3[e]		Transport, Extracellular	(1836.1 or 1811.1 or 5172.1 or 115111.1 or 115111.2 or 116369.1 or 116369.2 or 115019.1 or 115019.2)
CLI2tex	chloride transport via iodide countertransport	cl[e] + (2) i[c] --> cl[c] + (2) i[e]		Transport, Extracellular	5172.1
CLOHtex2	chloride transport via hydroxide countertransport (2:1)	(2) cl[e] + oh1[c] --> (2) cl[c] + oh1[e]		Transport, Extracellular	(65010.1 or 65010.2 or 65010.3)
CLOXAtex2	chloride transport via oxalate countertransport (2:1)	(2) cl[e] + oxa[c] --> (2) cl[c] + oxa[e]		Transport, Extracellular	(65010.1 or 65010.2 or 65010.3)
CLPNDCOAtx	fatty acid intracellular transport	clpndcoa[c] <==> clpndcoa[x]		Transport, Peroxisomal	
CLPNDCPT1	carnitine O-palmitoyltransferase	[c] : clpndcoa + crn --> clpndcrn + coa	2.3.1.21	Carnitine shuttle	(1375.4 or 1374.1 or 126129.1 or 1375.3 or 1375.2 or 1375.1)
CLPNDCPT2	carnitine transferase	[m] : clpndcrn + coa --> clpndcoa + crn		Carnitine shuttle	1376.1
CLPNDCRNt	transport into the mitochondria (carnitine)	clpndcrn[c] --> clpndcrn[m]		Carnitine shuttle	788.1
CLPNDt	fatty acid transport via diffusion	clpnd[e] <==> clpnd[c]		Transport, Extracellular	
CLS_hs	cardiolipin synthase (homo sapiens)	[c] : cdpdag_hs + pglyc_hs --> clpn_hs + cmp + h		Glycerophospholipid Metabolism	54675.1
CMPACNAtg	CMP-Sia Golgi transport via CMP antiport	cmp[g] + cmpacna[c] <==> cmp[c] + cmpacna[g]		Transport, Golgi Apparatus	10559.1
CMPACNAtn	CMP-Sia nuclear export	cmpacna[n] --> cmpacna[c]		Transport, Nuclear	
CMPSAS	CMP sialic acid synthase	[c] : acnam + ctp --> cmpacna + ppi	2.7.7.43	Aminosugar Metabolism	55907.1
CMPSASn	CMP sialic acid synthase, nuclear	[n] : acnam + ctp --> cmpacna + ppi	2.7.7.43	Aminosugar Metabolism	55907.1
CO2t	CO2 transporter via diffusion	co2[e] <==> co2[c]		Transport, Extracellular	
CO2ter	CO2 endoplasmic reticular transport via diffusion	co2[c] <==> co2[r]		Transport, Endoplasmic Reticular	
CO2tg	CO2 Golgi transport	co2[c] <==> co2[g]		Transport, Golgi Apparatus	
CO2tm	CO2 transport (diffusion), mitochondrial	co2[c] <==> co2[m]		Transport, Mitochondrial	
CO2tn	CO2 nuclear transport via diffusion	co2[n] <==> co2[c]		Transport, Nuclear	
CO2tp	CO2 peroxisomal transport	co2[c] <==> co2[x]		Transport, Peroxisomal	
COAtl	CoA transport in lysosome via diffusion	coa[c] <==> coa[l]		Transport, Lysosomal	
COAtm	CoA transporter	coa[c] <==> coa[m]		Transport, Mitochondrial	8034.1
COAtn	coenzyme A transport, nuclear	coa[c] <==> coa[n]		Transport, Nuclear	
COAtp	coenzyme A transport, peroxisomal	coa[c] <==> coa[x]		Transport, Peroxisomal	
COAtr	COA transporter, endoplasmic reticulum	coa[c] <==> coa[r]		Transport, Endoplasmic Reticular	
COKECBESr	Carboxylesterase (cocaine) (er)	[r] : coke + h2o --> bz + egme + h	3.1.1.1	Alkaloid biosynthesis II	8824.1
COQ3m	methyltransferase COQ3	[m] : 2dpmhobq + amet --> ahcys + h + q10		Ubiquinone Biosynthesis	51805.1
COQ5m	Ubiquinone biosynthesis methyltransferase COQ5	[m] : 2dp6mobq + amet --> 2dp6mobq_me + ahcys + h		Ubiquinone Biosynthesis	
COQ6m	Ubiquinone biosynthesis monooxgenase COQ6	[m] : 2dp6mep + o2 --> 2dp6mobq + h2o		Ubiquinone Biosynthesis	(51004.1 or 51004.2)
COQ7m	Ubiquinone biosynthesis COQ7	[m] : 2dp6mobq_me + h + nadph + o2 --> 2dpmhobq + h2o + nadp		Ubiquinone Biosynthesis	10229.1
CORE2GTg	Core 2 acetylglucosaminyltransferase, Golgi apparatus	[g] : T_antigen + uacgam --> core2 + h + udp	2.4.1.102	O-Glycan Biosynthesis	(2650.1 or 9245.1 or 51301.1)
CORE3GTg	Core 3 beta-GlcNAc-transferase, Golgi apparatus	[g] : Tn_antigen + uacgam --> core3 + h + udp	2.4.1.147	O-Glycan Biosynthesis	192134.1
CORE4GTg	Core 4 beta6-GalNAc-transferase, Golgi apparatus	[g] : core3 + uacgam --> core4 + h + udp	2.4.1.148	O-Glycan Biosynthesis	9245.1
CORE5GTg	Core 5 alpha-GalNAc-transferase, Golgi apparatus	[g] : Tn_antigen + udpacgal --> core5 + h + udp		O-Glycan Biosynthesis	
CORE6GTg	Core 6 beta-GlcNAc-transferase A, Golgi apparatus	[g] : Tn_antigen + uacgam --> core6 + h + udp	2.4.1.102	O-Glycan Biosynthesis	2650.1
CORE7GTg	Core 7 alpha-GalNAc-transferase, Golgi apparatus	[g] : Tn_antigen + udpacgal --> core7 + h + udp		O-Glycan Biosynthesis	
CORE8GTg	N-acetylgalactosamine 3-alpha-galactosyltransferase, Golgi apparatus	[g] : Tn_antigen + udpgal --> core8 + h + udp		O-Glycan Biosynthesis	
COt	CO transporter via diffusion	co[c] <==> co[e]		Transport, Extracellular	
COUCOAFm	p-coumaroyl-CoA formation	[m] : T4hcinnm + atp + coa --> amp + coucoa + ppi		Ubiquinone Biosynthesis	
COUMARINte	xenobiotic transport	coumarin[e] <==> coumarin[c]		Transport, Extracellular	
CPCTDTX	choline-phosphate cytidylyltransferase	[c] : ctp + h + ntm2amep --> cmpntm2amep + ppi	2.7.7.15	Glycerophospholipid Metabolism	(9468.1 or 5130.1)
CPPPGO	coproporphyrinogen oxidase (O2 required)	[c] : cpppg3 + (2) h + o2 --> (2) co2 + (2) h2o + pppg9	1.3.3.3	Heme Biosynthesis	1371.1
CREATt4(2)r	Creatine transport (sodium symport) (2:1)	creat[e] + (2) na1[e] <==> creat[c] + (2) na1[c]		Transport, Extracellular	(6535.1 or 6537.1)
CREATtmdiffir	Creatine transport to/from mitochondria via diffusion	creat[c] --> creat[m]		Urea cycle/amino group metabolism	
CRMPte	crmp_hs transport	crmp_hs[c] <==> crmp_hs[e]		Transport, Extracellular	
CRNCAR3tp	carnitine-propcarnitine carrier, peroxisomal	crn[c] + pcrn[x] --> crn[x] + pcrn[c]		Transport, Peroxisomal	
CRNCARtp	carnitine-acetylcarnitine carrier, peroxisomal	acrn[x] + crn[c] --> acrn[c] + crn[x]		Transport, Peroxisomal	
CRNt	L-carnitine reversible transport	crn[e] <==> crn[c]		Transport, Extracellular	6584.1
CRNtHa	L-carnitine outward transport (H+ antiport)	crn[c] + h[e] --> crn[e] + h[c]		Transport, Extracellular	6583.1
CRNtim	L-carnitine transport out of mitochondria via diffusion	crn[m] --> crn[c]		Transport, Mitochondrial	788.1
CRNtuIR	L-carnitine inward uniport	crn[e] --> crn[c]		Transport, Extracellular	6583.1
CRNtuNa	L-carnitine inward transport by Na+ symport	crn[e] + na1[e] --> crn[c] + na1[c]		Transport, Extracellular	6584.1

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
CRNtx	carnitine transport peroxisome to mitochondria	dmnoncrn[x] <==> dmnoncrn[m]		Transport, Peroxisomal	
CRTNsyn	Creatinine synthase	[c] : pcreat --> crtn + h + pi		Urea cycle/amino group metabolism	
CRTSLtm	cortisol intracellular transport	crtsl[c] <==> crtsl[m]		Transport, Mitochondrial	
CRTSLtr	cortisol intracellular transport	crtsl[c] <==> crtsl[r]		Transport, Endoplasmic Reticular	
CRTSTRNtm	corticosterone intracellular transport	crtstrn[c] <==> crtstrn[m]		Transport, Mitochondrial	
CRTSTRNtr	corticosterone intracellular transport	crtstrn[c] <==> crtstrn[r]		Transport, Endoplasmic Reticular	
CRVNCtr	fatty acid transport via diffusion	crvnc[e] <==> crvnc[c]		Transport, Extracellular	
CSAPASEly	chondroitin sulfate A proteoglycan protease, lysosome (endosome)	[l] : cspg_a + h2o --> Ser-Gly/Ala-X-Gly + cs_a		Chondroitin sulfate degradation	
CSBPASEly	chondroitin sulfate B proteoglycan protease, lysosome (endosome)	[l] : cspg_b + h2o --> Ser-Gly/Ala-X-Gly + cs_b		Chondroitin sulfate degradation	
CSCPASEly	chondroitin sulfate C proteoglycan protease, lysosome (endosome)	[l] : cspg_c + h2o --> Ser-Gly/Ala-X-Gly + cs_c		Chondroitin sulfate degradation	
CSDPASEly	chondroitin sulfate D proteoglycan protease, lysosome (endosome)	[l] : cspg_d + h2o --> Ser-Gly/Ala-X-Gly + cs_d		Chondroitin sulfate degradation	
CSEPASEly	chondroitin sulfate E proteoglycan protease, lysosome (endosome)	[l] : cspg_e + h2o --> Ser-Gly/Ala-X-Gly + cs_e		Chondroitin sulfate degradation	
CSm	citrate synthase	[m] : accoa + h2o + oaa --> cit + coa + h		Citric Acid Cycle	(1431.1 or 1431.2)
CSNAT2m	carnitine O-aceyltransferase, mitochondrial	[m] : coa + pcrn <==> crn + ppcoa	2.3.1.7	Carnitine shuttle	1384.1
CSNAT2x	carnitine dimethyl nonanoyl transferase, revsible, peroxisomal	[x] : crn + dmnoncoa <==> coa + dmnoncrn	2.3.1.7	Fatty Acid Metabolism	(54677.1 or 1384.2)
CSNAT3x	carnitine O-aceyltransferase, peroxisomal	[x] : crn + ppcoa <==> coa + pcrn	2.3.1.7	Carnitine shuttle	1384.2
CSNATer	carnitine O-acetyltransferase, endolasmic reticulum	[r] : accoa + crn <==> acrn + coa	2.3.1.7	Fatty Acid Metabolism	1384.3
CSNATm	carnitine O-aceyltransferase, mitochondrial	[m] : acrn + coa <==> accoa + crn	2.3.1.7	Fatty Acid Metabolism	1384.1
CSNATp	carnitine O-acetyltransferase, reverse direction, peroxisomal	[x] : accoa + crn <==> acrn + coa	2.3.1.7	Fatty Acid Metabolism	1384.2
CSNATr	carnitine O-acetyltransferase	[c] : accoa + crn <==> acrn + coa	2.3.1.7	Carnitine shuttle	
CSND	Cytosine deaminase	[c] : csn + h + h2o --> nh4 + ura	3.5.4.1	Pyrimidine Catabolism	
CSNt	cytosine transport via facilated diffusion	csn[e] <==> csn[c]		Transport, Extracellular	3177.1
CSPG_At	chondroitin sulfate A transport, golgi to extracellular	cspg_a[g] --> cspg_a[e]		Transport, Extracellular	
CSPG_Atly	chondroitin sulfate A transport, extracellular to lysosome	cspg_a[e] --> cspg_a[l]		Transport, Lysosomal	
CSPG_Bt	chondroitin sulfate B transport, golgi to extracellular	cspg_b[g] --> cspg_b[e]		Transport, Extracellular	
CSPG_Btly	chondroitin sulfate B transport, extracellular to lysosome	cspg_b[e] --> cspg_b[l]		Transport, Lysosomal	
CSPG_Ct	chondroitin sulfate C transport, golgi to extracellular	cspg_c[g] --> cspg_c[e]		Transport, Extracellular	
CSPG_Ctly	chondroitin sulfate C transport, extracellular to lysosome	cspg_c[e] --> cspg_c[l]		Transport, Lysosomal	
CSPG_Dt	chondroitin sulfate D transport, golgi to extracellular	cspg_d[g] --> cspg_d[e]		Transport, Extracellular	
CSPG_Dtly	chondroitin sulfate D transport, extracellular to lysosome	cspg_d[e] --> cspg_d[l]		Transport, Lysosomal	
CSPG_Et	chondroitin sulfate E transport, golgi to extracellular	cspg_e[g] --> cspg_e[e]		Transport, Extracellular	
CSPG_Etly	chondroitin sulfate E transport, extracellular to lysosome	cspg_e[e] --> cspg_e[l]		Transport, Lysosomal	
CTPS1	CTP synthase (NH3)	[c] : atp + nh4 + utp --> adp + ctp + (2) h + pi	6.3.4.2	Nucleotides	1503.1
CTPS2	CTP synthase (glutamine)	[c] : atp + gln-L + h2o + utp --> adp + ctp + glu-L + (2) h + pi	6.3.4.2	Pyrimidine Biosynthesis	(56474.1 or 56474.2)
CTPtn	CTP diffusion in nucleus	ctp[c] <==> ctp[n]		Transport, Nuclear	
CYANSTm	Cyanide sulfurtransferase, mitochondrial	[m] : cyan + tsul --> h + so3 + tcynt	2.8.1.1	Cysteine Metabolism	7263.1
CYANt	Cyanide transport via diffusion (extracellular to cytosol)	cyan[e] <==> cyan[c]		Transport, Extracellular	
CYANtm	Cyanide transport via diffusion (mitochondrial)	cyan[c] <==> cyan[m]		Transport, Mitochondrial	
CYOOm3	cytochrome c oxidase, mitochondrial Complex IV	(4) focytC[m] + (7.92) h[m] + o2[m] --> (4) ficytC[m] + (4) h[c] + (1.96) h2o[m] + (0.02) o2s[m]	1.9.3.1	Oxidative Phosphorylation	(9377.1 and 1347.1 and 84701.1 and 125965.1 and 1337.1 and 1350.1 and 1340.1 and 1351.1 and 1349.1 and 1327.1 and 1345.1 and 341947.1 and 1339.1 and 1346.1 and 4512.1 and 170712.1 and 9167.1 and 4514.1 and 4513.1 and 1329.1)
CYOR-u10m	ubiquinol-6 cytochrome c reductase, Complex III	(2) ficytC[m] + (2) h[m] + q10h2[m] --> (2) focytC[m] + (4) h[c] + q10[m]	1.10.2.2	Oxidative Phosphorylation	((7385.1 and 7388.1 and 7384.1 and 29796.2 and 7386.1 and 7381.1 and 10975.1 and 1537.1 and 27089.1 and 4519.1) or (7385.1 and 7388.1 and 4519.1 and 7381.1 and 1537.1 and 10975.1 and 7384.1 and 7386.1 and 29796.1 and 27089.1))
CYSALANaEx	L-alanine/L-cysteine Na-dependent exchange (Cys-L in)	ala-L[c] + cys-L[e] + na1[e] --> ala-L[e] + cys-L[c] + na1[c]		Transport, Extracellular	(6509.1 or 6510.1)
CYSAMO	Cysteamine oxygenase	[c] : cysam + o2 --> (2) h + hyptaur		Taurine and hypotaurine metabolism	
CYSASNNaEx	L-cysteine/L-asparagine Na-dependent exchange (Cys-L in)	asn-L[c] + cys-L[e] + na1[e] --> asn-L[e] + cys-L[c] + na1[c]		Transport, Extracellular	6510.1
CYSGLNNaEx	L-cysteine/L-glutamine Na-dependent exchange (Cys-L in)	cys-L[e] + gln-L[c] + na1[e] --> cys-L[c] + gln-L[e] + na1[c]		Transport, Extracellular	6510.1
CYSGLTH	Glutathione:cystine oxidoreductase	[c] : Lcystin + (2) gthrd <==> (2) cys-L + gthox	1.8.4.4	Cysteine Metabolism	
CYSGLUexR	L-cysteine/L-glutamine reversible exchanger	cys-L[e] + gln-L[c] <==> cys-L[c] + gln-L[e]		Transport, Extracellular	(56301.1 and 6520.1)

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
CYSGLYex	L-cysteine/glycine exchanger	cys-L[c] + gly[e] --> cys-L[e] + gly[c]		Transport, Extracellular	((6520.1 and 23428.1) or (23428.2 and 6520.1))
CYSGLYexR	L-cysteine/glycine reversible exchanger	cys-L[c] + gly[e] <==> cys-L[e] + gly[c]		Transport, Extracellular	(6520.1 and 56301.1)
CYSLYSL	L-Cystine Lysteine-lyase (deaminating)	[c] : Lcystin + h2o --> nh4 + pyr + thcys	4.4.1.1	Cysteine Metabolism	
CYSO	cysteine oxidase	[c] : cys-L + o2 --> 3sala + (2) h	1.13.11.20	Taurine and hypotaurine metabolism	1036.1
CYSSERNaEx	L-serine/L-cysteine Na-dependent exchange (Cys-L in)	cys-L[e] + na1[e] + ser-L[c] --> cys-L[c] + na1[c] + ser-L[e]		Transport, Extracellular	(6509.1 or 6510.1)
CYSt4	L-cysteine reversible transport via sodium symport	cys-L[e] + na1[e] --> cys-L[c] + na1[c]		Transport, Extracellular	11254.1
CYSTA	cysteine transaminase	[c] : akg + cys-L <==> glu-L + mercppyr	2.6.1.3	Cysteine Metabolism	2805.1
CYSTAm	cysteine transaminase (mitochondrial)	[m] : akg + cys-L <==> glu-L + mercppyr	2.6.1.3	Cysteine Metabolism	2806.1
CYStec	L-cysteine transport via diffusion (extracellular to cytosol)	cys-L[e] <==> cys-L[c]		Transport, Extracellular	124935.1
CYSTGL	cystathionine g-lyase	[c] : cyst-L + h2o --> 2obut + cys-L + nh4	4.4.1.1	Cysteine Metabolism	(1491.1 or 1491.2)
CYSTGLUex	L-cystine/L-glutamate exchanger	Lcystin[e] + glu-L[c] --> Lcystin[c] + glu-L[e]		Transport, Extracellular	(23657.1 and 6520.1)
CYSTHRNaEx	L-cysteine/L-threonine Na-dependent exchange (Cys-L in)	cys-L[e] + na1[e] + thr-L[c] --> cys-L[c] + na1[c] + thr-L[e]		Transport, Extracellular	(6509.1 or 6510.1)
CYSTS	cystathionine beta-synthase	[c] : hcys-L + ser-L --> cyst-L + h2o	4.2.1.22	Methionine Metabolism	875.1
CYSTSERex	L-cystine/glycine exchanger (cystine in)	Lcystin[e] + ser-L[c] --> Lcystin[c] + ser-L[e]		Transport, Extracellular	(6519.1 and 11136.1)
CYTD	cytidine deaminase	[c] : cytd + h + h2o --> nh4 + uri	3.5.4.5	Pyrimidine Catabolism	(978.1 or 57379.1)
CYTDK1	cytidine kinase (ATP)	[c] : atp + cytd --> adp + cmp + h		Nucleotides	(7371.1 or 83549.1)
CYTDK2m	cytidine kinase (ATP), mitochondrial	[m] : atp + cytd --> adp + cmp + h		Nucleotides	
CYTDn	cytidine deaminase, nuclear	[n] : cytd + h + h2o --> nh4 + uri	3.5.4.5	Nucleotides	57379.1
CYTDt	cytidine facilated transport in cytosol	cytd[e] <==> cytd[c]		Transport, Extracellular	(3177.1 or 2030.1)
CYTDt4	cytidine transport in via sodium symport	cytd[e] + na1[e] --> cytd[c] + na1[c]		Transport, Extracellular	(9154.1 or 64078.1 or 9154.2)
CYTDt5	cytidine transport (1:2 Na/cytd cotransport)	cytd[e] + (2) na1[e] --> cytd[c] + (2) na1[c]		Transport, Extracellular	64078.1
CYTDtl	Cytidine facilated transport from lysosome	cytd[l] <==> cytd[c]		Transport, Lysosomal	55315.1
CYTDtm	cytidine facilated transport in mitochondria	cytd[c] <==> cytd[m]		Transport, Mitochondrial	2030.1
CYTDtn	cytidine transport in nucleus	cytd[c] <==> cytd[n]		Transport, Nuclear	
CYTK1	cytidylate kinase (CMP)	[c] : atp + cmp <==> adp + cdp	2.7.4.14	Nucleotides	51727.1
CYTK10	cytidylate kinase (CMP,dGTP)	[c] : cmp + dgtp <==> cdp + dgdp	2.7.4.14	Nucleotides	51727.1
CYTK10n	cytidylate kinase (CMP,dGTP),nuclear	[n] : cmp + dgtp <==> cdp + dgdp	2.7.4.14	Nucleotides	51727.1
CYTK11	cytidylate kinase (dCMP,dGTP)	[c] : dcmp + dgtp <==> dcdp + dgdp	2.7.4.14	Nucleotides	51727.1
CYTK11n	cytidylate kinase (dCMP,dGTP),nuclear	[n] : dcmp + dgtp <==> dcdp + dgdp	2.7.4.14	Nucleotides	51727.1
CYTK12	cytidylate kinase (dCMP,dCTP)	[c] : dcmp + dctp <==> (2) dcdp	2.7.4.14	Nucleotides	51727.1
CYTK12n	cytidylate kinase (dCMP,dCTP),nuclear	[n] : dcmp + dctp <==> (2) dcdp	2.7.4.14	Nucleotides	51727.1
CYTK13	cytidylate kinase (dCMP,dATP)	[c] : datp + dcmp <==> dadp + dcdp	2.7.4.14	Nucleotides	51727.1
CYTK13n	cytidylate kinase (dCMP,dATP),nuclear	[n] : datp + dcmp <==> dadp + dcdp	2.7.4.14	Nucleotides	51727.1
CYTK14	cytidylate kinase (dCMP,UTP)	[c] : dcmp + utp <==> dcdp + udp	2.7.4.14	Nucleotides	51727.1
CYTK14n	cytidylate kinase (dCMP,CTP),nuclear	[n] : dcmp + utp <==> dcdp + udp	2.7.4.14	Nucleotides	51727.1
CYTK1m	cytidylate kinase (CMP),mitochondrial	[m] : atp + cmp <==> adp + cdp	2.7.4.14	Nucleotides	
CYTK1n	cytidylate kinase (CMP),nuclear	[n] : atp + cmp <==> adp + cdp	2.7.4.14	Nucleotides	51727.1
CYTK2	cytidylate kinase (dCMP)	[c] : atp + dcmp <==> adp + dcdp	2.7.4.14	Nucleotides	51727.1
CYTK2n	cytidylate kinase (dCMP),nuclear	[n] : atp + dcmp <==> adp + dcdp	2.7.4.14	Nucleotides	51727.1
CYTK3	cytidylate kinase (CMP)(GTP)	[c] : cmp + gtp <==> cdp + gdp		Nucleotides	(26289.1 or 26289.2)
CYTK3n	cytidylate kinase (dCMP,CTP),nuclear	[n] : ctp + dcmp <==> cdp + dcdp	2.7.4.14	Nucleotides	51727.1
CYTK4	cytidylate kinase (dCMP)(GTP)	[c] : dcmp + gtp <==> dcdp + gdp		Nucleotides	(26289.1 or 26289.2)
CYTK4n	cytidylate kinase (dCMP,GTP),nuclear	[n] : dcmp + gtp <==> dcdp + gdp	2.7.4.14	Nucleotides	51727.1
CYTK5	cytidylate kinase (dCMP)	[c] : ctp + dcmp <==> cdp + dcdp	2.7.4.14	Nucleotides	51727.1
CYTK5n	cytidylate kinase (CMP),nuclear	[n] : cmp + gtp <==> cdp + gdp	2.7.4.14	Nucleotides	51727.1
CYTK6	cytidylate kinase (CMP,CTP)	[c] : cmp + ctp <==> (2) cdp	2.7.4.14	Nucleotides	51727.1
CYTK6n	cytidylate kinase (CMP,CTP),nuclear	[n] : cmp + ctp <==> (2) cdp	2.7.4.14	Nucleotides	51727.1
CYTK7	cytidylate kinase (CMP,UTP)	[c] : cmp + utp <==> cdp + udp	2.7.4.14	Nucleotides	51727.1
CYTK7n	cytidylate kinase (CMP,UTP),nuclear	[n] : cmp + utp <==> cdp + udp	2.7.4.14	Nucleotides	51727.1
CYTK8	cytidylate kinase (CMP,dATP)	[c] : cmp + datp <==> cdp + dadp	2.7.4.14	Nucleotides	51727.1
CYTK8n	cytidylate kinase (CMP,dATP),nuclear	[n] : cmp + datp <==> cdp + dadp	2.7.4.14	Nucleotides	51727.1
CYTK9	cytidylate kinase (CMP,dCTP)	[c] : cmp + dctp <==> cdp + dcdp	2.7.4.14	Nucleotides	51727.1
CYTK9n	cytidylate kinase (CMP,dCTP),nuclear	[n] : cmp + dctp <==> cdp + dcdp	2.7.4.14	Nucleotides	51727.1
D-3AIBt	D-3-amino-isobutyrate transport	3aib-D[c] --> 3aib-D[e]		Transport, Extracellular	
D3AIBTm	D-3-Amino-isobutanoate:pyruvate aminotransferase, mitochondrial	[m] : 3aib-D + pyr <==> 2mop + ala-L	2.6.1.40	Pyrimidine Catabolism	
DADA	Deoxyadenosine deaminase	[c] : dad-2 + h + h2o --> din + nh4		Nucleotides	100.1
DADAe	Deoxyadenosine deaminase, extracellular	[e] : dad-2 + h + h2o --> din + nh4		Nucleotides	100.1
DADNK	deoxyadenosine kinase	[c] : atp + dad-2 --> adp + damp + h	2.7.1.76	Nucleotides	
DADNt4	deoxyadenosine transport via diffusion	dad-2[e] <==> dad-2[c]		Transport, Extracellular	
DAG_HSter	diacylglycerol ER export	dag_hs[r] --> dag_hs[c]		Transport, Endoplasmic Reticular	
DAGK_hs	Diacylglycerol phosphate kinase (homo sapiens)	[c] : atp + dag_hs <==> adp + h + pa_hs	2.7.1.107	Glycerophospholipid Metabolism	(8526.1 or 8525.1 or 8525.2 or 8525.3 or 1609.1 or 9162.1 or 160851.1 or 160851.2 or 1608.1 or 8527.2 or 1607.1 or 1607.2 or 1607.1 or 1606.1 or 8527.1)
DAGKn_hs	Diacylglycerol phosphate kinase (homo sapiens)	[n] : atp + dag_hs <==> adp + h + pa_hs	2.7.1.107	Glycerophospholipid Metabolism	(8525.1 or 9162.1)
DALAOXx	D-Alanine Oxidase (x)	[x] : ala-D + h2o + o2 --> h2o2 + nh4 + pyr	1.4.3.3	D-alanine metabolism	1610.1
DALAt2r	D-alanine transport via proton symport	ala-D[e] + h[e] <==> ala-D[c] + h[c]		Transport, Extracellular	206358.1
DALAt2rL	D-alanine transport via proton symport (lysosome)	ala-D[l] + h[l] <==> ala-D[c] + h[c]		Transport, Lysosomal	206358.1
DALAxt	D-Alanine transport to perixosome	ala-D[c] --> ala-D[x]		D-alanine metabolism	
DARGOp	D-arginine oxidase, perixosomal	[x] : arg-D + h2o + o2 --> 5g2oxpt + h2o2 + nh4	1.4.3.3	D-arg and D-orn metabolism	1610.1
DASCBH	L-Dehydroascorbate lactonohydrolase	[c] : dhdascb + h2o --> 23doguln + h	3.1.1.17	Ascorbate and Aldarate Metabolism	
DASCBR	dehydroascorbate reductase	[c] : dhdascb + h + nadph --> ascb-L + nadp	1.6.5.4	Ascorbate and Aldarate Metabolism	(2745.1 or 51022.1 or 51022.2)
DASPO1p	D-aspartate oxidase, peroxisomal	[x] : asp-D + h2o + o2 --> h2o2 + nh4 + oaa	1.4.3.1	Alanine and Aspartate Metabolism	(8528.2 or 8528.1)
DATPtn	dATP diffusion in nucleus	datp[c] <==> datp[n]		Transport, Nuclear	

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
DClm	dodecenoyl-Coenzyme A delta isomerase	[m] : dd2coa <==> dd3coa	5.3.3.8	Fatty Acid Metabolism	1632.1
DCK1m	Deoxycytidine kinase, mitochondrial (ATP)	[m] : atp + dcyt <==> adp + dcmp + h	2.7.1.74	Nucleotides	
DCK1n	Deoxycytidine kinase, nuclear (ATP)	[n] : atp + dcyt <==> adp + dcmp + h	2.7.1.74	Nucleotides	1633.1
DCK2n	Deoxycytidine kinase, nuclear (UTP)	[n] : dcyt + utp <==> dcmp + h + udp	2.7.1.74	Nucleotides	1633.1
DCMPDA	dCMP deaminase	[c] : dcmp + h + h2o <==> dump + nh4	3.5.4.12	Pyrimidine Catabolism	1635.1
DCSPTN1COAtx	fatty acid intracellular transport	dcsptn1coa[c] <==> dcsptn1coa[x]		Transport, Peroxisomal	
DCSPTN1CPT1	carnitine O-palmitoyltransferase	[c] : crn + dcsptn1coa --> coa + dcsptn1crn	2.3.1.21	Carnitine shuttle	(1375.4 or 1374.1 or 126129.1 or 1375.3 or 1375.2 or 1375.1)
DCSPTN1CPT2	carnitine transferase	[m] : coa + dcsptn1crn --> crn + dcsptn1coa		Carnitine shuttle	1376.1
DCSPTN1CRNt	transport into the mitochondria (carnitine)	dcsptn1crn[c] --> dcsptn1crn[m]		Carnitine shuttle	788.1
DCSPTN1t	fatty acid transport via diffusion	dcsptn1[e] <==> dcsptn1[c]		Transport, Extracellular	
DCT	Dopachrome tautomerase	[c] : L-dpchrm <==> 56dihindlcrbxlt	5.3.3.12	Tyrosine metabolism	1638.1
DCTPtn	dCTP diffusion in nucleus	dctp[c] <==> dctp[n]		Transport, Nuclear	
DCYTD	deoxycytidine deaminase	[c] : dcyt + h + h2o --> duri + nh4	3.5.4.14	Pyrimidine Catabolism	(978.1 or 57379.1)
DCYTDn	deoxycytidine deaminase, nuclear	[n] : dcyt + h + h2o --> duri + nh4	3.5.4.14	Nucleotides	57379.1
DCYTt	deoxycytidine transport via diffusion	dcyt[e] <==> dcyt[c]		Transport, Extracellular	
DDPGAm	2-dehydro-3-deoxy-phosphogluconate aldolase, mitochondrial	[m] : 4h2oglt <==> glx + pyr	4.1.2.14	Arginine and Proline Metabolism	
DEBRISOQUINEt	debrisoquine uniport	debrisoquine[e] <==> debrisoquine[c]		Transport, Extracellular	(6582.1 or 6582.2)
DECDPtm	lipid, flip-flop intracellular transport	decdp[c] <==> decdp[m]		Transport, Mitochondrial	
DEDOLP1_L	dehydrodolichol diphosphate phosphatase (liver)	[c] : (0.1) dedoldp_L + h2o --> (0.1) dedolp_L + h + pi		N-Glycan Biosynthesis	
DEDOLP1_U	dehydrodolichol diphosphate phosphatase (uterus)	[c] : (0.1) dedoldp_U + h2o --> (0.1) dedolp_U + h + pi		N-Glycan Biosynthesis	
DEDOLP2_L	dehydrodolichol phosphate phosphatase (liver)	[c] : (0.1) dedolp_L + h2o --> (0.1) dedol_L + pi		N-Glycan Biosynthesis	
DEDOLP2_U	dehydrodolichol phosphate phosphatase (uterus)	[c] : (0.1) dedolp_U + h2o --> (0.1) dedol_U + pi		N-Glycan Biosynthesis	
DEDOLR_L	dehydrodolichol reductase (liver)	[c] : (0.1) dedol_L + h + nadph --> (0.1) dolichol_L + nadp		N-Glycan Biosynthesis	
DEDOLR_U	dehydrodolichol reductase (uterus)	[c] : (0.1) dedol_U + h + nadph --> (0.1) dolichol_U + nadp		N-Glycan Biosynthesis	
DESAT16_2	palmitoyl-CoA desaturase (n-C16:0CoA -> n-C16:1CoA)	[c] : h + nadh + o2 + pmtcoa --> (2) h2o + hdcoa + nad	1.14.19.1	Fatty acid elongation	6319.1
DESAT18_10	fatty acyl-CoA desaturase (n-C18:2CoA -> n-C18:3CoA)	[c] : h + lnlncacoa + nadh + o2 --> (2) h2o + nad + strdnccoa	1.14.19.1	Fatty acid elongation	9415.1
DESAT18_3	stearoyl-CoA desaturase (n-C18:0CoA -> n-C18:1CoA)	[c] : h + nadh + o2 + stcoa --> (2) h2o + nad + odecoa	1.14.19.1	Fatty acid elongation	6319.1
DESAT18_4	stearoyl-CoA desaturase (n-C18:0CoA -> n-C18:1CoA)	[c] : h + nadh + o2 + stcoa --> (2) h2o + nad + vacccoa	1.14.19.1	Fatty acid elongation	6319.1
DESAT18_5	stearoyl-CoA desaturase (n-C18:0CoA -> n-C18:1CoA)	[c] : h + nadh + o2 + stcoa --> (2) h2o + nad + od2coa	1.14.19.1	Fatty acid elongation	6319.1
DESAT18_6	fatty acyl-CoA desaturase (n-C18:1CoA -> n-C18:2CoA)	[c] : h + nadh + o2 + odecoa --> (2) h2o + lneldccoa + nad	1.14.19.1	Fatty acid elongation	9415.1
DESAT18_7	fatty acyl-CoA desaturase (n-C18:1CoA -> n-C18:2CoA)	[c] : h + nadh + o2 + vacccoa --> (2) h2o + lneldccoa + nad	1.14.19.1	Fatty acid elongation	9415.1
DESAT18_8	fatty acyl-CoA desaturase (n-C18:1CoA -> n-C18:2CoA)	[c] : h + nadh + o2 + od2coa --> (2) h2o + lneldccoa + nad	1.14.19.1	Fatty acid elongation	9415.1
DESAT18_9	fatty acyl-CoA desaturase (n-C18:2CoA -> n-C18:3CoA)	[c] : h + lnlccoa + nadh + o2 --> (2) h2o + lnlncgcoa + nad	1.14.19.1	Fatty acid elongation	9415.1
DESAT20_1	fatty acyl-CoA desaturase (n-C20:3CoA -> n-C20:4CoA)	[c] : dlnlcgcoa + h + nadh + o2 --> arachdcoa + (2) h2o + nad	1.14.19.1	Fatty acid elongation	3992.1
DESAT20_2	fatty acyl-CoA desaturase (n-C20:4CoA -> n-C20:5CoA)	[c] : eicostetcoa + h + nadh + o2 --> (2) h2o + nad + tmndnccoa	1.14.19.1	Fatty acid elongation	3992.1
DESAT22_1p	fatty acyl-CoA desaturase (n-C22:4CoA -> n-C22:5CoA)	[x] : admcoa + h + nadh + o2 --> dcsptn1coa + (2) h2o + nad	1.14.19.1	Fatty acid elongation	
DESAT22_2p	fatty acyl-CoA desaturase (n-C22:5CoA -> n-C22:6CoA)	[x] : clpndcoa + h + nadh + o2 --> c226coa + (2) h2o + nad	1.14.19.1	Fatty acid elongation	
DESAT24_1	fatty acyl-CoA desaturase (n-C24:5CoA -> n-C24:6CoA)	[c] : h + nadh + o2 + tetpent3coa --> (2) h2o + nad + tethex3coa	1.14.19.1	Fatty acid elongation	9415.1
DGAT	diacylglycerol acyltransferase	[c] : Rtotal3coa + dag_hs --> coa + tag_hs		Triacylglycerol Synthesis	(8694.1 or 84649.1)
DGCHOLte	bile acid intracellular transport	dgchol[e] <==> dgchol[c]		Transport, Extracellular	
DGCHOLtx	bile acid intracellular transport	dgchol[x] <==> dgchol[c]		Transport, Peroxisomal	
DGK1	deoxyguanylate kinase (dGMP:ATP)	[c] : atp + dgmp <==> adp + dgdp	2.7.4.8	Nucleotides	2987.1
DGK2m	deoxyguanylate kinase (dGMP:dATP) (mitochondrial)	[m] : datp + dgmp <==> dadp + dgdp	2.7.4.8	Nucleotides	
DGNSKm	deoxyguanosine kinase	[m] : atp + dgsn --> adp + dgmp + h	2.7.1.113	Nucleotides	(1716.1 or 1716.2 or 1716.4 or 1716.5 or 1716.3)
DGSNt	deoyguanosine transport via diffusion	dgsn[e] <==> dgsn[c]		Transport, Extracellular	
DGSNtm	deoyguanosine transport in mitochondria	dgsn[c] <==> dgsn[m]		Transport, Mitochondrial	
DGTPtn	dGTP diffusion in nucleus	dgtp[c] <==> dgtp[n]		Transport, Nuclear	
DGULND	dehydro-L-gulonate decarboxylase	[c] : 3dhguln + h <==> co2 + xylu-L	4.1.1.34	Pentose and Glucuronate Interconversions	
DHAAt1r	dehydroascorbate transport (uniport)	dhdascb[e] <==> dhdascb[c]		Transport, Extracellular	(6515.1 or 6517.1 or 6513.1)
DHAPA	dihydroxyacetone phosphate acyltransferase	[c] : Rtotalcoa + dhap --> adhap_hs + coa	2.3.1.42	Triacylglycerol Synthesis	8443.1
DHAPAx	dihydroxyacetone phosphate acyltransferase	[x] : Rtotalcoa + dhap --> adhap_hs + coa	2.3.1.42	Triacylglycerol Synthesis	8443.1
DHCHOLESTANATEtm	lipid, flip-flop intracellular transport	dhcholestanate[m] <==> dhcholestanate[x]		Transport, Peroxisomal	
DHCR241r	24-dehydrocholesterol reductase [Precursor]	[r] : fadh2 + zymst --> fad + zymstnl		Cholesterol Metabolism	1718.1
DHCR242r	24-dehydrocholesterol reductase [Precursor]	[r] : chlstol + fadh2 --> fad + lthstrl		Cholesterol Metabolism	1718.1
DHCR243r	24-dehydrocholesterol reductase [Precursor]	[r] : dsmsterol + fadh2 --> chsterol + fad		Cholesterol Metabolism	1718.1
DHCR71r	7-dehydrocholesterol reductase	[r] : ddsmsterol + h + nadph --> dsmsterol + nadp	1.3.1.21	Cholesterol Metabolism	1717.1
DHCR72r	7-dehydrocholesterol reductase	[r] : 7dhchsterol + h + nadph --> chsterol + nadp	1.3.1.21	Cholesterol Metabolism	1717.1
DHCRD1	dihydroceramide desaturase	[c] : dhcrm_hs + nadp --> crm_hs + h + nadph		Sphingolipid Metabolism	(8560.1 or 8560.2)
DHCRD2	dihydroceramide desaturase	[c] : dhcrm_hs + fad --> crm_hs + fadh2		Sphingolipid Metabolism	(8560.1 or 8560.2)
DHDPBMTm	dihydroxydecaprenylbenzoate methyltransferase	[m] : 3dpdhb + amet --> 3dpdhb_me + ahcys + h		Ubiquinone Biosynthesis	51805.1
DHEASt	dehydroepiandrosterone sulfate transport via bicarbonate countertransport	dheas[e] + hco3[c] <==> dheas[c] + hco3[e]		Transport, Extracellular	(6579.1 or 10599.1 or 28234.1 or 11309.1)
DHEAStr	dheas intracellular transport	dheas[r] <==> dheas[c]		Transport, Extracellular	
DHEASULT	Dehydroepiandrosterone sulfotransferase	[c] : dhea + paps --> dheas + h + pap	2.8.2.2	Steroid Metabolism	(6783.1 or 6822.1)
DHFR	dihydrofolate reductase	[c] : dhf + h + nadph <==> nadp + thf	1.5.1.3	Folate Metabolism	1719.1
DHFtl	dihydrofolate reversible lysosomal transport	dhf[c] <==> dhf[l]		Transport, Lysosomal	

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
DHFtm	dihydrofolate reversible mitochondrial transport	dhf[c] <==> dhf[m]		Transport, Mitochondrial	
DHORD9	dihydoorotic acid dehydrogenase (quinone10)	dhor-S[c] + q10[m] --> orot[c] + q10h2[m]		Pyrimidine Biosynthesis	1723.1
DHORTS	dihydroorotase	[c] : dhor-S + h2o <==> cbasp + h	3.5.2.3	Pyrimidine Biosynthesis	790.1
DHPM1	dihydropyrimidinase (5,6-dihydrouracil)	[c] : 56dura + h2o --> cala + h	3.5.2.2	Pyrimidine Catabolism	(1807.1 or 1808.1 or 1809.1)
DHPM2	dihydropyrimidinase (dihydrothymine)	[c] : 56dthm + h2o --> 3uib + h	3.5.2.2	Pyrimidine Catabolism	
DHPR	6,7-dihydropteridine reductase	[c] : dhbpt + h + nadh --> nad + thbpt		Tetrahydrobiopterin	5860.1
DHPR2	6,7-dihydropteridine reduction	[c] : 5mthf + dhbpt --> h + mlthf + thbpt		Tetrahydrobiopterin	
DIDPtn	dIDP nuclear transport	didp[c] <==> didp[n]		Transport, Nuclear	
DIGALSGALSIDEte	digalsgalside_hs transport	digalsgalside_hs[c] <==> digalsgalside_hs[e]		Transport, Extracellular	
DIGALSGALSIDEtg	digalsgalside_hs intracellular transport	digalsgalside_hs[c] <==> digalsgalside_hs[g]		Transport, Golgi Apparatus	
DIGALSIDEtg	digalside_hs intracellular transport	digalside_hs[c] <==> digalside_hs[g]		Transport, Golgi Apparatus	
DIGALSIDEtl	digalside_hs intracellular transport	digalside_hs[c] <==> digalside_hs[l]		Transport, Lysosomal	
DINt	deoxyinosine transport via diffusion	din[e] <==> din[c]		Transport, Extracellular	
DITPtn	dITP nuclear transport	ditp[c] <==> ditp[n]		Transport, Nuclear	
DKMPPD	2,3-diketo-5-methylthio-1-phosphopentane degradation reaction	[c] : dkmpp + h2o + o2 --> 2kmb + for + (2) h + pi		Arginine and Proline Metabolism	
D-LACt2	D-lactate transport via proton symport	h[e] + lac-D[e] <==> h[c] + lac-D[c]		Transport, Extracellular	(6566.1 or 9194.1 or 23539.1 or 9123.1)
D-LACtm	D-lactate transport, mitochondrial	h[c] + lac-D[c] <==> h[m] + lac-D[m]		Transport, Mitochondrial	6566.1
DLNLCGCPT1	carnitine O-palmitoyltransferase	[c] : crn + dlnlcgcoa --> coa + dlnlcgcrn	2.3.1.21	Carnitine shuttle	(1375.4 or 1374.1 or 126129.1 or 1375.3 or 1375.2 or 1375.1)
DLNLCGCPT2	carnitine transferase	[m] : coa + dlnlcgcrn --> crn + dlnlcgcoa		Carnitine shuttle	1376.1
DLNLCGCRNt	transport into the mitochondria (carnitine)	dlnlcgcrn[c] --> dlnlcgcrn[m]		Carnitine shuttle	788.1
DLNLCGt	fatty acid transport via diffusion	dlnlcg[e] <==> dlnlcg[c]		Transport, Extracellular	
DMANTIPYRINEte	xenobiotic transport	dmantipyrine[e] <==> dmantipyrine[c]		Transport, Extracellular	
DMATT	dimethylallyltranstransferase	[c] : dmpp + ipdp --> grdp + ppi	2.5.1.1	Cholesterol Metabolism	9453.1
DMATTx	dimethylallyltranstransferase	[x] : dmpp + ipdp --> grdp + ppi	2.5.1.1	Cholesterol Metabolism	2224.1
DMGDHm	dimethylglycine dehydrogenase, mitochondrial	[m] : dmgly + fad + h2o --> fadh2 + fald + sarcs	1.5.99.2	Glycine, Serine, and Threonine Metabolism	29958.1
DMGtm	dimethylglycine transport via diffusion (cytosol to mitochondria)	dmgly[c] <==> dmgly[m]		Transport, Mitochondrial	
DMHPTCRNCPT1	carnitine fatty-acyl transferase	[c] : crn + dmhptcoa <==> coa + dmhptcrn	2.3.1.21	Carnitine shuttle	
DMHPTCRNCPT2	2,6 dimethylheptanoly CoA carnitine transferase	[m] : coa + dmhptcrn <==> crn + dmhptcoa		Carnitine shuttle	
DMHPTCRNt	2,6 dimethylheptanoyl crn transport	dmhptcrn[c] <==> dmhptcrn[m]		Carnitine shuttle	
DMHPTCRNte	2,6 dimethylheptanoyl carnitine transport	dmhptcrn[c] <==> dmhptcrn[e]		Transport, Extracellular	
DNADDP	Deaminido NAD diphosphatase	[c] : dnad + h2o --> amp + (2) h + nicrnt	3.6.1.9	NAD Metabolism	(5167.1 or 5168.1 or 5169.1)
DNADtn	dNAD transport, nuclear trhough pore	dnad[c] <==> dnad[n]		Transport, Nuclear	
DNAMTn	DNA (cytosine-5-)-methyltransferase, nucleus	[n] : amet + dna --> ahcys + dna5mtc + h	2.1.1.37	Methionine Metabolism	(1786.1 or 1787.1 or 1787.2 or 1787.3 or 1787.4 or 1787.5 or 1787.6 or 1788.1 or 1788.2 or 1788.3 or 1788.4 or 1789.1 or 1789.2 or 1789.3 or 1789.4)
DNAMTSEn	DNA (cytosine-5-)-methyltransferase, nucleus	[n] : dna + seasmet --> dna5mtc + h + seahcys	2.1.1.37	Selenoamino acid metabolism	(1786.1 or 1787.1 or 1787.2 or 1787.3 or 1787.4 or 1787.5 or 1787.6 or 1788.1 or 1788.2 or 1788.3 or 1788.4 or 1789.1 or 1789.2 or 1789.3 or 1789.4)
DNDPt10m	dADP transport via dCDP antiport	dadp[c] + dcdp[m] --> dadp[m] + dcdp[c]		Transport, Mitochondrial	60386.1
DNDPt11m	dADP transport via dGDP antiport	dadp[c] + dgdp[m] --> dadp[m] + dgdp[c]		Transport, Mitochondrial	60386.1
DNDPt12m	dADP transport via ADP antiport	adp[m] + dadp[c] --> adp[c] + dadp[m]		Transport, Mitochondrial	60386.1
DNDPt13m	dADP transport via ATP antiport	atp[m] + dadp[c] --> atp[c] + dadp[m]		Transport, Mitochondrial	60386.1
DNDPt14m	dUDP transport via dTDP antiport	dtdp[m] + dudp[c] --> dtdp[c] + dudp[m]		Transport, Mitochondrial	60386.1
DNDPt15m	dUDP transport via dGDP antiport	dgdp[m] + dudp[c] --> dgdp[c] + dudp[m]		Transport, Mitochondrial	60386.1
DNDPt16m	dUDP transport via dADP antiport	dadp[m] + dudp[c] --> dadp[c] + dudp[m]		Transport, Mitochondrial	60386.1
DNDPt17m	dUDP transport via dCDP antiport	dcdp[m] + dudp[c] --> dcdp[c] + dudp[m]		Transport, Mitochondrial	60386.1
DNDPt18m	dUDP transport via ADP antiport	adp[m] + dudp[c] --> adp[c] + dudp[m]		Transport, Mitochondrial	60386.1
DNDPt19m	dUDP transport via ATP antiport	atp[m] + dudp[c] --> atp[c] + dudp[m]		Transport, Mitochondrial	60386.1
DNDPt1m	dATP transport via ADP antiport	adp[m] + datp[c] --> adp[c] + datp[m]		Transport, Mitochondrial	60386.1
DNDPt20m	dTDP transport via ATP antiport	atp[m] + dtdp[c] --> atp[c] + dtdp[m]		Transport, Mitochondrial	60386.1
DNDPt21m	dTDP transport via ADP antiport	adp[m] + dtdp[c] --> adp[c] + dtdp[m]		Transport, Mitochondrial	60386.1
DNDPt22m	dTDP transport via dUDP antiport	dtdp[c] + dudp[m] --> dtdp[m] + dudp[c]		Transport, Mitochondrial	60386.1
DNDPt23m	dTDP transport via dGTP antiport	dgdp[m] + dtdp[c] --> dgdp[c] + dtdp[m]		Transport, Mitochondrial	60386.1
DNDPt24m	dTDP transport via dADP antiport	dadp[m] + dtdp[c] --> dadp[c] + dtdp[m]		Transport, Mitochondrial	60386.1
DNDPt25m	dTDP transport via dCDP antiport	dcdp[m] + dtdp[c] --> dcdp[c] + dtdp[m]		Transport, Mitochondrial	60386.1
DNDPt26m	dCDP transport via dUDP antiport	dcdp[c] + dudp[m] --> dcdp[m] + dudp[c]		Transport, Mitochondrial	60386.1
DNDPt27m	dCDP transport via dTDP antiport	dcdp[c] + dtdp[m] --> dcdp[m] + dtdp[c]		Transport, Mitochondrial	60386.1
DNDPt28m	dCDP transport via dGDP antiport	dcdp[c] + dgdp[m] --> dcdp[m] + dgdp[c]		Transport, Mitochondrial	60386.1
DNDPt29m	dCDP transport via dADP antiport	dadp[m] + dcdp[c] --> dadp[c] + dcdp[m]		Transport, Mitochondrial	60386.1
DNDPt2m	dATP transport via ATP antiport	atp[m] + datp[c] --> atp[c] + datp[m]		Transport, Mitochondrial	60386.1
DNDPt30m	dCDP transport via ADP antiport	adp[m] + dcdp[c] --> adp[c] + dcdp[m]		Transport, Mitochondrial	60386.1
DNDPt31m	dCDP transport via ATP antiport	atp[m] + dcdp[c] --> atp[c] + dcdp[m]		Transport, Mitochondrial	60386.1
DNDPt32m	dGDP transport via ATP antiport	atp[m] + dgdp[c] --> atp[c] + dgdp[m]		Transport, Mitochondrial	60386.1
DNDPt33m	dGDP transport via dUDP antiport	dgdp[c] + dudp[m] --> dgdp[m] + dudp[c]		Transport, Mitochondrial	60386.1
DNDPt34m	dGDP transport via dTDP antiport	dgdp[c] + dtdp[m] --> dgdp[m] + dtdp[c]		Transport, Mitochondrial	60386.1
DNDPt35m	dGDP transport via dADP antiport	dadp[m] + dgdp[c] --> dadp[c] + dgdp[m]		Transport, Mitochondrial	60386.1
DNDPt36m	dGDP transport via dCDP antiport	dcdp[m] + dgdp[c] --> dcdp[c] + dgdp[m]		Transport, Mitochondrial	60386.1
DNDPt37m	dUTP transport via dTDP antiport	dtdp[m] + dutp[c] --> dtdp[c] + dutp[m]		Transport, Mitochondrial	60386.1
DNDPt38m	dUTP transport via dUDP antiport	dudp[m] + dutp[c] --> dudp[c] + dutp[m]		Transport, Mitochondrial	60386.1
DNDPt39m	dUTP transport via dGDP antiport	dgdp[m] + dutp[c] --> dgdp[c] + dutp[m]		Transport, Mitochondrial	60386.1
DNDPt3m	dATP transport via dCDP antiport	datp[c] + dcdp[m] --> datp[m] + dcdp[c]		Transport, Mitochondrial	60386.1
DNDPt40m	dUTP transport via dADP antiport	dadp[m] + dutp[c] --> dadp[c] + dutp[m]		Transport, Mitochondrial	60386.1
DNDPt41m	dUTP transport via dCDP antiport	dcdp[m] + dutp[c] --> dcdp[c] + dutp[m]		Transport, Mitochondrial	60386.1
DNDPt42m	dUTP transport via ADP antiport	adp[m] + dutp[c] --> adp[c] + dutp[m]		Transport, Mitochondrial	60386.1

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
DNDPt43m	dUTP transport via ATP antiport	atp[m] + dutp[c] --> atp[c] + dutp[m]		Transport, Mitochondrial	60386.1
DNDPt44m	dTTP transport via ATP antiport	atp[m] + dttp[c] --> atp[c] + dttp[m]		Transport, Mitochondrial	60386.1
DNDPt45m	dTTP transport via ADP antiport	adp[m] + dttp[c] --> adp[c] + dttp[m]		Transport, Mitochondrial	60386.1
DNDPt46m	dTTP transport via dUDP antiport	dttp[c] + dudp[m] --> dttp[m] + dudp[c]		Transport, Mitochondrial	60386.1
DNDPt47m	dTTP transport via dTDP antiport	dtdp[m] + dttp[c] --> dtdp[c] + dttp[m]		Transport, Mitochondrial	60386.1
DNDPt48m	dTTP transport via dGDP antiport	dgdp[m] + dttp[c] --> dgdp[c] + dttp[m]		Transport, Mitochondrial	60386.1
DNDPt49m	dTTP transport via dADP antiport	dadp[m] + dttp[c] --> dadp[c] + dttp[m]		Transport, Mitochondrial	60386.1
DNDPt4m	dATP transport via dUDP antiport	datp[c] + dudp[m] --> datp[m] + dudp[c]		Transport, Mitochondrial	60386.1
DNDPt50m	dTTP transport via dCDP antiport	dcdp[m] + dttp[c] --> dcdp[c] + dttp[m]		Transport, Mitochondrial	60386.1
DNDPt51m	dCTP transport via dCDP antiport	dcdp[m] + dctp[c] --> dcdp[c] + dctp[m]		Transport, Mitochondrial	60386.1
DNDPt52m	dCTP transport via dUDP antiport	dctp[c] + dudp[m] --> dctp[m] + dudp[c]		Transport, Mitochondrial	60386.1
DNDPt53m	dCTP transport via dGDP antiport	dctp[c] + dgdp[m] --> dctp[m] + dgdp[c]		Transport, Mitochondrial	60386.1
DNDPt54m	dCTP transport via dADP antiport	dadp[m] + dctp[c] --> dadp[c] + dctp[m]		Transport, Mitochondrial	60386.1
DNDPt55m	dCTP transport via ADP antiport	adp[m] + dctp[c] --> adp[c] + dctp[m]		Transport, Mitochondrial	60386.1
DNDPt56m	dCTP transport via ATP antiport	atp[m] + dctp[c] --> atp[c] + dctp[m]		Transport, Mitochondrial	60386.1
DNDPt57m	dGTP transport via ATP antiport	atp[m] + dgtp[c] --> atp[c] + dgtp[m]		Transport, Mitochondrial	60386.1
DNDPt58m	dGTP transport via ADP antiport	adp[m] + dgtp[c] --> adp[c] + dgtp[m]		Transport, Mitochondrial	60386.1
DNDPt59m	dGTP transport via dADP antiport	dadp[m] + dgtp[c] --> dadp[c] + dgtp[m]		Transport, Mitochondrial	60386.1
DNDPt5m	dATP transport via dTDP antiport	datp[c] + dtdp[m] --> datp[m] + dtdp[c]		Transport, Mitochondrial	60386.1
DNDPt60m	dGTP transport via dUDP antiport	dgtp[c] + dudp[m] --> dgtp[m] + dudp[c]		Transport, Mitochondrial	60386.1
DNDPt61m	dGTP transport via dTDP antiport	dgtp[c] + dtdp[m] --> dgtp[m] + dtdp[c]		Transport, Mitochondrial	60386.1
DNDPt62m	dGTP transport via dGDP antiport	dgdp[m] + dgtp[c] --> dgdp[c] + dgtp[m]		Transport, Mitochondrial	60386.1
DNDPt63m	dGTP transport via dCDP antiport	dcdp[m] + dgtp[c] --> dcdp[c] + dgtp[m]		Transport, Mitochondrial	60386.1
DNDPt6m	dATP transport via dGDP antiport	datp[c] + dgdp[m] --> datp[m] + dgdp[c]		Transport, Mitochondrial	60386.1
DNDPt7m	dATP transport via dADP antiport	dadp[m] + datp[c] --> dadp[c] + datp[m]		Transport, Mitochondrial	60386.1
DNDPt8m	dADP transport via dUDP antiport	dadp[c] + dudp[m] --> dadp[m] + dudp[c]		Transport, Mitochondrial	60386.1
DNDPt9m	dADP transport via dTDP antiport	dadp[c] + dtdp[m] --> dadp[m] + dtdp[c]		Transport, Mitochondrial	60386.1
DOGULND1	2,3-dioxo-L-gulonate decarboxylase (L-lyxonate-forming)	[c] : 23doguln + h2o --> co2 + lyxnt		Ascorbate and Aldarate Metabolism	
DOGULND2	2,3-dioxo-L-gulonate decarboxylase (L-xylonate-forming)	[c] : 23doguln + h2o --> co2 + xylnt		Ascorbate and Aldarate Metabolism	
DOGULNO1	2,3-dioxo-L-gulonate:hydrogen peroxide oxireductase	[c] : 23doguln + h2o2 --> (2) h + oxa + thrnt		Ascorbate and Aldarate Metabolism	
DOGULNO2	2,3-dioxo-L-gulonate:hydrogen peroxide oxireductase	[c] : 23doguln + h2o --> eryth + h + oxa		Ascorbate and Aldarate Metabolism	
DOLASNT_Ler	Dolichyl-diphosphooligosaccharide:protein-L-asparagine oligopolysaccharidotransferase (liver)	[r] : Asn-X-Ser/Thr + (0.1) g3m8mpdol_L --> (0.1) doldp_L + g3m8masn + h	2.4.1.119	N-Glycan Biosynthesis	(6185.1 and 1650.1 and 1603.1 and 6184.1)
DOLASNT_Uer	Dolichyl-diphosphooligosaccharide:protein-L-asparagine oligopolysaccharidotransferase (uterus)	[r] : Asn-X-Ser/Thr + (0.1) g3m8mpdol_U --> (0.1) doldp_U + g3m8masn + h	2.4.1.119	N-Glycan Biosynthesis	(6185.1 and 1650.1 and 1603.1 and 6184.1)
DOLDPP_Ler	Dolichyl-diphosphate phosphohydrolase, human (liver)	[r] : (0.1) doldp_L + h2o --> (0.1) dolp_L + h + pi	3.6.1.43	N-Glycan Biosynthesis	57171.1
DOLDPP_Uer	Dolichyl-diphosphate phosphohydrolase, human (uterus)	[r] : (0.1) doldp_U + h2o --> (0.1) dolp_U + h + pi	3.6.1.43	N-Glycan Biosynthesis	57171.1
DOLGLCP_Lter	Dolichyl beta-D-glucosyl phosphate flippase (liver)	(0.1) dolglcp_L[c] --> (0.1) dolglcp_L[r]		N-Glycan Biosynthesis	
DOLGLCP_Uter	Dolichyl beta-D-glucosyl phosphate flippase (uterus)	(0.1) dolglcp_U[c] --> (0.1) dolglcp_U[r]		N-Glycan Biosynthesis	
DOLGPP_Ler	Dolichyl-beta-D-glucosyl-phosphate dolichylphosphohydrolase (liver)	[r] : (0.1) dolglcp_L + h2o --> (0.1) dolp_L + glc-D + h	3.1.4.48	N-Glycan Biosynthesis	
DOLGPP_Uer	Dolichyl-beta-D-glucosyl-phosphate dolichylphosphohydrolase (uterus)	[r] : (0.1) dolglcp_U + h2o --> (0.1) dolp_U + glc-D + h	3.1.4.48	N-Glycan Biosynthesis	
DOLICHOL_Lter	dolichol diffusion, human (liver)	(0.1) dolichol_L[r] <==> (0.1) dolichol_L[c]		N-Glycan Biosynthesis	
DOLICHOL_Uter	dolichol diffusion, human (uterus)	(0.1) dolichol_U[r] <==> (0.1) dolichol_U[c]		N-Glycan Biosynthesis	
DOLK_L	Dolichol kinase, human (liver)	[c] : ctp + (0.1) dolichol_L --> cdp + (0.1) dolp_L + h	2.7.1.108	N-Glycan Biosynthesis	
DOLK_U	Dolichol kinase, human (uterus)	[c] : ctp + (0.1) dolichol_U --> cdp + (0.1) dolp_U + h	2.7.1.108	N-Glycan Biosynthesis	
DOLMANP_Lter	dolichol-phosphate mannose flippase (liver)	(0.1) dolmanp_L[c] --> (0.1) dolmanp_L[r]		N-Glycan Biosynthesis	
DOLMANP_Uter	dolichol-phosphate mannose flippase (uterus)	(0.1) dolmanp_U[c] --> (0.1) dolmanp_U[r]		N-Glycan Biosynthesis	
DOLP_Lter	dolichol phosphate flippase (liver)	(0.1) dolp_L[r] --> (0.1) dolp_L[c]		N-Glycan Biosynthesis	
DOLP_Uter	dolichol phosphate flippase (uterus)	(0.1) dolp_U[r] --> (0.1) dolp_U[c]		N-Glycan Biosynthesis	
DOLPGT1_Ler	dolichyl-phosphate-glucose-glycolipid alpha-glucosyltransferase (liver)	[r] : (0.1) dolglcp_L + (0.1) m8mpdol_L --> (0.1) dolp_L + (0.1) g1m8mpdol_L + h		N-Glycan Biosynthesis	29929.1
DOLPGT1_Uer	dolichyl-phosphate-glucose-glycolipid alpha-glucosyltransferase (uterus)	[r] : (0.1) dolglcp_U + (0.1) m8mpdol_U --> (0.1) dolp_U + (0.1) g1m8mpdol_U + h		N-Glycan Biosynthesis	29929.1
DOLPGT2_Ler	dolichyl-phosphate-glucose-glycolipid alpha-glucosyltransferase (liver)	[r] : (0.1) dolglcp_L + (0.1) g1m8mpdol_L --> (0.1) dolp_L + (0.1) g2m8mpdol_L + h		N-Glycan Biosynthesis	(79053.1 or 79053.2 or 79053.3)
DOLPGT2_Uer	dolichyl-phosphate-glucose-glycolipid alpha-glucosyltransferase (uterus)	[r] : (0.1) dolglcp_U + (0.1) g1m8mpdol_U --> (0.1) dolp_U + (0.1) g2m8mpdol_U + h		N-Glycan Biosynthesis	(79053.1 or 79053.2 or 79053.3)
DOLPGT3_Ler	dolichyl-phosphate-glucose-glycolipid alpha-glucosyltransferase (liver)	[r] : (0.1) dolglcp_L + (0.1) g2m8mpdol_L --> (0.1) dolp_L + (0.1) g3m8mpdol_L + h		N-Glycan Biosynthesis	84920.1
DOLPGT3_Uer	dolichyl-phosphate-glucose-glycolipid alpha-glucosyltransferase (uterus)	[r] : (0.1) dolglcp_U + (0.1) g2m8mpdol_U --> (0.1) dolp_U + (0.1) g3m8mpdol_U + h		N-Glycan Biosynthesis	84920.1
DOLPH_Ler	Dolichol-phosphate phosphohydrolase, human (liver)	[r] : (0.1) dolp_L + h2o --> (0.1) dolichol_L + pi	3.1.3.51	N-Glycan Biosynthesis	
DOLPH_Uer	Dolichol-phosphate phosphohydrolase, human (uterus)	[r] : (0.1) dolp_U + h2o --> (0.1) dolichol_U + pi	3.1.3.51	N-Glycan Biosynthesis	
DOLPMT_L	Dolichyl-phosphate D-mannosyltransferase (liver)	[c] : (0.1) dolp_L + gdpmann --> (0.1) dolmanp_L + gdp	2.4.1.83	N-Glycan Biosynthesis	((8813.1 and 8818.2 and 54344.1) or (54344.2 and 8818.2 and 8813.1) or (8813.1 and 54344.2 and 8818.1) or (54344.1 and 8813.1 and 8818.1))
DOLPMT_U	Dolichyl-phosphate D-mannosyltransferase (uterus)	[c] : (0.1) dolp_U + gdpmann --> (0.1) dolmanp_U + gdp	2.4.1.83	N-Glycan Biosynthesis	((8813.1 and 8818.2 and 54344.1) or (54344.2 and 8818.2 and 8813.1) or (8813.1 and 54344.2 and 8818.1) or (54344.1 and 8813.1 and 8818.1))
DOLPMT1_Ler	dolichyl-phosphate-mannose-glycolipid alpha-mannosyltransferase (liver)	[r] : (0.1) dolmanp_L + (0.1) m4mpdol_L --> (0.1) dolp_L + h + (0.1) m5mpdol_L	2.4.1.130	N-Glycan Biosynthesis	(10195.1 or 10195.2 or 10195.3 or 10195.4)

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
DOLPMT1_Uer	dolichyl-phosphate-mannose-glycolipid alpha-mannosyltransferase (uterus)	[r] : (0.1) dolmanp_U + (0.1) m4mpdol_U --> (0.1) dolp_U + h + (0.1) m5mpdol_U	2.4.1.130	N-Glycan Biosynthesis	(10195.1 or 10195.2 or 10195.3 or 10195.4)
DOLPMT2_Ler	dolichyl-phosphate-mannose-glycolipid alpha-mannosyltransferase (liver)	[r] : (0.1) dolmanp_L + (0.1) m5mpdol_L --> (0.1) dolp_L + h + (0.1) m6mpdol_L	2.4.1.130	N-Glycan Biosynthesis	
DOLPMT2_Uer	dolichyl-phosphate-mannose-glycolipid alpha-mannosyltransferase (uterus)	[r] : (0.1) dolmanp_U + (0.1) m5mpdol_U --> (0.1) dolp_U + h + (0.1) m6mpdol_U	2.4.1.130	N-Glycan Biosynthesis	
DOLPMT3_Ler	dolichyl-phosphate-mannose-glycolipid alpha-mannosyltransferase (liver)	[r] : (0.1) dolmanp_L + (0.1) m6mpdol_L --> (0.1) dolp_L + h + (0.1) m7mpdol_L	2.4.1.130	N-Glycan Biosynthesis	79087.1
DOLPMT3_Uer	dolichyl-phosphate-mannose-glycolipid alpha-mannosyltransferase (uterus)	[r] : (0.1) dolmanp_U + (0.1) m6mpdol_U --> (0.1) dolp_U + h + (0.1) m7mpdol_U	2.4.1.130	N-Glycan Biosynthesis	79087.1
DOLPMT4_Ler	dolichyl-phosphate-mannose-glycolipid alpha-mannosyltransferase (liver)	[r] : (0.1) dolmanp_L + (0.1) m7mpdol_L --> (0.1) dolp_L + h + (0.1) m8mpdol_L	2.4.1.130	N-Glycan Biosynthesis	
DOLPMT4_Uer	dolichyl-phosphate-mannose-glycolipid alpha-mannosyltransferase (uterus)	[r] : (0.1) dolmanp_U + (0.1) m7mpdol_U --> (0.1) dolp_U + h + (0.1) m8mpdol_U	2.4.1.130	N-Glycan Biosynthesis	
DOPABMO	dopamine beta-monooxygenase	[c] : ascb-L + dopa + o2 --> dhdascb + h2o + nrpphr	1.14.17.1	Tyrosine metabolism	(26002.1 or 1621.1)
DOPACHRMISO	L-dopachrome isomerase 1	[c] : (2) 2c23dh56dhoxin + o2 --> (2) L-dpchrm + (2) h2o		Tyrosine metabolism	7299.1
DOPAMT	Dopamine:amet O-methyltransferase	[c] : amet + dopa --> 3moxtyr + ahcys + h	2.1.1.6	Tyrosine metabolism	(1312.1 or 1312.2)
DOPAQNISO1	Dopaquinone isomerase 1	[c] : dopaqn <==> 2c23dh56dhoxin + h		Tyrosine metabolism	
DOPASFt	Dopamine 3-0-sulfate transport (diffusion)	dopasf[c] --> dopasf[e]		Transport, Extracellular	
DOPASULT	Dopamine Sulfotransferase	[c] : dopa + paps --> dopasf + h + pap	2.8.2.1	Tyrosine metabolism	(6817.1 or 6817.2 or 6817.3 or 6817.4 or 6817.5 or 6799.1 or 6799.2 or 6818.1 or 6818.2 or 6818.3)
DOPAt4(2)r	Dopamine reversible transport in via sodium symport (1:2)	dopa[e] + (2) na1[e] <==> dopa[c] + (2) na1[c]		Transport, Extracellular	(6530.1 or 6531.1)
DOPAtu	Dopamine uniport	dopa[e] <==> dopa[c]		Transport, Extracellular	(6582.1 or 6582.2 or 6581.1)
DOPAVESSEC	Dopamine secretion via secretory vesicle (ATP driven)	(2) atp[c] + (3) dopa[c] + (2) h2o[c] --> (2) adp[c] + (3) dopa[e] + (2) h[c] + (2) pi[c]		Transport, Extracellular	(6570.1 or 6571.1)
DORNOp	D-ornithine oxidase, perixosomal	[x] : h2o + o2 + orn-D --> 5a2opntn + h2o2 + nh4	1.4.3.3	D-arg and D-orn metabolism	1610.1
DPCOAK	dephospho-CoA kinase	[c] : atp + dpcoa --> adp + coa + h	2.7.1.24	CoA Biosynthesis	80347.1
DPCOAPP	pyrophasphatase (dephospho-CoA)	[c] : dpcoa + h2o --> amp + (2) h + pan4p		CoA Catabolism	
DPCOAtl	dephospho-CoA transport from lysosome via diffusion	dpcoa[l] <==> dpcoa[c]		Transport, Lysosomal	
DPGase	Diphosphoglycerate phosphatase	[c] : 23dpg + h2o --> 3pg + pi	3.1.3.13	Glycolysis/Gluconeogenesis	(5223.1 or 5224.1 or 5224.2 or 669.2 or 669.1)
DPGM	Diphosphoglyceromutase	[c] : 13dpg <==> 23dpg + h		Glycolysis/Gluconeogenesis	(5223.1 or 5224.1 or 5224.2 or 669.1 or 669.2)
DPHMBDCm	3-Decaprenyl-4-hydroxy-5-methoxybenzoate decarboxylation	[m] : 3dpdhb_me + h --> 2dp6mep + co2		Ubiquinone Biosynthesis	
DPMVDx	diphosphomevalonate decarboxylase	[x] : 5dpmev + atp --> adp + co2 + ipdp + pi	4.1.1.33	Cholesterol Metabolism	4597.1
DPPS	decaprenyl synthase	[c] : frdp + (7) ipdp --> decdp + (7) ppi		Miscellaneous	
DPROOp	D-proline oxidase, perixosomal	[x] : o2 + pro-D --> 1p2cbxl + h + h2o2		Arginine and Proline Metabolism	1610.1
DRBK	Deoxyribokinase	[c] : atp + drib --> 2dr5p + adp + h	2.7.1.15	Pentose Phosphate Pathway	64080.1
DRIBt	deoxyribose transport via diffusion	drib[e] <==> drib[c]		Transport, Extracellular	
DRPA	deoxyribose-phosphate aldolase	[c] : 2dr5p --> acald + g3p	4.1.2.4	Pentose Phosphate Pathway	
DSAT	dihydrosphingosine N-acyltransferase	[c] : Rtotalcoa + sphgn --> coa + dhcrm_hs + h		Sphingolipid Metabolism	
DTDPtn	dTDP nuclear transport	dtdp[c] <==> dtdp[n]		Transport, Nuclear	
DTMPK	dTMP kinase	[c] : atp + dtmp <==> adp + dtdp	2.7.4.9	Nucleotides	1841.1
DTTPtn	dTTP diffusion in nucleus	dttp[c] <==> dttp[n]		Transport, Nuclear	
DUDPtn	dUDP nuclear transport	dudp[c] <==> dudp[n]		Transport, Nuclear	
DUMPtn	dUMP nuclear transport	dump[c] <==> dump[n]		Transport, Nuclear	
DURAD	dihydrouracil dehydrogenase (NADP)	[c] : 56dura + nadp <==> h + nadph + ura	1.3.1.2	Pyrimidine Catabolism	1806.1
DURAD2	dihydrothymin dehydrogenase (NADP)	[c] : 56dthm + nadp <==> h + nadph + thym	1.3.1.2	Pyrimidine Catabolism	1806.1
DURIK1	deoxyuridine kinase (ATP:Deoxyuridine)	[c] : atp + duri --> adp + dump + h		Nucleotides	(7083.1 or 7084.1)
DURIK1m	deoxyuridine kinase (ATP:Deoxyuridine), mitochondrial	[m] : atp + duri --> adp + dump + h		Nucleotides	7084.1
DURIPP	deoxyuridine phosphorylase	[c] : duri + pi <==> 2dr1p + ura		Nucleotides	(4860.1 or 151531.1)
DURIt	deoxyuridine transport via diffusion	duri[e] <==> duri[c]		Transport, Extracellular	
DURItn	deoxyuridine transport in nucleus	duri[c] <==> duri[n]		Transport, Nuclear	
DUTPDPm	dUTP diphosphatase	[m] : dutp + h2o --> dump + h + ppi	3.6.1.23	Nucleotides	1854.1
DUTPDPn	dUTP diphosphatase, nuclear	[n] : dutp + h2o --> dump + h + ppi	3.6.1.23	Nucleotides	1854.1
EAFLATOXINte	xenobiotic transport	eaflatoxin[e] <==> eaflatoxin[c]		Transport, Extracellular	
EBASTINEOHte	xenobiotic transport	ebastineoh[e] <==> ebastineoh[c]		Transport, Extracellular	
EBASTINEOHtr	xenobiotic transport	ebastineoh[r] <==> ebastineoh[c]		Transport, Endoplasmic Reticular	
EBASTINEte	xenobiotic transport	ebastine[e] <==> ebastine[c]		Transport, Extracellular	
EBASTINEtr	xenobiotic transport	ebastine[r] <==> ebastine[c]		Transport, Endoplasmic Reticular	
EBP1r	3-beta-hydroxysteroid-delta(8),delta(7)-isomerase	[r] : zymst --> chlstol	5.3.3.5	Cholesterol Metabolism	10682.1
EBP2r	3-beta-hydroxysteroid-delta(8),delta(7)-isomerase	[r] : zymstnl --> lthstrl	5.3.3.5	Cholesterol Metabolism	10682.1
ECGISOr	Ecgonine isomerase (ER)	[r] : ecgon <==> pecgon		Alkaloid biosynthesis II	
ECOAH12m	3-hydroxyacyl-CoA dehydratase (3-hydroxyisobutyryl-CoA) (mitochondria)	[m] : 2mp2coa + h2o <==> 3hibutcoa	4.2.1.17	Valine, Leucine, and Isoleucine Metabolism	(1892.1 or (3030.1 and 3032.1))
ECOAH1m	3-hydroxyacyl-CoA dehydratase (3-hydroxybutanoyl-CoA) (mitochondria)	[m] : 3hbcoa <==> b2coa + h2o	4.2.1.17	Tryptophan metabolism	(549.1 or 1892.1 or (3032.1 and 3030.1))
ECOAH1x	3-hydroxyacyl-CoA dehydratase (3-hydroxybutanoyl-CoA) (perioxisome)	[x] : 3hbcoa <==> b2coa + h2o	4.2.1.17	Tryptophan metabolism	(1891.1 or 1962.1)
ECOAH9m	2-Methylprop-2-enoyl-CoA (2-Methylbut-2-enoyl-CoA), mitochondrial	[m] : 2mb2coa + h2o <==> 3hmbcoa	4.2.1.17	Valine, Leucine, and Isoleucine Metabolism	(1892.1 or (3030.1 and 3032.1))
EGMESTr	ecgonine methyl esterase (ER)	[r] : egme + h2o --> ecgon + h + meoh		Alkaloid biosynthesis II	13.1
EHGLAT	L-erythro-4-Hydroxyglutamate:2-oxoglutarate aminotransferase	[c] : akg + e4hglu --> 4h2oglt + glu-L	2.6.1.1	Arginine and Proline Metabolism	2805.1
EHGLAT2m	L-erythro-4-Hydroxyglutamate:2-oxoglutarate aminotransferase 2, mitochondrial	[m] : e4hglu + oaa --> 4h2oglt + asp-L	2.6.1.21	Arginine and Proline Metabolism	2806.1
EHGLATm	L-erythro-4-Hydroxyglutamate:2-oxoglutarate aminotransferase, mitochondrial	[m] : akg + e4hglu --> 4h2oglt + glu-L	2.6.1.1	Arginine and Proline Metabolism	2806.1
EICOSTETCPT1	carnitine O-palmitoyltransferase	[c] : crn + eicostetcoa --> coa + eicostetcrn	2.3.1.21	Carnitine shuttle	(1375.4 or 1374.1 or 126129.1 or 1375.3 or 1375.2 or 1375.1)

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
EICOSTETCPT2	carnitine transferase	[m] : coa + eicostetcrn --> crn + eicostetcoa		Carnitine shuttle	1376.1
EICOSTETCRNt	transport into the mitochondria (carnitine)	eicostetcrn[c] --> eicostetcrn[m]		Carnitine shuttle	788.1
EICOSTETt	fatty acid transport via diffusion	eicostet[e] <==> eicostet[c]		Transport, Extracellular	
ELAIDCPT1	carnitine O-palmitoyltransferase	[c] : crn + od2coa --> coa + elaidcrn	2.3.1.21	Carnitine shuttle	(1375.4 or 1374.1 or 126129.1 or 1375.3 or 1375.2 or 1375.1)
ELAIDCPT2	carnitine transferase	[m] : coa + elaidcrn --> crn + od2coa		Carnitine shuttle	1376.1
ELAIDCRNt	transport into the mitochondria (carnitine)	elaidcrn[c] --> elaidcrn[m]		Carnitine shuttle	788.1
ELAIDt	fatty acid transport via diffusion	elaid[e] <==> elaid[c]		Transport, Extracellular	
ENGASE	endo-beta-N-acetylglucosaminidase	[c] : h2o + s2l2n2m2m --> acgam + s2l2n2m2mn	3.2.1.96	N-Glycan Degradation	64772.1
ENGASE2	endo-beta-N-acetylglucosaminidase	[c] : h2o + n2m2nm --> acgam + n2m2nmn	3.2.1.96	N-Glycan Degradation	64772.1
ENGASE2ly	endo-beta-N-acetylglucosaminidase, lysosomal	[l] : h2o + n2m2nm --> acgam + n2m2nmn	3.2.1.96	N-Glycan Degradation	
ENGASE3ly	endo-beta-N-acetylglucosaminidase, lysosomal	[l] : h2o + ksi_deg2 --> acgam + ksi_deg3	3.2.1.96	Keratan sulfate degradation	
ENGASEly	endo-beta-N-acetylglucosaminidase, lysosomal	[l] : h2o + s2l2n2m2m --> acgam + s2l2n2m2mn	3.2.1.96	N-Glycan Degradation	
ENMAN1g	Endomannosidase (glc1man-producing), Golgi apparatus	[g] : g1m8masn + h2o --> glc1man + m7masnA		N-Glycan Biosynthesis	
ENMAN2g	Endomannosidase (glc2man-producing), Golgi apparatus	[g] : g2m8masn + h2o --> glc2man + m7masnA		N-Glycan Biosynthesis	
ENMAN3g	Endomannosidase (glc3man-producing), Golgi apparatus	[g] : g3m8masn + h2o --> glc3man + m7masnA		N-Glycan Biosynthesis	
ENMAN4g	Endomannosidase (m6masnC-producing), Golgi apparatus	[g] : g1m7masnC + h2o --> glc1man + m6masnC		N-Glycan Biosynthesis	
ENMAN5g	Endomannosidase (m6masnB2-producing), Golgi apparatus	[g] : g1m7masnB + h2o --> glc1man + m6masnB2		N-Glycan Biosynthesis	
ENMAN6g	Endomannosidase (m5masnB1-producing), Golgi apparatus	[g] : g1m6masnB1 + h2o --> glc1man + m5masnB1		N-Glycan Biosynthesis	
ENO	enolase	[c] : 2pg <==> h2o + pep	4.2.1.11	Glycolysis/Gluconeogenesis	(2027.1 or 2027.2 or 26237.1 or 2023.1 or 2026.1)
EPCTX	ethanolamine-phosphate cytidylyltransferase	[c] : 2ameph + ctp + h --> cmp2amep + ppi	2.7.7.14	Glycerophospholipid Metabolism	5833.1
ESTRADIOLGLCt	estradiol glucuronide transport via bicarbonate countertransport	estradiolglc[e] + hco3[c] <==> estradiolglc[c] + hco3[e]		Transport, Extracellular	(28231.1 or 6579.1 or 10599.1 or 28234.1 or 53919.1)
ESTRADIOLGLCt2	17-beta-D-glucuronide transport (ATP-dependent)	atp[c] + estradiolglc[c] + h2o[c] --> adp[c] + estradiolglc[e] + h[c] + pi[c]		Transport, Extracellular	10257.1
ESTRADIOLGLCtr	glucuronidated compound transport	estradiolglc[c] <==> estradiolglc[r]		Transport, Endoplasmic Reticular	
ESTRADIOLtr	estradiol intracellular transport	estradiol[r] <==> estradiol[c]		Transport, Endoplasmic Reticular	
ESTRIOLGLCte	glucuronidated compound transport	atp[c] + estriolglc[c] + h2o[c] --> adp[c] + estriolglc[e] + h[c] + pi[c]		Transport, Extracellular	4363.1
ESTRIOLGLCtr	glucuronidated compound transport	estriolglc[c] <==> estriolglc[r]		Transport, Endoplasmic Reticular	
ESTRIOLtr	estriol intracellular transport	estriol[r] <==> estriol[c]		Transport, Endoplasmic Reticular	
ESTRONEGLCt	ABC transporter	atp[c] + estroneglc[c] + h2o[c] --> adp[c] + estroneglc[e] + h[c] + pi[c]		Transport, Extracellular	(8714.1 or 8714.2 or 8714.3)
ESTRONEGLCtr	glucuronidated compound transport	estroneglc[c] <==> estroneglc[r]		Transport, Endoplasmic Reticular	
ESTRONESt	estrone 3-sulfate transport via bicarbonate countertransport	estrones[e] + hco3[c] <==> estrones[c] + hco3[e]		Transport, Extracellular	(28231.1 or 6579.1 or 10599.1 or 28234.1 or 11309.1 or 28232.1 or 53919.1)
ESTRONESt2	estrone-3-sulfate transport via sodium cotransport	estrones[e] + (2) na1[e] --> estrones[c] + (2) na1[c]		Transport, Extracellular	6554.1
ESTRONEtr	estrone intracellular transport	estrone[r] <==> estrone[c]		Transport, Endoplasmic Reticular	
ESTSULT	Estrogen sulfotransferase	[c] : estrone + paps --> estrones + h + pap	2.8.2.4	Steroid Metabolism	(6817.1 or 6817.2 or 6817.3 or 6817.4 or 6817.5 or 6783.1)
ETF	electron transfer flavoprotein	[m] : etfox + fadh2 --> etfrd + fad		Fatty acid oxidation	((2108.1 and 2109.2) or (2108.1 and 2109.1))
ETFQO	Electron transfer flavoprotein-ubiquinone oxidoreductase	[m] : etfrd + q10 --> etfox + q10h2	1.5.5.1	Fatty acid oxidation	2110.1
ETHAK	Ethanolamine kinase	[c] : atp + etha --> adp + ethamp + h	2.7.1.82	Glycerophospholipid Metabolism	(55500.1 or 55224.1 or 1119.1 or 1119.2)
ETHP	ethanolamine phosphate phosphatase	[c] : ethamp + h2o --> etha + pi		Glycerophospholipid Metabolism	162466.1
ETOHMO	ethanol monooxygenase	[c] : etoh + h + nadph + o2 --> acald + (2) h2o + nadp		Glycolysis/Gluconeogenesis	1571.1
ETOHt	ethanol reversible transport	etoh[e] <==> etoh[c]		Transport, Extracellular	
ETOHtx	ethanol reversible peroxisomal transport	etoh[c] <==> etoh[x]		Transport, Peroxisomal	
F1PGT	fucose-1-phosphate guanylyltransferase	[c] : fuc1p-L + gtp + h <==> gdpfuc + ppi	2.7.7.30	Fructose and Mannose Metabolism	8790.1
F6Tg	glycoprotein 6-alpha-L-fucosyltransferase	[g] : gdpfuc + n2m2masn --> fn2m2masn + gdp + h	2.4.1.68	N-Glycan Biosynthesis	(2530.1 or 2530.2 or 2530.3 or 2530.4 or 2530.5)
FA120ACPH	fatty-acyl-ACP hydrolase	[c] : ddcaACP + h2o <==> ACP + ddca + h	3.1.2.14	Fatty Acid Metabolism	55301.1
FA140ACPH	fatty-acyl-ACP hydrolase	[c] : h2o + myrsACP <==> ACP + h + ttdca	3.1.2.14	Fatty Acid Metabolism	55301.1
FA141ACPH	fatty-acyl-ACP hydrolase	[c] : h2o + tdeACP <==> ACP + h + ttdcea	3.1.2.14	Fatty Acid Metabolism	55301.1
FA160ACPH	fatty-acyl-ACP hydrolase	[c] : h2o + palmACP <==> ACP + h + hdca	3.1.2.14	Fatty Acid Metabolism	55301.1
FA161ACPH	fatty-acyl-ACP hydrolase	[c] : h2o + hdeACP <==> ACP + h + hdcea	3.1.2.14	Fatty Acid Metabolism	55301.1
FA180ACPH	fatty-acyl-ACP hydrolase	[c] : h2o + ocdcaACP <==> ACP + h + ocdca	3.1.2.14	Fatty Acid Metabolism	55301.1
FA181ACPH	fatty-acyl-ACP hydrolase	[c] : h2o + octeACP <==> ACP + h + ocdcea	3.1.2.14	Fatty Acid Metabolism	55301.1
FA1821ACPH	fatty-acyl-ACP hydrolase	[c] : h2o + lnlcACP <==> ACP + h + lnlc	3.1.2.14	Fatty Acid Metabolism	
FA1822ACPH	fatty-acyl-ACP hydrolase	[c] : h2o + lneldcACP <==> ACP + h + lneldc	3.1.2.14	Fatty Acid Metabolism	
FA182ACPH	fatty-acyl-ACP hydrolase	[c] : h2o + ocdcyaACP <==> ACP + h + ocdcya	3.1.2.14	Fatty Acid Metabolism	55301.1
FACOAL140i	fatty-acid--CoA ligase (tetradecanoate)	[c] : atp + coa + ttdca --> amp + ppi + tdcoa	6.2.1.3	Fatty acid activation	2181.1
FACOAL150	fatty-acid--CoA ligase	[c] : atp + coa + ptdca <==> amp + ppi + ptdcacoa	6.2.1.3	Fatty acid activation	(2180.1 or 2181.1 or 2181.2 or 2182.1 or 22305.1 or 22305.2)
FACOAL160i	C160 fatty acid activation	[c] : atp + coa + hdca --> amp + pmtcoa + ppi	6.2.1.3	Fatty acid activation	(51703.1 or 2180.1 or 22305.1 or 22305.2 or 2181.1 or 2181.2)
FACOAL161	fatty-acid--CoA ligase (hexadecenoate)	[c] : atp + coa + hdcea <==> amp + hdcoa + ppi	6.2.1.3	Fatty acid activation	2180.1
FACOAL170	fatty-acid--CoA ligase	[c] : atp + coa + hpdca <==> amp + hpdcacoa + ppi	6.2.1.3	Fatty acid activation	(2180.1 or 2181.1 or 2181.2 or 2182.1 or 22305.1 or 22305.2)

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
FACOAL180i	C180 fatty acid activation	[c] : atp + coa + ocdca --> amp + ppi + stcoa	6.2.1.3	Fatty acid activation	(51703.1 or 2180.1 or 2181.1 or 2181.2 or 22305.1 or 22305.2)
FACOAL1812	fatty-acid--CoA ligase	[c] : atp + coa + vacc <==> amp + ppi + vaccoa	6.2.1.3	Fatty acid activation	2180.1
FACOAL1813	fatty-acid--CoA ligase	[c] : atp + coa + elaid <==> amp + od2coa + ppi	6.2.1.3	Fatty acid activation	2180.1
FACOAL181i	C181 fatty acid activation	[c] : atp + coa + ocdcea --> amp + odecoa + ppi	6.2.1.3	Fatty acid activation	(2180.1 or 2181.1 or 2181.2)
FACOAL1821	fatty-acid--CoA ligase	[c] : atp + coa + lnlc <==> amp + lnlccoa + ppi	6.2.1.3	Fatty acid activation	2180.1
FACOAL1822	fatty-acid--CoA ligase	[c] : atp + coa + lneldc <==> amp + lneldccoa + ppi	6.2.1.3	Fatty acid activation	2180.1
FACOAL1831	fatty-acid--CoA ligase	[c] : atp + coa + lnlncg <==> amp + lnlncgcoa + ppi	6.2.1.3	Fatty acid activation	2180.1
FACOAL1832	fatty-acid--CoA ligase	[c] : atp + coa + lnlnca <==> amp + lnlncacoa + ppi	6.2.1.3	Fatty acid activation	2180.1
FACOAL184	fatty-acid--CoA ligase	[c] : atp + coa + strdnc <==> amp + ppi + strdnccoa	6.2.1.3	Fatty acid activation	2180.1
FACOAL191	fatty-acid--CoA ligase	[c] : atp + coa + prist --> amp + ppi + pristcoa	6.2.1.3	Fatty acid activation	11001.1
FACOAL200	fatty-acid--CoA ligase	[c] : arach + atp + coa <==> amp + arachcoa + ppi	6.2.1.3	Fatty acid activation	2180.1
FACOAL203	fatty-acid--CoA ligase	[c] : atp + coa + dlnlcg <==> amp + dlnlcgcoa + ppi	6.2.1.3	Fatty acid activation	2180.1
FACOAL204	fatty-acid--CoA ligase	[c] : arachd + atp + coa <==> amp + arachdcoa + ppi	6.2.1.3	Fatty acid activation	2180.1
FACOAL2042	fatty-acid--CoA ligase	[c] : atp + coa + eicostet <==> amp + eicostetcoa + ppi	6.2.1.3	Fatty acid activation	2180.1
FACOAL204i	arachidonic acid activation	[c] : arachd + atp + coa --> amp + arachdcoa + ppi	6.2.1.3	Fatty acid activation	(2181.1 or 2182.1 or 2180.1 or 2181.2 or 2182.2 or 22305.1 or 22305.2)
FACOAL205	fatty-acid--CoA ligase	[c] : atp + coa + tmndnc <==> amp + ppi + tmndnccoa	6.2.1.3	Fatty acid activation	2180.1
FACOAL206	fatty-acid--CoA ligase	[c] : atp + coa + phyt <==> amp + phytcoa + ppi	6.2.1.3	Fatty acid activation	11001.1
FACOAL224	fatty-acid--CoA ligase	[c] : adrn + atp + coa <==> adrncoa + amp + ppi	6.2.1.3	Fatty acid activation	2180.1
FACOAL2251	fatty-acid--CoA ligase	[c] : atp + coa + dcsptn1 <==> amp + dcsptn1coa + ppi	6.2.1.3	Fatty acid activation	2180.1
FACOAL2252	fatty-acid--CoA ligase	[c] : atp + clpnd + coa <==> amp + clpndcoa + ppi	6.2.1.3	Fatty acid activation	2180.1
FACOAL226	fatty-acid--CoA ligase	[c] : atp + coa + crvnc <==> amp + c226coa + ppi	6.2.1.3	Fatty acid activation	2180.1
FACOAL226i	C226 fatty acid activation	[c] : atp + coa + crvnc --> amp + c226coa + ppi	6.2.1.3	Fatty acid activation	
FACOAL240	fatty-acid--CoA ligase	[c] : atp + coa + lgnc <==> amp + lgnccoa + ppi	6.2.1.3	Fatty acid activation	2180.1
FACOAL241	fatty-acid--CoA ligase	[c] : atp + coa + nrvnc <==> amp + nrvnccoa + ppi	6.2.1.3	Fatty acid activation	2180.1
FACOAL244_1	fatty-acid--CoA ligase	[c] : atp + coa + tettet6 <==> amp + ppi + tettet6coa	6.2.1.3	Fatty acid activation	2180.1
FACOAL245_1	fatty-acid--CoA ligase	[c] : atp + coa + tetpent6 <==> amp + ppi + tetpent6coa	6.2.1.3	Fatty acid activation	2180.1
FACOAL245_2	fatty-acid--CoA ligase	[c] : atp + coa + tetpent3 <==> amp + ppi + tetpent3coa	6.2.1.3	Fatty acid activation	2180.1
FACOAL246_1	fatty-acid--CoA ligase	[c] : atp + coa + tethex3 <==> amp + ppi + tethex3coa	6.2.1.3	Fatty acid activation	2180.1
FACOAL260	fatty-acid--CoA ligase (n-C26:0)	[c] : atp + coa + hexc <==> amp + hexccoa + ppi	6.2.1.3	Fatty acid activation	2180.1
FACOAL40im	fatty-acid--CoA ligase (butanoate), mitochondrial	[m] : atp + but + coa --> amp + btcoa + ppi	6.2.1.2	Fatty acid activation	116285.1
FACOAL80i	fatty-acid--CoA ligase (octanoate)	[c] : atp + coa + octa --> amp + occoa + ppi	6.2.1.2	Fatty acid activation	(2181.1 or 2181.2)
FADDP	FAD diphosphatase	[c] : fad + h2o --> amp + fmn + (2) h	3.6.1.9	Riboflavin Metabolism	5167.1
FADH2tru	FADH2 transporter, endoplasmic reticulum	fadh2[c] --> fadh2[r]		Transport, Endoplasmic Reticular	
FADH2tx	FADH2 transporter, peroxisomal	fadh2[c] <==> fadh2[x]		Transport, Peroxisomal	
FADtru	FAD transporter, endoplasmic reticulum	fad[r] --> fad[c]		Transport, Endoplasmic Reticular	
FADtx	FAD transporter, peroxisomal	fad[c] <==> fad[x]		Transport, Peroxisomal	
FAEL183	fatty-acyl-CoA elongation (n-C18:3CoA)	[c] : (5) h + lnlncgcoa + malcoa + (4) nadph + o2 --> co2 + coa + dlnlcgcoa + (3) h2o + (4) nadp	2.3.1.86	Fatty acid elongation	6785.1
FAEL184	fatty-acyl-CoA elongation (n-C20:4CoA)	[c] : (5) h + malcoa + (4) nadph + o2 + strdnccoa --> co2 + coa + eicostetcoa + (3) h2o + (4) nadp	2.3.1.86	Fatty acid elongation	6785.1
FAEL204	fatty-acyl-CoA elongation (n-C20:4CoA)	[c] : arachdcoa + (5) h + malcoa + (4) nadph + o2 --> adrncoa + co2 + coa + (3) h2o + (4) nadp	2.3.1.86	Fatty acid elongation	6785.1
FAEL205	fatty-acyl-CoA elongation (n-C20:5CoA)	[c] : (5) h + malcoa + (4) nadph + o2 + tmndnccoa --> clpndcoa + co2 + coa + (3) h2o + (4) nadp	2.3.1.86	Fatty acid elongation	6785.1
FAH1	Fatty acid omega-hydroxylase	[c] : ddca + h + nadph + o2 --> h2o + nadp + whddca		CYP Metabolism	1579.1
FAH2	Fatty acid omega-hydroxylase	[c] : h + nadph + o2 + ttdca --> h2o + nadp + whttdca		CYP Metabolism	1579.1
FAH3	Fatty acid omega-hydroxylase	[c] : h + hdca + nadph + o2 --> h2o + nadp + whhdca		CYP Metabolism	1579.1
FALDH	formaldehyde dehydrogenase	[c] : fald + gthrd + nad <==> Sfglutth + h + nadh	1.2.1.1	Tyrosine metabolism	128.1
FALDtly	formaldehyde transport via diffusion (lysosomall)	fald[l] <==> fald[c]		Transport, Lysosomal	
FALDtm	formaldehyde transport via diffusion (mitochondrial)	fald[m] <==> fald[c]		Transport, Mitochondrial	
FAOXC11	Beta oxidation of long chain fatty acid	[m] : coa + dmnoncoa + h2o + nad --> accoa + dmhptcoa + h + nadh	1.3.99.3	Fatty acid oxidation	34.1
FAOXC140	Beta oxidation of long chain fatty acid	[m] : (6) coa + (6) fad + (6) h2o + (6) nad + tdcoa --> (7) accoa + (6) fadh2 + (6) h + (6) nadh	1.3.99.3	Fatty acid oxidation	(35.1 or 34.1)
FAOXC150m	Beta oxidation of long chain fatty acid (odd chain)	[m] : (6) coa + (6) fad + (6) h2o + (6) nad + ptdcacoa --> (6) accoa + (6) fadh2 + (6) h + (6) nadh + ppcoa	1.3.99.3	Fatty acid oxidation	(35.1 or 34.1)
FAOXC160	Beta oxidation of long chain fatty acid	[m] : (7) coa + (7) fad + (7) h2o + (7) nad + pmtcoa --> (8) accoa + (7) fadh2 + (7) h + (7) nadh	1.3.99.3	Fatty acid oxidation	(34.1 or 35.1)
FAOXC16080m	Beta oxidation of long chain fatty acid	[m] : (4) coa + (4) fad + (4) h2o + (4) nad + pmtcoa --> (4) accoa + (4) fadh2 + (4) h + (4) nadh + occoa	1.3.99.3	Fatty acid oxidation	(35.1 or 34.1)
FAOXC16080x	Beta oxidation of long chain fatty acid	[x] : (4) coa + (4) h2o + (4) nad + (4) o2 + pmtcoa --> (4) accoa + (4) h + (4) h2o2 + (4) nadh + occoa	1.3.99.3	Fatty acid oxidation, peroxisome	((51.1 and 1962.1 and 30.1) or (51.2 and 30.1 and 3295.1) or (1962.1 and 51.2 and 30.1) or (51.1 and 30.1 and 3295.1))
FAOXC161802m	Beta oxidation fatty acid	[m] : (4) coa + (3) fad + (4) h2o + hdd2coa + (4) nad --> (4) accoa + (3) fadh2 + (4) h + (4) nadh + occoa	1.3.99.3	Fatty acid activation	(34.1 or 35.1)
FAOXC16180m	Beta oxidation fatty acid	[m] : (4) coa + (3) fad + (4) h2o + hdcoa + (4) nad --> (4) accoa + (3) fadh2 + (4) h + (4) nadh + occoa	1.3.99.3	Fatty acid oxidation	(35.1 or 34.1)
FAOXC170m	Beta oxidation of long chain fatty acid (odd chain)	[m] : (7) coa + (7) fad + (7) h2o + hpdcacoa + (7) nad --> (7) accoa + (7) fadh2 + (7) h + (7) nadh + ppcoa	1.3.99.3	Fatty acid oxidation	34.1
FAOXC180	Beta oxidation of long chain fatty acid	[m] : coa + fad + h2o + nad + stcoa --> accoa + fadh2 + h + nadh + pmtcoa	1.3.99.3	Fatty acid oxidation	(35.1 or 34.1 or 34.1 or 35.1)
FAOXC180x	Beta oxidation of long chain fatty acid	[x] : coa + h2o + nad + o2 + stcoa --> accoa + h + h2o2 + nadh + pmtcoa	1.3.99.3	Fatty acid oxidation, peroxisome	((51.1 and 1962.1 and 30.1) or (51.2 and 30.1 and 3295.1) or (1962.1 and 51.2 and 30.1) or (51.1 and 30.1 and 3295.1))
FAOXC1811601m	Beta oxidation fatty acid	[m] : (5) coa + (4) fad + (5) h2o + (5) nad + od2coa --> (5) accoa + (4) fadh2 + (5) h + (5) nadh + occoa	1.3.99.3	Fatty acid oxidation	(35.1 or 34.1)
FAOXC1811602m	Beta oxidation fatty acid	[m] : (5) coa + (4) fad + (5) h2o + (5) nad + vacccoa --> (5) accoa + (4) fadh2 + (5) h + (5) nadh + occoa	1.3.99.3	Fatty acid oxidation	(35.1 or 34.1)

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
FAOXC1811603m	Beta oxidation fatty acid	[m] : (5) coa + (4) fad + (5) h2o + (5) nad + odecoa --> (5) accoa + (4) fadh2 + (5) h + (5) nadh + occoa	1.3.99.3	Fatty acid oxidation	(34.1 or 35.1)
FAOXC182806m	Beta oxidation of fatty acid	[m] : (5) coa + (3) fad + (5) h2o + lnlccoa + (5) nad --> (5) accoa + (3) fadh2 + (5) h + (5) nadh + occoa	1.3.99.3	Fatty acid oxidation	(34.1 or 35.1)
FAOXC18280m	Beta oxidation of fatty acid	[m] : (5) coa + (3) fad + (5) h2o + lneldccoa + (5) nad --> (5) accoa + (3) fadh2 + (5) h + (5) nadh + occoa	1.3.99.3	Fatty acid oxidation	(34.1 or 35.1)
FAOXC183803m	Beta oxidation of fatty acid	[m] : (5) coa + (2) fad + (5) h2o + lnlncacoa + (5) nad --> (5) accoa + (2) fadh2 + (5) h + (5) nadh + occoa	1.3.99.3	Fatty acid oxidation	(34.1 or 35.1)
FAOXC183806m	Beta oxidation of fatty acid	[m] : (5) coa + (5) h2o + lnlncgcoa + (5) nad + (2) o2 --> (5) accoa + (5) h + (2) h2o2 + (5) nadh + occoa	1.3.99.3	Fatty acid oxidation	(34.1 or 35.1)
FAOXC183806x	Beta oxidation of long chain fatty acid	[x] : (5) coa + (5) h2o + lnlncgcoa + (5) nad + (2) o2 --> (5) accoa + (5) h + (2) h2o2 + (5) nadh + occoa	1.3.99.3	Fatty acid oxidation, peroxisome	((1962.1 and 51.2 and 30.1) or (51.1 and 1962.1 and 30.1) or (51.1 and 30.1 and 3295.1) or (51.2 and 30.1 and 3295.1))
FAOXC18480m	Beta oxidation of fatty acid	[m] : (5) coa + fad + (5) h2o + (5) nad + strdnccoa --> (5) accoa + fadh2 + (5) h + (5) nadh + occoa	1.3.99.3	Fatty acid oxidation	(34.1 or 35.1)
FAOXC18480x	Beta oxidation of long chain fatty acid	[x] : (5) coa + (5) h2o + (5) nad + o2 + strdnccoa --> (5) accoa + (5) h + h2o2 + (5) nadh + occoa	1.3.99.3	Fatty acid oxidation, peroxisome	((1962.1 and 51.2 and 30.1) or (51.2 and 30.1 and 3295.1) or (51.1 and 1962.1 and 30.1) or (51.1 and 30.1 and 3295.1))
FAOXC200180m	Beta oxidation of long chain fatty acid	[m] : arachcoa + coa + fad + h2o + nad --> accoa + fadh2 + h + nadh + stcoa	1.3.99.3	Fatty acid oxidation	(35.1 or 34.1)
FAOXC200180x	Beta oxidation of long chain fatty acid	[x] : arachcoa + coa + h2o + nad + o2 --> accoa + h + h2o2 + nadh + stcoa	1.3.99.3	Fatty acid oxidation, peroxisome	((51.1 and 1962.1 and 30.1) or (1962.1 and 51.2 and 30.1) or (51.1 and 30.1 and 3295.1) or (51.2 and 30.1 and 3295.1))
FAOXC2031836m	Beta oxidation of fatty acid	[m] : coa + dlnlcgcoa + fad + h2o + nad --> accoa + fadh2 + h + lnlncgcoa + nadh	1.3.99.3	Fatty acid oxidation	(35.1 or 34.1)
FAOXC204	Beta oxidation of long chain fatty acid	[m] : arachdcoa + (9) coa + (5) fad + (9) h2o + (9) nad --> (10) accoa + (5) fadh2 + (9) h + (9) nadh	1.3.99.3	Fatty acid oxidation	(34.1 or 35.1 or 35.1 or 34.1)
FAOXC204184m	Beta oxidation fatty acid	[m] : coa + eicostetcoa + fad + h2o + nad --> accoa + fadh2 + h + nadh + strdnccoa	1.3.99.3	Fatty acid oxidation	(35.1 or 34.1)
FAOXC2051843m	Beta oxidation of fatty acid	[m] : coa + h2o + nad + tmndnccoa --> accoa + h + nadh + strdnccoa	1.3.99.3	Fatty acid oxidation	(34.1 or 35.1)
FAOXC2051843x	Beta oxidation of long chain fatty acid	[x] : coa + h2o + nad + tmndnccoa --> accoa + h + nadh + strdnccoa	1.3.99.3	Fatty acid oxidation, peroxisome	((51.1 and 30.1 and 3295.1) or (51.2 and 30.1 and 3295.1) or (51.1 and 1962.1 and 30.1) or (1962.1 and 51.2 and 30.1))
FAOXC2242046m	Beta oxidation of long chain fatty acid	[m] : adrncoa + coa + fad + h2o + nad --> accoa + arachdcoa + fadh2 + h + nadh	1.3.99.3	Fatty acid oxidation	(34.1 or 35.1)
FAOXC2242046x	Beta oxidation of long chain fatty acid	[x] : adrncoa + coa + h2o + nad + o2 --> accoa + arachdcoa + h + h2o2 + nadh	1.3.99.3	Fatty acid oxidation, peroxisome	((51.1 and 1962.1 and 30.1) or (51.1 and 30.1 and 3295.1) or (1962.1 and 51.2 and 30.1) or (51.2 and 30.1 and 3295.1))
FAOXC2251836m	Beta oxidation of fatty acid	[m] : (2) coa + dcsptn1coa + (2) h2o + (2) nad --> (2) accoa + (2) h + lnlncgcoa + (2) nadh	1.3.99.3	Fatty acid oxidation	(34.1 or 35.1)
FAOXC2251836x	Beta oxidation of long chain fatty acid	[x] : (2) coa + dcsptn1coa + (2) h2o + (2) nad --> (2) accoa + (2) h + lnlncgcoa + (2) nadh	1.3.99.3	Fatty acid oxidation, peroxisome	((51.1 and 1962.1 and 30.1) or (1962.1 and 51.2 and 30.1) or (51.1 and 30.1 and 3295.1) or (51.2 and 30.1 and 3295.1))
FAOXC2252053m	Beta oxidation of long chain fatty acid	[m] : coa + dcsptn1coa + h2o + nad + o2 --> accoa + h + h2o2 + nadh + tmndnccoa	1.3.99.3	Fatty acid oxidation	(35.1 or 34.1)
FAOXC2252053x	Beta oxidation of long chain fatty acid	[x] : coa + dcsptn1coa + h2o + nad + o2 --> accoa + h + h2o2 + nadh + tmndnccoa	1.3.99.3	Fatty acid oxidation, peroxisome	((1962.1 and 51.2 and 30.1) or (51.2 and 30.1 and 3295.1) or (51.1 and 1962.1 and 30.1) or (51.1 and 30.1 and 3295.1))
FAOXC226	Beta oxidation of long chain fatty acid	[m] : c226coa + (10) coa + (4) fad + (10) h2o + (10) nad --> (11) accoa + (4) fadh2 + (10) h + (10) nadh	1.3.99.3	Fatty acid oxidation	(35.1 or 34.1)
FAOXC226205m	Beta oxidation of long chain fatty acid	[m] : c226coa + coa + h2o + nad --> accoa + h + nadh + tmndnccoa	1.3.99.3	Fatty acid oxidation	(35.1 or 34.1)
FAOXC226205x	Beta oxidation of long chain fatty acid	[x] : c226coa + coa + h2o + nad --> accoa + h + nadh + tmndnccoa	1.3.99.3	Fatty acid oxidation, peroxisome	((51.1 and 30.1 and 3295.1) or (51.1 and 1962.1 and 30.1) or (1962.1 and 51.2 and 30.1) or (51.2 and 30.1 and 3295.1))
FAOXC240200x	Beta oxidation of long chain fatty acid	[x] : (2) coa + (2) h2o + lgnccoa + (2) nad + (2) o2 --> (2) accoa + arachcoa + (2) h + (2) h2o2 + (2) nadh	1.3.99.3	Fatty acid oxidation, peroxisome	((1962.1 and 51.2 and 30.1) or (51.2 and 30.1 and 3295.1) or (51.1 and 1962.1 and 30.1) or (51.1 and 30.1 and 3295.1))
FAOXC241181x	Beta oxidation of long chain fatty acid	[x] : (3) coa + (3) h2o + (3) nad + nrvnccoa + (3) o2 --> (3) accoa + (3) h + (3) h2o2 + (3) nadh + odecoa	1.3.99.3	Fatty acid oxidation, peroxisome	((51.1 and 1962.1 and 30.1) or (1962.1 and 51.2 and 30.1) or (51.1 and 30.1 and 3295.1) or (51.2 and 30.1 and 3295.1))

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
FAOXC2442246x	Beta oxidation of long chain fatty acid	[x] : coa + h2o + nad + o2 + tettet6coa --> accoa + adrncoa + h + h2o2 + nadh	1.3.99.3	Fatty acid oxidation, peroxisome	((51.1 and 1962.1 and 30.1) or (51.2 and 30.1 and 3295.1) or (1962.1 and 51.2 and 30.1) or (51.1 and 30.1 and 3295.1))
FAOXC2452253x	Beta oxidation of long chain fatty acid	[x] : coa + h2o + nad + o2 + tetpent3coa --> accoa + clpndcoa + h + h2o2 + nadh	1.3.99.3	Fatty acid oxidation, peroxisome	((1962.1 and 51.2 and 30.1) or (51.1 and 30.1 and 3295.1) or (51.1 and 1962.1 and 30.1) or (51.2 and 30.1 and 3295.1))
FAOXC2452256x	Beta oxidation of long chain fatty acid	[x] : coa + h2o + nad + o2 + tetpent6coa --> accoa + dcsptn1coa + h + h2o2 + nadh	1.3.99.3	Fatty acid oxidation, peroxisome	((51.1 and 30.1 and 3295.1) or (51.1 and 1962.1 and 30.1) or (1962.1 and 51.2 and 30.1) or (51.2 and 30.1 and 3295.1))
FAOXC246226x	Beta oxidation of long chain fatty acid	[x] : coa + h2o + nad + o2 + tethex3coa --> accoa + c226coa + h + h2o2 + nadh	1.3.99.3	Fatty acid oxidation, peroxisome	((51.1 and 30.1 and 3295.1) or (51.1 and 1962.1 and 30.1) or (1962.1 and 51.2 and 30.1) or (51.2 and 30.1 and 3295.1))
FAOXC260240x	Beta oxidation of long chain fatty acid	[x] : coa + h2o + hexccoa + nad + o2 --> accoa + h + h2o2 + lgnccoa + nadh	1.3.99.3	Fatty acid oxidation, peroxisome	((51.1 and 1962.1 and 30.1) or (1962.1 and 51.2 and 30.1) or (51.1 and 30.1 and 3295.1) or (51.2 and 30.1 and 3295.1))
FAOXC80	Beta oxidation of med/long chain fatty acid	[m] : (3) coa + (3) fad + (3) h2o + (3) nad + occoa --> (4) accoa + (3) fadh2 + (3) h + (3) nadh	1.3.99.3	Fatty acid oxidation	(35.1 or 34.1)
FAS100COA	fatty acyl-CoA synthase (n-C10:0CoA)	[c] : (3) h + malcoa + (2) nadph + occoa --> co2 + coa + dcacoa + h2o + (2) nadp	2.3.1.86	Fatty acid elongation	2194.1
FAS120COA	fatty-acyl-CoA synthase (n-C12:0CoA)	[c] : dcacoa + (3) h + malcoa + (2) nadph --> co2 + coa + ddcacoa + h2o + (2) nadp	2.3.1.86	Fatty acid elongation	2194.1
FAS140COA	fatty-acyl-CoA synthase (n-C14:0CoA)	[c] : ddcacoa + (3) h + malcoa + (2) nadph --> co2 + coa + h2o + (2) nadp + tdcoa	2.3.1.86	Fatty acid elongation	2194.1
FAS160COA	fatty-acyl-CoA synthase (n-C16:0CoA)	[c] : (3) h + malcoa + (2) nadph + tdcoa --> co2 + coa + h2o + (2) nadp + pmtcoa	2.3.1.86	Fatty acid elongation	2194.1
FAS180COA	fatty-acyl-CoA synthase (n-C18:0CoA)	[c] : (3) h + malcoa + (2) nadph + pmtcoa --> co2 + coa + h2o + (2) nadp + stcoa	2.3.1.86	Fatty acid elongation	2194.1
FAS80COA_L	fatty acyl-CoA synthase (n-C8:0CoA), lumped reaction	[c] : accoa + (9) h + (3) malcoa + (6) nadph --> (3) co2 + (3) coa + (3) h2o + (6) nadp + occoa	2.3.1.86	Fatty acid elongation	2194.1
FATP1t	fatty acid electroneutral transport	hdca[c] + na1[c] <==> hdca[e] + na1[e]		Transport, Extracellular	(10999.1 or 11000.1 or 376497.1 or 376497.2)
FATP2t	fatty acid electroneutral transport	na1[c] + ocdcea[c] <==> na1[e] + ocdcea[e]		Transport, Extracellular	(376497.1 or 376497.2)
FATP3t	fatty acid electroneutral transport	na1[c] + ocdca[c] <==> na1[e] + ocdca[e]		Transport, Extracellular	(376497.1 or 376497.2)
FATP4t	fatty acid electroneutral transport	arach[c] + na1[c] <==> arach[e] + na1[e]		Transport, Extracellular	10998.1
FATP5t	fatty acid electroneutral transport	arachd[c] + na1[c] <==> arachd[e] + na1[e]		Transport, Extracellular	10998.1
FATP6t	fatty acid electroneutral transport	adrn[c] + na1[c] <==> adrn[e] + na1[e]		Transport, Extracellular	(10998.1 or 11001.1)
FATP7t	fatty acid electroneutral transport	crvnc[c] + na1[c] <==> crvnc[e] + na1[e]		Transport, Extracellular	(10998.1 or 11001.1)
FATP8t	fatty acid electroneutral transport	lgnc[c] + na1[c] <==> lgnc[e] + na1[e]		Transport, Extracellular	(10998.1 or 11001.1)
FATP9t	fatty acid electroneutral transport	na1[c] + nrvnc[c] <==> na1[e] + nrvnc[e]		Transport, Extracellular	(10998.1 or 11001.1)
FBA	fructose-bisphosphate aldolase	[c] : fdp <==> dhap + g3p	4.1.2.13	Glycolysis/Gluconeogenesis	(226.1 or 230.1 or 226.3 or 226.2 or 229.1)
FBA2	D-Fructose 1-phosphate D-glyceraldehyde-3-phosphate-lyase	[c] : f1p <==> dhap + glyald	4.1.2.13	Fructose and Mannose Metabolism	(226.1 or 229.1 or 226.3 or 226.2 or 230.1)
FBA4	D-Fructose 1-phosphate D-glyceraldehyde-3-phosphate-lyase	[c] : xu1p-D <==> dhap + gcald	4.1.2.13	Glyoxylate and Dicarboxylate Metabolism	(229.1 or 230.1 or 226.3 or 226.2 or 226.1)
FBA5	D-Tagatose 1-phosphate D-glyceraldehyde-3-phosphate-lyase	[c] : tag1p-D <==> dhap + glyald	4.1.2.13	Galactose metabolism	229.1
FBP	fructose-bisphosphatase	[c] : fdp + h2o --> f6p + pi	3.1.3.11	Glycolysis/Gluconeogenesis	(2203.1 or 8789.1)
FBP26	Fructose-2,6-bisphosphate 2-phosphatase	[c] : f26bp + h2o --> f6p + pi	3.1.3.46	Fructose and Mannose Metabolism	(5207.1 or 5208.1 or 5209.1 or 5210.1 or 8789.1 or 2203.1)
FCLTm	Ferrochelatase, mitochondrial	[m] : fe2 + ppp9 --> (2) h + pheme	4.99.1.1	Heme Biosynthesis	(2235.1 or 2235.2)
FCOAH	formyl coa hydrolase	[c] : formcoa + h2o --> coa + for + (5) h		Fatty Acid Metabolism	
FDH	formate dehydrogenase	[c] : for + nad --> co2 + nadh	1.2.1.2	Fatty Acid Metabolism	10840.1
FE2t	iron (II) transport	fe2[e] --> fe2[c]		Transport, Extracellular	
FE2tm	iron (II) transport	fe2[c] + h[c] --> fe2[m] + h[m]		Transport, Mitochondrial	
FE3R2e	Fe(III) reduction (ascorbate)	[e] : ascb-L + (2) fe3 --> dhdascb + (2) fe2 + (2) h		Heme Biosynthesis	79901.1
FK	Fucokinase	[c] : atp + fuc-L --> adp + fuc1p-L + h	2.7.1.52	Fructose and Mannose Metabolism	197258.1
FKYNH	N-Formyl-L-kynurenine amidohydrolase	[c] : Lfmkynr + h2o --> Lkynr + for + h	3.5.1.9	Tryptophan metabolism	
FMNAT	FMN adenylyltransferase	[c] : atp + fmn + h --> fad + ppi	2.7.7.2	Riboflavin Metabolism	(80308.1 or 80308.2)
FOLR2	folate reductase	[c] : fol + nadph --> dhf + nadp	1.5.1.3	Folate Metabolism	1719.1
FOLt2	folate transport via anion exchange	fol[e] + oh1[c] <==> fol[c] + oh1[e]		Transport, Extracellular	(6573.1 or 6573.2)
FORMCOAtx	formyl coa transport	formcoa[x] <==> formcoa[c]		Transport, Peroxisomal	
FORt2m	formate mitochondrial transport	for[m] <==> for[c]		Transport, Mitochondrial	
FORtr	FOR transporter, endoplasmic reticulum	for[c] <==> for[r]		Transport, Endoplasmic Reticular	
FORtrn	Formate transport, nuclear	for[c] <==> for[n]		Transport, Nuclear	
FPGS	folylpolyglutamate synthetase	[c] : (4) atp + (4) glu-L + thf --> 5thf + (4) adp + (4) h + (4) pi	6.3.2.17	Folate Metabolism	2356.1
FPGS2	folylpolyglutamate synthetase	[c] : 5thf + atp + glu-L --> 6thf + adp + h + pi	6.3.2.17	Folate Metabolism	2356.1

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
FPGS2m	folylpolyglutamate synthetase, mitochondrial	[m] : 5thf + atp + glu-L --> 6thf + adp + h + pi	6.3.2.17	Folate Metabolism	2356.1
FPGS3	folylpolyglutamate synthetase	[c] : 6thf + atp + glu-L --> 7thf + adp + h + pi	6.3.2.17	Folate Metabolism	2356.1
FPGS3m	folylpolyglutamate synthetase, mitochondrial	[m] : 6thf + atp + glu-L --> 7thf + adp + h + pi	6.3.2.17	Folate Metabolism	2356.1
FPGS4	folylpolyglutamate synthetase (DHF)	[c] : (4) atp + dhf + (4) glu-L --> 5dhf + (4) adp + (4) h + (4) pi	6.3.2.17	Folate Metabolism	2356.1
FPGS4m	folylpolyglutamate synthetase (DHF), mitochondrial	[m] : (4) atp + dhf + (4) glu-L --> 5dhf + (4) adp + (4) h + (4) pi	6.3.2.17	Folate Metabolism	2356.1
FPGS5	folylpolyglutamate synthetase (DHF)	[c] : 5dhf + atp + glu-L --> 6dhf + adp + h + pi	6.3.2.17	Folate Metabolism	2356.1
FPGS5m	folylpolyglutamate synthetase (DHF), mitochondrial	[m] : 5dhf + atp + glu-L --> 6dhf + adp + h + pi	6.3.2.17	Folate Metabolism	2356.1
FPGS6	folylpolyglutamate synthetase (DHF)	[c] : 6dhf + atp + glu-L --> 7dhf + adp + h + pi	6.3.2.17	Folate Metabolism	2356.1
FPGS6m	folylpolyglutamate synthetase (DHF), mitochondrial	[m] : 6dhf + atp + glu-L --> 7dhf + adp + h + pi	6.3.2.17	Folate Metabolism	2356.1
FPGS7	folylpolyglutamate synthetase (10fthf)	[c] : 10fthf + (4) atp + (4) glu-L --> 10fthf5glu + (4) adp + (4) h + (4) pi	6.3.2.17	Folate Metabolism	2356.1
FPGS7m	folylpolyglutamate synthetase (10fthf), mitochondrial	[m] : 10fthf + (4) atp + (4) glu-L --> 10fthf5glu + (4) adp + (4) h + (4) pi	6.3.2.17	Folate Metabolism	2356.1
FPGS8	folylpolyglutamate synthetase (10fthf)	[c] : 10fthf5glu + atp + glu-L --> 10fthf6glu + adp + h + pi	6.3.2.17	Folate Metabolism	2356.1
FPGS8m	folylpolyglutamate synthetase (10fthf), mitochondrial	[m] : 10fthf5glu + atp + glu-L --> 10fthf6glu + adp + h + pi	6.3.2.17	Folate Metabolism	2356.1
FPGS9	folylpolyglutamate synthetase (10fthf)	[c] : 10fthf6glu + atp + glu-L --> 10fthf7glu + adp + h + pi	6.3.2.17	Folate Metabolism	2356.1
FPGS9m	folylpolyglutamate synthetase (10fthf), mitochondrial	[m] : 10fthf6glu + atp + glu-L --> 10fthf7glu + adp + h + pi	6.3.2.17	Folate Metabolism	2356.1
FPGSm	folylpolyglutamate synthetase, mitochondrial	[m] : (4) atp + (4) glu-L + thf --> 5thf + (4) adp + (4) h + (4) pi	6.3.2.17	Folate Metabolism	2356.1
FRDPtc	lipid, flip-flop intracellular transport	frdp[x] <==> frdp[c]		Transport, Peroxisomal	
FRDPtr	lipid, flip-flop intracellular transport	frdp[x] <==> frdp[r]		Transport, Peroxisomal	
FRTT	farnesyltranstransferase	[c] : frdp + ipdp --> ggdp + ppi	2.5.1.29	Cholesterol Metabolism	9453.1
FRUt1r	D-fructose transport in via uniport	fru[e] <==> fru[c]		Transport, Extracellular	(6514.1 or 6518.1 or 155184.1 or 29988.1 or 66035.1)
FRUt4	D-fructose transport via sodium cotransport	fru[e] + na1[e] <==> fru[c] + na1[c]		Transport, Extracellular	200010.1
FT	farnesyltranstransferase (trans,trans,cis-geranylgeranyl diphosphate-generating)	[c] : frdp + ipdp --> ppi + ttc-ggdp		N-Glycan Biosynthesis	
FTCD	formimidoyltransferase cyclodeaminase	[c] : 5forthf + (2) h --> methf + nh4	4.3.1.4	Folate Metabolism	(10841.1 or 10841.2)
FTHFCL	5-formethyltetrahydrofolate cyclo-ligase	[c] : 5fthf + atp --> adp + methf + pi	6.3.3.2	Folate Metabolism	10588.1
FTHFDH	formyltetrahydrofolate dehydrogenase	[c] : 10fthf + h2o + nadp --> co2 + h + nadph + thf	1.5.1.6	Folate Metabolism	10840.1
FTHFL	formate-tetrahydrofolate ligase	[c] : atp + for + thf <==> 10fthf + adp + pi	6.3.4.3	Folate Metabolism	(4522.1 or 286297.1)
FTHFLm	formate-tetrahydrofolate ligase, mitochondrial	[m] : atp + for + thf <==> 10fthf + adp + pi	6.3.4.3	Folate Metabolism	25902.1
FUC13GALACGLCGAL14ACGLCGALGLUSIDEte	blood group intracellular transport	fuc13galacglcgal14acglcgalgluside_hs[e] <==> fuc13galacglcgal14acglcgalgluside_hs[c]		Transport, Extracellular	
FUC13GALACGLCGAL14ACGLCGALGLUSIDEtg	blood group intracellular transport	fuc13galacglcgal14acglcgalgluside_hs[g] <==> fuc13galacglcgal14acglcgalgluside_hs[c]		Transport, Golgi Apparatus	
FUC14GALACGLCGALGLUSIDEte	blood group intracellular transport	fuc14galacglcgalgluside_hs[e] <==> fuc14galacglcgalgluside_hs[c]		Transport, Extracellular	
FUC14GALACGLCGALGLUSIDEtg	blood group intracellular transport	fuc14galacglcgalgluside_hs[g] <==> fuc14galacglcgalgluside_hs[c]		Transport, Golgi Apparatus	
FUCACGALFUCGALACGLCGALGLUSIDEte	blood group intracellular transport	fucacgalfucgalacglcgalgluside_hs[e] <==> fucacgalfucgalacglcgalgluside_hs[c]		Transport, Extracellular	
FUCACGALFUCGALACGLCGALGLUSIDEtg	blood group intracellular transport	fucacgalfucgalacglcgalgluside_hs[g] <==> fucacgalfucgalacglcgalgluside_hs[c]		Transport, Golgi Apparatus	
FUCACNGAL14ACGLCGALGLUSIDEte	blood group intracellular transport	fucacngal14acglcgalgluside_hs[e] <==> fucacngal14acglcgalgluside_hs[c]		Transport, Extracellular	
FUCACNGAL14ACGLCGALGLUSIDEtg	blood group intracellular transport	fucacngal14acglcgalgluside_hs[g] <==> fucacngal14acglcgalgluside_hs[c]		Transport, Golgi Apparatus	
FUCACNGALACGLCGALGLUSIDEte	blood group intracellular transport	fucacngalacglcgalgluside_hs[e] <==> fucacngalacglcgalgluside_hs[c]		Transport, Extracellular	
FUCACNGALACGLCGALGLUSIDEtg	blood group intracellular transport	fucacngalacglcgalgluside_hs[g] <==> fucacngalacglcgalgluside_hs[c]		Transport, Golgi Apparatus	
FUCASE2e	alpha-fucosidase, extracellular	[e] : h2o + ksi --> fuc-L + ksi_deg1	3.2.1.51	Keratan sulfate degradation	2519.1
FUCASE2ly	alpha-fucosidase, lysosomal	[l] : h2o + ksi --> fuc-L + ksi_deg1	3.2.1.51	Keratan sulfate degradation	2517.1
FUCASEe	alpha-fucosidase, extracellular	[e] : h2o + s2l2fn2m2masn --> fuc-L + s2l2n2m2masn	3.2.1.51	N-Glycan Degradation	2519.1
FUCASEly	alpha-fucosidase, lysosomal	[l] : h2o + s2l2fn2m2masn --> fuc-L + s2l2n2m2masn	3.2.1.51	N-Glycan Degradation	2517.1
FUCFUC12GAL14ACGLCGALGLUSIDEte	blood group intracellular transport	fucfuc12gal14acglcgalgluside_hs[e] <==> fucfuc12gal14acglcgalgluside_hs[c]		Transport, Extracellular	
FUCFUC12GAL14ACGLCGALGLUSIDEtg	blood group intracellular transport	fucfuc12gal14acglcgalgluside_hs[g] <==> fucfuc12gal14acglcgalgluside_hs[c]		Transport, Golgi Apparatus	
FUCFUC132GALACGLCGAL14ACGLCGALGLUSIDEte	blood group intracellular transport	fucfuc132galacglcgal14acglcgalgluside_hs[e] <==> fucfuc132galacglcgal14acglcgalgluside_hs[c]		Transport, Extracellular	
FUCFUC132GALACGLCGAL14ACGLCGALGLUSIDEtg	blood group intracellular transport	fucfuc132galacglcgal14acglcgalgluside_hs[g] <==> fucfuc132galacglcgal14acglcgalgluside_hs[c]		Transport, Golgi Apparatus	
FUCFUCFUCGALACGLC13GALACGLCGAL14ACGLCGALGLUSIDEte	blood group intracellular transport	fucfucfucgalacglc13galacglcgal14acglcgalgluside_hs[e] <==> fucfucfucgalacglc13galacglcgal14acglcgalgluside_hs[c]		Transport, Extracellular	
FUCFUCFUCGALACGLC13GALACGLCGAL14ACGLCGALGLUSIDEtg	blood group intracellular transport	fucfucfucgalacglc13galacglcgal14acglcgalgluside_hs[g] <==> fucfucfucgalacglc13galacglcgal14acglcgalgluside_hs[c]		Transport, Golgi Apparatus	
FUCFUCFUCGALACGLCGAL14ACGLCGALGLUSIDEte	blood group intracellular transport	fucfucfucgalacglcgal14acglcgalgluside_hs[e] <==> fucfucfucgalacglcgal14acglcgalgluside_hs[c]		Transport, Extracellular	
FUCFUCFUCGALACGLCGAL14ACGLCGALGLUSIDEtg	blood group intracellular transport	fucfucfucgalacglcgal14acglcgalgluside_hs[g] <==> fucfucfucgalacglcgal14acglcgalgluside_hs[c]		Transport, Golgi Apparatus	
FUCFUCGALACGLCGALGLUSIDEte	blood group intracellular transport	fucfucgalacglcgalgluside_hs[e] <==> fucfucgalacglcgalgluside_hs[c]		Transport, Extracellular	

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
FUCFUCGALACGLCGALGLUSIDEtg	blood group intracellular transport	fucfucgalacglcgalgluside_hs[g] <==> fucfucgalacglcgalgluside_hs[c]		Transport, Golgi Apparatus	
FUCGAL14ACGLCGALGLUSIDEte	blood group intracellular transport	fucgal14acglcgalgluside_hs[e] <==> fucgal14acglcgalgluside_hs[c]		Transport, Extracellular	
FUCGAL14ACGLCGALGLUSIDEtg	blood group intracellular transport	fucgal14acglcgalgluside_hs[g] <==> fucgal14acglcgalgluside_hs[c]		Transport, Golgi Apparatus	
FUCGALFUCGALACGLCGALGLUSIDEte	blood group intracellular transport	fucgalfucgalacglcgalgluside_hs[e] <==> fucgalfucgalacglcgalgluside_hs[c]		Transport, Extracellular	
FUCGALFUCGALACGLCGALGLUSIDEtg	blood group intracellular transport	fucgalfucgalacglcgalgluside_hs[g] <==> fucgalfucgalacglcgalgluside_hs[c]		Transport, Golgi Apparatus	
FUCGALGBSIDEte	fucgalgbside_hs transport	fucgalgbside_hs[c] <==> fucgalgbside_hs[e]		Transport, Extracellular	
FUCGALGBSIDEtg	fucgalgbside_hs intracellular transport	fucgalgbside_hs[c] <==> fucgalgbside_hs[g]		Transport, Golgi Apparatus	
FUCtly	L-fucose efflux from lysosome	fuc-L[l] --> fuc-L[c]		Transport, Lysosomal	
FUM	fumarase	[c] : fum + h2o <==> mal-L	4.2.1.2	Citric Acid Cycle	2271.1
FUMAC	fumarylacetoacetase	[c] : 4fumacac + h2o --> acac + fum + h	3.7.1.2	Tyrosine metabolism	2184.1
FUMm	fumarase, mitochondrial	[m] : fum + h2o <==> mal-L	4.2.1.2	Citric Acid Cycle	2271.1
FUMSO3tm	Fumarate:sulfite antiport, mitochondrial	fum[c] + so3[m] <==> fum[m] + so3[c]		Transport, Mitochondrial	1468.1
FUMSO4tm	Fumarate:sulfate antiport, mitochondrial	fum[c] + so4[m] <==> fum[m] + so4[c]		Transport, Mitochondrial	1468.1
FUMtm	fumarate transport, mitochondrial	fum[c] + pi[m] <==> fum[m] + pi[c]		Transport, Mitochondrial	1468.1
FUMTSULtm	Fumarate:thiosulfate antiport, mitochondrial	fum[c] + tsul[m] <==> fum[m] + tsul[c]		Transport, Mitochondrial	1468.1
FUT11g	Galactoside 2-alpha-L-fucosyltransferase 1	[g] : galgbside_hs + gdpfuc --> fucgalgbside_hs + gdp + h	2.4.1.69	Sphingolipid Metabolism	2523.1
FUT12g	Galactoside 2-alpha-L-fucosyltransferase 1	[g] : galacglcgalgluside_hs + gdpfuc --> fucgalacglcgalgluside_hs + gdp + h	2.4.1.69	Blood Group Biosynthesis	2523.1
FUT14g	Galactoside 2-alpha-L-fucosyltransferase 1	[g] : gal14acglcgalgluside_hs + gdpfuc --> fuc12gal14acglcgalgluside_hs + gdp + h	2.4.1.69	Blood Group Biosynthesis	2523.1
FUT15g	Galactoside 2-alpha-L-fucosyltransferase 1	[g] : galacgalfuc12gal14acglcgalgluside_hs + gdpfuc --> fucgalacgalfuc12gal14acglcgalgluside_hs + gdp + h	2.4.1.69	Blood Group Biosynthesis	2523.1
FUT16g	Galactoside 2-alpha-L-fucosyltransferase 1	[g] : galacglcgal14acglcgalgluside_hs + gdpfuc --> fucgalacglcgal14acglcgalgluside_hs + gdp + h	2.4.1.69	Blood Group Biosynthesis	2523.1
FUT17g	Galactoside 2-alpha-L-fucosyltransferase 1	[g] : galacgalfucgalacglcgal14acglcgalgluside_hs + gdpfuc --> fucgalacgalfucgalacglcgal14acglcgalgluside_hs + gdp + h	2.4.1.69	Blood Group Biosynthesis	2523.1
FUT18g	Galactoside 2-alpha-L-fucosyltransferase 1	[g] : galacglcgalacglcgal14acglcgalgluside_hs + (2) gdpfuc --> fucfucgalacglcgalacglcgal14acglcgalgluside_hs + (2) gdp + (2) h	2.4.1.69	Blood Group Biosynthesis	2523.1
FUT31g	fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood group included) 1	[g] : galacglcgalgluside_hs + gdpfuc --> fuc14galacglcgalgluside_hs + gdp + h	2.4.1.65	Blood Group Biosynthesis	2525.1
FUT32g	fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood group included) 1	[g] : acngalacglcgalgluside_hs + gdpfuc --> fucacngalacglcgalgluside_hs + gdp + h	2.4.1.65	Blood Group Biosynthesis	2525.1
FUT33g	fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood group included) 1	[g] : acgalfucgalacglcgalgluside_hs + gdpfuc --> fucacgalfucgalacglcgalgluside_hs + gdp + h	2.4.1.65	Blood Group Biosynthesis	2525.1
FUT34g	fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood group included) 1	[g] : fucgalacglcgalgluside_hs + gdpfuc --> fucfucgalacglcgalgluside_hs + gdp + h	2.4.1.65	Blood Group Biosynthesis	2525.1
FUT35g	fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood group included) 1	[g] : galfucgalacglcgalgluside_hs + gdpfuc --> fucgalfucgalacglcgalgluside_hs + gdp + h	2.4.1.65	Blood Group Biosynthesis	2525.1
FUT910g	Alpha-(1,3)-fucosyltransferase	[g] : fucgalacglc13galacglcgal14acglcgalgluside_hs + gdpfuc --> fucfucgalacglc13galacglcgal14acglcgalgluside_hs + gdp + h	2.4.1.152	Blood Group Biosynthesis	10690.1
FUT911g	Alpha-(1,3)-fucosyltransferase	[g] : fucfucgalacglc13galacglcgal14acglcgalgluside_hs + gdpfuc --> fucfucfucgalacglc13galacglcgal14acglcgalgluside_hs + gdp + h	2.4.1.152	Blood Group Biosynthesis	10690.1
FUT91g	Alpha-(1,3)-fucosyltransferase	[g] : gal14acglcgalgluside_hs + gdpfuc --> fucgal14acglcgalgluside_hs + gdp + h	2.4.1.152	Blood Group Biosynthesis	10690.1
FUT92g	Alpha-(1,3)-fucosyltransferase	[g] : acngal14acglcgalgluside_hs + gdpfuc --> fucacngal14acglcgalgluside_hs + gdp + h	2.4.1.152	Blood Group Biosynthesis	10690.1
FUT93g	Alpha-(1,3)-fucosyltransferase	[g] : fuc12gal14acglcgalgluside_hs + gdpfuc --> fucfuc12gal14acglcgalgluside_hs + gdp + h	2.4.1.152	Blood Group Biosynthesis	10690.1
FUT94g	Alpha-(1,3)-fucosyltransferase	[g] : fucgalacglcgal14acglcgalgluside_hs + gdpfuc --> fucfucgalacglcgal14acglcgalgluside_hs + gdp + h	2.4.1.152	Blood Group Biosynthesis	10690.1
FUT95g	Alpha-(1,3)-fucosyltransferase	[g] : fucfucgalacglcgal14acglcgalgluside_hs + gdpfuc --> fucfucfucgalacglcgal14acglcgalgluside_hs + gdp + h	2.4.1.152	Blood Group Biosynthesis	10690.1
FUT96g	Alpha-(1,3)-fucosyltransferase	[g] : galacglcgal14acglcgalgluside_hs + gdpfuc --> fuc132galacglcgal14acglcgalgluside_hs + gdp + h	2.4.1.152	Blood Group Biosynthesis	10690.1
FUT97g	Alpha-(1,3)-fucosyltransferase	[g] : fuc132galacglcgal14acglcgalgluside_hs + gdpfuc --> fucfuc132galacglcgal14acglcgalgluside_hs + gdp + h	2.4.1.152	Blood Group Biosynthesis	10690.1
FUT98g	Alpha-(1,3)-fucosyltransferase	[g] : galacglcgal14acglcgalgluside_hs + gdpfuc --> fuc13galacglcgal14acglcgalgluside_hs + gdp + h	2.4.1.152	Blood Group Biosynthesis	10690.1
FUT99g	Alpha-(1,3)-fucosyltransferase	[g] : galacglc13galacglcgal14acglcgalgluside_hs + gdpfuc --> fucgalacglc13galacglcgal14acglcgalgluside_hs + gdp + h	2.4.1.152	Blood Group Biosynthesis	10690.1
G12MT1_L	Glycolipid 1,2-alpha-D-mannosyltransferase (liver)	[c] : gdpmann + (0.1) m2mpdol_L --> gdp + h + (0.1) m3mpdol_L	2.4.1.131	N-Glycan Biosynthesis	
G12MT1_U	Glycolipid 1,2-alpha-D-mannosyltransferase (uterus)	[c] : gdpmann + (0.1) m2mpdol_U --> gdp + h + (0.1) m3mpdol_U	2.4.1.131	N-Glycan Biosynthesis	
G12MT2_L	Glycolipid 1,2-alpha-D-mannosyltransferase (liver)	[c] : gdpmann + (0.1) m3mpdol_L --> gdp + h + (0.1) m4mpdol_L	2.4.1.131	N-Glycan Biosynthesis	
G12MT2_U	Glycolipid 1,2-alpha-D-mannosyltransferase (uterus)	[c] : gdpmann + (0.1) m3mpdol_U --> gdp + h + (0.1) m4mpdol_U	2.4.1.131	N-Glycan Biosynthesis	
G13MT_L	Glycolipid 1,3-alpha-D-mannosyltransferase (liver)	[c] : gdpmann + (0.1) mpdol_L --> gdp + h + (0.1) m1mpdol_L	2.4.1.132	N-Glycan Biosynthesis	(85365.1 or 85365.2)
G13MT_U	Glycolipid 1,3-alpha-D-mannosyltransferase (uterus)	[c] : gdpmann + (0.1) mpdol_U --> gdp + h + (0.1) m1mpdol_U	2.4.1.132	N-Glycan Biosynthesis	(85365.2 or 85365.1)
G14T10g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	[g] : ksi_pre14 + udpgal --> h + ksi_pre15 + udp	2.4.1.38	Keratan sulfate biosynthesis	(2683.1 or 8704.2 or 8703.1 or 9334.1 or 8704.1)
G14T11g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	[g] : ksi_pre17 + udpgal --> h + ksi_pre18 + udp	2.4.1.38	Keratan sulfate biosynthesis	(8704.2 or 2683.1 or 8704.1 or 8703.1 or 9334.1)
G14T12g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	[g] : ksi_pre20 + udpgal --> h + ksi_pre21 + udp	2.4.1.38	Keratan sulfate biosynthesis	(2683.1 or 8704.1 or 8704.2 or 8703.1 or 9334.1)
G14T13g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	[g] : ksi_pre23 + udpgal --> h + ksi_pre24 + udp	2.4.1.38	Keratan sulfate biosynthesis	(2683.1 or 8704.1 or 8704.2 or 8703.1 or 9334.1)

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
G14T14g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	[g] : ksi_pre26 + udpgal --> h + ksi_pre27 + udp	2.4.1.38	Keratan sulfate biosynthesis	(8704.2 or 2683.1 or 8704.1 or 8703.1 or 9334.1)
G14T15g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	[g] : ksi_pre29 + udpgal --> h + ksi_pre30 + udp	2.4.1.38	Keratan sulfate biosynthesis	(2683.1 or 8704.1 or 8704.2 or 8703.1 or 9334.1)
G14T16g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	[g] : ksi_pre32 + udpgal --> h + ksi_pre33 + udp	2.4.1.38	Keratan sulfate biosynthesis	(8704.1 or 8704.2 or 8703.1 or 9334.1 or 2683.1)
G14T17g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	[g] : ksi_pre35 + udpgal --> h + ksi_pre36 + udp	2.4.1.38	Keratan sulfate biosynthesis	(8704.2 or 2683.1 or 8704.1 or 8703.1 or 9334.1)
G14T18g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	[g] : core4 + (2) udpgal --> (2) h + ksii_core4_pre1 + (2) udp	2.4.1.38	Keratan sulfate biosynthesis	(8704.2 or 2683.1 or 8704.1 or 8703.1 or 9334.1)
G14T19g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	[g] : ksii_core4_pre3 + udpgal --> h + ksii_core4_pre4 + udp	2.4.1.38	Keratan sulfate biosynthesis	(2683.1 or 8704.1 or 8704.2 or 8703.1 or 9334.1)
G14T20g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	[g] : ksii_core4_pre6 + udpgal --> h + ksii_core4_pre7 + udp	2.4.1.38	Keratan sulfate biosynthesis	(2683.1 or 8704.1 or 8704.2 or 8703.1 or 9334.1)
G14T21g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	[g] : ksii_core4_pre9 + udpgal --> h + ksii_core4_pre10 + udp	2.4.1.38	Keratan sulfate biosynthesis	(2683.1 or 8704.1 or 8704.2 or 8703.1 or 9334.1)
G14T2g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	[g] : ksii_core2_pre1 + udpgal --> h + ksii_core2_pre2 + udp	2.4.1.38	Keratan sulfate biosynthesis	(2683.1 or 8704.1 or 8704.2 or 8703.1 or 9334.1)
G14T3g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	[g] : ksii_core2_pre3 + udpgal --> h + ksii_core2_pre4 + udp	2.4.1.38	Keratan sulfate biosynthesis	(2683.1 or 8704.1 or 8704.2 or 8703.1 or 9334.1)
G14T4g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	[g] : ksii_core2_pre6 + udpgal --> h + ksii_core2_pre7 + udp	2.4.1.38	Keratan sulfate biosynthesis	(2683.1 or 8704.1 or 8704.2 or 8703.1 or 9334.1)
G14T5g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	[g] : ksii_core2_pre9 + udpgal --> h + ksii_core2_pre10 + udp	2.4.1.38	Keratan sulfate biosynthesis	(2683.1 or 8704.1 or 8704.2 or 9334.1 or 8703.1)
G14T6g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	[g] : ksi_pre2 + udpgal --> h + ksi_pre3 + udp	2.4.1.38	Keratan sulfate biosynthesis	(2683.1 or 8704.1 or 8704.2 or 8703.1 or 9334.1)
G14T7g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	[g] : ksi_pre5 + udpgal --> h + ksi_pre6 + udp	2.4.1.38	Keratan sulfate biosynthesis	(2683.1 or 8704.1 or 8704.2 or 8703.1 or 9334.1)
G14T8g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	[g] : ksi_pre8 + udpgal --> h + ksi_pre9 + udp	2.4.1.38	Keratan sulfate biosynthesis	(2683.1 or 8704.1 or 8704.2 or 8703.1 or 9334.1)
G14T9g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	[g] : ksi_pre11 + udpgal --> h + ksi_pre12 + udp	2.4.1.38	Keratan sulfate biosynthesis	(2683.1 or 8704.1 or 8704.2 or 8703.1 or 9334.1)
G14Tg	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase	[g] : fn2m2masn + (2) udpgal --> (2) h + l2fn2m2masn + (2) udp	2.4.1.38	N-Glycan Biosynthesis	(2683.1 or 8703.1 or 8704.1 or 9334.1 or 8704.2)
G16MT_L	Glycolipid 1,6-alpha-D-mannosyltransferase (liver)	[c] : gdpmann + (0.1) m1mpdol_L --> gdp + h + (0.1) m2mpdol_L		N-Glycan Biosynthesis	
G16MT_U	Glycolipid 1,6-alpha-D-mannosyltransferase (uterus)	[c] : gdpmann + (0.1) m1mpdol_U --> gdp + h + (0.1) m2mpdol_U		N-Glycan Biosynthesis	
G1M6MASNB1terg	g1m6masnB1 endoplasmic reticulum to Golgi transport	g1m6masnB1[r] --> g1m6masnB1[g]		N-Glycan Biosynthesis	
G1M7MASNBterg	g1m7masnC endoplasmic reticulum to Golgi transport	g1m7masnB[r] --> g1m7masnB[g]		N-Glycan Biosynthesis	
G1M7MASNCterg	g1m7masnC endoplasmic reticulum to Golgi transport	g1m7masnC[r] --> g1m7masnC[g]		N-Glycan Biosynthesis	
G1M8MASNterg	g1m8masn transport from endoplasmic reticulum to Golgi apparatus	g1m8masn[r] --> g1m8masn[g]		N-Glycan Biosynthesis	
G1PTT	glucose-1-phosphate thymidylyltransferase	[c] : dttp + g1p + h --> dtdpglu + ppi	2.7.7.24	Nucleotide Sugar Metabolism	
G2M8MASNterg	g2m8masn transport from endoplasmic reticulum to Golgi apparatus	g2m8masn[r] --> g2m8masn[g]		N-Glycan Biosynthesis	
G3M8MASNterg	g3m8masn transport from endoplasmic reticulum to Golgi apparatus	g3m8masn[r] --> g3m8masn[g]		N-Glycan Biosynthesis	
G3PD1	glycerol-3-phosphate dehydrogenase (NAD)	[c] : glyc3p + nad <==> dhap + h + nadh	1.1.1.94	Glycerophospholipid Metabolism	2819.1
G3PD2m	glycerol-3-phosphate dehydrogenase (FAD), mitochondrial	fad[m] + glyc3p[c] --> dhap[c] + fadh2[m]	1.1.99.5	Glycolysis/Gluconeogenesis	2820.1
G5SADrm	L-glutamate 5-semialdehyde dehydratase, reversible, mitochondrial	[m] : glu5sa <==> 1pyr5c + h + h2o		Arginine and Proline Metabolism	
G5SADs	L-glutamate 5-semialdehyde dehydratase (spontaneous)	[c] : glu5sa --> 1pyr5c + h + h2o		Urea cycle/amino group metabolism	
G5SDym	glutamate-5-semialdehyde dehydrogenase (m)	[m] : glu5p + h + nadph --> glu5sa + nadp + pi	1.2.1.41	Urea cycle/amino group metabolism	5832.1
G6PDA	glucosamine-6-phosphate deaminase	[c] : gam6p + h2o --> f6p + nh4	3.5.99.6	Aminosugar Metabolism	(10007.1 or 132789.1)
G6PDH1er	glucose-6-phosphate dehydrogenase, endoplasmic reticulum	[r] : g6p + nad --> 6pgl + h + nadh		Pentose Phosphate Pathway	9563.1
G6PDH1rer	glucose-6-phosphate dehydrogenase, endoplasmic reticulum	[r] : g6p + nad <==> 6pgl + h + nadh		Pentose Phosphate Pathway	9563.1
G6PDH2r	glucose 6-phosphate dehydrogenase	[c] : g6p + nadp <==> 6pgl + h + nadph	1.1.1.49	Pentose Phosphate Pathway	2539.1
G6PDH2rer	glucose 6-phosphate dehydrogenase, endoplasmic reticulum	[r] : g6p + nadp <==> 6pgl + h + nadph		Pentose Phosphate Pathway	9563.1
G6PPer	glucose-6-phosphate phosphatase, edoplasmic reticular	[r] : g6p + h2o --> glc-D + pi	3.1.3.9	Glycolysis/Gluconeogenesis	(57818.1 or 92579.1 or 2538.1)
G6Pter	glucose 6-phosphate endoplasmic reticular transport via diffusion	g6p[c] <==> g6p[r]		Transport, Endoplasmic Reticular	2542.1
GABAVESSEC	GABA secretion via secretory vesicle (ATP driven)	(3) 4abut[c] + atp[c] + h2o[c] --> (3) 4abut[e] + adp[c] + h[c] + pi[c]		Transport, Extracellular	140679.1
GACMTRc	guanidinoacetate N-methyltransferase (c)	[c] : amet + gudac <==> ahcys + creat + h	2.1.1.2	Urea cycle/amino group metabolism	(2593.1 or 2593.2)
GACPAILter	glucosaminyl-acylphosphatidylinositol ER flippase	gacpail_hs[c] --> gacpail_hs[r]		Transport, Endoplasmic Reticular	
GAL3ST11	Galactosylceramide sulfotransferase	[g] : galside_hs + paps --> h + pap + sgalside_hs	2.8.2.11	Sphingolipid Metabolism	9514.1
GAL3ST12	Galactosylceramide sulfotransferase	[g] : digalside_hs + paps --> digalsgalside_hs + h + pap	2.8.2.11	Sphingolipid Metabolism	9514.1
GALACGLCGALGBSIDEte	galacglcgalgbside_hs transport	galacglcgalgbside_hs[c] <==> galacglcgalgbside_hs[e]		Transport, Extracellular	
GALACGLCGALGBSIDEtg	galacglcgalgbside_hs intracellular transport	galacglcgalgbside_hs[c] <==> galacglcgalgbside_hs[g]		Transport, Golgi Apparatus	

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
GALASE10ly	beta-galactosidase, lysosomal	[l] : h2o + ksi_deg26 --> gal + ksi_deg27	3.2.1.23	Keratan sulfate degradation	((2720.1 and 4758.1 and 2588.1 and 5476.1) or (2720.1 and 5476.1))
GALASE11ly	beta-galactosidase, lysosomal	[l] : h2o + ksi_deg29 --> gal + ksi_deg30	3.2.1.23	Keratan sulfate degradation	((4758.1 and 2588.1 and 5476.1 and 2720.1) or (2720.1 and 5476.1))
GALASE12ly	beta-galactosidase, lysosomal	[l] : h2o + ksi_deg32 --> gal + ksi_deg33	3.2.1.23	Keratan sulfate degradation	((5476.1 and 2720.1 and 2588.1 and 4758.1) or (2720.1 and 5476.1))
GALASE13ly	beta-galactosidase, lysosomal	[l] : h2o + ksi_deg35 --> gal + ksi_deg36	3.2.1.23	Keratan sulfate degradation	((2720.1 and 4758.1 and 2588.1 and 5476.1) or (2720.1 and 5476.1))
GALASE14ly	beta-galactosidase, lysosomal	[l] : h2o + ksi_deg38 --> gal + ksi_deg39	3.2.1.23	Keratan sulfate degradation	((5476.1 and 4758.1 and 2588.1 and 2720.1) or (2720.1 and 5476.1))
GALASE15ly	beta-galactosidase, lysosomal	[l] : h2o + ksi_deg40 --> gal + ksi_deg41	3.2.1.23	Keratan sulfate degradation	((2720.1 and 4758.1 and 2588.1 and 5476.1) or (5476.1 and 2720.1))
GALASE16ly	beta-galactosidase, lysosomal	[l] : (2) h2o + ksii_core2_deg2 --> (2) gal + ksii_core2_deg3	3.2.1.23	Keratan sulfate degradation	((2720.1 and 2588.1 and 5476.1 and 4758.1) or (2720.1 and 5476.1))
GALASE17ly	beta-galactosidase, lysosomal	[l] : h2o + ksii_core2_deg5 --> gal + ksii_core2_deg6	3.2.1.23	Keratan sulfate degradation	((2720.1 and 4758.1 and 5476.1 and 2588.1) or (5476.1 and 2720.1))
GALASE18ly	beta-galactosidase, lysosomal	[l] : h2o + ksii_core2_deg8 --> gal + ksii_core2_deg9	3.2.1.23	Keratan sulfate degradation	((2720.1 and 4758.1 and 5476.1 and 2588.1) or (2720.1 and 5476.1))
GALASE19ly	beta-galactosidase, lysosomal	[l] : f1a + h2o --> core6 + gal	3.2.1.23	Keratan sulfate degradation	((2720.1 and 4758.1 and 2588.1 and 5476.1) or (2720.1 and 5476.1))
GALASE1ly	beta-galactosidase, lysosomal	[l] : (2) h2o + l2n2m2mn --> (2) gal + n2m2mn	3.2.1.23	N-Glycan Degradation	((2720.1 and 4758.1 and 2588.1 and 5476.1) or (2720.1 and 5476.1))
GALASE20ly	beta-galactosidase, lysosomal	[l] : (2) h2o + ksii_core4_deg2 --> (2) gal + ksii_core4_deg3	3.2.1.23	Keratan sulfate degradation	((2588.1 and 5476.1 and 2720.1 and 4758.1) or (5476.1 and 2720.1))
GALASE3ly	beta-galactosidase, lysosomal	[l] : (2) h2o + ksi_deg5 --> (2) gal + ksi_deg6	3.2.1.23	Keratan sulfate degradation	((2588.1 and 5476.1 and 2720.1 and 4758.1) or (2720.1 and 5476.1))
GALASE4ly	beta-galactosidase, lysosomal	[l] : h2o + ksi_deg8 --> gal + ksi_deg9	3.2.1.23	Keratan sulfate degradation	((2720.1 and 2588.1 and 4758.1 and 5476.1) or (2720.1 and 5476.1))
GALASE5ly	beta-galactosidase, lysosomal	[l] : h2o + ksi_deg11 --> gal + ksi_deg12	3.2.1.23	Keratan sulfate degradation	((2720.1 and 2588.1 and 4758.1 and 5476.1) or (2720.1 and 5476.1))
GALASE6ly	beta-galactosidase, lysosomal	[l] : h2o + ksi_deg14 --> gal + ksi_deg15	3.2.1.23	Keratan sulfate degradation	((5476.1 and 2588.1 and 2720.1 and 4758.1) or (5476.1 and 2720.1))
GALASE7ly	beta-galactosidase, lysosomal	[l] : h2o + ksi_deg17 --> gal + ksi_deg18	3.2.1.23	Keratan sulfate degradation	((4758.1 and 2720.1 and 2588.1 and 5476.1) or (2720.1 and 5476.1))
GALASE8ly	beta-galactosidase, lysosomal	[l] : h2o + ksi_deg20 --> gal + ksi_deg21	3.2.1.23	Keratan sulfate degradation	((2588.1 and 4758.1 and 5476.1 and 2720.1) or (2720.1 and 5476.1))
GALASE9ly	beta-galactosidase, lysosomal	[l] : h2o + ksi_deg23 --> gal + ksi_deg24	3.2.1.23	Keratan sulfate degradation	((2720.1 and 5476.1 and 2588.1 and 4758.1) or (2720.1 and 5476.1))
GALC	Galactocerebrosidase	[l] : galside_hs + h2o --> crm_hs + gal	3.2.1.46	Sphingolipid Metabolism	2581.1
GALFUC12GAL14ACGLCGALGLUSIDEte	blood group intracellular transport	galfuc12gal14acglcgalgluside_hs[e] <==> galfuc12gal14acglcgalgluside_hs[c]		Transport, Extracellular	
GALFUC12GAL14ACGLCGALGLUSIDEtg	blood group intracellular transport	galfuc12gal14acglcgalgluside_hs[g] <==> galfuc12gal14acglcgalgluside_hs[c]		Transport, Golgi Apparatus	
GALFUCGALACGLCGAL14ACGLCGALGLUSIDEte	blood group intracellular transport	galfucgalacglcgal14acglcgalgluside_hs[e] <==> galfucgalacglcgal14acglcgalgluside_hs[c]		Transport, Extracellular	
GALFUCGALACGLCGAL14ACGLCGALGLUSIDEtg	blood group intracellular transport	galfucgalacglcgal14acglcgalgluside_hs[g] <==> galfucgalacglcgal14acglcgalgluside_hs[c]		Transport, Golgi Apparatus	
GALGALFUCFUCGALACGLCGALACGLCGAL14ACGLCGALGLUSIDEte	blood group intracellular transport	galgalfucfucgalacglcgalacglcgal14acglcgalgluside_hs[e] <==> galgalfucfucgalacglcgalacglcgal14acglcgalgluside_hs[c]		Transport, Extracellular	
GALGALFUCFUCGALACGLCGALACGLCGAL14ACGLCGALGLUSIDEtg	blood group intracellular transport	galgalfucfucgalacglcgalacglcgal14acglcgalgluside_hs[g] <==> galgalfucfucgalacglcgalacglcgal14acglcgalgluside_hs[c]		Transport, Golgi Apparatus	
GALGALGALTHCRMte	galgalgalthcrm_hs transport	galgalgalthcrm_hs[c] <==> galgalgalthcrm_hs[e]		Transport, Extracellular	
GALGALGALTHCRMtg	galgalgalthcrm_hs intracellular transport	galgalgalthcrm_hs[c] <==> galgalgalthcrm_hs[g]		Transport, Golgi Apparatus	
GALGLUSIDEtg	galgluside_hs intracellular transport	galgluside_hs[c] <==> galgluside_hs[g]		Transport, Golgi Apparatus	
GALGLUSIDEtl	galgluside_hs intracellular transport	galgluside_hs[c] <==> galgluside_hs[l]		Transport, Lysosomal	
GALGT1	Beta-1,4 N-acetylgalactosaminyltransferase	[g] : galgluside_hs + udpacgal --> ga2_hs + h + udp	2.4.1.92	Sphingolipid Metabolism	2583.1

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
GALGT2	Beta-1,4 N-acetylgalactosaminyltransferase	[g] : gm3_hs + udpacgal --> gm2_hs + h + udp	2.4.1.92	Sphingolipid Metabolism	2583.1
GALGT3	Beta-1,4 N-acetylgalactosaminyltransferase	[g] : gd3_hs + udpacgal --> gd2_hs + h + udp	2.4.1.92	Sphingolipid Metabolism	2583.1
GALGT4	Beta-1,4 N-acetylgalactosaminyltransferase	[g] : gt3_hs + udpacgal --> gt2_hs + h + udp	2.4.1.92	Sphingolipid Metabolism	2583.1
GALK	galactokinase	[c] : atp + gal --> adp + gal1p + h	2.7.1.6	Galactose metabolism	(2584.1 or 2585.1 or 2585.2)
GALNACT1g	UDPGal-chondroitin acetylgalactosaminyltransferase I, Golgi	[g] : cs,hs_linkage + udpacgal --> cs_pre + h + udp	2.4.1.174	Chondroitin / heparan sulfate biosynthesis	(55790.1 or 55454.1)
GALNACT2g	uridine diphosphoacetylgalactosamine-chondroitin acetylgalactosaminyltransferase II, Golgi	[g] : cs_a,b_pre2 + uacgam --> cs_a,b_pre3 + h + udp	2.4.1.175	Chondroitin / heparan sulfate biosynthesis	((79586.1 and 22856.1) or 337876.1 or 55454.1 or 55790.1)
GALNACT3g	uridine diphosphoacetylgalactosamine-chondroitin acetylgalactosaminyltransferase II, Golgi	[g] : cs_c_pre2 + uacgam --> cs_c_pre3 + h + udp	2.4.1.175	Chondroitin / heparan sulfate biosynthesis	((79586.1 and 22856.1) or 337876.1 or 55454.1 or 55790.1)
GALNACT4g	uridine diphosphoacetylgalactosamine-chondroitin acetylgalactosaminyltransferase II, Golgi	[g] : cs_d_pre3 + uacgam --> cs_d_pre4 + h + udp	2.4.1.175	Chondroitin / heparan sulfate biosynthesis	((79586.1 and 22856.1) or 337876.1 or 55454.1 or 55790.1)
GALNACT5g	uridine diphosphoacetylgalactosamine-chondroitin acetylgalactosaminyltransferase II, Golgi	[g] : cs_e_pre3 + uacgam --> cs_e_pre4 + h + udp	2.4.1.175	Chondroitin / heparan sulfate biosynthesis	((79586.1 and 22856.1) or 337876.1 or 55454.1 or 55790.1)
GALNTg	GalNAc transferase, Golgi apparatus	[g] : Ser/Thr + udpacgal --> Tn_antigen + h + udp	2.4.1.41	O-Glycan Biosynthesis	(2590.1 or 11226.1 or 2589.1 or 51809.1 or 2591.1 or 26290.1 or 50614.1 or 55568.1 or 8693.1 or 63917.1 or 79695.1 or 114805.1 or 79623.1 or 11227.1 or 117248.1 or 26290.1 or 55568.2)
GALOR	D-Galactose:NADP+ 1-oxidoreductase	[c] : gal + h + nadph <==> galt + nadp	1.1.1.21	Galactose metabolism	(231.1 or 10327.1 or 10327.2)
GALSIDEtg	galactocerebroside intracellular transport	galside_hs[c] <==> galside_hs[g]		Transport, Golgi Apparatus	
GALSIDEtl	galactocerebroside intracellular transport	galside_hs[c] <==> galside_hs[l]		Transport, Lysosomal	
GALT	galactose-1-phosphate uridylyltransferase	[c] : gal1p + h + utp <==> ppi + udpgal	2.7.7.10	Galactose metabolism	(2592.1 or 2592.2 or 2592.3)
GALt1r	galactose transport (uniport)	gal[e] <==> gal[c]		Transport, Extracellular	(6513.1 or 6514.1 or 6515.1 or 29988.1 or 81031.1)
GALt2_2	D-galactose transport via proton symport	gal[e] + (2) h[e] <==> gal[c] + (2) h[c]		Transport, Extracellular	6523.1
GALT2g	UDP-D-galactose:galactosylxylose galactosyltransferase, Golgi apparatus	[g] : lxser + udpgal --> h + l2xser + udp	2.4.1.134	Chondroitin / heparan sulfate biosynthesis	126792.1
GALt4	galactose transport via sodium symport	gal[e] + na1[e] <==> gal[c] + na1[c]		Transport, Extracellular	200010.1
GALt4_2	galactose transport via sodium symport	gal[e] + (2) na1[e] <==> gal[c] + (2) na1[c]		Transport, Extracellular	6523.1
GALTg	UDP-D-galactose:D-xylose galactosyltransferase, Golgi apparatus	[g] : udpgal + xser --> h + lxser + udp	2.4.1.133	Chondroitin / heparan sulfate biosynthesis	11285.1
GALtly	galactose efflux from lysosome	gal[l] --> gal[c]		Transport, Lysosomal	
GALU	UTP-glucose-1-phosphate uridylyltransferase	[c] : g1p + h + utp <==> ppi + udpg	2.7.7.9	Galactose metabolism	(7360.1 or 7360.2 or 7359.1)
GAMt1r	glucosamine transport (uniport)	gam[e] <==> gam[c]		Transport, Extracellular	(6513.1 or 6514.1 or 6517.1)
GAMYe	glucoamylase, extracellular (glygn5 -> malt)	[e] : glygn5 + h2o --> Tyr-ggn + malt	3.2.1.3	Starch and Sucrose Metabolism	8972.1
GAO1	Ganglioside O-acetylation	[c] : accoa + gd3_hs --> coa + oagd3_hs		Sphingolipid Metabolism	9197.1
GAO1g	Ganglioside O-acetylation	[g] : accoa + gd3_hs --> coa + oagd3_hs		Sphingolipid Metabolism	9197.1
GAO2	Ganglioside O-acetylation	[c] : accoa + gt3_hs --> coa + oagt3_hs		Sphingolipid Metabolism	9197.1
GAO2g	Ganglioside O-acetylation	[g] : accoa + gt3_hs --> coa + oagt3_hs		Sphingolipid Metabolism	9197.1
GAPD	glyceraldehyde-3-phosphate dehydrogenase	[c] : g3p + nad + pi <==> 13dpg + h + nadh	1.2.1.12	Glycolysis/Gluconeogenesis	(2597.1 or 26330.1)
GARFT	phosphoribosylglycinamide formyltransferase	[c] : 10fthf + gar <==> fgam + h + thf	2.1.2.2	IMP Biosynthesis	(2618.1 or 2618.2)
GASNASE2ly	glycosylasparaginase, lysosomal	[l] : h2o + n2m2nmasn --> Asn-X-Ser/Thr + n2m2nm	3.5.1.26	N-Glycan Degradation	175.1
GASNASE3ly	glycosylasparaginase, lysosomal	[l] : h2o + ksi_deg1 --> Asn-X-Ser/Thr + ksi_deg2	3.5.1.26	Keratan sulfate degradation	175.1
GASNASEly	glycosylasparaginase, lysosomal	[l] : h2o + s2l2n2m2masn --> Asn-X-Ser/Thr + s2l2n2m2m	3.5.1.26	N-Glycan Degradation	175.1
GBA	Glucosylceramidase	[c] : gluside_hs + h2o --> crm_hs + glc-D	3.2.1.45	Sphingolipid Metabolism	(2629.3 or 2629.5 or 2629.4 or 2629.2 or 2629.1)
GBAl	Glucosylceramidase	[l] : gluside_hs + h2o --> crm_hs + glc-D	3.2.1.45	Sphingolipid Metabolism	(2629.1 or 2629.2 or 2629.3 or 2629.4 or 2629.5)
GBGT1	globoside alpha-1,3-N-acetylgalactosaminyltransferase 1	[g] : gbside_hs + udpacgal --> acgagbside_hs + h + udp		Sphingolipid Metabolism	26301.1
GBSIDEte	globoside transport	gbside_hs[c] <==> gbside_hs[e]		Transport, Extracellular	
GBSIDEtl	globoside intracellular transport	gbside_hs[c] <==> gbside_hs[l]		Transport, Lysosomal	
GCALDD	Glycolaldehyde dehydrogenase	[c] : gcald + h2o + nad --> glyclt + (2) h + nadh	1.2.1.21	Glyoxylate and Dicarboxylate Metabolism	(216.1 or 8854.1 or 8854.2 or 8854.3 or 220.1 or 218.1 or 224.1 or 221.1 or 222.1 or 501.1 or 223.1)
GCALDDm	Glycolaldehyde dehydrogenase, mitochondrial	[m] : gcald + h2o + nad --> glyclt + (2) h + nadh	1.2.1.21	Glyoxylate and Dicarboxylate Metabolism	(5832.1 or 219.1 or 217.1 or 8659.1 or 8659.2 or 7915.1 or 7915.2 or 4329.1)
GCC2am	glycine-cleavage complex (lipoamide), mitochondrial	[m] : gly + h + lpam <==> alpam + co2	1.4.4.2	Glycine, Serine, and Threonine Metabolism	(2731.1 and 2653.1 and 1738.1 and 275.1)
GCC2bim	glycine-cleavage system (lipoamide) irreversible, mitochondrial	[m] : alpam + thf --> dhlam + mlthf + nh4	2.1.2.10	Glycine, Serine, and Threonine Metabolism	(1738.1 and 275.1 and 2653.1 and 2731.1)
GCC2cm	glycine-cleavage complex (lipoamide), mitochondrial	[m] : dhlam + nad <==> h + lpam + nadh	1.8.1.4	Glycine, Serine, and Threonine Metabolism	(1738.1 and 275.1 and 2731.1 and 2653.1)
GCCam	glycine-cleavage complex (lipoylprotein), mitochondrial	[m] : gly + h + lpro <==> alpro + co2	1.4.4.2	Glycine, Serine, and Threonine Metabolism	(1738.1 and 2731.1 and 275.1 and 2653.1)
GCCbim	glycine-cleavage complex (lipoylprotein) irreversible, mitochondrial	[m] : alpro + thf --> dhlpro + mlthf + nh4	2.1.2.10	Glycine, Serine, and Threonine Metabolism	(275.1 and 2653.1 and 1738.1 and 2731.1)

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
GCCcm	glycine-cleavage complex (lipoylprotein), mitochondrial	[m] : dhlpro + nad <==> h + lpro + nadh	1.8.1.4	Glycine, Serine, and Threonine Metabolism	(1738.1 and 2653.1 and 2731.1 and 275.1)
GCHOLAt	glycocholate transport via bicarbonate countertransport	gchola[e] + hco3[c] <==> gchola[c] + hco3[e]		Transport, Extracellular	(6579.1 or 10599.1 or 28234.1)
GCHOLAt2	glycocholate transport via sodium cotransport	gchola[e] + (2) na1[e] --> gchola[c] + (2) na1[c]		Transport, Extracellular	(6554.1 or 6555.1)
GCHOLAt3	ABC bile acid transporter	atp[c] + gchola[c] + h2o[c] --> adp[c] + gchola[e] + h[c] + pi[c]		Transport, Extracellular	(8647.1 or 8714.1 or 8714.2 or 8714.3)
GCHOLAte	bile acid intracellular transport	gchola[e] <==> gchola[c]		Transport, Extracellular	
GCHOLAtx	bile acid intracellular transport	gchola[x] <==> gchola[c]		Transport, Peroxisomal	
GCNTg	N-acetyllactosaminide beta-1,6-N-acetylglucosaminyltransferase	[g] : galacglcgal14acglcgalgluside_hs + uacgam --> acglcgalacglcgal14acglcgalgluside_hs + h + udp	2.4.1.150	Blood Group Biosynthesis	2651.1
GD1B2te	gd1b2_hs transport	gd1b2_hs[c] <==> gd1b2_hs[e]		Transport, Extracellular	
GD1B2tg	gd1b2_hs intracellular transport	gd1b2_hs[c] <==> gd1b2_hs[g]		Transport, Golgi Apparatus	
GD1Cte	gd1c_hs transport	gd1c_hs[c] <==> gd1c_hs[e]		Transport, Extracellular	
GD1Ctg	gd1c_hs intracellular transport	gd1c_hs[c] <==> gd1c_hs[g]		Transport, Golgi Apparatus	
GDCHOLAte	bile acid intracellular transport	gdchola[e] <==> gdchola[c]		Transport, Extracellular	
GDCHOLAtx	bile acid intracellular transport	gdchola[x] <==> gdchola[c]		Transport, Peroxisomal	
GDPFUCtg	GDPFuc Golgi transport via CMP antiport	gdpfuc[c] + gmp[g] <==> gdpfuc[g] + gmp[c]		Transport, Golgi Apparatus	55343.1
GDPtg	GDP intracellular transport	gdp[c] <==> gdp[g]		Transport, Golgi Apparatus	
GF6PTA	glutamine-fructose-6-phosphate transaminase	[c] : f6p + gln-L --> gam6p + glu-L	2.6.1.16	Aminosugar Metabolism	(2673.1 or 9945.1)
GFUCS	GDP-L-fucose synthase	[c] : gdpddman + h + nadph --> gdpfuc + nadp	1.1.1.271	Fructose and Mannose Metabolism	7264.1
GGH-10FTHF5GLUe	Gamma-glutamyl hydrolase (10FTHF5GLU), extracellular	[e] : 10fthf5glu + (4) h2o --> 10fthf + (4) glu-L		Folate Metabolism	8836.1
GGH-10FTHF5GLUl	Gamma-glutamyl hydrolase (10FTHF5GLU), lysosomal	[l] : 10fthf5glu + (4) h2o --> 10fthf + (4) glu-L		Folate Metabolism	8836.1
GGH-10FTHF6GLUe	Gamma-glutamyl hydrolase (10FTHF6GLU), extracellular	[e] : 10fthf6glu + h2o --> 10fthf5glu + glu-L		Folate Metabolism	8836.1
GGH-10FTHF6GLUl	Gamma-glutamyl hydrolase (10FTHF6GLU), lysosomal	[l] : 10fthf6glu + h2o --> 10fthf5glu + glu-L		Folate Metabolism	8836.1
GGH-10FTHF7GLUe	Gamma-glutamyl hydrolase (10FTHF7GLU), extracellular	[e] : 10fthf7glu + h2o --> 10fthf6glu + glu-L		Folate Metabolism	8836.1
GGH-10FTHF7GLUl	Gamma-glutamyl hydrolase (10FTHF7GLU), lysosomal	[l] : 10fthf7glu + h2o --> 10fthf6glu + glu-L		Folate Metabolism	8836.1
GGH-5DHFe	Gamma-glutamyl hydrolase (5DHF), extracellular	[e] : 5dhf + (4) h2o --> dhf + (4) glu-L		Folate Metabolism	8836.1
GGH-5DHFl	Gamma-glutamyl hydrolase (5DHF), lysosomal	[l] : 5dhf + (4) h2o --> dhf + (4) glu-L		Folate Metabolism	8836.1
GGH-5THFe	Gamma-glutamyl hydrolase (5THF), extracellular	[e] : 5thf + (4) h2o --> (4) glu-L + thf		Folate Metabolism	8836.1
GGH-5THFl	Gamma-glutamyl hydrolase (5THF), lysosomal	[l] : 5thf + (4) h2o --> (4) glu-L + thf		Folate Metabolism	8836.1
GGH-6DHFe	Gamma-glutamyl hydrolase (6DHF), extracellular	[e] : 6dhf + h2o --> 5dhf + glu-L		Folate Metabolism	8836.1
GGH-6DHFl	Gamma-glutamyl hydrolase (6DHF), lysosomal	[l] : 6dhf + h2o --> 5dhf + glu-L		Folate Metabolism	8836.1
GGH-6THFe	Gamma-glutamyl hydrolase (6THF), extracellular	[e] : 6thf + h2o --> 5thf + glu-L		Folate Metabolism	8836.1
GGH-6THFl	Gamma-glutamyl hydrolase (6THF), lysosomal	[l] : 6thf + h2o --> 5thf + glu-L		Folate Metabolism	8836.1
GGH-7DHFe	Gamma-glutamyl hydrolase (7DHF), extracellular	[e] : 7dhf + h2o --> 6dhf + glu-L		Folate Metabolism	8836.1
GGH-7DHFl	Gamma-glutamyl hydrolase (7DHF), lysosomal	[l] : 7dhf + h2o --> 6dhf + glu-L		Folate Metabolism	8836.1
GGH-7THFe	Gamma-glutamyl hydrolase (7THF), extracellular	[e] : 7thf + h2o --> 6thf + glu-L		Folate Metabolism	8836.1
GGH-7THFl	Gamma-glutamyl hydrolase (7THF), lysosomal	[l] : 7thf + h2o --> 6thf + glu-L		Folate Metabolism	8836.1
GGLUCT	gamma-glutamylcyclotransferase	gluala[e] --> 5oxpro[c] + ala-L[c]	2.3.2.4	Glutathione Metabolism	2655.1
GGNG	glycogenin self-glucosylation	[c] : Tyr-ggn + (8) udpg --> ggn + (8) h + (8) udp		Starch and Sucrose Metabolism	((2992.1 and 2998.1) or (2997.1 and 8908.1) or (2992.1 and 2997.1) or (8908.1 and 2998.1))
GGT_L	geranylgeranyltransferase (liver)	[c] : (17.6) ipdp + ttc-ggdp --> (0.1) dedoldp_L + (17.6) ppi		N-Glycan Biosynthesis	
GGT_U	geranylgeranyltransferase (uterus)	[c] : (16.5) ipdp + ttc-ggdp --> (0.1) dedoldp_U + (16.5) ppi		N-Glycan Biosynthesis	
GGT5r	Gamma-glutamyltransferase 5	[r] : h2o + leuktrC4 <==> glu-L + leuktrD4	2.3.2.2	Eicosanoid Metabolism	2687.1
GGT6	Gamma-glutamyltransferase	[c] : glu-L + leuktrE4 <==> h2o + leuktrF4	2.3.2.2	Eicosanoid Metabolism	
GHMT2r	glycine hydroxymethyltransferase, reversible	[c] : ser-L + thf <==> gly + h2o + mlthf	2.1.2.1	Glycine, Serine, and Threonine Metabolism	(6470.1 or 6470.2)
GHMT2rm	glycine hydroxymethyltransferase, reversible, mitochondrial	[m] : ser-L + thf <==> gly + h2o + mlthf	2.1.2.1	Glycine, Serine, and Threonine Metabolism	6472.1
GHMT3	glycine hydroxymethyltransferase	[c] : 3htmelys + h --> 4tmeabut + gly	2.1.2.1	Lysine Metabolism	(6470.1 or 6470.2)
GHMT3m	glycine hydroxymethyltransferase, mitochondrial	[m] : 3htmelys + h --> 4tmeabut + gly	2.1.2.1	Lysine Metabolism	6472.1
GK1	guanylate kinase (GMP:ATP)	[c] : atp + gmp <==> adp + gdp	2.7.4.8	Nucleotides	2987.1
GK1m	guanylate kinase (GMP:ATP), mitochondrial	[m] : atp + gmp <==> adp + gdp	2.7.4.8	Nucleotides	
GLACO	D-Glucuronolactone:NAD+ oxidoreductase	[c] : glac + (2) h2o + nad --> glcr + (3) h + nadh	1.2.1.3	Ascorbate and Aldarate Metabolism	(216.1 or 218.1 or 220.1 or 221.1 or 222.1 or 223.1 or 224.1 or 8854.1 or 8854.2 or 8854.3)
GLACOm	D-Glucuronolactone:NAD+ oxidoreductase, mitochondrial	[m] : glac + (2) h2o + nad --> glcr + (3) h + nadh	1.2.1.3	Ascorbate and Aldarate Metabolism	(217.1 or 219.1 or 8659.1 or 8659.2)
GLACter	D-glucurono-6,3-lactone transport, endoplasmic reticulum	glac[c] <==> glac[r]		Transport, Endoplasmic Reticular	
GLAl	galactosidase, alpha	[l] : digalside_hs + h2o --> gal + galside_hs	3.2.1.22	Sphingolipid Metabolism	2717.1
GLB1	Beta-galactosidase	[l] : galgluside_hs + h2o --> gal + gluside_hs	3.2.1.23	Sphingolipid Metabolism	((4758.1 and 2588.1 and 2720.1 and 5476.1) or (5476.1 and 2720.1))
GLBRAN	1,4-alpha-glucan branching enzyme (glygn1 -> glygn2)	[c] : glygn1 --> glygn2	2.4.1.18	Starch and Sucrose Metabolism	2632.1
GLCAASE1ly	beta-glucuronidase, lysosomal	[l] : h2o + hs_deg9 --> glcur + hs_deg10	3.2.1.31	Heparan sulfate degradation	2990.1
GLCAASE4ly	beta-glucuronidase, lysosomal	[l] : cs_a_deg2 + h2o --> cs_a_deg3 + glcur	3.2.1.31	Chondroitin sulfate degradation	2990.1

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
GLCAASE5ly	beta-glucuronidase, lysosomal	[l] : cs_c_deg2 + h2o --> cs_c_deg3 + glcur	3.2.1.31	Chondroitin sulfate degradation	2990.1
GLCAASE6ly	beta-glucuronidase, lysosomal	[l] : cs_d_deg3 + h2o --> cs_d_deg4 + glcur	3.2.1.31	Chondroitin sulfate degradation	2990.1
GLCAASE7ly	beta-glucuronidase, lysosomal	[l] : cs_e_deg3 + h2o --> cs_e_deg4 + glcur	3.2.1.31	Chondroitin sulfate degradation	2990.1
GLCAASE8ly	beta-glucuronidase, lysosomal	[l] : h2o + ha --> glcur + ha_deg1	3.2.1.31	Hyaluronan Metabolism	2990.1
GLCAASE9ly	beta-glucuronidase, lysosomal	[l] : (2) h2o + ha_pre1 --> acgam + glcur	3.2.1.31	Hyaluronan Metabolism	2990.1
GLCAE1g	chondroitin-glucuronate 5-epimerase	[g] : cs_a,b_pre3 --> cs_b_pre4	5.1.3.19	Chondroitin / heparan sulfate biosynthesis	
GLCAE2g	heparosan-N-sulfate-glucuronate 5-epimerase	[g] : hs_pre10 --> hs_pre11	5.1.3.17	Chondroitin / heparan sulfate biosynthesis	26035.1
GLCAT2g	chondroitin glucuronyltransferase II, Golgi apparatus	[g] : cs_a,b,e_pre1 + udpglcur --> cs_a,b_pre2 + h + udp		Chondroitin / heparan sulfate biosynthesis	(54480.1 or (79586.1 and 22856.1) or 337876.1)
GLCAT3g	chondroitin glucuronyltransferase II, Golgi apparatus	[g] : cs_c,d,e_pre1 + udpglcur --> cs_c_pre2 + h + udp		Chondroitin / heparan sulfate biosynthesis	(54480.1 or (79586.1 and 22856.1) or 337876.1)
GLCAT4g	chondroitin glucuronyltransferase II, Golgi apparatus	[g] : cs_d_pre2 + udpglcur --> cs_d_pre3 + h + udp		Chondroitin / heparan sulfate biosynthesis	(54480.1 or (79586.1 and 22856.1) or 337876.1)
GLCAT5g	chondroitin glucuronyltransferase II, Golgi apparatus	[g] : cs_e_pre2 + udpglcur --> cs_e_pre3 + h + udp		Chondroitin / heparan sulfate biosynthesis	(54480.1 or (22856.1 and 79586.1) or 337876.1)
GLCAT6g	heparan glucuronyltransferase II	[g] : hs_pre1 + udpglcur --> h + hs_pre2 + udp		Chondroitin / heparan sulfate biosynthesis	((2131.1 and 2132.1) or (2132.2 and 2131.1))
GLCAT7g	heparan glucuronyltransferase II	[g] : hs_pre3 + udpglcur --> h + hs_pre4 + udp		Chondroitin / heparan sulfate biosynthesis	((2131.1 and 2132.1) or (2132.2 and 2131.1))
GLCAT8g	heparan glucuronyltransferase II	[g] : hs_pre5 + udpglcur --> h + hs_pre6 + udp		Chondroitin / heparan sulfate biosynthesis	((2131.1 and 2132.1) or (2132.2 and 2131.1))
GLCAT9g	heparan glucuronyltransferase II	[g] : hs_pre7 + udpglcur --> h + hs_pre8 + udp		Chondroitin / heparan sulfate biosynthesis	((2131.1 and 2132.1) or (2132.2 and 2131.1))
GLCATg	UDP-D-glucuronate:galactosylgalactosylxylose glucuronosyltransferase, Golgi apparatus	[g] : l2xser + udpglcur --> cs,hs_linkage + h + udp	2.4.1.135	Chondroitin / heparan sulfate biosynthesis	(135152.1 or 26229.1 or 27087.1 or 27087.2)
GLCMter	glucose transport via membrane vesicle	glc-D[r] --> glc-D[e]		Transport, Extracellular	
GLCNACASE1ly	alpha-N-acetylglucosaminidase, lysosomal	[l] : h2o + hs_deg3 --> acgam + hs_deg4	3.2.1.50	Heparan sulfate degradation	4669.1
GLCNACASE2ly	alpha-N-acetylglucosaminidase, lysosomal	[l] : h2o + hs_deg8 --> acgam + hs_deg9	3.2.1.50	Heparan sulfate degradation	4669.1
GLCNACASE3ly	alpha-N-acetylglucosaminidase, lysosomal	[l] : h2o + hs_deg14 --> acgam + hs_deg15	3.2.1.50	Heparan sulfate degradation	4669.1
GLCNACASE4ly	alpha-N-acetylglucosaminidase, lysosomal	[l] : h2o + hs_deg20 --> acgam + hs_deg21	3.2.1.50	Heparan sulfate degradation	4669.1
GLCNACASE5ly	alpha-N-acetylglucosaminidase, lysosomal	[l] : h2o + hs_deg24 --> acgam + hs_deg25	3.2.1.50	Heparan sulfate degradation	4669.1
GLCNACDASg	GlcNAc N-deacetylase / N-sulfotransferase	[g] : (4) h2o + hs_pre9 + (4) paps --> (4) ac + (4) h + hs_pre10 + (4) pap		Chondroitin / heparan sulfate biosynthesis	(3340.1 or 8509.1 or 9348.1 or 64579.1)
GLCNACPT_L	UDP-GlcNAc:dolichol-phosphate GlcNAc phosphotransferase (liver)	[c] : (0.1) dolp_L + uacgam --> (0.1) naglc2p_L + ump	2.7.8.15	N-Glycan Biosynthesis	(1798.2 or 1798.1)
GLCNACPT_U	UDP-GlcNAc:dolichol-phosphate GlcNAc phosphotransferase (uterus)	[c] : (0.1) dolp_U + uacgam --> (0.1) naglc2p_U + ump	2.7.8.15	N-Glycan Biosynthesis	(1798.1 or 1798.2)
GLCNACT_L	UDP-GlcNAc:N-acetyl-D-glucosaminyl diphosphodolichol N-acetyl-D-glucosaminyltransferase (liver)	[c] : (0.1) naglc2p_L + uacgam --> (0.1) chito2pdol_L + h + udp	2.4.1.141	N-Glycan Biosynthesis	
GLCNACT_U	UDP-GlcNAc:N-acetyl-D-glucosaminyl diphosphodolichol N-acetyl-D-glucosaminyltransferase (uterus)	[c] : (0.1) naglc2p_U + uacgam --> (0.1) chito2pdol_U + h + udp	2.4.1.141	N-Glycan Biosynthesis	
GLCNACT1g	alpha-N-acetylglucosaminyltransferase I, Golgi apparatus	[g] : cs,hs_linkage + uacgam --> h + hs_pre1 + udp		Chondroitin / heparan sulfate biosynthesis	(2137.1 or 2135.1)
GLCNACT2g	alpha-N-acetylglucosaminyltransferase II	[g] : hs_pre2 + uacgam --> h + hs_pre3 + udp		Chondroitin / heparan sulfate biosynthesis	(2137.1 or 2134.1 or (2131.1 and 2132.1) or (2132.2 and 2131.1))
GLCNACT3g	alpha-N-acetylglucosaminyltransferase II	[g] : hs_pre4 + uacgam --> h + hs_pre5 + udp		Chondroitin / heparan sulfate biosynthesis	(2137.1 or 2134.1 or (2131.1 and 2132.1) or (2132.2 and 2131.1))
GLCNACT4g	alpha-N-acetylglucosaminyltransferase II	[g] : hs_pre6 + uacgam --> h + hs_pre7 + udp		Chondroitin / heparan sulfate biosynthesis	(2137.1 or 2134.1 or (2131.1 and 2132.1) or (2132.2 and 2131.1))
GLCNACT5g	alpha-N-acetylglucosaminyltransferase II	[g] : hs_pre8 + uacgam --> h + hs_pre9 + udp		Chondroitin / heparan sulfate biosynthesis	(2137.1 or 2134.1 or (2131.1 and 2132.1) or (2132.2 and 2131.1))
GLCt1r	glucose transport (uniport)	glc-D[e] <==> glc-D[c]		Transport, Extracellular	(155184.1 or 29988.1 or 56606.1 or 56606.2 or 81031.1 or 66035.1 or 154091.1 or 6514.1 or 6513.1 or 6515.1 or 6517.1 or 11182.1 or 144195.1)
GLCt2_2	D-glucose transport in via proton symport	glc-D[e] + (2) h[e] <==> glc-D[c] + (2) h[c]		Transport, Extracellular	6523.1
GLCt2r	D-glucose transport in via proton symport	glc-D[e] + h[e] <==> glc-D[c] + h[c]		Transport, Extracellular	6524.1
GLCt4	glucose transport via sodium symport	glc-D[e] + na1[e] <==> glc-D[c] + na1[c]		Transport, Extracellular	(159963.1 or 125206.1 or 6524.1 or 6526.1 or 200010.1)
GLCt4_2	glucose transport via sodium symport	glc-D[e] + (2) na1[e] <==> glc-D[c] + (2) na1[c]		Transport, Extracellular	6523.1
GLCter	glucose transport, endoplasmic reticulum	glc-D[c] <==> glc-D[r]		Transport, Endoplasmic Reticular	
GLCtg	glucose transport, Golgi apparatus	glc-D[c] <==> glc-D[g]		Transport, Golgi Apparatus	6513.1
GLCtly	glucose efflux from lysosome	glc-D[l] --> glc-D[c]		Transport, Lysosomal	
GLCURter	glucuronate endoplasmic reticular transport	glcur[c] --> glcur[r]		Transport, Endoplasmic Reticular	
GLCURtly	glucuronate transport into lysososme	glcur[c] + h[c] <==> glcur[l] + h[l]		Transport, Lysosomal	26503.1
GLDBRAN	glycogen debranching enzyme	[c] : dxtrn + h2o --> glc-D + glygn3	3.2.1.33	Starch and Sucrose Metabolism	(178.1 or 178.2 or 178.3 or 178.5 or 178.6 or 178.4)
GLGNS1	glycogen synthase (ggn -> glygn1)	[c] : ggn + (3) udpg --> glygn1 + (3) h + (3) udp	2.4.1.11	Starch and Sucrose Metabolism	((2998.1 and 2992.1) or (8908.1 and 2998.1) or (2992.1 and 2997.1) or (2997.1 and 8908.1))

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
GLNALANaEx	L-alanine/L-glutamine Na-dependent exchange (Gln-L in)	ala-L[c] + gln-L[e] + na1[e] --> ala-L[e] + gln-L[c] + na1[c]		Transport, Extracellular	6510.1
GLNASNNaEx	L-glutamine/L-asparagine Na-dependent exchange (Gln-L in)	asn-L[c] + gln-L[e] + na1[e] --> asn-L[e] + gln-L[c] + na1[c]		Transport, Extracellular	6510.1
GLNCYSNaEx	L-cysteine/L-glutamine Na-dependent exchange (Gln-L in)	cys-L[c] + gln-L[e] + na1[e] --> cys-L[e] + gln-L[c] + na1[c]		Transport, Extracellular	6510.1
GLNLASEer	gluconolactonase, endoplasmic reticulum	[r] : guln + h <==> gullac + h2o	3.1.1.17	Ascorbate and Aldarate Metabolism	
GLNS	glutamine synthetase	[c] : atp + glu-L + nh4 --> adp + gln-L + h + pi	6.3.1.2	Glutamate metabolism	(2752.1 or 51557.1)
GLNSERNaEx	L-serine/L-glutamine Na-dependent exchange (Gln-L in)	gln-L[e] + na1[e] + ser-L[c] --> gln-L[c] + na1[c] + ser-L[e]		Transport, Extracellular	6510.1
GLNt4	L-glutamine reversible transport via sodium symport	gln-L[e] + na1[e] --> gln-L[c] + na1[c]		Transport, Extracellular	(11254.1 or 55089.1 or 54407.1 or 81539.1)
GLNTHRNaEx	L-threonine/L-glutamine Na-dependent exchange (Gln-L in)	gln-L[e] + na1[e] + thr-L[c] --> gln-L[c] + na1[c] + thr-L[e]		Transport, Extracellular	6510.1
GLNtm	L-glutamine transport via electroneutral transporter	gln-L[c] --> gln-L[m]		Transport, Mitochondrial	
GLNtN1	Glutamine transport (Na, H coupled)	gln-L[e] + h[c] + (2) na1[e] <==> gln-L[c] + h[e] + (2) na1[c]		Transport, Extracellular	(92745.1 or 10991.1)
GLPASE1	glycogen phosphorylase (glygn2 -> dxtrn)	[c] : glygn2 + (3) pi --> dxtrn + (3) g1p	2.4.1.1	Starch and Sucrose Metabolism	(5834.1 or 5836.1 or 5837.1)
GLPASE2	glycogen phosphorylase (amyls -> glc-D)	[c] : glygn3 + (7) h2o --> Tyr-ggn + (7) glc-D	2.4.1.1	Starch and Sucrose Metabolism	(5836.1 or 5834.1 or 5837.1)
GLRASE	glucuronolactone reductase	[c] : gullac + nadp <==> glac + h + nadph	1.1.1.20	Ascorbate and Aldarate Metabolism	
GLU5Km	glutamate 5-kinase (m)	[m] : atp + glu-L --> adp + glu5p	2.7.2.11	Urea cycle/amino group metabolism	5832.1
GLUCYS	gamma-glutamylcysteine synthetase	[c] : atp + cys-L + glu-L --> adp + glucys + h + pi	6.3.2.2	Glutathione Metabolism	(2730.1 and 2729.1)
GLUDC	Glutamate Decarboxylase	[c] : glu-L + h --> 4abut + co2	4.1.1.15	Glutamate metabolism	(2571.1 or 2571.2 or 2572.1)
GLUDxm	glutamate dehydrogenase (NAD) (mitochondrial)	[m] : glu-L + h2o + nad <==> akg + h + nadh + nh4	1.4.1.2	Glutamate metabolism	(2747.1 or 2746.1)
GLUDym	glutamate dehydrogenase (NADP), mitochondrial	[m] : glu-L + h2o + nadp <==> akg + h + nadph + nh4	1.4.1.4	Glutamate metabolism	(2747.1 or 2746.1)
GluForTx	Glutamate formimidoyltransferase	[c] : forglu + h + thf --> 5forthf + glu-L	2.1.2.5	Histidine Metabolism	(10841.1 or 10841.2)
GLUNm	glutaminase (mitochondrial)	[m] : gln-L + h2o --> glu-L + nh4	3.5.1.2	Glutamate metabolism	(2744.1 or 27165.1 or 27165.2)
GLUPRT	glutamine phosphoribosyldiphosphate amidotransferase	[c] : gln-L + h2o + prpp --> glu-L + ppi + pram	2.4.2.14	IMP Biosynthesis	5471.1
GLUt2m	L-glutamate reversible transport via proton symport, mitochondrial	glu-L[c] + h[c] <==> glu-L[m] + h[m]		Transport, Mitochondrial	(8604.1 or 10165.1 or 79751.1 or 83733.1)
GLUt6	Glutamate transport via Na, H symport and K antiport	glu-L[e] + h[e] + k[c] + (3) na1[e] --> glu-L[c] + h[c] + k[e] + (3) na1[c]		Transport, Extracellular	(6505.1 or 6506.1 or 6507.1 or 6511.1 or 6512.1)
GLUt7l	Glutamate transport, lysosomal	glu-L[l] --> glu-L[c]		Transport, Lysosomal	
GLUTCOADHm	glutaryl-CoA dehydrogenase (mitochondria)	[m] : fad + glutcoa + h --> b2coa + co2 + fadh2	1.3.99.7	Tryptophan metabolism	(2639.1 or 2639.2)
GLUtr	intracellular transport	glu-L[c] <==> glu-L[r]		Transport, Endoplasmic Reticular	
GLUVESSEC	L-glutamate secretion via secretory vesicle (ATP driven)	atp[c] + glu-L[c] + h2o[c] --> adp[c] + glu-L[e] + h[c] + pi[c]		Transport, Extracellular	(57084.1 or 57030.1 or 246213.1)
GLXO1	glyoxylate oxidase	[c] : glx + h2o + nad --> (2) h + nadh + oxa		Glyoxylate and Dicarboxylate Metabolism	(160287.1 or 92483.1 or 55293.1 or 3948.1 or 3948.2 or 3939.1 or (3945.1 and 3939.1) or 3945.1 or 197257.1 or 197257.2)
GLXO2p	glyoxylate oxidase, peroxisomal	[x] : glx + h2o + o2 --> h + h2o2 + oxa		Glyoxylate and Dicarboxylate Metabolism	(54363.1 or 51179.1 or 51179.2)
GLXtm	glyoxylate transport, mitochondrial	glx[c] <==> glx[m]		Transport, Mitochondrial	
GLXtp	glyoxylate transport, peroxisomal	glx[c] <==> glx[x]		Transport, Peroxisomal	
GLYAMDTRc	glycine amidinotransferase (c)	[c] : arg-L + gly <==> gudac + orn	2.1.4.1	Urea cycle/amino group metabolism	2628.1
GLYATm	glycine C-acetyltransferase	[m] : accoa + gly <==> 2aobut + coa	2.3.1.29	Glycine, Serine, and Threonine Metabolism	23464.1
GLYBt4(2)r	Betaine transport (sodium symport) (2:1)	glyb[e] + (2) na1[e] <==> glyb[c] + (2) na1[c]		Transport, Extracellular	6539.1
GLYBtm	Glycine betaine transport via diffusion (mitochondria to cytosol)	glyb[m] <==> glyb[c]		Transport, Mitochondrial	
GLYC3Ptm	glycerol-3-phosphate shuttle	glyc3p[c] --> glyc3p[m]		Transport, Mitochondrial	
GLYCK2	glycerate kinase	[c] : atp + glyc-R --> 2pg + adp + h	2.7.1.31	Glyoxylate and Dicarboxylate Metabolism	
GLYCLTDy	Glycolate dehydrogenase (NADP)	[c] : glx + h + nadph --> glyclt + nadp		Glyoxylate and Dicarboxylate Metabolism	9380.1
GLYCLTDym	Glycolate dehydrogenase (NADP), mitochondrial	[m] : glx + h + nadph --> glyclt + nadp		Glyoxylate and Dicarboxylate Metabolism	
GLYCLTtp	glycolate transport into peroxisome	glyclt[c] --> glyclt[x]		Transport, Peroxisomal	
GLYC-St	L-glycerate export	glyc-S[c] --> glyc-S[e]		Transport, Extracellular	
GLYCt	glycerol transport via channel	glyc[c] <==> glyc[e]		Transport, Extracellular	
GLYCtm	glycerol transport	glyc[c] <==> glyc[m]		Transport, Mitochondrial	
GLYCTO1p	Glycolate oxidase, peroxisome	[x] : glyclt + o2 --> glx + h2o2		Glyoxylate and Dicarboxylate Metabolism	(51179.1 or 51179.2 or 54363.1)
GLYK	glycerol kinase	[c] : atp + glyc --> adp + glyc3p + h	2.7.1.30	Glycerophospholipid Metabolism	(2712.1 or 2713.1 or 2710.1 or 2710.2)
GLYKm	glycerol kinase	[m] : atp + glyc --> adp + glyc3p + h	2.7.1.30	Glycerophospholipid Metabolism	(2712.1 or 2713.1 or 2710.1 or 2710.2)
GLYOp	glycine oxidase, perixosomal	[x] : gly + h2o + o2 --> glx + h2o2 + nh4		Glycine, Serine, and Threonine Metabolism	
GLYOX	hydroxyacylglutathione hydrolase	[c] : h2o + lgt-S --> gthrd + h + lac-D	3.1.2.6	Pyruvate Metabolism	(3029.1 or 84264.1 or 84264.2)
GLYOXm	hydroxyacylglutathione hydrolase, mitochondrial	[m] : h2o + lgt-S --> gthrd + h + lac-D	3.1.2.6	Pyruvate Metabolism	3029.1
GLYt2r	glycine reversible transport via proton symport	gly[e] + h[e] <==> gly[c] + h[c]		Transport, Extracellular	206358.1
GLYt2rL	glycine reversible transport via proton symport (lysosome)	gly[l] + h[l] <==> gly[c] + h[c]		Transport, Lysosomal	206358.1
GLYt4	glycine transport via sodium symport	gly[e] + na1[e] --> gly[c] + na1[c]		Transport, Extracellular	(11254.1 or 55089.1 or 54407.1 or 81539.1)
GLYt7(211)r	glycine reversible transport via sodium and chloride symport (2:1:1)	cl[e] + gly[e] + (2) na1[e] <==> cl[c] + gly[c] + (2) na1[c]		Transport, Extracellular	(6536.1 or 6536.2)
GLYt7(311)r	glycine reversible transport via sodium and chloride symport (3:1:1)	cl[e] + gly[e] + (3) na1[e] <==> cl[c] + gly[c] + (3) na1[c]		Transport, Extracellular	9152.1
GLYtm	glycine passive transport to mitochondria	gly[c] <==> gly[m]		Transport, Mitochondrial	

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
GLYtp	glycine passive transport to peroxisome	gly[c] <==> gly[x]		Transport, Peroxisomal	
GLYVESSEC	Glycine secretion via secretory vesicle (ATP driven)	atp[c] + (3) gly[c] + h2o[c] --> adp[c] + (3) gly[e] + h[c] + pi[c]		Transport, Extracellular	140679.1
GMAND	GDP-D-mannose dehydratase	[c] : gdpmann --> gdpddman + h2o	4.2.1.47	Fructose and Mannose Metabolism	2762.1
GMPR	GMP reductase	[c] : gmp + (2) h + nadph --> imp + nadp + nh4	1.7.1.7	Nucleotides	(51292.1 or 51292.2 or 51292.3 or 2766.1)
GMPS2	GMP synthase	[c] : atp + gln-L + h2o + xmp --> amp + glu-L + gmp + (2) h + ppi	6.3.5.2	Nucleotides	8833.1
GMPtn	GMP nuclear transport	gmp[c] <==> gmp[n]		Transport, Nuclear	
GND	phosphogluconate dehydrogenase	[c] : 6pgc + nadp --> co2 + nadph + ru5p-D	1.1.1.44	Pentose Phosphate Pathway	5226.1
GNDer	phosphogluconate dehydrogenase, endoplasmic reticulum	[r] : 6pgc + nadp --> co2 + nadph + ru5p-D	1.1.1.44	Pentose Phosphate Pathway	
GNMT	glycine N-methyltransferase	[c] : amet + gly --> ahcys + h + sarcs	2.1.1.20	Glycine, Serine, and Threonine Metabolism	27232.1
GP1CALPHAte	gp1calpha_hs transport	gp1calpha_hs[c] <==> gp1calpha_hs[e]		Transport, Extracellular	
GP1CALPHAtg	gp1calpha_hs intracellular transport	gp1calpha_hs[c] <==> gp1calpha_hs[g]		Transport, Golgi Apparatus	
GP1Cte	gp1c_hs transport	gp1c_hs[c] <==> gp1c_hs[e]		Transport, Extracellular	
GP1Ctg	gp1c_hs intracellular transport	gp1c_hs[c] <==> gp1c_hs[g]		Transport, Golgi Apparatus	
GPAM_hs	glycerol-3-phosphate acyltransferase	[c] : Rtotalcoa + glyc3p --> alpa_hs + coa	2.3.1.15	Triacylglycerol Synthesis	57678.1
GPAMm_hs	glycerol-3-phosphate acyltransferase	[m] : Rtotalcoa + glyc3p --> alpa_hs + coa	2.3.1.15	Triacylglycerol Synthesis	57678.1
GPDDA1	Glycerophosphodiester phosphodiesterase (Glycerophosphocholine)	[c] : g3pc + h2o --> chol + glyc3p + h	3.1.4.46	Glycerophospholipid Metabolism	
GPIAT	glucosaminylphosphatidyl inositol acetyltransferase	[c] : gpail_hs + pmtcoa --> coa + gacpail_hs		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	284098.1
GPIDA2er	glycophosphatidylinositol (GPI) deacylase, endoplasmic reticulum	[r] : em2emgacpail_prot_hs + h2o --> dem2emgacpail_prot_hs + h + hdca		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	80055.1
GPIDAer	glycophosphatidylinositol (GPI) deacylase, endoplasmic reticulum	[r] : gpi_prot_hs + h2o --> dgpi_prot_hs + h + hdca		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	80055.1
GPIMTer_L	GlcN-acylPI mannosyltransferase, endoplasmic reticulum	[r] : (0.1) dolmanp_L + gacpail_hs --> (0.1) dolp_L + h + mgacpail_hs		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	(54965.1 and 93183.1)
GPIMTer_U	GlcN-acylPI mannosyltransferase, endoplasmic reticulum	[r] : (0.1) dolmanp_U + gacpail_hs --> (0.1) dolp_U + h + mgacpail_hs		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	(93183.1 and 54965.1)
GQ1BALPHAte	gq1balpha_hs transport	gq1balpha_hs[c] <==> gq1balpha_hs[e]		Transport, Extracellular	
GQ1BALPHAtg	gq1balpha_hs intracellular transport	gq1balpha_hs[c] <==> gq1balpha_hs[g]		Transport, Golgi Apparatus	
GQ1Bte	gq1b_hs transport	gq1b_hs[c] <==> gq1b_hs[e]		Transport, Extracellular	
GQ1Btg	gq1b_hs intracellular transport	gq1b_hs[c] <==> gq1b_hs[g]		Transport, Golgi Apparatus	
GRTT	geranyltranstransferase	[c] : grdp + ipdp --> frdp + ppi	2.5.1.10	Cholesterol Metabolism	9453.1
GRTTx	geranyltranstransferase	[x] : grdp + ipdp --> frdp + ppi	2.5.1.10	Cholesterol Metabolism	2224.1
GSNKm	guanosine kinase (mitochondrial)	[m] : atp + gsn --> adp + gmp + h		Nucleotides	
GSNt	guanosine facilated transport in cytosol	gsn[e] <==> gsn[c]		Transport, Extracellular	(3177.1 or 2030.1)
GSNt4	guanosine transport in via sodium symport	gsn[e] + na1[e] --> gsn[c] + na1[c]		Transport, Extracellular	(9153.1 or 64078.1)
GSNt5	guanosine transport in via sodium (1:2) symport	gsn[e] + (2) na1[e] --> gsn[c] + (2) na1[c]		Transport, Extracellular	64078.1
GSNtl	guanosine facilated transport from lysosome	gsn[l] <==> gsn[c]		Transport, Lysosomal	55315.1
GSNtm	guanosine facilated transport in mitochondria	gsn[c] <==> gsn[m]		Transport, Mitochondrial	2030.1
GT1Ate	gt1a_hs transport	gt1a_hs[c] <==> gt1a_hs[e]		Transport, Extracellular	
GT1Atg	gt1a_hs intracellular transport	gt1a_hs[c] <==> gt1a_hs[g]		Transport, Golgi Apparatus	
GTHDH	Glutathione dehydrogenase (dehydroascorbate reductase)	[c] : dhdascb + (2) gthrd --> ascb-L + gthox	1.8.5.1	Ascorbate and Aldarate Metabolism	
GTHO	glutathione oxidoreductase	[c] : gthox + h + nadph --> (2) gthrd + nadp	1.8.1.7	Glutamate metabolism	2936.1
GTHOm	glutathione oxidoreductase	[m] : gthox + h + nadph --> (2) gthrd + nadp	1.8.1.7	Glutamate metabolism	2936.1
GTHP	glutathione peridoxase	[c] : (2) gthrd + h2o2 <==> gthox + (2) h2o	1.11.1.9	Glutathione Metabolism	(5052.1 or 5052.2 or 5052.3 or 7001.1 or 7001.2 or 7001.3 or 2877.1 or 2876.1 or 2876.2 or 2879.1)
GTHPe	glutathione peroxidase (e)	[e] : (2) gthrd + h2o2 <==> gthox + (2) h2o	1.11.1.9	Glutathione Metabolism	(2878.1 or 257202.1)
GTHPm	glutathione peroxidase, mitochondria	[m] : (2) gthrd + h2o2 <==> gthox + (2) h2o	1.11.1.9	Glutathione Metabolism	(10935.1 or 10935.2 or 2879.1)
GTHRDt	Glutathione transport into mitochondria	atp[c] + gthrd[c] + h2o[c] <==> adp[c] + gthrd[m] + h[c] + pi[c]		Glutathione Metabolism	
GTHRDtr	glutathione transport via diffusion	gthrd[c] <==> gthrd[r]		Transport, Endoplasmic Reticular	
GTHS	glutathione synthetase	[c] : atp + glucys + gly --> adp + gthrd + h + pi	6.3.2.3	Glutathione Metabolism	2937.1
GTMLTe	g-glutamyltransferase (e)	ala-L[c] + gthrd[c] --> cgly[e] + gluala[e]	2.3.2.2	Glutathione Metabolism	(2678.1 or 2678.2 or 2678.3 or 2679.1)
GTPCI	GTP cyclohydrolase I	[c] : gtp + h2o --> ahdt + for + h	3.5.4.16	Tetrahydrobiopterin	2643.1
GTPCIn	GTP cyclohydrolase I, nuclear	[n] : gtp + h2o --> ahdt + for + h	3.5.4.16	Tetrahydrobiopterin	2643.1
GTPtn	GTP diffusion in nucleus	gtp[c] <==> gtp[n]		Transport, Nuclear	
GUACYC	guanylate cyclase	[c] : gtp --> 35cgmp + ppi	4.6.1.2	Nucleotides	(4881.1 or 4882.1 or 4882.2 or (2974.1 and 2977.1) or (2983.1 and 2982.1) or (2977.1 and 2983.1) or (2982.1 and 2974.1) or 2984.1 or 2986.1 or 3000.1)
GUAD	guanine deaminase	[c] : gua + h + h2o --> nh4 + xan	3.5.4.3	Purine Catabolism	9615.1
GUAPRT	guanine phosphoribosyltransferase	[c] : gua + prpp --> gmp + ppi	2.4.2.8	Salvage Pathway	3251.1
GUAt	Guanine transport	gua[e] <==> gua[c]		Transport, Extracellular	3177.1
GULLACter	gulonolactone endoplasmic reticular transport	gullac[c] --> gullac[r]		Transport, Endoplasmic Reticular	
GULN3D	L-gulonate 3-dehydrogenase	[c] : guln + nad <==> 3dhguln + h + nadh	1.1.1.45	Pentose and Glucuronate Interconversions	
GULNDer	gulonate dehydrogenase, endoplasmic reticulum	[r] : glcur + h + nadph <==> guln + nadp	1.1.1.19	Pentose and Glucuronate Interconversions	
GULNter	L-gulonate endoplasmic reticular export	guln[r] --> guln[c]		Transport, Endoplasmic Reticular	
GUR1PP	Glucuronate 1-phosphate phosphatase	[c] : glcur1p + h2o --> glcur + pi		Pentose and Glucuronate Interconversions	
H2CO3D	carboxylic acid dissociation	[c] : co2 + h2o <==> h2co3	4.2.1.1	Miscellaneous	(771.2 or 23632.1 or 377677.1 or 759.1 or 760.1 or 761.1 or 762.1 or 766.1 or 766.2 or 768.1 or 771.1)
H2CO3D2	carboxylic acid dissociation	[c] : h + hco3 <==> h2co3		Miscellaneous	

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
H2CO3D2m	carboxylic acid dissociation, mitochondrial	[m] : h + hco3 <==> h2co3		Miscellaneous	
H2CO3Dm	carboxylic acid dissociation	[m] : co2 + h2o <==> h2co3	4.2.1.1	Miscellaneous	(763.1 or 11238.1)
H2ETer	H2 phosphoethanolaminyl transferase, endoplasmic reticulum	[r] : mgacpail_hs + pe_hs --> dag_hs + emgacpail_hs		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	(23556.1 or 23556.2)
H2MTer_L	H2 mannosyltransferase, endoplasmic reticulum	[r] : (0.1) dolmanp_L + mgacpail_hs --> (0.1) dolp_L + h + m2gacpail_hs		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	55650.1
H2MTer_U	H2 mannosyltransferase, endoplasmic reticulum	[r] : (0.1) dolmanp_U + mgacpail_hs --> (0.1) dolp_U + h + m2gacpail_hs		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	55650.1
H2O2syn	Hydrogen peroxide synthesis (NADPH dependent)	[c] : h + nadph + o2 --> h2o2 + nadp		Tyrosine metabolism	(53905.1 or 53905.2 or 50506.1)
H2O2t	hydrogen peroxide transport via diffusion	h2o2[e] <==> h2o2[c]		Transport, Extracellular	
H2O2tly	hydrogen peroxide lysosomal transport via diffusion	h2o2[c] <==> h2o2[l]		Transport, Lysosomal	
H2O2tm	hydrogen peroxide mitochondrial transport	h2o2[c] <==> h2o2[m]		Transport, Mitochondrial	
H2O2tn	hydrogen peroxide nuclear transport	h2o2[c] <==> h2o2[n]		Transport, Nuclear	
H2O2tp	hydrogen peroxide peroxisomal transport via diffusion	h2o2[c] <==> h2o2[x]		Transport, Peroxisomal	
H2Ot	H2O transport via diffusion	h2o[e] <==> h2o[c]		Transport, Extracellular	6523.1
H2Oter	H2O endoplasmic reticulum transport	h2o[c] <==> h2o[r]		Transport, Endoplasmic Reticular	
H2Otg	H2O transport, Golgi apparatus	h2o[c] <==> h2o[g]		Transport, Golgi Apparatus	
H2Otly	H2O transport, lysosomal	h2o[c] <==> h2o[l]		Transport, Lysosomal	
H2Otm	H2O transport, mitochondrial	h2o[c] <==> h2o[m]		Transport, Mitochondrial	343.1
H2Otn	H2O transport, nuclear	h2o[n] <==> h2o[c]		Transport, Nuclear	
H2Otp	H2O transport, peroxisomal	h2o[c] <==> h2o[x]		Transport, Peroxisomal	
H3ETer	H3 phosphoethanolaminyl transferase, endoplasmic reticulum	[r] : m2gacpail_hs + pe_hs --> dag_hs + memgacpail_hs		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	(23556.1 or 23556.2)
H3MTer_L	H3 mannosyltransferase, endoplasmic reticulum	[r] : (0.1) dolmanp_L + m2gacpail_hs --> (0.1) dolp_L + h + m3gacpail_hs		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	9488.1
H3MTer_U	H3 mannosyltransferase, endoplasmic reticulum	[r] : (0.1) dolmanp_U + m2gacpail_hs --> (0.1) dolp_U + h + m3gacpail_hs		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	9488.1
H4ET3er	H4 phosphoethanolaminyl transferase, endoplasmic reticulum	[r] : m3gacpail_hs + pe_hs --> dag_hs + em3gacpail_hs		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	((5281.2 and 84720.1) or (5281.2 and 84720.2) or (5281.1 and 84720.1) or (5281.1 and 84720.2))
H4ETer	H4 phosphoethanolaminyl transferase, endoplasmic reticulum	[r] : m3gacpail_hs + pe_hs --> dag_hs + m2emgacpail_hs		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	(23556.1 or 23556.2)
H5MTer_L	H5 mannosyltransferase, endoplasmic reticulum	[r] : (0.1) dolmanp_L + emgacpail_hs --> (0.1) dolp_L + h + memgacpail_hs		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	55650.1
H5MTer_U	H5 mannosyltransferase, endoplasmic reticulum	[r] : (0.1) dolmanp_U + emgacpail_hs --> (0.1) dolp_U + h + memgacpail_hs		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	55650.1
H6'ET2er	H6' phosphoethanolaminyl transferase, endoplasmic reticulum	[r] : em3gacpail_hs + pe_hs --> dag_hs + emem2gacpail_hs		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	((5281.1 and 54872.1) or (54872.1 and 5281.2))
H6ET3er	H6 phosphoethanolaminyl transferase, endoplasmic reticulum	[r] : m2emgacpail_hs + pe_hs --> dag_hs + em2emgacpail_hs		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	((5281.2 and 84720.1) or (5281.2 and 84720.2) or (5281.1 and 84720.1) or (5281.1 and 84720.2))
H6'ETer	H6' phosphoethanolaminyl transferase, endoplasmic reticulum	[r] : em3gacpail_hs + pe_hs --> dag_hs + em2emgacpail_hs		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	(23556.1 or 23556.2)
H6MTer_L	H6 mannosyltransferase, endoplasmic reticulum	[r] : (0.1) dolmanp_L + m2emgacpail_hs --> (0.1) dolp_L + h + m3emgacpail_hs		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	80235.1
H6MTer_U	H6 mannosyltransferase, endoplasmic reticulum	[r] : (0.1) dolmanp_U + m2emgacpail_hs --> (0.1) dolp_U + h + m3emgacpail_hs		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	80235.1
H7ET2er	H7 phosphoethanolaminyl transferase, endoplasmic reticulum	[r] : em2emgacpail_hs + pe_hs --> dag_hs + gpi_hs		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	((5281.1 and 54872.1) or (54872.1 and 5281.2))
H7'ETer	H7' phosphoethanolaminyl transferase, endoplasmic reticulum	[r] : emem2gacpail_hs + pe_hs --> dag_hs + gpi_hs		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	(23556.1 or 23556.2)
H7MTer_L	H7 mannosyltransferase, endoplasmic reticulum	[r] : (0.1) dolmanp_L + em2emgacpail_hs --> (0.1) dolp_L + h + mem2emgacpail_hs		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	80235.1
H7MTer_U	H7 mannosyltransferase, endoplasmic reticulum	[r] : (0.1) dolmanp_U + em2emgacpail_hs --> (0.1) dolp_U + h + mem2emgacpail_hs		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	80235.1
H7'TAer	H7' transamidase, endoplasmic reticulum	[r] : em2emgacpail_hs + pre_prot --> em2emgacpail_prot_hs + gpi_sig		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	(94005.1 and 10026.1 and 128869.1 and 8733.1 and 51604.1)
H8MTer_L	H8 mannosyltransferase, endoplasmic reticulum	[r] : (0.1) dolmanp_L + gpi_hs --> (0.1) dolp_L + h + m(em)3gacpail_hs		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	80235.1
H8MTer_U	H8 mannosyltransferase, endoplasmic reticulum	[r] : (0.1) dolmanp_U + gpi_hs --> (0.1) dolp_U + h + m(em)3gacpail_hs		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	80235.1
H8TAer	H8 transamidase, endoplasmic reticulum	[r] : gpi_hs + pre_prot --> gpi_prot_hs + gpi_sig		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	(94005.1 and 8733.1 and 10026.1 and 51604.1 and 128869.1)
HACD1m	3-hydroxyacyl-CoA dehydrogenase (acetoacetyl-CoA) (mitochondria)	[m] : aacoa + h + nadh <==> 3hbcoa + nad	1.1.1.35	Tryptophan metabolism	(3028.1 or (3032.1 and 3030.1) or 3033.1)
HACD1x	3-hydroxyacyl-CoA dehydrogenase (acetoacetyl-CoA) (peroxisome)	[x] : aacoa + h + nadh <==> 3hbcoa + nad	1.1.1.35	Tryptophan metabolism	(1962.1 or 3295.1)
HACD9m	3-hydroxyacyl-CoA dehydrogenase (2-Methylacetoacetyl-CoA), mitochondrial	[m] : 3hmbcoa + nad <==> 2maacoa + h + nadh	1.1.1.35	Valine, Leucine, and Isoleucine Metabolism	3028.1
HAS1	hyaluronan synthase	uacgam[c] + udpglcur[c] --> (2) h[c] + ha_pre1[e] + (2) udp[c]	2.4.1.212	Hyaluronan Metabolism	(3036.1 or 3037.1 or 3038.1 or 3038.2)
HAS2	hyaluronan synthase	ha_pre1[e] + uacgam[c] + udpglcur[c] --> (2) h[c] + ha[e] + (2) udp[c]	2.4.1.212	Hyaluronan Metabolism	(3036.1 or 3037.1 or 3038.1 or 3038.2)
HAtly	hyaluronan transport, extracellular to lysosome	ha[e] --> ha[l]		Transport, Lysosomal	
HBZOPT10m	Hydroxybenzoate Decaprenyltransferase	[m] : 4hbz + decdp --> 3dphb + ppi		Ubiquinone Biosynthesis	27235.1
HCO3_CLt	bicarbonate transport (Cl-/HCO3- exchange)	cl[c] + hco3[e] <==> cl[e] + hco3[c]		Transport, Extracellular	(83697.1 or 6508.2 or 6521.1 or 6522.1 or 6508.1)
HCO3_NAt	bicarbonate transport (Na/HCO3 cotransport)	hco3[e] + na1[e] <==> hco3[c] + na1[c]		Transport, Extracellular	9497.1

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
HCO3Em	HCO3 equilibration reaction	[m] : co2 + h2o <==> h + hco3		Urea cycle/amino group metabolism	
HCOUMARINte	xenobiotic transport	hcoumarin[e] <==> hcoumarin[c]		Transport, Extracellular	
HDCAter	palmitate ER export	hdca[r] --> hdca[c]		Transport, Endoplasmic Reticular	
HDCAtr	fatty acid transport via diffusion	hdca[e] <==> hdca[c]		Transport, Extracellular	
HDCEAtr	fatty acid transport via diffusion	hdcea[e] <==> hdcea[c]		Transport, Extracellular	
HDD2COAtx	hdd2coa intracellular transport	hdd2coa[c] <==> hdd2coa[x]		Transport, Peroxisomal	
HESTRATRIOLte	hydroxylated estrogen derivative transport	hestratriol[c] <==> hestratriol[e]		Transport, Extracellular	
HESTRATRIOLtr	hydroxylated estrogen derivative transport	hestratriol[c] <==> hestratriol[r]		Transport, Endoplasmic Reticular	
HEX1	hexokinase (D-glucose:ATP)	[c] : atp + glc-D --> adp + g6p + h	2.7.1.1	Glycolysis/Gluconeogenesis	(2645.1 or 2645.2 or 2645.3 or 3098.1 or 3098.2 or 3098.3 or 3098.4 or 3098.5 or 3099.1 or 3101.1 or 80201.1)
HEX10	hexokinase (D-glucosamine:ATP)	[c] : atp + gam --> adp + gam6p + h	2.7.1.1	Aminosugar Metabolism	(3098.1 or 3098.2 or 3098.3 or 3098.4 or 3098.5 or 2645.1 or 2645.2 or 2645.3 or 80201.1 or 3101.1 or 3099.1)
HEX4	hexokinase (D-mannose:ATP)	[c] : atp + man --> adp + h + man6p	2.7.1.7	Fructose and Mannose Metabolism	(2645.1 or 3098.2 or 2645.3 or 3098.5 or 3098.4 or 80201.1 or 2645.2 or 3099.1 or 3098.3 or 3101.1 or 3098.1)
HEX7	hexokinase (D-fructose:ATP)	[c] : atp + fru --> adp + f6p + h	2.7.1.1	Fructose and Mannose Metabolism	(2645.1 or 2645.2 or 3098.1 or 3098.2 or 3098.3 or 3098.4 or 3098.5 or 3099.1 or 3101.1 or 80201.1 or 2645.3)
HEXCCOAtx	fatty acid intracellular transport	hexccoa[c] <==> hexccoa[x]		Transport, Peroxisomal	
HEXCCPT1	carnitine O-palmitoyltransferase	[c] : crn + hexccoa --> coa + hexccrn	2.3.1.21	Carnitine shuttle	(1375.4 or 1374.1 or 126129.1 or 1375.3 or 1375.2 or 1375.1)
HEXCCPT2	carnitine transferase	[m] : coa + hexccrn --> crn + hexccoa		Carnitine shuttle	1376.1
HEXCCRNt	transport into the mitochondria (carnitine)	hexccrn[c] --> hexccrn[m]		Carnitine shuttle	788.1
HEXCt	fatty acid transport via diffusion	hexc[e] <==> hexc[c]		Transport, Extracellular	
HGNTOR	Homogentisate:oxygen 1,2-oxidoreductase (decyclizing)	[c] : hgentis + o2 --> 4mlacac + h	1.13.11.5	Tyrosine metabolism	3081.1
HIBDm	3-hydroxyisobutyrate dehydrogenase, mitochondrial	[m] : 3hmp + nad <==> 2mop + h + nadh	1.1.1.31	Valine, Leucine, and Isoleucine Metabolism	11112.1
HISD	histidase	[c] : his-L --> nh4 + urcan	4.3.1.3	Histidine Metabolism	3034.1
HISDC	histidine decarboxylase	[c] : h + his-L --> co2 + hista	4.1.1.22	Histidine Metabolism	(1644.1 or 3067.1)
HISt4	L-histidine transport in via sodium symport	his-L[e] + na1[e] --> his-L[c] + na1[c]		Transport, Extracellular	(11254.1 or 54407.1)
HISTASE	Histaminase	[c] : h2o + hista + o2 --> h2o2 + im4act + nh4	1.4.3.6	Histidine Metabolism	(26.1 or 314.2 or 314.1)
HISTAtu	Histamine uniport	hista[e] <==> hista[c]		Transport, Extracellular	(6582.1 or 6582.2 or 6581.1)
HISTAVESSEC	Histamine secretion via secretory vesicle (ATP driven)	(2) atp[c] + (2) h2o[c] + (3) hista[c] --> (2) adp[c] + (2) h[c] + (3) hista[e] + (2) pi[c]		Transport, Extracellular	(6570.1 or 6571.1)
HIStiDF	L-histidine transport via diffusion (extracellular to cytosol)	his-L[e] --> his-L[c]		Transport, Extracellular	55089.1
HIStN1	Histidine transport (Na, H coupled)	h[c] + his-L[e] + (2) na1[e] <==> h[e] + his-L[c] + (2) na1[c]		Transport, Extracellular	10991.1
HKt	H+/K+ gastric/non-gastric P-ATPase and ABC ATPase	atp[c] + h2o[c] + k[e] --> adp[c] + h[e] + k[c] + pi[c]	3.6.3.10	Transport, Extracellular	(496.1 and 495.1)
HKYNH	3-Hydroxy-L-kynurenine hydrolase	[c] : h2o + hLkynr --> 3hanthrn + ala-L	3.7.1.3	Tryptophan metabolism	8942.1
HMBS	hydroxymethylbilane synthase	[c] : h2o + (4) ppbng --> hmbil + (4) nh4	4.3.1.8	Heme Biosynthesis	3145.1
HMGCOARr	Hydroxymethylglutaryl CoA reductase (ir)	[r] : (2) h + hmgcoa + (2) nadph --> coa + mev-R + (2) nadp	1.1.1.34	Cholesterol Metabolism	3156.1
HMGCOARx	Hydroxymethylglutaryl CoA reductase (ir)	[x] : (2) h + hmgcoa + (2) nadph --> coa + mev-R + (2) nadp	1.1.1.34	Cholesterol Metabolism	3156.1
HMGCOASi	Hydroxymethylglutaryl CoA synthase (ir)	[c] : aacoa + accoa + h2o --> coa + h + hmgcoa	4.1.3.5	Cholesterol Metabolism	(3157.2 or 3157.1)
HMGCOASim	Hydroxymethylglutaryl CoA synthase (ir)	[m] : aacoa + accoa + h2o --> coa + h + hmgcoa	4.1.3.5	Cholesterol Metabolism	3158.1
HMGCOAtm	Hydroxymethylglutaryl-CoA reversible mitochondria transport	hmgcoa[c] <==> hmgcoa[m]		Transport, Mitochondrial	
HMGCOAtx	Hydroxymethylglutaryl-CoA reversible peroxisomal transport	hmgcoa[c] <==> hmgcoa[x]		Transport, Peroxisomal	
HMGLm	hydroxymethylglutaryl-CoA lyase	[m] : hmgcoa --> acac + accoa	4.1.3.4	Cholesterol Metabolism	(3155.1 or 54511.1)
HMGLx	hydroxymethylglutaryl-CoA lyase	[x] : hmgcoa --> acac + accoa	4.1.3.4	Cholesterol Metabolism	3155.1
HOMt4	L-homoserine via sodium symport	hom-L[e] + na1[e] --> hom-L[c] + na1[c]		Transport, Extracellular	(6541.1 or 6542.1 or 84889.1)
HOXG	Heme oxygenase 1	[c] : (5) h + (3) nadph + (3) o2 + pheme --> biliverd + co + fe2 + (3) h2o + (3) nadp	1.14.99.3	Heme Degradation	(3162.1 or 3163.1)
HPACtr	hydroxyphenylacetate transport via diffusion	4hphac[c] <==> 4hphac[e]		Transport, Extracellular	
HPCLx	2-hydroxyphytanoyl-CoA lyase	[x] : (4) h + phyt2ohcoa --> formcoa + pristanal		Fatty Acid Metabolism	26062.1
HPDCACRNCPT1	carnitine fatty-acyl transferase	[c] : crn + hpdcacoa --> coa + hpdcacrn	2.3.1.21	Carnitine shuttle	(1375.3 or 126129.1 or 1374.1 or 1375.2 or 1375.1)
HPDCACRNCPT2	heptadecanoate transport into the mitochondria	[m] : coa + hpdcacrn --> crn + hpdcacoa		Carnitine shuttle	1376.1
HPDCACRNt	heptadecanoate transport into the mitochondria	hpdcacrn[c] --> hpdcacrn[m]		Carnitine shuttle	788.1
HPDCAt	fatty acid transport via diffusion	hpdca[e] <==> hpdca[c]		Transport, Extracellular	
HPROxm	L-hydroxyproline dehydrogenase (NAD), mitochondrial	[m] : 4hpro-LT + nad --> 1p3h5c + (2) h + nadh	1.5.1.12	Arginine and Proline Metabolism	(8659.1 or 8659.2)
HPYRDC	hydroxypyruvate decarboxylase	[c] : h + hpyr --> co2 + gcald	4.1.1.40	Glyoxylate and Dicarboxylate Metabolism	
HPYRDCm	hydroxypyruvate decarboxylase, mitochondria	[m] : h + hpyr --> co2 + gcald	4.1.1.40	Glyoxylate and Dicarboxylate Metabolism	

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
HPYRR2x	hydroxypyruvate reductase (NADH)	[c] : h + hpyr + nadh --> glyc-S + nad		Glyoxylate and Dicarboxylate Metabolism	(197257.1 or 197257.2 or 3948.2 or 3948.1 or 3945.1 or 92483.1 or 160287.1 or 3939.1 or (3945.1 and 3939.1))
HPYRRy	Hydroxypyruvate reductase (NADPH)	[c] : h + hpyr + nadph --> glyc-R + nadp		Glyoxylate and Dicarboxylate Metabolism	9380.1
HPYRtp	hydroxypyruate transport, peroxisomal	hpyr[c] <==> hpyr[x]		Transport, Peroxisomal	
HRETNtn	4-hydroxyretinoic acid transport, Nuclear	hretn[c] <==> hretn[n]		Transport, Nuclear	
HS1ly	heparan-N-sulfatase, lysosomal	[l] : h2o + hs_deg1 --> h + hs_deg2 + so4	3.10.1.1	Heparan sulfate degradation	6448.1
HS2ly	heparan-N-sulfatase, lysosomal	[l] : h2o + hs_deg6 --> h + hs_deg7 + so4	3.10.1.1	Heparan sulfate degradation	6448.1
HS3ly	heparan-N-sulfatase, lysosomal	[l] : h2o + hs_deg12 --> h + hs_deg13 + so4	3.10.1.1	Heparan sulfate degradation	6448.1
HS4ly	heparan-N-sulfatase, lysosomal	[l] : h2o + hs_deg18 --> h + hs_deg19 + so4	3.10.1.1	Heparan sulfate degradation	6448.1
HSAT1ly	heparan-glucosaminide N-acetyltransferase, lysosomal	accoa[c] + hs_deg2[l] --> coa[c] + h[l] + hs_deg3[l]	2.3.1.78	Heparan sulfate degradation	
HSAT2ly	heparan-glucosaminide N-acetyltransferase, lysosomal	accoa[c] + hs_deg7[l] --> coa[c] + h[l] + hs_deg8[l]	2.3.1.78	Heparan sulfate degradation	
HSAT3ly	heparan-glucosaminide N-acetyltransferase, lysosomal	accoa[c] + hs_deg13[l] --> coa[c] + h[l] + hs_deg14[l]	2.3.1.78	Heparan sulfate degradation	
HSAT4ly	heparan-glucosaminide N-acetyltransferase, lysosomal	accoa[c] + hs_deg19[l] --> coa[c] + h[l] + hs_deg20[l]	2.3.1.78	Heparan sulfate degradation	
HSD11B1r	11-beta-hydroxysteroid dehydrogenase type 1	[r] : cortsn + h + nadph <==> crtsl + nadp		Steroid Metabolism	(3290.1 or 3290.2)
HSD11B2r	11-beta-hydroxysteroid dehydrogenase type 2	[r] : cortsn + h + nadh <==> crtsl + nad		Steroid Metabolism	3291.1
HSD17B1	testicular 17-beta-hydroxysteroid dehydrogenase	[c] : estrone + h + nadph <==> estradiol + nadp	1.1.1.62	Steroid Metabolism	(3292.1 or 7923.1)
HSD17B2r	17-beta-hydroxysteroid dehydrogenase	[r] : andrstndn + h + nadh --> nad + tststerone	1.1.1.62	Steroid Metabolism	3294.1
HSD17B3r	testicular 17-beta-hydroxysteroid dehydrogenase	[r] : andrstndn + h + nadph --> nadp + tststerone	1.1.1.62	Steroid Metabolism	3293.1
HSD17B42x	hydroxysteroid (17-beta) dehydrogenase 4	[x] : h + nadph + o2 + thcholoylcoa --> dhocholoylcoa + (2) h2o + nadp		Bile Acid Biosynthesis	3295.1
HSD17B4x	hydroxysteroid (17-beta) dehydrogenase 4	[x] : cholcoads + h + nadph + o2 --> cholcoaone + h2o + nadp		Bile Acid Biosynthesis	3295.1
HSD17B7r	testicular 17-beta-hydroxysteroid dehydrogenase	[r] : estrone + h + nadph --> estradiol + nadp	1.1.1.62	Steroid Metabolism	51478.1
HSD17B8r	17-beta-hydroxysteroid dehydrogenase	[r] : estrone + h + nadh --> estradiol + nad	1.1.1.62	Steroid Metabolism	3294.1
HSD17B9r	17-beta-hydroxysteroid dehydrogenase (type 7)	[r] : andrstrn + h + nadph + (1.5) o2 --> eandrstrn + (2) h2o + nadp		Steroid Metabolism	51478.1
HSD3A1r	3 alpha-hydroxysteroid dehydrogenase (type 3)	[r] : andrstandn + h + nadh <==> andrstrn + nad		Steroid Metabolism	1109.1
HSD3A2r	3 alpha-hydroxysteroid dehydrogenase (type 3)	[r] : andrstandn + h + nadph <==> andrstrn + nadp		Steroid Metabolism	1109.1
HSD3B11	3 beta-hydroxysteroid dehydrogenase/delta 5-->4-isomerase type I	[c] : nad + prgnlone --> h + nadh + prgstrn		Steroid Metabolism	3283.1
HSD3B11r	3 beta-hydroxysteroid dehydrogenase/delta 5-->4-isomerase type I	[r] : nad + prgnlone --> h + nadh + prgstrn		Steroid Metabolism	3284.1
HSD3B12r	3 beta-hydroxysteroid dehydrogenase/delta 5-->4-isomerase type I	[r] : dhea + nad --> andrstndn + h + nadh		Steroid Metabolism	3284.1
HSD3B13	3 beta-hydroxysteroid dehydrogenase/delta 5-->4-isomerase type I	[c] : 17ahprgnlone + nad --> 17ahprgstrn + h + nadh		Steroid Metabolism	3283.1
HSD3B13r	3 beta-hydroxysteroid dehydrogenase/delta 5-->4-isomerase type I	[r] : 17ahprgnlone + nad --> 17ahprgstrn + h + nadh		Steroid Metabolism	3284.1
HSD3B2r	3 beta-hydroxysteroid dehydrogenase type 1	[r] : eandrstrn + h + nadh --> andrstandn + h2o + nad		Steroid Metabolism	3284.1
HSD3B3r	3 beta-hydroxysteroid dehydrogenase type 1	[r] : eandrstrn + h + nadph --> andrstandn + h2o + nadp		Steroid Metabolism	3284.1
HSD3B7	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	[r] : nad + xol7a --> h + nadh + xol7aone		Bile Acid Biosynthesis	80270.1
HSD3B7P	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	[r] : nadp + xol7a --> h + nadph + xol7aone		Bile Acid Biosynthesis	80270.1
HSPASEly	heparan sulfate proteoglycan protease, lysosome (endosome)	[l] : h2o + hspg --> Ser-Gly/Ala-X-Gly + hs		Heparan sulfate degradation	
HSPGt	heparan sulfate transport, golgi to extracellular	hspg[g] --> hspg[e]		Transport, Extracellular	
HSPGtly	heparan sulfate transport, extracellular to lysosome	hspg[e] --> hspg[l]		Transport, Lysosomal	
HTAXOLte	xenobiotic transport	htaxol[e] <==> htaxol[c]		Transport, Extracellular	
Htm	Uncoupling protein	h[c] --> h[m]		Transport, Mitochondrial	(7352.1 or 7350.1 or 7351.1 or 7352.2 or 9481.1 or 9016.1 or 9016.2)
Htr	H transporter, endoplasmic reticulum	h[c] <==> h[r]		Transport, Endoplasmic Reticular	
Htx	H transporter, peroxisome	h[c] <==> h[x]		Transport, Peroxisomal	
HXANtl	hypoxanthine facilated transport from lysosome	hxan[l] <==> hxan[c]		Transport, Lysosomal	55315.1
HXANtx	hypoxanthine diffusion in peroxisome	hxan[c] --> hxan[x]		Transport, Peroxisomal	
HXPRT	hypoxanthine phosphoribosyltransferase (Hypoxanthine)	[c] : hxan + prpp --> imp + ppi	2.4.2.8	Salvage Pathway	3251.1
HYPOE	hypothetical enyme	[c] : h2o + pyam5p --> pi + pydam		Vitamin B6 Metabolism	57026.1
HYPTROX	Hypotaurine oxidase	[c] : (2) h + (2) hyptaur + o2 --> (2) taur		Taurine and hypotaurine metabolism	
HYXNt	Hypoxanthine transport	hxan[e] <==> hxan[c]		Transport, Extracellular	3177.1
ICDHxm	Isocitrate dehydrogenase (NAD+)	[m] : icit + nad --> akg + co2 + nadh	1.1.1.41	Citric Acid Cycle	((3421.1 and 3419.1 and 3420.1) or (3421.1 and 3420.2 and 3419.1) or (3421.1 and 3419.1 and 3420.3) or (3421.1 and 3419.1 and 3420.1) or (3420.2 and 3419.1 and 3421.2) or (3419.1 and 3421.2 and 3420.3))
ICDHy	isocitrate dehydrogenase (NADP)	[c] : icit + nadp --> akg + co2 + nadph	1.1.1.42	Citric Acid Cycle	3417.1
ICDHyp	Isocitrate dehydrogenase (NADP+)	[x] : icit + nadp --> akg + co2 + nadph	1.1.1.42	Citric Acid Cycle	3417.1
ICDHyrm	Isocitrate dehydrogenase (NADP+)	[m] : icit + nadp <==> akg + co2 + nadph	1.1.1.42	Citric Acid Cycle	3418.1
IDHPOXOX2b	Iodide:hydrogen-peroxide oxidoreductase 2	[c] : 3ityr-L + iodine --> 35diotyr + h + i	1.11.1.8	Tyrosine metabolism	(7173.1 or 7173.2 or 7173.3 or 7173.4 or 7173.5)

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
IDHPOXOX3	Iodide:hydrogen-peroxide oxidoreductase 3	[c] : 35diotyr + 3ityr-L + h2o2 --> 2amac + (2) h2o + triodthy	1.11.1.8	Tyrosine metabolism	(7173.1 or 7173.2 or 7173.3 or 7173.4 or 7173.5)
IDHPOXOX4	Iodide:hydrogen-peroxide oxidoreductase 4	[c] : (2) 35diotyr + h2o2 --> 2amac + (2) h2o + thyox-L	1.11.1.8	Tyrosine metabolism	(7173.1 or 7173.2 or 7173.3 or 7173.4 or 7173.5)
IDHPOXOXb	Iodide:hydrogen-peroxide oxidoreductase	[c] : iodine + tyr-L --> 3ityr-L + h + i	1.11.1.8	Tyrosine metabolism	(7173.1 or 7173.2 or 7173.3 or 7173.4 or 7173.5)
IDOAASE1ly	alpha-L-iduronidase, lysosomal	[l] : h2o + hs_deg4 --> hs_deg5 + idour	3.2.1.76	Heparan sulfate degradation	3425.1
IDOAASE2ly	alpha-L-iduronidase, lysosomal	[l] : h2o + hs_deg16 --> hs_deg17 + idour	3.2.1.76	Heparan sulfate degradation	3425.1
IDOAASE3ly	alpha-L-iduronidase, lysosomal	[l] : h2o + hs_deg22 --> hs_deg23 + idour	3.2.1.76	Heparan sulfate degradation	3425.1
IDOAASE4ly	alpha-L-iduronidase, lysosomal	[l] : cs_b_deg3 + h2o --> cs_a_deg3 + idour	3.2.1.76	Chondroitin sulfate degradation	3425.1
IDOURtly	iduronate transport into lysososme	h[c] + idour[c] <==> h[l] + idour[l]		Transport, Lysosomal	26503.1
IDPtn	IDP nuclear transport	idp[c] <==> idp[n]		Transport, Nuclear	
ILEt4	L-isoleucine transport in via sodium symport	ile-L[e] + na1[e] --> ile-L[c] + na1[c]		Transport, Extracellular	11254.1
ILEt5m	Isoleucine mitochondrial transport	ile-L[c] <==> ile-L[m]		Transport, Mitochondrial	
ILETA	isoleucine transaminase	[c] : akg + ile-L <==> 3mop + glu-L	2.6.1.42	Valine, Leucine, and Isoleucine Metabolism	586.1
ILETAm	isoleucine transaminase, mitochondrial	[m] : akg + ile-L <==> 3mop + glu-L	2.6.1.42	Valine, Leucine, and Isoleucine Metabolism	587.1
ILEtec	L-isoleucine transport via diffusion (extracellular to cytosol)	ile-L[e] <==> ile-L[c]		Transport, Extracellular	(8501.1 or 124935.1)
IMACTD	Imidazole acetaldeyde dehydrogenase	[c] : h2o + im4act + nad --> (2) h + im4ac + nadh	1.2.1.3	Histidine Metabolism	(224.1 or 501.1 or 8854.2 or 8854.1 or 8854.3 or 216.1 or 223.1)
IMACTD_m	Imidazole acetaldeyde dehydrogenase (mito)	[m] : h2o + im4act + nad --> (2) h + im4ac + nadh	1.2.1.3	Histidine Metabolism	(8659.1 or 8659.2 or 217.1 or 219.1)
IMPC	IMP cyclohydrolase	[c] : h2o + imp <==> fprica	3.5.4.10	IMP Biosynthesis	471.1
IMPD	IMP dehydrogenase	[c] : h2o + imp + nad --> h + nadh + xmp	1.1.1.205	Nucleotides	(3614.1 or 3614.2 or 3615.1)
INOSTO	inositol oxygenase	[c] : inost + o2 --> glcur + h + h2o	1.13.99.1	Inositol Phosphate Metabolism	55586.1
INSKm	insosine kinase, mitochondrial	[m] : atp + ins --> adp + h + imp	2.7.1.73	Nucleotides	
INSt	Inosine transport (diffusion)	ins[e] <==> ins[c]		Transport, Extracellular	(3177.1 or 2030.1)
INSt4	inosine transport in via sodium symport	ins[e] + na1[e] --> ins[c] + na1[c]		Transport, Extracellular	(9153.1 or 64078.1)
INSt5	inosine transport in via sodium (1:2) symport	ins[e] + (2) na1[e] --> ins[c] + (2) na1[c]		Transport, Extracellular	64078.1
INStl	inosine facilated transport from lysosome	ins[l] <==> ins[c]		Transport, Lysosomal	55315.1
INStm	inosine facilated transport in mitochondria	ins[c] <==> ins[m]		Transport, Mitochondrial	2030.1
INSTt2r	inositol transport in via proton symport	h[e] + inost[e] <==> h[c] + inost[c]		Transport, Extracellular	114134.1
INSTt4	inositol transport via sodium symport	inost[e] + na1[e] <==> inost[c] + na1[c]		Transport, Extracellular	6526.1
INSTt4_2	inositol transport via sodium symport	inost[e] + (2) na1[e] <==> inost[c] + (2) na1[c]		Transport, Extracellular	115584.1
IPDDIx	isopentenyl-diphosphate D-isomerase	[x] : ipdp <==> dmpp	5.3.3.2	Cholesterol Metabolism	(3422.1 or 91734.1)
It	Iodide uniport	i[e] <==> i[c]		Transport, Extracellular	160728.1
ITCOAL1m	Itaconate--CoA ligase (GDP-forming), mitochondrial	[m] : coa + gtp + itacon <==> gdp + itaccoa + pi	6.2.1.4	C5-Branched dibasic acid metabolism	(8802.1 and 8801.1)
ITCOALm	Itaconate--CoA ligase (ADP-forming), mitochondrial	[m] : atp + coa + itacon <==> adp + itaccoa + pi	6.2.1.5	C5-Branched dibasic acid metabolism	(8802.1 and 8803.1)
ITPtn	ITP nuclear transport	itp[c] <==> itp[n]		Transport, Nuclear	
IZPN	imidazolonepropionase	[c] : 4izp + h2o --> forglu + h	3.5.2.7	Histidine Metabolism	
KAS8	b-ketoacyl synthetase (palmitate, n-C16:0)	[c] : accoa + (20) h + (7) malcoa + (14) nadph --> (7) co2 + (8) coa + (6) h2o + hdca + (14) nadp	2.3.1.41	Fatty acid elongation	2194.1
KCC2t	K+-Cl- cotransporter (NH4+)	cl[e] + nh4[e] <==> cl[c] + nh4[c]		Transport, Extracellular	(6560.1 or 9990.1 or 10723.1)
KCCt	K+-Cl- cotransport	cl[e] + k[e] <==> cl[c] + k[c]		Transport, Extracellular	(57468.1 or 6560.1 or 9990.1 or 10723.1)
KDNH	2-keto-3deoxy-D-glycero-D-galactononic acid phosphohydrolase	[c] : h2o + kdnp --> kdn + pi		Aminosugar Metabolism	
KHK	ketohexokinase	[c] : atp + fru --> adp + f1p + h	2.7.1.3	Fructose and Mannose Metabolism	(3795.1 or 3795.2)
KHK2	ketohexokinase (D-xylulose)	[c] : atp + xylu-D --> adp + h + xu1p-D	2.7.1.3	Glyoxylate and Dicarboxylate Metabolism	(3795.1 or 3795.2)
KHK3	ketohexokinase (D-tagatose)	[c] : atp + tagat-D --> adp + h + tag1p-D	2.7.1.3	Galactose metabolism	(3795.1 or 3795.2)
KSII_CORE2t	keratan sulfate II (core2) transport, golgi to extracellular	ksii_core2[g] --> ksii_core2[e]		Transport, Extracellular	
KSII_CORE2tly	keratan sulfate II (core 2) transport, extracellular to lysosome	ksii_core2[e] --> ksii_core2[l]		Transport, Lysosomal	
KSII_CORE4t	keratan sulfate II (core4) transport, golgi to extracellular	ksii_core4[g] --> ksii_core4[e]		Transport, Extracellular	
KSII_CORE4tly	keratan sulfate II (core 4) transport, extracellular to lysosome	ksii_core4[e] --> ksii_core4[l]		Transport, Lysosomal	
KSIt	keratan sulfate I transport, golgi to extracellular	ksi[g] --> ksi[e]		Transport, Extracellular	
KSItly	keratan sulfate I transport, extracellular to lysosome	ksi[e] --> ksi[l]		Transport, Lysosomal	
Kt3g	potassium transport via proton antiport	h[g] + k[c] <==> h[c] + k[g]		Transport, Golgi Apparatus	(84679.1 or 23315.1)
KYN	kynureninase	[c] : Lkynr + h2o --> ala-L + anth + h	3.7.1.3	Tryptophan metabolism	8942.1
KYN3OX	kynurenine 3-monooxygenase	[c] : Lkynr + h + nadph + o2 --> h2o + hLkynr + nadp	1.14.13.9	Tryptophan metabolism	8564.1
KYNAKGAT	L-Kynurenine:2-oxoglutarate aminotransferase	[c] : Lkynr + akg --> 4aphdob + glu-L	2.6.1.7	Tryptophan metabolism	(51166.1 or 51166.2 or 883.1)
KYNATESYN	4-(2-Aminophenyl)-2,4-dioxobutanoate dehydratase	[c] : 4aphdob --> h2o + kynate		Tryptophan metabolism	
LACZe	b-galactosidase, extracellular	[e] : h2o + lcts --> gal + glc-D	3.2.1.23	Galactose metabolism	3938.1
LACZly	b-galactosidase,lysosomal	[l] : h2o + lcts --> gal + glc-D	3.2.1.23	Galactose metabolism	((2588.1 and 4758.1 and 5476.1 and 2720.1) or (2720.1 and 5476.1))
LALDD	D-lactaldehyde dehydrogenase	[c] : lald-D + nadp <==> h + mthgxl + nadph	1.1.1.79	Pyruvate Metabolism	9380.1
LALDO	D-Lactaldehyde:NAD+ oxidoreductase (glutathione-formylating)	[c] : gthrd + lald-D + nad <==> h + lgt-S + nadh		Pyruvate Metabolism	128.1
LALDO2	D-Lactaldehyde:NADP+ 1-oxidoreductase	[c] : h + mthgxl + nadph --> lald-D + nadp	1.1.1.21	Pyruvate Metabolism	(8574.1 or 231.1 or 10327.2 or 10327.1)
LALDO2x	D-Lactaldehyde:NAD+ 1-oxidoreductase	[c] : h + mthgxl + nadh --> lald-D + nad	1.1.1.21	Pyruvate Metabolism	8574.1
LAPCOAl	lysosomal acid phosphorylase (CoA)	[l] : coa + h2o --> dpcoa + pi		CoA Catabolism	53.1

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
LCADi	lactaldehyde dehydrogenase	[c] : h2o + lald-L + nad --> (2) h + lac-L + nadh	1.2.1.21	Pyruvate Metabolism	(216.1 or 8854.1 or 8854.2 or 8854.3 or 220.1 or 218.1 or 224.1 or 221.1 or 222.1 or 501.1 or 223.1)
LCADi_D	lactaldehyde dehydrogenase	[c] : h2o + lald-D + nad --> (2) h + lac-D + nadh	1.2.1.21	Pyruvate Metabolism	(216.1 or 8854.1 or 8854.2 or 8854.3 or 220.1 or 218.1 or 224.1 or 221.1 or 222.1 or 501.1 or 223.1)
LCADi_Dm	lactaldehyde dehydrogenase, mitochondrial	[m] : h2o + lald-D + nad --> (2) h + lac-D + nadh	1.2.1.21	Pyruvate Metabolism	(5832.1 or 219.1 or 217.1 or 8659.1 or 8659.2 or 7915.1 or 7915.2 or 4329.1)
LCADim	lactaldehyde dehydrogenase, mitochondrial	[m] : h2o + lald-L + nad --> (2) h + lac-L + nadh	1.2.1.21	Pyruvate Metabolism	(5832.1 or 219.1 or 217.1 or 8659.1 or 8659.2 or 7915.1 or 7915.2 or 4329.1)
LCAT1e	Lecithin-cholesterol acyltransferase	[e] : chsterol + pchol_hs --> lpchol_hs + xolest2_hs	2.3.1.43	Fatty Acid Metabolism	3931.1
LCTStg	lactose transport from Golgi to extracellular (via vesicle)	lcts[g] --> lcts[e]		Transport, Extracellular	
LCTStl	lactose transport from cytosol to lysosome (via autophagocytosis)	lcts[c] --> lcts[l]		Transport, Lysosomal	
LCYSTAT	L-Cysteate:2-oxoglutarate aminotransferase	[c] : Lcyst + akg <==> 3spyr + glu-L		Cysteine Metabolism	2805.1
LCYSTATm	L-Cysteate:2-oxoglutarate aminotransferase, mitochondrial	[m] : Lcyst + akg <==> 3spyr + glu-L		Cysteine Metabolism	2806.1
LCYSTCBOXL	3-Sulfoalanine carboxy-lyase	[c] : Lcyst + h --> co2 + taur	4.1.1.15	Taurine and hypotaurine metabolism	(2571.1 or 2571.2 or 2572.1 or 51380.1)
LDH_D	D-lactate dehydrogenase	[c] : lac-D + nad <==> h + nadh + pyr	1.1.1.28	Pyruvate Metabolism	(197257.1 or 197257.2)
LDH_L	L-lactate dehydrogenase	[c] : lac-L + nad <==> h + nadh + pyr	1.1.1.27	Glycolysis/Gluconeogenesis	(3939.1 or 3945.1 or 3948.1 or 3948.2 or 92483.1 or 160287.1 or 55293.1 or (3945.1 and 3939.1))
LDH_Lm	L-lactate dehydrogenase	[m] : lac-L + nad <==> h + nadh + pyr	1.1.1.27	Pyruvate Metabolism	3939.1
LEUKTRA4tr	leukotriene intracellular transport	leuktrA4[c] <==> leuktrA4[r]		Transport, Endoplasmic Reticular	
LEUKTRB4tr	leukotriene intracellular transport	leuktrB4[c] <==> leuktrB4[r]		Transport, Endoplasmic Reticular	
LEUKTRC4t	leukotriene C4 transport via bicarbonate countertransport	hco3[c] + leuktrC4[e] <==> hco3[e] + leuktrC4[c]		Transport, Extracellular	(10599.1 or 28234.1)
LEUKTRD4tr	leukotriene intracellular transport	leuktrD4[c] <==> leuktrD4[r]		Transport, Endoplasmic Reticular	
LEUt4	L-leucine transport in via sodium symport	leu-L[e] + na1[e] --> leu-L[c] + na1[c]		Transport, Extracellular	(11254.1 or 6520.1 or 55089.1 or 81539.1 or 6541.1 or 6542.1 or 84889.1)
LEUt5m	leucine mitochondrial transport	leu-L[c] <==> leu-L[m]		Transport, Mitochondrial	
LEUTA	leucine transaminase	[c] : akg + leu-L <==> 4mop + glu-L	2.6.1.6	Valine, Leucine, and Isoleucine Metabolism	586.1
LEUTAm	leucine transaminase, mitochondrial	[m] : akg + leu-L <==> 4mop + glu-L	2.6.1.6	Valine, Leucine, and Isoleucine Metabolism	587.1
LEUtec	L-leucine transport via diffusion (extracellular to cytosol)	leu-L[e] <==> leu-L[c]		Transport, Extracellular	(8501.1 or 124935.1)
LFORKYNHYD	L-Formylkynurenine hydrolase	[c] : Lfmkynr + h2o --> ala-L + h + nformanth	3.7.1.3	Tryptophan metabolism	8942.1
LGNCCOAtx	fatty acid intracellular transport	lgnccoa[c] <==> lgnccoa[x]		Transport, Peroxisomal	
LGNCCPT1	carnitine O-palmitoyltransferase	[c] : crn + lgnccoa --> coa + lgnccrn	2.3.1.21	Carnitine shuttle	(1375.4 or 1374.1 or 126129.1 or 1375.3 or 1375.2 or 1375.1)
LGNCCPT2	transport into the mitochondria (carnitine)	[m] : coa + lgnccrn --> crn + lgnccoa		Carnitine shuttle	1376.1
LGNCCRNt	transport into the mitochondria (carnitine)	lgnccrn[c] --> lgnccrn[m]		Carnitine shuttle	788.1
LGNCt	fatty acid transport via diffusion	lgnc[e] <==> lgnc[c]		Transport, Extracellular	
LGTHL	lactoylglutathione lyase	[c] : gthrd + mthgxl --> lgt-S	4.4.1.5	Pyruvate Metabolism	2739.1
LIMNENte	xenobiotic transport	limnen[e] <==> limnen[c]		Transport, Extracellular	
LINKDEG11ly	degradation of proteoglycan linkage region, lysosomal	[l] : (3) h2o + hs_deg25 --> (2) gal + glcur + xyl-D		Heparan sulfate degradation	
LINKDEG2ly	degradation of proteoglycan linkage region, lysosomal	[l] : cs_a_deg5 + (4) h2o --> (2) gal + glcur + h + so4 + xyl-D		Chondroitin sulfate degradation	
LINKDEG3ly	degradation of proteoglycan linkage region, lysosomal	[l] : cs_c_deg5 + (4) h2o --> (2) gal + glcur + h + so4 + xyl-D		Chondroitin sulfate degradation	
LINKDEG4ly	degradation of proteoglycan linkage region, lysosomal	[l] : cs_e_deg7 + (5) h2o --> (2) gal + glcur + (2) h + (2) so4 + xyl-D		Chondroitin sulfate degradation	
LIPOti	Lipoate transport via sodium symport	atp[c] + h2o[c] + lipoate[e] + (2) na1[e] --> adp[c] + h[c] + lipoate[c] + (2) na1[c] + pi[c]		Transport, Extracellular	8884.1
L-LACDcm	L-Lactate dehydrogenase, cytosolic/mitochondrial	(2) ficytC[m] + lac-L[c] --> (2) focytC[m] + (2) h[c] + pyr[c]	1.1.2.3	Pyruvate Metabolism	124637.1
L-LACt2r	L-lactate reversible transport via proton symport	h[e] + lac-L[e] <==> h[c] + lac-L[c]		Transport, Extracellular	(6566.1 or 9194.1 or 23539.1 or 9123.1)
L-LACt4r	L-lactate reversible transport via sodium symport	lac-L[e] + na1[e] <==> lac-L[c] + na1[c]		Transport, Extracellular	
L-LACtcm	L-lactate transport via diffusion (cytosol to mitochondria)	lac-L[c] --> lac-L[m]		Transport, Mitochondrial	366.1
L-LACtm	L-lactate transport, mitochondrial	h[c] + lac-L[c] <==> h[m] + lac-L[m]		Transport, Mitochondrial	6566.1
LNELDCCPT1	carnitine O-palmitoyltransferase	[c] : crn + lneldccoa --> coa + lneldccrn	2.3.1.21	Carnitine shuttle	(1375.4 or 1374.1 or 126129.1 or 1375.3 or 1375.2 or 1375.1)
LNELDCCPT2	carnitine transferase	[m] : coa + lneldccrn --> crn + lneldccoa		Carnitine shuttle	1376.1
LNELDCCRNt	transport into the mitochondria (carnitine)	lneldccrn[c] --> lneldccrn[m]		Carnitine shuttle	788.1
LNELDCt	fatty acid transport via diffusion	lneldc[e] <==> lneldc[c]		Transport, Extracellular	
LNLCCPT1	carnitine O-palmitoyltransferase	[c] : crn + lnlccoa --> coa + lnlccrn	2.3.1.21	Carnitine shuttle	(1375.4 or 1374.1 or 126129.1 or 1375.3 or 1375.2 or 1375.1)
LNLCCPT2	carnitine transferase	[m] : coa + lnlccrn --> crn + lnlccoa		Carnitine shuttle	1376.1
LNLCCRNt	transport into the mitochondria (carnitine)	lnlccrn[c] --> lnlccrn[m]		Carnitine shuttle	788.1
LNLCt	Linoleic acid (n-C18:2) transport in via diffusion	lnlc[e] <==> lnlc[c]		Transport, Extracellular	
LNLNCACPT1	carnitine O-palmitoyltransferase	[c] : crn + lnlncacoa --> coa + lnlncacrn	2.3.1.21	Carnitine shuttle	(1375.4 or 1374.1 or 126129.1 or 1375.3 or 1375.2 or 1375.1)
LNLNCACPT2	carnitine transferase	[m] : coa + lnlncacrn --> crn + lnlncacoa		Carnitine shuttle	1376.1

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
LNLNCACRNt	transport into the mitochondria (carnitine)	lnlncacrn[c] --> lnlncacrn[m]		Carnitine shuttle	788.1
LNLNCAt	fatty acid transport via diffusion	lnlnca[e] <==> lnlnca[c]		Transport, Extracellular	
LNLNCGCPT1	carnitine O-palmitoyltransferase	[c] : crn + lnlncgcoa --> coa + lnlncgcrn	2.3.1.21	Carnitine shuttle	(1375.4 or 1374.1 or 126129.1 or 1375.3 or 1375.2 or 1375.1)
LNLNCGCPT2	carnitine transferase	[m] : coa + lnlncgcrn --> crn + lnlncgcoa		Carnitine shuttle	1376.1
LNLNCGCRNt	transport into the mitochondria (carnitine)	lnlncgcrn[c] --> lnlncgcrn[m]		Carnitine shuttle	788.1
LNLNCGt	fatty acid transport via diffusion	lnlncg[e] <==> lnlncg[c]		Transport, Extracellular	
LNS14DM	cytochrome P450 lanosterol 14-alpha-demethylase (NADP)	[c] : (2) h + lanost + (3) nadph + (3) o2 --> 44mctr + for + (4) h2o + (3) nadp	1.14.14.1	Cholesterol Metabolism	11283.1
LNS14DMr	cytochrome P450 lanosterol 14-alpha-demethylase	[r] : (2) h + lanost + (3) nadph + (3) o2 --> 44mctr + for + (4) h2o + (3) nadp	1.14.14.1	Cholesterol Metabolism	1595.1
LNSTLSr	lanosterol synthase	[r] : Ssq23epx --> lanost	5.4.99.7	Cholesterol Metabolism	4047.1
LPASE	lysophospholipase	[c] : h2o + lpchol_hs --> Rtotal + g3pc + h		Glycerophospholipid Metabolism	(5321.1 or 29124.1 or 1178.1)
LPCOXp	L-pipecolate oxidase, peroxisomal	[x] : Lpipecol + o2 --> h + h2o2 + thp2c	1.5.3.7	Lysine Metabolism	51268.1
LPS	lipase	[c] : h2o + tag_hs --> Rtotal3 + dag_hs + h	3.1.1.3	Triacylglycerol Synthesis	4023.1
LPS2	lipase	[c] : dag_hs + h2o --> Rtotal + h + mag_hs	3.1.1.3	Triacylglycerol Synthesis	4023.1
LPS2e	lipase, extracellular	[e] : dag_hs + h2o --> Rtotal + h + mag_hs	3.1.1.3	Fatty Acid Metabolism	3990.1
LPS3	lipase	[c] : h2o + mag_hs --> Rtotal2 + glyc + h	3.1.1.23	Triacylglycerol Synthesis	(11343.1 or 11343.2)
LPS3e	lipase, extracellular	[e] : h2o + mag_hs --> Rtotal2 + glyc + h	3.1.1.23	Fatty Acid Metabolism	3990.1
LPS4e	phospholipase	[e] : h2o + pglyc_hs --> 1glyc_hs + Rtotal2 + h		Triacylglycerol Synthesis	50487.1
LPSe	lipase	[e] : h2o + tag_hs --> Rtotal3 + dag_hs + h	3.1.1.3	Triacylglycerol Synthesis	(5407.1 or 5408.1 or 8513.1 or 9388.1 or 5406.1 or 3990.1)
LRAT	Lecithin retinol acyltransferase	[c] : pchol_hs + retinol --> lpchol_hs + retfa		Vitamin A Metabolism	9227.1
LRAT1	Lecithin retinol acyltransferase (11-cis)	[c] : pchol_hs + retinol-cis-11 --> 11-cis-retfa + lpchol_hs		Vitamin A Metabolism	
LRAT2	Lecithin retinol acyltransferase (9-cis)	[c] : pchol_hs + retinol-9-cis --> 9-cis-retfa + lpchol_hs		Vitamin A Metabolism	
LS3	Lumisterol 3 formation	[c] : pd3 <==> lum3		Vitamin D	
LSTO1r	Lathosterol oxidase	[r] : chlstol + h + nadph + o2 --> ddsmsterol + (2) h2o + nadp	1.3.3.2	Cholesterol Metabolism	6309.1
LSTO2r	Lathosterol oxidase	[r] : h + lthstrl + nadph + o2 --> 7dhchsterol + (2) h2o + nadp	1.3.3.2	Cholesterol Metabolism	6309.1
LTA4H	Leukotriene A-4 hydrolase	[c] : h2o + leuktrA4 --> leuktrB4	3.3.2.6	Eicosanoid Metabolism	4048.1
LTC4CP	Leukotriene C4 carboxypeptidase	[c] : h2o + leuktrC4 <==> gly + leuktrF4	2.3.2.2	Eicosanoid Metabolism	
LTC4Sr	Leukotriene C4 synthase	[r] : gthrd + leuktrA4 --> leuktrC4		Eicosanoid Metabolism	(4259.1 or 4258.1 or 4056.2 or 4056.1)
LTD4DP	Leukotriene D4 dipeptidase	[c] : h2o + leuktrD4 <==> gly + leuktrE4	2.3.2.2	Eicosanoid Metabolism	
LTDCL	L-Tryptophan decarboxy-lyase	[c] : h + trp-L --> co2 + trypta	4.1.1.28	Tryptophan metabolism	1644.1
LYSMTF1n	histone-lysine N-methyltransferase, nuclear	[n] : amet + peplys --> Nmelys + ahcys	2.1.1.43	Lysine Metabolism	(10919.2 or 83852.1 or 79723.1 or 79813.1 or 387893.1 or 80854.1 or 10919.1 or 6839.1 or 9869.1 or 58508.1 or 58508.2 or 84444.1)
LYSMTF2n	histone-lysine N-methyltransferase, nuclear	[n] : Nmelys + amet --> Ndmelys + ahcys	2.1.1.43	Lysine Metabolism	(10919.1 or 10919.2 or 83852.1 or 79723.1 or 79813.1 or 387893.1 or 80854.1 or 6839.1 or 9869.1 or 58508.1 or 58508.2 or 84444.1)
LYSMTF3n	histone-lysine N-methyltransferase, nuclear	[n] : Ndmelys + amet --> Ntmelys + ahcys	2.1.1.43	Lysine Metabolism	(10919.1 or 10919.2 or 83852.1 or 79723.1 or 79813.1 or 387893.1 or 80854.1 or 6839.1 or 9869.1 or 58508.1 or 58508.2 or 84444.1)
LYSOXp	L-lysine oxidase, peroxisomal	[x] : h2o + lys-L + o2 --> 6a2ohxnt + h2o2 + nh4	1.4.3.14	Lysine Metabolism	
LYSt4	L-lysine transport in via sodium symport	lys-L[e] + na1[e] --> lys-L[c] + na1[c]		Transport, Extracellular	(11254.1 or 6584.1)
LYStiDF	L-lysine transport via diffusion (extracellular to cytosol)	lys-L[e] --> lys-L[c]		Transport, Extracellular	(55089.1 or 6541.1 or 6542.1 or 84889.1)
LYStip	L-lysine transport, peroxisomal (irreversible)	lys-L[c] --> lys-L[x]		Transport, Peroxisomal	
LYStm	Lysine mitochondrial transport via ornithine carrier	h[m] + lys-L[c] <==> h[c] + lys-L[m]		Transport, Mitochondrial	(83884.1 or 10166.1)
LYStn	L-lysine transport, nuclear	lys-L[c] <==> lys-L[n]		Transport, Nuclear	
M1316Mg	mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase	[g] : (2) h2o + nm4masn --> (2) man + nm2masn	3.2.1.114	N-Glycan Biosynthesis	(4124.1 or 4122.1)
M13N2Tg	alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase	[g] : m4masn + uacgam --> h + nm4masn + udp	2.4.1.101	N-Glycan Biosynthesis	4245.1
M13N4Tg	alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase	[g] : n2m2masn + uacgam --> h + n3m2masn + udp	2.4.1.145	N-Glycan Biosynthesis	(11320.1 or 11282.1 or 11282.2)
M14NTg	beta-1,4-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase	[g] : n2m2masn + uacgam --> h + n2m2nmasn + udp	2.4.1.144	N-Glycan Biosynthesis	4248.1
M16N4Tg	alpha-1,6-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase	[g] : n4m2masn + uacgam --> h + n5m2masn + udp	2.4.1.201	N-Glycan Biosynthesis	
M16N6Tg	alpha-1,6-mannosyl-glycoprotein 6-beta-N-acetylglucosaminyltransferase	[g] : n3m2masn + uacgam --> h + n4m2masn + udp	2.4.1.155	N-Glycan Biosynthesis	4249.1
M16NTg	alpha-1,6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase	[g] : nm2masn + uacgam --> h + n2m2masn + udp	2.4.1.143	N-Glycan Biosynthesis	4247.1
M4ATAer	M4A transamidase, endoplasmic reticulum	[r] : m(em)3gacpail_hs + pre_prot --> gpi_sig + m(em)3gacpail_prot_hs		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	(94005.1 and 128869.1 and 8733.1 and 10026.1)
M4BET2er	M4B phosphoethanolaminyl transferase, endoplasmic reticulum	[r] : mem2emgacpail_hs + pe_hs --> dag_hs + m(em)3gacpail_hs		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	((54872.1 and 5281.1) or (5281.2 and 54872.1))
M4BTAer	M4B transamidase, endoplasmic reticulum	[r] : mem2emgacpail_hs + pre_prot --> gpi_sig + mem2emgacpail_prot_hs		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	(8733.1 and 10026.1 and 51604.1 and 94005.1 and 128869.1)

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
M4CET3er	M4C phosphoethanolaminyl transferase, endoplasmic reticulum	[r] : m3emgacpail_hs + pe_hs --> dag_hs + mem2emgacpail_hs		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	((5281.1 and 84720.1) or (5281.1 and 84720.2) or (5281.2 and 84720.1) or (84720.2 and 5281.2))
M4MPDOL_Lter	m4mpdol flippase	m4mpdol_L[c] --> m4mpdol_L[r]		N-Glycan Biosynthesis	
M4MPDOL_Uter	m4mpdol flippase	m4mpdol_U[c] --> m4mpdol_U[r]		N-Glycan Biosynthesis	
M7MASNBterg	m7masnB transport from endoplasmic reticulum to Golgi apparatus	m7masnB[r] --> m7masnB[g]		N-Glycan Biosynthesis	
M8MASNterg	m8masn transport from ER to Golgi apparatus	m8masn[r] --> m8masn[g]		N-Glycan Biosynthesis	
MACACI	maleylacetoacetate isomerase	[c] : 4mlacac --> 4fumacac	5.2.1.2	Tyrosine metabolism	(2954.1 or 2954.2 or 2954.3)
MACOXO	3-Methylimidazole acetaldehyde:NAD+ oxidoreductase	[c] : 3mldz + h2o + nad --> 3mlda + (2) h + nadh	1.2.1.5	Histidine Metabolism	(4129.1 or 218.1 or 220.1 or 221.1 or 222.1)
MALSO3tm	Malate:sulfite antiport, mitochondrial	mal-L[c] + so3[m] <==> mal-L[m] + so3[c]		Transport, Mitochondrial	1468.1
MALSO4tm	Malate:sulfate antiport, mitochondrial	mal-L[c] + so4[m] <==> mal-L[m] + so4[c]		Transport, Mitochondrial	1468.1
MALT	alpha-glucosidase	[c] : h2o + malt --> (2) glc-D	3.2.1.20	Starch and Sucrose Metabolism	2595.1
MALTe	alpha-glucosidase, extracellular	[e] : h2o + malt --> (2) glc-D	3.2.1.20	Starch and Sucrose Metabolism	8972.1
MALTly	alpha-glucosidase, lysosomal	[l] : h2o + malt --> (2) glc-D	3.2.1.20	Starch and Sucrose Metabolism	2548.1
MALtm	malate transport, mitochondrial	mal-L[c] + pi[m] <==> mal-L[m] + pi[c]		Transport, Mitochondrial	1468.1
MALTSULtm	Malate:thiosulfate antiport, mitochondrial	mal-L[c] + tsul[m] <==> mal-L[m] + tsul[c]		Transport, Mitochondrial	1468.1
MALTt1r	maltose transport (uniport)	malt[e] <==> malt[c]		Transport, Extracellular	6515.1
MAN1_6B1er	mannosidase I, endoplasmic reticulum (g1m6masnB1-producing)	[r] : g1m7masnC + h2o --> g1m6masnB1 + man		N-Glycan Biosynthesis	11253.1
MAN1_7Ber	mannosidase I, endoplasmic reticulum (g1m7masnB-producing)	[r] : g1m8masn + h2o --> g1m7masnB + man		N-Glycan Biosynthesis	11253.1
MAN1PT2	mannose-1-phosphate guanylyltransferase (GDP)	[c] : gdp + h + man1p --> gdpmann + pi	2.7.7.22	Fructose and Mannose Metabolism	(29926.1 or 29925.1 or 29925.2 or 29926.2)
MAN2_6B1er	mannosidase II, endoplasmic reticulum (g1m6masnB1-producing)	[r] : g1m7masnB + h2o --> g1m6masnB1 + man		N-Glycan Biosynthesis	
MAN2_7Cer	mannosidase II, endoplasmic reticulum (g1m7masnC-producing)	[r] : g1m8masn + h2o --> g1m7masnC + man		N-Glycan Biosynthesis	
MAN6PI	mannose-6-phosphate isomerase	[c] : man6p <==> f6p	5.3.1.8	Fructose and Mannose Metabolism	4351.1
MANt1r	mannose transport (uniport)	man[e] <==> man[c]		Transport, Extracellular	(6513.1 or 6514.1 or 6515.1)
MANt4	D-mannose transport via sodium cotransport	man[e] + na1[e] <==> man[c] + na1[c]		Transport, Extracellular	200010.1
MANter	mannose efflux from endoplasmic reticulum	man[r] --> man[c]		Transport, Endoplasmic Reticular	
MANtg	mannose efflux from Golgi apparatus	man[g] --> man[c]		Transport, Golgi Apparatus	
MANtly	mannose efflux from lysosome	man[l] --> man[c]		Transport, Lysosomal	
MAOLNOR	monoamine oxidase (L-Normetanephrine)	[c] : h2o + normete-L + o2 --> 3m4hpga + h2o2 + nh4	1.4.3.4	Tyrosine metabolism	(4128.1 or 4129.1)
MAOX	Methylamine oxidase	[c] : h2o + mma + o2 --> fald + h2o2 + nh4	1.4.3.6	Tyrosine metabolism	(26.1 or 314.1 or 314.2 or 8639.1)
MCCCrm	methylcrotonoyl-CoA carboxylase, mitochondrial	[m] : 3mb2coa + atp + hco3 <==> 3mgcoa + adp + h + pi	6.4.1.4	Valine, Leucine, and Isoleucine Metabolism	(64087.1 and 56922.1)
MCD	Malonyl-CoA Decarboxylase cytoplasmic	[c] : h + malcoa --> accoa + co2	4.1.1.9	Fatty Acid Metabolism	23417.1
MCDm	Malonyl-CoA Decarboxylase, mitochondrial	[m] : h + malcoa --> accoa + co2	4.1.1.9	Fatty Acid Metabolism	23417.1
MCDp	Malonyl-CoA Decarboxylase peroxisomal	[x] : h + malcoa --> accoa + co2	4.1.1.9	Fatty Acid Metabolism	23417.1
MCITS	2-methylcitrate synthase	[c] : h2o + oaa + ppcoa --> 2mcit + coa + h	4.1.3.31	Propanoate Metabolism	
MCLACCYSR	3-mercaptolactate:cysteine reductase	[c] : cys-L + mercplac + nad --> h + mercplaccys + nadh		Cysteine Metabolism	
MCLOR	3-Mercaptolactate:NAD+ oxidoreductase	[c] : mercplac + nad <==> h + mercppyr + nadh	1.1.1.27	Cysteine Metabolism	(3948.2 or 160287.1 or 3948.1 or 55293.1 or 3939.1 or (3945.1 and 3939.1) or 3945.1 or 92483.1)
MCOATA	Malonyl-CoA-ACP transacylase	[c] : ACP + malcoa <==> coa + malACP	2.3.1.39	Fatty Acid Metabolism	2194.1
MCOATAm	Malonyl-CoA-ACP transacylase, mitochondrial	[m] : ACP + malcoa <==> coa + malACP	2.3.1.39	Fatty Acid Metabolism	(27349.1 or 27349.2)
MCPST	3-mercaptopyruvate sulfurtransferase	[c] : cyan + mercppyr --> h + pyr + tcynt	2.8.1.2	Cysteine Metabolism	4357.1
MDH	malate dehydrogenase	[c] : mal-L + nad <==> h + nadh + oaa	1.1.1.37	Citric Acid Cycle	(130752.1 or 4190.1)
MDHm	malate dehydrogenase, mitochondrial	[m] : mal-L + nad <==> h + nadh + oaa	1.1.1.37	Citric Acid Cycle	4191.1
MDRPD	5-Methylthio-5-deoxy-D-ribulose 1-phosphate dehydratase	[c] : 5mdru1p --> dkmpp + h2o		Arginine and Proline Metabolism	
ME1m	malic enzyme (NAD), mitochondrial	[m] : mal-L + nad --> co2 + nadh + pyr	1.1.1.38	Pyruvate Metabolism	4200.1
ME2	malic enzyme (NADP)	[c] : mal-L + nadp --> co2 + nadph + pyr	1.1.1.40	Pyruvate Metabolism	4199.1
ME2m	malic enzyme (NADP), mitochondrial	[m] : mal-L + nadp --> co2 + nadph + pyr	1.1.1.40	Pyruvate Metabolism	(4200.1 or 10873.1)
MECOALm	mesaconate--CoA ligase (ADP-forming), mitochondrial	[m] : atp + coa + mescon <==> adp + mescoa + pi	6.2.1.5	C5-Branched dibasic acid metabolism	(8802.1 and 8803.1)
MECOAS1m	mesaconate--CoA ligase (GDP-forming)	[m] : coa + gtp + mescon <==> gdp + mescoa + pi	6.2.1.4	C5-Branched dibasic acid metabolism	(8802.1 and 8801.1)
MELATN23DOX	Melatonin:oxygen 2,3-dioxygenase (indole-decyclizing)	[c] : melatn + o2 --> fna5moxam	1.13.11.42	Tryptophan metabolism	3620.1
MELATNOX	Melatonin:NADP oxidoreductase	[c] : h + melatn + nadph + o2 --> 6hoxmelatn + h2o + nadp	1.14.14.1	Tryptophan metabolism	(1543.1 or 1544.1 or 1545.1 or 1557.1)
MEOHt2	Methanol diffusion	meoh[e] <==> meoh[c]		Transport, Extracellular	
MEOHtly	Methanol transporter, lysosome	meoh[c] <==> meoh[l]		Transport, Lysosomal	
MEOHtr	Methanol transporter, endoplasmic reticulum	meoh[c] <==> meoh[r]		Transport, Endoplasmic Reticular	
MEPIVESSte	metanephrine secretion via secretory vesicle (ATP driven)	(2) atp[c] + (2) h2o[c] + (3) mepi[c] --> (2) adp[c] + (2) h[c] + (3) mepi[e] + (2) pi[c]		Transport, Extracellular	
MERCPLACCYSt	3-mercaptolactate-cysteine disulfide transport, extracellular	mercplaccys[c] --> mercplaccys[e]		Transport, Extracellular	
MESCOALm	Mesaconyl-CoA pyruvate-lyase	[m] : h2o + mescoa --> accoa + pyr	4.1.3.25	C5-Branched dibasic acid metabolism	
METAT	methionine adenosyltransferase	[c] : atp + h2o + met-L --> amet + pi + ppi	2.5.1.6	Methionine Metabolism	(4143.1 or (27430.1 and 4144.1) or (27430.2 and 4144.1))
METLEUex	Methionine/Leucine exchange (Met in)	leu-L[c] + met-L[e] --> leu-L[e] + met-L[c]		Transport, Extracellular	(6520.1 and 8140.1)
METS	methionine synthase	[c] : 5mthf + hcys-L --> h + met-L + thf	2.1.1.13	Methionine Metabolism	4548.1

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
METt4	L-methionine transport in via sodium symport	met-L[e] + na1[e] --> met-L[c] + na1[c]		Transport, Extracellular	(11254.1 or 6584.1 or 54407.1 or 81539.1)
METtec	L-methionine transport via diffusion (extracellular to cytosol)	met-L[e] <==> met-L[c]		Transport, Extracellular	(8501.1 or 124935.1)
MEVK1x	mevalonate kinase (atp)	[x] : atp + mev-R --> 5pmev + adp + h	2.7.1.36	Cholesterol Metabolism	4598.1
MG1er	mannosyl-oligosaccharide glucosidase, endoplasmic reticulum	[r] : g3m8masn + h2o --> g2m8masn + glc-D	3.2.1.106	N-Glycan Biosynthesis	7841.1
MG2er	mannosyl-oligosaccharide glucosidase, endoplasmic reticulum	[r] : g2m8masn + h2o --> g1m8masn + glc-D		N-Glycan Biosynthesis	
MG3er	mannosyl-oligosaccharide glucosidase, endoplasmic reticulum	[r] : g1m8masn + h2o --> glc-D + m8masn		N-Glycan Biosynthesis	
MGACONm	methylglutaconase, mitochondrial	[m] : citmcoa-L <==> h2o + mescoa		C5-Branched dibasic acid metabolism	
MGCHrm	methylglutaconyl-CoA hydratase (reversible), mitochondrial	[m] : 3mgcoa + h2o <==> hmgcoa	4.2.1.18	Valine, Leucine, and Isoleucine Metabolism	549.1
MGSA	methylglyoxal synthase	[c] : dhap --> mthgxl + pi	4.2.3.3	Pyruvate Metabolism	
MGSA2	methyglyoxylate synthase 2 (from g3p)	[c] : g3p --> mthgxl + pi	4.2.3.3	Pyruvate Metabolism	
MHISOR	N-Methylhistamine:oxygen oxidoreductase (deaminating)	[c] : h2o + mhista + o2 --> 3mldz + h2o2 + nh4	1.4.3.4	Histidine Metabolism	(314.1 or 314.2 or 8639.1 or 26.1)
MI13456PK	inositol-1,3,4,5,6-pentakisphosphate 2-kinase	[c] : atp + mi13456p --> adp + h + minohp		Inositol Phosphate Metabolism	
MI13456Ptn	inositol 1,3,4,5,6-pentakisphosphate nuclear transport (diffusion)	mi13456p[c] <==> mi13456p[n]		Transport, Nuclear	
MI1345PKn	inositol-1,3,4,5-triphosphate 6-kinase, nucleus	[n] : atp + mi1345p --> adp + h + mi13456p		Inositol Phosphate Metabolism	253430.1
MI1345PP	inositol-1,3,4,5-trisphosphate 5-phosphatase	[c] : h2o + mi1345p --> mi134p + pi	3.1.3.56	Inositol Phosphate Metabolism	(3633.1 or 8867.1 or 8867.2 or 56623.1 or 3632.1 or 3635.1 or 3636.1 or 27124.1 or 27124.2)
MI1346PKn	inositol-1,3,4,6-tetrakisphosphate 5-kinase, nucleus	[n] : atp + mi1346p --> adp + h + mi13456p	2.7.1.140	Inositol Phosphate Metabolism	253430.1
MI1346Ptn	1D-myo-Inositol 1,3,4,6-tetrakisphosphate nuclear transport (diffusion)	mi1346p[c] <==> mi1346p[n]		Transport, Nuclear	
MI134P4P	inositol-1,3,4-trisphosphate 4-phosphatase	[c] : h2o + mi134p --> mi13p + pi		Inositol Phosphate Metabolism	
MI134PK	inositol-1,3,4-trisphosphate 6-kinase	[c] : atp + mi134p --> adp + h + mi1346p	2.7.1.134	Inositol Phosphate Metabolism	
MI134PP	inositol-1,3,4-trisphosphate 1-phosphatase	[c] : h2o + mi134p --> mi34p + pi	3.1.3.57	Inositol Phosphate Metabolism	3628.1
MI13PP	inositol-1,3-bisphosphate 3-phosphatase	[c] : h2o + mi13p --> mi1p-D + pi	3.1.3.64	Inositol Phosphate Metabolism	
MI1456PKn	inositol-1,4,5,6- tetrakisphosphate 3-kinase, nucleus	[n] : atp + mi1456p --> adp + h + mi13456p	2.7.1.151	Inositol Phosphate Metabolism	253430.1
MI145P6Kn	inositol-1,4,5-triphosphate 6-kinase, nucleus	[n] : atp + mi145p --> adp + h + mi1456p	2.7.1.151	Inositol Phosphate Metabolism	253430.1
MI145PK	inositol-1,4,5-trisphosphate 3-kinase	[c] : atp + mi145p --> adp + h + mi1345p	2.7.1.127	Inositol Phosphate Metabolism	(3706.1 or 3707.1 or 80271.1)
MI145PKn	inositol-1,4,5-trisphosphate 3-kinase, nucleus	[n] : atp + mi145p --> adp + h + mi1345p	2.7.1.127	Inositol Phosphate Metabolism	253430.1
MI145PP	inositol-1,4,5-trisphosphate 5-phosphatase	[c] : h2o + mi145p --> mi14p + pi	3.1.3.56	Inositol Phosphate Metabolism	(3633.1 or 8867.1 or 8867.2 or 56623.1 or 3632.1 or 3635.1 or 3636.1 or 27124.1 or 27124.2)
MI14P4P	inositol-1,4-bisphosphate 4-phosphatase	[c] : h2o + mi14p --> mi1p-D + pi		Inositol Phosphate Metabolism	
MI14PP	inositol-1,4-bisphosphate 1-phosphatase	[c] : h2o + mi14p --> mi4p-D + pi	3.1.3.57	Inositol Phosphate Metabolism	3628.1
MI14Ptn	inositol 1,4-bisphosphate nuclear transport (diffusion)	mi14p[c] <==> mi14p[n]		Transport, Nuclear	
MI1P-Dtn	inositol 1-phosphate nuclear transport (diffusion)	mi1p-D[c] <==> mi1p-D[n]		Transport, Nuclear	
MI1PP	myo-inositol 1-phosphatase	[c] : h2o + mi1p-D --> inost + pi	3.1.3.25	Inositol Phosphate Metabolism	(3612.1 or 3613.1)
MI1PS	myo-Inositol-1-phosphate synthase	[c] : g6p --> mi1p-D	5.5.1.4	Inositol Phosphate Metabolism	51477.1
MI3456PK	inositol-3,4,5,6-tetrakisphosphate 1-kinase	[c] : atp + mi3456p --> adp + h + mi13456p	2.7.1.134	Inositol Phosphate Metabolism	
MI34PP	inositol-3,4-bisphosphate 4-phosphatase	[c] : h2o + mi34p --> mi3p-D + pi	3.1.3.66	Inositol Phosphate Metabolism	(3631.2 or 8821.1 or 3631.1)
MI3PP	myo-inositol 3-phosphatase	[c] : h2o + mi3p-D --> inost + pi	3.1.3.25	Inositol Phosphate Metabolism	(3612.1 or 3613.1)
MI4PP	myo-inositol 4-phosphatase	[c] : h2o + mi4p-D --> inost + pi	3.1.3.25	Inositol Phosphate Metabolism	(3612.1 or 3613.1)
MICITDr	2-methylisocitrate dehydratase	[c] : 2mcacn + h2o <==> micit	4.2.1.99	Propanoate Metabolism	
MINOHPtn	inositol hexakisphosphate nuclear transport (diffusion)	minohp[c] <==> minohp[n]		Transport, Nuclear	
MLTG1	Maltodextrin glucosidase (maltotriose)	[c] : h2o + malttr --> glc-D + malt		Starch and Sucrose Metabolism	2595.1
MLTG1e	Maltodextrin glucosidase (maltotriose), extracellular	[e] : h2o + malttr --> glc-D + malt		Starch and Sucrose Metabolism	8972.1
MLTG1ly	Maltodextrin glucosidase (maltotriose), lysosome	[l] : h2o + malttr --> glc-D + malt		Starch and Sucrose Metabolism	2548.1
MM5ag	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus	[g] : h2o + m5masnC --> m4masn + man	3.2.1.113	N-Glycan Biosynthesis	(4121.1 or 10905.1 or 57134.1)
MM5bg	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus	[g] : h2o + m5masnB1 --> m4masn + man	3.2.1.113	N-Glycan Biosynthesis	(4121.1 or 10905.1 or 57134.1)
MM5cg	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus	[g] : h2o + m5masnB2 --> m4masn + man	3.2.1.113	N-Glycan Biosynthesis	(10905.1 or 57134.1 or 4121.1)
MM6ag	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus	[g] : h2o + m6masnA --> m5masnC + man	3.2.1.113	N-Glycan Biosynthesis	57134.1
MM6B1ag	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus	[g] : h2o + m6masnB1 --> m5masnB1 + man	3.2.1.113	N-Glycan Biosynthesis	(4121.1 or 10905.1 or 57134.1)
MM6B1bg	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus	[g] : h2o + m6masnB2 --> m5masnB1 + man	3.2.1.113	N-Glycan Biosynthesis	(4121.1 or 57134.1 or 10905.1)
MM6B2g	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus	[g] : h2o + m6masnB2 --> m5masnB2 + man	3.2.1.113	N-Glycan Biosynthesis	(10905.1 or 57134.1 or 4121.1)
MM6bg	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus	[g] : h2o + m6masnC --> m5masnC + man	3.2.1.113	N-Glycan Biosynthesis	(4121.1 or 10905.1 or 57134.1)
MM7Ag	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus	[g] : h2o + m7masnA --> m6masnA + man	3.2.1.113	N-Glycan Biosynthesis	57134.1
MM7B1g	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus	[g] : h2o + m7masnB --> m6masnB1 + man	3.2.1.113	N-Glycan Biosynthesis	(4121.1 or 10905.1 or 57134.1)
MM7B2g	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus	[g] : h2o + m7masnB --> m6masnB2 + man	3.2.1.113	N-Glycan Biosynthesis	(4121.1 or 10905.1 or 57134.1)
MM7Cag	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus	[g] : h2o + m7masnA --> m6masnC + man	3.2.1.113	N-Glycan Biosynthesis	(4121.1 or 10905.1 or 57134.1)
MM7Cbg	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus	[g] : h2o + m7masnC --> m6masnC + man	3.2.1.113	N-Glycan Biosynthesis	(4121.1 or 10905.1 or 57134.1)
MM8Ag	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus	[g] : h2o + m8masn --> m7masnA + man	3.2.1.113	N-Glycan Biosynthesis	(4121.1 or 10905.1 or 57134.1)

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
MM8Ber	mannosyl-oligosaccharide 1,2-alpha-mannosidase, endoplasmic reticulum	[r] : h2o + m8masn --> m7masnB + man	3.2.1.113	N-Glycan Biosynthesis	11253.1
MM8Cg	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus	[g] : h2o + m8masn --> m7masnC + man	3.2.1.113	N-Glycan Biosynthesis	(4121.1 or 10905.1 or 57134.1)
MMCD	Methylmalonyl-CoA decarboxylase	[c] : h + mmcoa-S --> co2 + ppcoa	4.1.1.41	Valine, Leucine, and Isoleucine Metabolism	23417.1
MMCDm	Methylmalonyl-CoA decarboxylase, mitochondrial	[m] : h + mmcoa-S --> co2 + ppcoa	4.1.1.41	Valine, Leucine, and Isoleucine Metabolism	23417.1
MMCDp	Methylmalonyl-CoA decarboxylase, peroxisomal	[x] : h + mmcoa-S --> co2 + ppcoa	4.1.1.41	Valine, Leucine, and Isoleucine Metabolism	23417.1
MMEm	methylmalonyl-CoA epimerase/racemase	[m] : mmcoa-R <==> mmcoa-S	5.1.99.1	Valine, Leucine, and Isoleucine Metabolism	84693.1
MMMm	methylmalonyl-CoA mutase	[m] : mmcoa-R <==> succoa	5.4.99.2	Valine, Leucine, and Isoleucine Metabolism	4594.1
MMSAD1m	methylmalonate-semialdehyde dehydrogenase	[m] : 2mop + coa + nad --> co2 + nadh + ppcoa	1.2.1.27	Valine, Leucine, and Isoleucine Metabolism	4329.1
MMSAD3m	methylmalonate-semialdehyde dehydrogenase (malonic semialdehyde), mitochondrial	[m] : coa + msa + nad --> accoa + co2 + nadh	1.2.1.27	Propanoate Metabolism	4329.1
MMTSADm	malonate-semialdehyde dehydrogenase (acetylating), mitochondrial	[m] : 2mop + coa + nad --> h + mmcoa-R + nadh	1.2.1.18	Valine, Leucine, and Isoleucine Metabolism	
MOGAT	monoacylglycerol acyltransferase	[c] : Rtotalcoa + mag_hs --> coa + dag_hs		Triacylglycerol Synthesis	(116255.1 or 80168.1)
MTAP	5'-methylthioadenosine phosphorylase	[c] : 5mta + pi --> 5mdr1p + ade	2.4.2.28	Arginine and Proline Metabolism	4507.1
MTHFC	methenyltetrahydrofolate cyclohydrolase	[c] : h2o + methf <==> 10fthf + h	3.5.4.9	Folate Metabolism	(4522.1 or 80068.1 or 285216.1)
MTHFCm	methenyltetrahydrifikate cyclohydrolase, mitochondrial	[m] : h2o + methf <==> 10fthf + h	3.5.4.9	Folate Metabolism	(25902.1 or 10797.1)
MTHFD	methylenetetrahydrofolate dehydrogenase (NADP)	[c] : mlthf + nadp <==> methf + nadph	1.5.1.5	Folate Metabolism	4522.1
MTHFD2	methylenetetrahydrofolate dehydrogenase (NAD)	[c] : mlthf + nad <==> methf + nadh	1.5.1.5	Folate Metabolism	(285216.1 or 80068.1)
MTHFD2m	methylenetetrahydrofolate dehydrogenase (NAD), mitochondrial	[m] : mlthf + nad <==> methf + nadh	1.5.1.5	Folate Metabolism	10797.1
MTHFDm	methylenetetrahydrofolate dehydrogenase (NADP), mitochondrial	[m] : mlthf + nadp <==> methf + nadph	1.5.1.5	Folate Metabolism	(25902.1 or 10797.1)
MTHFR3	5,10-methylenetetrahydrofolatereductase (NADPH)	[c] : (2) h + mlthf + nadph --> 5mthf + nadp	1.5.1.20	Folate Metabolism	4524.1
MTHGXLt	Methylglyoxal transport (cytosol to extracellular)	mthgxl[c] --> mthgxl[e]		Transport, Extracellular	
MTRI	5-methylthioribose-1-phosphate isomerase	[c] : 5mdr1p <==> 5mdru1p	5.3.1.23	Arginine and Proline Metabolism	
N2M2NMASNt	n2m2nmasn transport, Golgi to extracellular	n2m2nmasn[g] --> n2m2nmasn[e]		Transport, Extracellular	
N2M2NMASNtly	n2m2nmasn transport, extracellular to lysosome	n2m2nmasn[e] --> n2m2nmasn[l]		Transport, Lysosomal	
N3Tg	N-acetylgalactosamine 3-beta-galactosyltransferase, Golgi apparatus	[g] : Tn_antigen + udpgal --> T_antigen + h + udp	2.4.1.122	O-Glycan Biosynthesis	56913.1
N4Tg	N-acetylgalactosamine 4-beta-galactosyltransferase, Golgi apparatus	[g] : core6 + udpgal --> f1a + h + udp		O-Glycan Biosynthesis	
NABTNO	N4-Acetylaminobutanal:NAD+ oxidoreductase	[c] : h2o + n4abutn + nad --> 4aabutn + (2) h + nadh	1.2.1.3	Arginine and Proline Metabolism	(216.1 or 223.1 or 224.1 or 501.1 or 8854.1 or 8854.2 or 8854.3)
NABTNOm	N4-Acetylaminobutanal:NAD+ oxidoreductase (m)	[m] : h2o + n4abutn + nad --> 4aabutn + (2) h + nadh	1.2.1.3	Arginine and Proline Metabolism	(217.1 or 219.1 or 8659.1)
NACASPAH	N-Acetyl-L-aspartate amidohydrolase	[c] : Nacasp + h2o --> ac + asp-L	3.5.1.15	Alanine and Aspartate Metabolism	(443.1 or 91703.1)
NACASPtm	N-acetyl-L-aspartate transport (mitochondria to cytosol)	Nacasp[m] --> Nacasp[c]		Transport, Mitochondrial	
NACHEX10ly	beta-N-acetylhexosaminidase, lysosomal	[l] : (2) h2o + ksi_deg7 --> (2) acgam + ksi_deg8	3.2.1.52	Keratan sulfate degradation	(3074.1 or (3074.1 and 3073.1) or 3073.1)
NACHEX11ly	beta-N-acetylhexosaminidase, lysosomal	[l] : h2o + ksi_deg10 --> acgam + ksi_deg11	3.2.1.52	Keratan sulfate degradation	(3073.1 or 3074.1 or (3074.1 and 3073.1))
NACHEX12ly	beta-N-acetylhexosaminidase, lysosomal	[l] : h2o + ksi_deg13 --> acgam + ksi_deg14	3.2.1.52	Keratan sulfate degradation	(3074.1 or (3074.1 and 3073.1) or 3073.1)
NACHEX13ly	beta-N-acetylhexosaminidase, lysosomal	[l] : h2o + ksi_deg16 --> acgam + ksi_deg17	3.2.1.52	Keratan sulfate degradation	(3074.1 or (3074.1 and 3073.1) or 3073.1)
NACHEX14ly	beta-N-acetylhexosaminidase, lysosomal	[l] : h2o + ksi_deg19 --> acgam + ksi_deg20	3.2.1.52	Keratan sulfate degradation	((3074.1 and 3073.1) or 3073.1 or 3074.1)
NACHEX15ly	beta-N-acetylhexosaminidase, lysosomal	[l] : h2o + ksi_deg22 --> acgam + ksi_deg23	3.2.1.52	Keratan sulfate degradation	((3074.1 and 3073.1) or 3073.1 or 3074.1)
NACHEX16ly	beta-N-acetylhexosaminidase, lysosomal	[l] : h2o + ksi_deg25 --> acgam + ksi_deg26	3.2.1.52	Keratan sulfate degradation	((3074.1 and 3073.1) or 3073.1 or 3074.1)
NACHEX17ly	beta-N-acetylhexosaminidase, lysosomal	[l] : h2o + ksi_deg28 --> acgam + ksi_deg29	3.2.1.52	Keratan sulfate degradation	(3074.1 or (3074.1 and 3073.1) or 3073.1)
NACHEX18ly	beta-N-acetylhexosaminidase, lysosomal	[l] : h2o + ksi_deg31 --> acgam + ksi_deg32	3.2.1.52	Keratan sulfate degradation	(3073.1 or 3074.1 or (3074.1 and 3073.1))
NACHEX19ly	beta-N-acetylhexosaminidase, lysosomal	[l] : h2o + ksi_deg34 --> acgam + ksi_deg35	3.2.1.52	Keratan sulfate degradation	(3074.1 or 3073.1 or (3074.1 and 3073.1))
NACHEX1ly	beta-N-acetylhexosaminidase, lysosomal	[l] : cs_a_deg1 + h2o --> acgal + cs_a_deg2	3.2.1.52	Chondroitin sulfate degradation	((3074.1 and 3073.1) or 3074.1 or 3073.1)
NACHEX20ly	beta-N-acetylhexosaminidase, lysosomal	[l] : h2o + ksi_deg37 --> acgam + ksi_deg38	3.2.1.52	Keratan sulfate degradation	((3074.1 and 3073.1) or 3073.1 or 3074.1)
NACHEX21ly	beta-N-acetylhexosaminidase, lysosomal	[l] : h2o + ksi_deg39 --> acgam + ksi_deg40	3.2.1.52	Keratan sulfate degradation	(3074.1 or (3074.1 and 3073.1) or 3073.1)
NACHEX22ly	beta-N-acetylhexosaminidase, lysosomal	[l] : h2o + ksi_deg41 --> acgam + m2mn	3.2.1.52	Keratan sulfate degradation	(3074.1 or 3073.1 or (3074.1 and 3073.1))
NACHEX23ly	beta-N-acetylhexosaminidase, lysosomal	[l] : h2o + ksii_core2_deg4 --> acgam + ksii_core2_deg5	3.2.1.52	Keratan sulfate degradation	((3074.1 and 3073.1) or 3074.1 or 3073.1)

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
NACHEX24ly	beta-N-acetylhexosaminidase, lysosomal	[l] : h2o + ksii_core2_deg7 --> acgam + ksii_core2_deg8	3.2.1.52	Keratan sulfate degradation	(3074.1 or (3074.1 and 3073.1) or 3073.1)
NACHEX25ly	beta-N-acetylhexosaminidase, lysosomal	[l] : h2o + ksii_core2_deg9 --> acgam + f1a	3.2.1.52	Keratan sulfate degradation	((3074.1 and 3073.1) or 3074.1 or 3073.1)
NACHEX26ly	beta-N-acetylhexosaminidase, lysosomal	[l] : (2) h2o + ksii_core4_deg4 --> (2) acgam + ksii_core2_deg5	3.2.1.52	Keratan sulfate degradation	((3074.1 and 3073.1) or 3074.1 or 3073.1)
NACHEX27ly	beta-N-acetylhexosaminidase, lysosomal	[l] : h2o + ha_deg1 --> acgam + ha_pre1	3.2.1.52	Hyaluronan Metabolism	((3074.1 and 3073.1) or 3074.1 or 3073.1)
NACHEX2ly	beta-N-acetylhexosaminidase, lysosomal	[l] : cs_a_deg4 + h2o --> acgal + cs_a_deg5	3.2.1.52	Chondroitin sulfate degradation	((3074.1 and 3073.1) or 3074.1 or 3073.1)
NACHEX3ly	beta-N-acetylhexosaminidase, lysosomal	[l] : cs_b_deg1 + h2o --> acgal + cs_b_deg2	3.2.1.52	Chondroitin sulfate degradation	(3073.1 or 3074.1 or (3074.1 and 3073.1))
NACHEX4ly	beta-N-acetylhexosaminidase, lysosomal	[l] : cs_c_deg1 + h2o --> acgal + cs_c_deg2	3.2.1.52	Chondroitin sulfate degradation	(3073.1 or 3074.1 or (3074.1 and 3073.1))
NACHEX5ly	beta-N-acetylhexosaminidase, lysosomal	[l] : cs_c_deg4 + h2o --> acgal + cs_c_deg5	3.2.1.52	Chondroitin sulfate degradation	(3073.1 or 3074.1 or (3074.1 and 3073.1))
NACHEX6ly	beta-N-acetylhexosaminidase, lysosomal	[l] : cs_d_deg1 + h2o --> acgal + cs_d_deg2	3.2.1.52	Chondroitin sulfate degradation	((3074.1 and 3073.1) or 3073.1 or 3074.1)
NACHEX7ly	beta-N-acetylhexosaminidase, lysosomal	[l] : cs_d_deg5 + h2o --> acgal + cs_d_deg6	3.2.1.52	Chondroitin sulfate degradation	((3074.1 and 3073.1) or 3073.1 or 3074.1)
NACHEX8ly	beta-N-acetylhexosaminidase, lysosomal	[l] : cs_e_deg2 + h2o --> acgal + cs_e_deg3	3.2.1.52	Chondroitin sulfate degradation	((3074.1 and 3073.1) or 3073.1 or 3074.1)
NACHEX9ly	beta-N-acetylhexosaminidase, lysosomal	[l] : cs_e_deg6 + h2o --> acgal + cs_e_deg7	3.2.1.52	Chondroitin sulfate degradation	((3074.1 and 3073.1) or 3073.1 or 3074.1)
NACHEXA10ly	beta-N-acetylhexosaminidase A, lysosomal	[l] : (2) h2o + ksi_deg9 --> acgam + h + ksi_deg11 + so4		Keratan sulfate degradation	(3073.1 or (3074.1 and 3073.1))
NACHEXA11ly	beta-N-acetylhexosaminidase A, lysosomal	[l] : (2) h2o + ksi_deg12 --> acgam + h + ksi_deg14 + so4		Keratan sulfate degradation	(3073.1 or (3074.1 and 3073.1))
NACHEXA12ly	beta-N-acetylhexosaminidase A, lysosomal	[l] : (2) h2o + ksi_deg15 --> acgam + h + ksi_deg17 + so4		Keratan sulfate degradation	(3073.1 or (3074.1 and 3073.1))
NACHEXA13ly	beta-N-acetylhexosaminidase A, lysosomal	[l] : (2) h2o + ksi_deg18 --> acgam + h + ksi_deg20 + so4		Keratan sulfate degradation	(3073.1 or (3074.1 and 3073.1))
NACHEXA14ly	beta-N-acetylhexosaminidase A, lysosomal	[l] : (2) h2o + ksi_deg21 --> acgam + h + ksi_deg23 + so4		Keratan sulfate degradation	(3073.1 or (3074.1 and 3073.1))
NACHEXA15ly	beta-N-acetylhexosaminidase A, lysosomal	[l] : (2) h2o + ksi_deg24 --> acgam + h + ksi_deg26 + so4		Keratan sulfate degradation	(3073.1 or (3074.1 and 3073.1))
NACHEXA16ly	beta-N-acetylhexosaminidase A, lysosomal	[l] : (2) h2o + ksi_deg27 --> acgam + h + ksi_deg29 + so4		Keratan sulfate degradation	(3073.1 or (3074.1 and 3073.1))
NACHEXA17ly	beta-N-acetylhexosaminidase A, lysosomal	[l] : (2) h2o + ksi_deg30 --> acgam + h + ksi_deg32 + so4		Keratan sulfate degradation	(3073.1 or (3074.1 and 3073.1))
NACHEXA18ly	beta-N-acetylhexosaminidase A, lysosomal	[l] : (2) h2o + ksi_deg33 --> acgam + h + ksi_deg35 + so4		Keratan sulfate degradation	(3073.1 or (3074.1 and 3073.1))
NACHEXA19ly	beta-N-acetylhexosaminidase A, lysosomal	[l] : (2) h2o + ksi_deg36 --> acgam + h + ksi_deg38 + so4		Keratan sulfate degradation	(3073.1 or (3074.1 and 3073.1))
NACHEXA1ly	beta-N-acetylhexosaminidase A, lysosomal	[l] : cs_a + (2) h2o --> acgal + cs_a_deg2 + h + so4		Chondroitin sulfate degradation	(3073.1 or (3074.1 and 3073.1))
NACHEXA20ly	beta-N-acetylhexosaminidase A, lysosomal	[l] : (2) h2o + ksii_core2_deg3 --> acgam + h + ksii_core2_deg5 + so4		Keratan sulfate degradation	(3073.1 or (3074.1 and 3073.1))
NACHEXA21ly	beta-N-acetylhexosaminidase A, lysosomal	[l] : (2) h2o + ksii_core2_deg6 --> acgam + h + ksii_core2_deg8 + so4		Keratan sulfate degradation	(3073.1 or (3074.1 and 3073.1))
NACHEXA22ly	beta-N-acetylhexosaminidase A, lysosomal	[l] : (3) h2o + ksii_core4_deg3 --> (2) acgam + h + ksii_core2_deg5 + so4		Keratan sulfate degradation	(3073.1 or (3074.1 and 3073.1))
NACHEXA2ly	beta-N-acetylhexosaminidase A, lysosomal	[l] : cs_b + (2) h2o --> acgal + cs_b_deg2 + h + so4		Chondroitin sulfate degradation	(3073.1 or (3074.1 and 3073.1))
NACHEXA3ly	beta-N-acetylhexosaminidase A, lysosomal	[l] : cs_c + (2) h2o --> acgal + cs_c_deg2 + h + so4		Chondroitin sulfate degradation	(3073.1 or (3074.1 and 3073.1))
NACHEXA4ly	beta-N-acetylhexosaminidase A, lysosomal	[l] : cs_c_deg3 + (2) h2o --> acgal + cs_c_deg5 + h + so4		Chondroitin sulfate degradation	(3073.1 or (3074.1 and 3073.1))
NACHEXA5ly	beta-N-acetylhexosaminidase A, lysosomal	[l] : cs_d + (2) h2o --> acgal + cs_d_deg2 + h + so4		Chondroitin sulfate degradation	(3073.1 or (3074.1 and 3073.1))
NACHEXA6ly	beta-N-acetylhexosaminidase A, lysosomal	[l] : cs_d_deg4 + (2) h2o --> acgal + cs_d_deg6 + h + so4		Chondroitin sulfate degradation	(3073.1 or (3074.1 and 3073.1))
NACHEXA7ly	beta-N-acetylhexosaminidase A, lysosomal	[l] : cs_e + (3) h2o --> acgal + cs_e_deg3 + (2) h + (2) so4		Chondroitin sulfate degradation	(3073.1 or (3074.1 and 3073.1))
NACHEXA8ly	beta-N-acetylhexosaminidase A, lysosomal	[l] : cs_e_deg4 + (3) h2o --> acgal + cs_e_deg7 + (2) h + (2) so4		Chondroitin sulfate degradation	(3073.1 or (3074.1 and 3073.1))
NACHEXA9ly	beta-N-acetylhexosaminidase A, lysosomal	[l] : (3) h2o + ksi_deg6 --> (2) acgam + h + ksi_deg8 + so4		Keratan sulfate degradation	(3073.1 or (3074.1 and 3073.1))
NACUP	Nicotinic acid uptake	nac[e] --> nac[c]		Transport, Extracellular	

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
NADH2-u10m	NADH dehydrogenase, mitochondrial	(5) h[m] + nadh[m] + q10[m] --> (4) h[c] + nad[m] + q10h2[m]	1.6.99.3	Oxidative Phosphorylation	((4720.1 and 4706.1 and 4704.1 and 4535.1 and 4722.1 and 4705.1 and 4716.1 and 4723.1 and 4698.1 and 4702.1 and 7991.1 and 4694.1 and 4695.1 and 126328.1 and 4719.1 and 4710.1 and 4540.1 and 51079.1 and 4720.1 and 4538.1 and 4711.1 and 4709.1 and 4715.1 and 4708.1 and 4714.1 and 4539.1 and 55967.1 and 4718.1 and 4536.1 and 4541.1 and 4706.1 and 4731.1 and 4537.1 and 4696.1 and 374291.1 and 4713.1 and 4707.1 and 4728.1 and 4717.1 and 4725.1 and 4701.1 and 4729.1 and 4697.1 and 4712.2 and 4724.1) or (4726.1 and 55967.1 and 4697.1 and 4696.1 and 7991.1 and 4694.1 and 4719.1 and 4710.1 and 4540.1 and 4538.1 and 4711.1 and 4729.1 and 4535.1 and 4713.1 and 4707.1 and 4716.1 and 4701.1 and 4724.1 and 4536.1 and 4537.1 and 4731.2 and 4698.1 and 4709.1 and 4700.1 and 4704.1 and 4728.1 and 126328.1 and 4712.1 and 4539.1 and 374291.1 and 4722.1 and
NADHtpu	NADH transporter, peroxisome	nadh[c] --> nadh[x]		Transport, Peroxisomal	
NADHtru	NADH transporter, endoplasmic reticulum	nadh[c] --> nadh[r]		Transport, Endoplasmic Reticular	
NADK	NAD kinase	[c] : atp + nad --> adp + h + nadp	2.7.1.23	NAD Metabolism	65220.1
NADN	NAD nucleosidase	[c] : h2o + nad --> adprib + h + ncam	3.2.2.5	NAD Metabolism	
NADNe	NAD nucleosidase,extracellular	[e] : h2o + nad --> adprib + h + ncam	3.2.2.5	NAD Metabolism	952.1
NADPHtru	NADPH transporter, endoplasmic reticulum	nadph[c] --> nadph[r]		Transport, Endoplasmic Reticular	
NADPHtxu	NADPH transporter, peroxisome	nadph[c] --> nadph[x]		Transport, Peroxisomal	
NADPN	NADP nucleosidase	[c] : h2o + nadp --> adprbp + h + ncam	3.2.2.6	NAD Metabolism	
NADPNe	NADP nucleosidase,extracellular	[e] : h2o + nadp --> adprbp + h + ncam	3.2.2.6	NAD Metabolism	952.1
NADPtru	NADP transporter, endoplasmic reticulum	nadp[r] --> nadp[c]		Transport, Endoplasmic Reticular	
NADPtxu	NADP transporter, peroxisome	nadp[x] --> nadp[c]		Transport, Peroxisomal	
NADS2	NAD synthase (glutamine-hydrolysing)	[c] : atp + dnad + gln-L + h2o --> amp + glu-L + h + nad + ppi	6.3.5.1	NAD Metabolism	55191.1
NADtn	NAD transport, nuclear through pores	nad[n] <==> nad[c]		Transport, Nuclear	
NADtpu	NAD transporter, peroxisome	nadh[x] --> nadh[c]		Transport, Peroxisomal	
NADtru	NAD transporter, endoplasmic reticulum	nad[r] --> nad[c]		Transport, Endoplasmic Reticular	
NAGA2ly	N-acetylgalactosaminidase, alpha-	[l] : Tn_antigen + h + udp --> Ser/Thr + udpacgal	3.2.1.49	Keratan sulfate degradation	4668.1
NAGAlby	N-acetylgalactosaminidase, beta-	[l] : acgbgbside_hs + h + udp --> gbside_hs + udpacgal		Sphingolipid Metabolism	
NAGAly	N-acetylgalactosaminidase, alpha-	[l] : acgagbside_hs + h + udp --> gbside_hs + udpacgal	3.2.1.49	Sphingolipid Metabolism	4668.1
NAGLCAly	N-acetylglucosaminidase, lysosomal	[l] : core6 + h2o --> Tn_antigen + acgam		Keratan sulfate degradation	
NAHCO3_HCLt	bicarbonate transport (HCl/NaHCO3 exchange)	cl[c] + h[c] + hco3[e] + na1[e] <==> cl[e] + h[e] + hco3[c] + na1[c]		Transport, Extracellular	(9498.1 or 57282.1)
NAIt	Na+ / iodide cotransport	i[e] + (2) na1[e] <==> i[c] + (2) na1[c]		Transport, Extracellular	6528.1
NaKt	Na+/K+ exchanging ATPase	atp[c] + h2o[c] + (2) k[e] + (3) na1[c] --> adp[c] + h[c] + (2) k[c] + (3) na1[e] + pi[c]	3.6.3.9	Transport, Extracellular	((481.1 and 476.1) or (476.1 and 482.1) or (476.1 and 483.1) or (476.1 and 23439.1) or (481.1 and 477.1) or (478.1 and 481.1) or (481.1 and 480.1) or (477.1 and 482.1) or (478.1 and 482.1) or (480.1 and 23439.1) or (23439.1 and 477.1))
NAt	sodium transport (uniport)	na1[e] <==> na1[c]		Transport, Extracellular	(6526.1 or 6528.1 or 6523.1)
NAt3_1	sodium proton antiporter (H:NA is 1:1)	h[e] + na1[c] <==> h[c] + na1[e]		Transport, Extracellular	(6549.1 or 6550.1 or 389015.1 or 6553.1 or 6548.1)
NAt3_1g	sodium proton antiporter (H:NA is 1:1)	h[g] + na1[c] <==> h[c] + na1[g]		Transport, Golgi Apparatus	(84679.1 or 23315.1)
NAt5	sodium/ammonium proton antiporter	na1[c] + nh4[e] <==> na1[e] + nh4[c]		Transport, Extracellular	(6549.1 or 6550.1 or 6548.1)
NAtx	sodium transport via diffusion (perioxisome)	na1[c] <==> na1[x]		Transport, Peroxisomal	
NBAHH_ir	Nalpha-(beta-alanyl)-L-histidine hydrolase IR	[c] : carn + h2o --> ala-B + his-L	3.4.13.3	beta-Alanine metabolism	84735.1
NCAMUP	Nicotinamide acid uptake	ncam[e] --> ncam[c]		Transport, Extracellular	
NCCt	Na+-Cl- cotransport	cl[e] + na1[e] --> cl[c] + na1[c]		Transport, Extracellular	6559.1
NCKt	Na+/Ca2+-K+ exchange	ca2[e] + k[e] + (4) na1[c] <==> ca2[c] + k[c] + (4) na1[e]		Transport, Extracellular	(9187.1 or 25769.1 or 123041.3 or 57419.1 or 123041.1 or 123041.2)
NCNt	Na+/Ca2+-NH4+ exchange	ca2[e] + (4) na1[c] + nh4[e] <==> ca2[c] + (4) na1[e] + nh4[c]		Transport, Extracellular	(9187.1 or 25769.1)
NDP10ex	nucleoside-diphosphatase (IDP), extracellular	[e] : h2o + idp --> h + imp + pi	3.6.1.6	Nucleotides	124583.1
NDP3ex	nucleoside-diphosphatase (GDP), extracellular	[e] : gdp + h2o --> gmp + h + pi	3.6.1.6	Nucleotides	124583.1
NDP6	nucleoside-diphosphatase (dCDP)	[c] : dcdp + h2o --> dcmp + h + pi	3.6.1.6	Nucleotides	
NDP7er	nucleoside-diphosphatase (UDP), endoplasmic reticulum	[r] : h2o + udp --> h + pi + ump	3.6.1.6	Nucleotides	

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
NDP7ex	nucleoside-diphosphatase (UDP), extracellular	[e] : h2o + udp --> h + pi + ump	3.6.1.6	Nucleotides	124583.1
NDP7g	nucleoside-diphosphatase (UDP), Golgi apparatus	[g] : h2o + udp --> h + pi + ump	3.6.1.6	Nucleotides	9583.1
NDP8	nucleoside-diphosphatase (dUDP)	[c] : dudp + h2o --> dump + h + pi	3.6.1.6	Nucleotides	1841.1
NDP8ex	nucleoside-diphosphatase (UTP), extracellular	[e] : h2o + utp --> h + pi + udp	3.6.1.6	Nucleotides	124583.1
NDPK1	nucleoside-diphosphate kinase (ATP:GDP)	[c] : atp + gdp <==> adp + gtp	2.7.4.6	Nucleotides	((4831.1 and 4830.1) or (4830.2 and 4831.1) or 4832.1 or 29922.2 or 10201.1 or 29922.1)
NDPK10	nucleoside-diphosphate kinase (ATP:dIDP)	[c] : atp + didp <==> adp + ditp	2.7.4.6	Nucleotides	((4831.1 and 4830.1) or (4830.2 and 4831.1) or 4832.1 or 10201.1 or 29922.1 or 29922.2)
NDPK10m	nucleoside-diphosphate kinase (ATP:dIDP), mitochondrial	[m] : atp + didp <==> adp + ditp	2.7.4.6	Nucleotides	4833.1
NDPK10n	nucleoside-diphosphate kinase (ATP:dIDP), nuclear	[n] : atp + didp <==> adp + ditp	2.7.4.6	Nucleotides	((4831.1 and 4830.1) or (4831.1 and 4830.2))
NDPK1m	nucleoside-diphosphate kinase (ATP:GDP), mitochondrial	[m] : atp + gdp <==> adp + gtp	2.7.4.6	Nucleotides	4833.1
NDPK1n	nucleoside-diphosphate kinase (ATP:GDP), nuclear	[n] : atp + gdp <==> adp + gtp	2.7.4.6	Nucleotides	((4831.1 and 4830.1) or (4831.1 and 4830.2))
NDPK2	nucleoside-diphosphate kinase (ATP:UDP)	[c] : atp + udp <==> adp + utp	2.7.4.6	Nucleotides	((4831.1 and 4830.1) or (4830.2 and 4831.1) or 4832.1 or 10201.1 or 29922.1 or 29922.2)
NDPK2m	nucleoside-diphosphate kinase (ATP:UDP), mitochondrial	[m] : atp + udp <==> adp + utp	2.7.4.6	Nucleotides	4833.1
NDPK2n	nucleoside-diphosphate kinase (ATP:UDP), nuclear	[n] : atp + udp <==> adp + utp	2.7.4.6	Nucleotides	((4831.1 and 4830.1) or (4831.1 and 4830.2))
NDPK3	nucleoside-diphosphate kinase (ATP:CDP)	[c] : atp + cdp <==> adp + ctp	2.7.4.6	Nucleotides	((4831.1 and 4830.1) or (4830.2 and 4831.1) or 4832.1 or 10201.1 or 29922.1 or 29922.2)
NDPK3m	nucleoside-diphosphate kinase (ATP:CDP), mitochondrial	[m] : atp + cdp <==> adp + ctp	2.7.4.6	Nucleotides	4833.1
NDPK3n	nucleoside-diphosphate kinase (ATP:CDP),nuclear	[n] : atp + cdp <==> adp + ctp	2.7.4.6	Nucleotides	((4831.1 and 4830.1) or (4831.1 and 4830.2))
NDPK4	nucleoside-diphosphate kinase (ATP:dTDP)	[c] : atp + dtdp <==> adp + dttp	2.7.4.6	Nucleotides	((4831.1 and 4830.1) or (4830.2 and 4831.1) or 4832.1 or 10201.1 or 29922.1 or 29922.2)
NDPK4m	nucleoside-diphosphate kinase (ATP:dTDP), mitochondrial	[m] : atp + dtdp <==> adp + dttp	2.7.4.6	Nucleotides	4833.1
NDPK4n	nucleoside-diphosphate kinase (ATP:dTDP), nuclear	[n] : atp + dtdp <==> adp + dttp	2.7.4.6	Nucleotides	((4831.1 and 4830.1) or (4831.1 and 4830.2))
NDPK5	nucleoside-diphosphate kinase (ATP:dGDP)	[c] : atp + dgdp <==> adp + dgtp	2.7.4.6	Nucleotides	((4830.2 and 4831.1) or (4831.1 and 4830.1) or 4832.1 or 10201.1 or 29922.1 or 29922.2)
NDPK5m	nucleoside-diphosphate kinase (ATP:dGDP), mitochondrial	[m] : atp + dgdp <==> adp + dgtp	2.7.4.6	Nucleotides	4833.1
NDPK5n	nucleoside-diphosphate kinase (ATP:dGDP), nuclear	[n] : atp + dgdp <==> adp + dgtp	2.7.4.6	Nucleotides	((4831.1 and 4830.1) or (4831.1 and 4830.2))
NDPK6	nucleoside-diphosphate kinase (ATP:dUDP)	[c] : atp + dudp <==> adp + dutp	2.7.4.6	Nucleotides	((4831.1 and 4830.1) or (4830.2 and 4831.1) or 4832.1 or 10201.1 or 29922.1 or 29922.2)
NDPK6m	nucleoside-diphosphate kinase (ATP:dUDP), mitochondrial	[m] : atp + dudp <==> adp + dutp	2.7.4.6	Nucleotides	4833.1
NDPK6n	nucleoside-diphosphate kinase (ATP:dUDP), nuclear	[n] : atp + dudp <==> adp + dutp	2.7.4.6	Nucleotides	((4831.1 and 4830.1) or (4831.1 and 4830.2))
NDPK7	nucleoside-diphosphate kinase (ATP:dCDP)	[c] : atp + dcdp <==> adp + dctp	2.7.4.6	Nucleotides	((4831.1 and 4830.1) or (4830.2 and 4831.1) or 4832.1 or 10201.1 or 29922.1 or 29922.2)
NDPK7m	nucleoside-diphosphate kinase (ATP:dCDP), mitochondrial	[m] : atp + dcdp <==> adp + dctp	2.7.4.6	Nucleotides	4833.1
NDPK7n	nucleoside-diphosphate kinase (ATP:dCDP), nuclear	[n] : atp + dcdp <==> adp + dctp	2.7.4.6	Nucleotides	((4831.1 and 4830.1) or (4831.1 and 4830.2))
NDPK8	nucleoside-diphosphate kinase (ATP:dADP)	[c] : atp + dadp <==> adp + datp	2.7.4.6	Nucleotides	((4831.1 and 4830.1) or (4830.2 and 4831.1) or 4832.1 or 10201.1 or 29922.1 or 29922.2)
NDPK8m	nucleoside-diphosphate kinase (ATP:dADP), mitochondrial	[m] : atp + dadp <==> adp + datp	2.7.4.6	Nucleotides	4833.1
NDPK8n	nucleoside-diphosphate kinase (ATP:dADP), nuclear	[n] : atp + dadp <==> adp + datp	2.7.4.6	Nucleotides	((4831.1 and 4830.1) or (4831.1 and 4830.2))
NDPK9	nucleoside-diphosphate kinase (ATP:IDP)	[c] : atp + idp <==> adp + itp	2.7.4.6	Nucleotides	((4831.1 and 4830.1) or (4830.2 and 4831.1) or 4832.1 or 10201.1 or 29922.1 or 29922.2)

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
NDPK9m	nucleoside-diphosphate kinase (ATP:IDP), mitochondrial	[m] : atp + idp <==> adp + itp	2.7.4.6	Nucleotides	4833.1
NDPK9n	nucleoside-diphosphate kinase (ATP:IDP), nuclear	[n] : atp + idp <==> adp + itp	2.7.4.6	Nucleotides	((4831.1 and 4830.1) or (4831.1 and 4830.2))
NH4t3r	ammonia transport via proton antiport	h[e] + nh4[c] <==> h[c] + nh4[e]		Transport, Extracellular	(6005.1 or 57127.1)
NH4tn	ammonia nuclear transport	nh4[c] <==> nh4[n]		Transport, Nuclear	
NH4tp	ammonia peroxisomal transport	nh4[c] <==> nh4[x]		Transport, Peroxisomal	
NICRNS	NICRNS	[c] : atp + nicrns --> adp + h + nicrnt		NAD Metabolism	
NICRNTtn	NICRNT transport, nuclear trhough pore	nicrnt[c] <==> nicrnt[n]		Transport, Nuclear	
NIFEDIPINEte	xenobiotic transport	nifedipine[e] <==> nifedipine[c]		Transport, Extracellular	
NKCC2t	Na+-K+-Cl- cotransport (NH4+)	(2) cl[e] + na1[e] + nh4[e] <==> (2) cl[c] + na1[c] + nh4[c]		Transport, Extracellular	(6557.1 or 6558.1)
NKCCt	Na+-K+-Cl- cotransport	(2) cl[e] + k[e] + na1[e] <==> (2) cl[c] + k[c] + na1[c]		Transport, Extracellular	(6557.1 or 6558.1)
NMNATm	nicotinamide-nucleotide adenylyltransferase, mitochondrial	[m] : atp + h + nmn --> nad + ppi	2.7.7.1	NAD Metabolism	349565.1
NMNATn	nicotinamide-nucleotide adenylyltransferase	[n] : atp + h + nmn --> nad + ppi	2.7.7.1	NAD Metabolism	64802.1
NMNATr	nicotinamide-nucleotide adenylyltransferase	[c] : atp + h + nmn <==> nad + ppi	2.7.7.1	NAD Metabolism	(349565.1 or 23057.2 or 23057.1)
NMNS	NMN synthetase	[c] : h + ncam + prpp --> nmn + ppi	2.4.2.12	NAD Metabolism	
NMNtn	NMN transport, nuclear trhough pore	nmn[c] <==> nmn[n]		Transport, Nuclear	
NMPTRCOX	N-Methylputrescine:oxygen oxidoreductase (deaminating)	[c] : nmptrc + o2 --> 1mpyr + h2o2 + nh4	1.4.3.6	Alkaloid biosynthesis II	(314.1 or 314.2 or 8639.1 or 26.1)
NNAT	nicotinate-nucleotide adenylyltransferase	[c] : atp + h + nicrnt --> dnad + ppi	2.7.7.18	NAD Metabolism	(5167.1 or 5168.1 or 5169.1)
NNATm	nicotinate-nucleotide adenylyltransferase, mitochondrial	[m] : atp + h + nicrnt --> dnad + ppi	2.7.7.18	NAD Metabolism	349565.1
NNATn	nicotinate-nucleotide adenylyltransferase	[n] : atp + h + nicrnt --> dnad + ppi	2.7.7.18	NAD Metabolism	64802.1
NNATr	nicotinate-nucleotide adenylyltransferase	[c] : atp + h + nicrnt <==> dnad + ppi	2.7.7.18	NAD Metabolism	(349565.1 or 23057.1 or 23057.2)
NNDPR	nicotinate-nucleotide diphosphorylase (carboxylating)	[c] : (2) h + prpp + quln --> co2 + nicrnt + ppi	2.4.2.19	NAD Metabolism	23475.1
NNMT	Nicotinamide N-methyltransferase	[c] : amet + ncam --> 1mncam + ahcys	2.1.1.1	NAD Metabolism	4837.1
NORANMT	noradrenaline N-methyltransferase	[c] : amet + nrpphr --> adrnl + ahcys + h	2.1.1.28	Tyrosine metabolism	5409.1
NOS1	Nitric Oxide Synthase (intermediate forming)	[c] : arg-L + h + nadph + o2 --> h2o + nadp + nwharg	1.14.13.39	Arginine and Proline Metabolism	(4842.1 or 4843.1 or 4843.2 or 4844.1 or 4845.1 or 4846.1)
NOS2	Nitric Oxide Synthase (NO forming)	[c] : nadph + (2) nwharg + (2) o2 --> (2) citr-L + h + (2) h2o + nadp + (2) no	1.14.13.39	Arginine and Proline Metabolism	(4842.1 or 4843.1 or 4843.2 or 4844.1 or 4845.1 or 4846.1)
NOt	NO transport (diffusion)	no[e] <==> no[c]		Transport, Extracellular	
NP1	nucleotide phosphatase	[c] : h + nac + r1p --> nicrns + pi	2.4.2.1	NAD Metabolism	4860.1
NPTHLte	xenobiotic transport	npthl[e] <==> npthl[c]		Transport, Extracellular	
NRPPHRSFt	norepinephrine sulfate transport (diffusion)	nrpphrsf[c] --> nrpphrsf[e]		Transport, Extracellular	
NRPPHRSULT	Norepinephrine Sulfotransferase	[c] : nrpphr + paps --> h + nrpphrsf + pap	2.8.2.1	Tyrosine metabolism	(6818.1 or 6818.2 or 6818.3)
NRPPHRt4(2)r	Norepinephrine reversible transport in via sodium symport (1:2)	(2) na1[e] + nrpphr[e] <==> (2) na1[c] + nrpphr[c]		Transport, Extracellular	(6530.1 or 6531.1)
NRPPHRtu	Norepinephrine uniport	nrpphr[e] <==> nrpphr[c]		Transport, Extracellular	(6582.1 or 6582.2 or 6581.1)
NRPPHRVESSEC	Noradrenaline secretion via secretory vesicle (ATP driven)	(2) atp[c] + (2) h2o[c] + (3) nrpphr[c] --> (2) adp[c] + (2) h[c] + (3) nrpphr[e] + (2) pi[c]		Transport, Extracellular	(6570.1 or 6571.1)
NRVNCCOAtx	fatty acid intracellular transport	nrvnccoa[c] <==> nrvnccoa[x]		Transport, Peroxisomal	
NRVNCCPT1	carnitine O-palmitoyltransferase	[c] : crn + nrvnccoa --> coa + nrvnccrn	2.3.1.21	Carnitine shuttle	(1375.4 or 1374.1 or 126129.1 or 1375.3 or 1375.2 or 1375.1)
NRVNCCPT2	carnitine transferase	[m] : coa + nrvnccrn --> crn + nrvnccoa		Carnitine shuttle	1376.1
NRVNCCRNt	transport into the mitochondria (carnitine)	nrvnccrn[c] --> nrvnccrn[m]		Carnitine shuttle	788.1
NRVNCt	fatty acid transport via diffusion	nrvnc[e] <==> nrvnc[c]		Transport, Extracellular	
NS26T2g	alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase	[g] : cmpacna + sT_antigen --> cmp + dsT_antigen + h	2.4.99.3	O-Glycan Biosynthesis	55808.1
NS26Tg	alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase	[g] : Tn_antigen + cmpacna --> cmp + h + sTn_antigen	2.4.99.3	O-Glycan Biosynthesis	55808.1
NT5C	5'-nucleotidase	[c] : h2o + nicrnt --> nicrns + pi	3.1.3.5	NAD Metabolism	22978.1
NTD1	5'-nucleotidase (dUMP)	[c] : dump + h2o --> duri + pi	3.1.3.5	Pyrimidine Catabolism	30833.1
NTD10	5'-nucleotidase (XMP)	[c] : h2o + xmp --> pi + xtsn	3.1.3.5	Nucleotides	22978.1
NTD11	5'-nucleotidase (IMP)	[c] : h2o + imp --> ins + pi	3.1.3.5	Purine Catabolism	(22978.1 or 93034.1 or 93034.2)
NTD12	5'-nucleotidase (dIMP)	[c] : dimp + h2o --> din + pi	3.1.3.5	Nucleotides	30833.1
NTD1m	5'-nucleotidase (dUMP),mitochondrial	[m] : dump + h2o --> duri + pi	3.1.3.5	Nucleotides	56953.1
NTD2	5'-nucleotidase (UMP)	[c] : h2o + ump --> pi + uri	3.1.3.5	Pyrimidine Catabolism	51251.1
NTD2e	5'-nucleotidase (UMP), extracellular	[e] : h2o + ump --> pi + uri	3.1.3.5	Nucleotides	4907.1
NTD2l	5'-nucleotidase (UMP), lysosome	[l] : h2o + ump --> pi + uri	3.1.3.5	Nucleic acid degradation	53.1
NTD2m	5'-nucleotidase (UMP), mitochondrial	[m] : h2o + ump --> pi + uri	3.1.3.5	Nucleotides	56953.1
NTD3	5'-nucleotidase (dCMP)	[c] : dcmp + h2o --> dcyt + pi	3.1.3.5	Pyrimidine Catabolism	(93034.1 or 93034.2 or 30833.1)
NTD3l	5'-nucleotidase (dCMP), lysosomal	[l] : dcmp + h2o --> dcyt + pi	3.1.3.5	Nucleic acid degradation	53.1
NTD4	5'-nucleotidase (CMP)	[c] : cmp + h2o --> cytd + pi	3.1.3.5	Pyrimidine Catabolism	51251.1
NTD4e	5'-nucleotidase (CMP), extracellular	[e] : cmp + h2o --> cytd + pi	3.1.3.5	Nucleotides	4907.1
NTD4l	5'-nucleotidase (CMP), lysosome	[l] : cmp + h2o --> cytd + pi	3.1.3.5	Nucleic acid degradation	53.1
NTD5	5'-nucleotidase (dTMP)	[c] : dtmp + h2o --> pi + thymd	3.1.3.5	Pyrimidine Catabolism	30833.1
NTD5l	5'-nucleotidase (dTMP), lysosomal	[l] : dtmp + h2o --> pi + thymd	3.1.3.5	Nucleic acid degradation	53.1
NTD5m	5'-nucleotidase (dTMP), mitochondrial	[m] : dtmp + h2o --> pi + thymd	3.1.3.5	Nucleotides	56953.1
NTD6	5'-nucleotidase (dAMP)	[c] : damp + h2o --> dad-2 + pi	3.1.3.5	Nucleotides	22978.1
NTD6l	5'-nucleotidase (dAMP), lysosome	[l] : damp + h2o --> dad-2 + pi	3.1.3.5	Nucleic acid degradation	53.1
NTD7	5'-nucleotidase (AMP)	[c] : amp + h2o --> adn + pi	3.1.3.5	Nucleotides	(22978.1 or 93034.1 or 93034.2)
NTD7e	5'-nucleotidase (AMP), extracellular	[e] : amp + h2o --> adn + pi	3.1.3.5	Nucleotides	4907.1
NTD7l	5'-nucleotidase (AMP), lysosome	[l] : amp + h2o --> adn + pi	3.1.3.5	Nucleic acid degradation	53.1
NTD8	5'-nucleotidase (dGMP)	[c] : dgmp + h2o --> dgsn + pi	3.1.3.5	Nucleotides	(22978.1 or 30833.1)
NTD8l	5'-nucleotidase (dGMP), lysosomal	[l] : dgmp + h2o --> dgsn + pi	3.1.3.5	Nucleic acid degradation	53.1
NTD9	5'-nucleotidase (GMP)	[c] : gmp + h2o --> gsn + pi	3.1.3.5	Nucleotides	22978.1
NTD9e	5'-nucleotidase (GMP), extracellular	[e] : gmp + h2o --> gsn + pi	3.1.3.5	Nucleotides	4907.1
NTD9l	5'-nucleotidase (GMP), lysosome	[l] : gmp + h2o --> gsn + pi	3.1.3.5	Nucleic acid degradation	53.1
NTMELYStner	protein trimethyl lysine transport (nucleus to ER)	Ntmelys[n] --> Ntmelys[r]		Transport, Nuclear	

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
NTP3e	nucleoside-triphosphatase (GTP)	[e] : gtp + h2o --> gdp + h + pi	3.6.1.15	Nucleotides	124583.1
NTPP10	Nucleoside triphosphate pyrophosphorylase (ditp)	[c] : ditp + h2o --> dimp + h + ppi	3.6.1.19	Nucleotides	(3704.1 or 3704.2)
NTPP11	Nucleoside triphosphate pyrophosphorylase (xtp)	[c] : h2o + xtp --> h + ppi + xmp	3.6.1.19	Nucleotides	(3704.1 or 3704.2)
NTPP9	Nucleoside triphosphate pyrophosphorylase (itp)	[c] : h2o + itp --> h + imp + ppi	3.6.1.19	Nucleotides	(3704.1 or 3704.2)
O16G1e	oligo-1,6-glucosidase (glygn4 -> glygn5), extracellular	[e] : glygn4 + h2o --> glc-D + glygn5	3.2.1.10	Starch and Sucrose Metabolism	6476.1
O16G2e	oligo-1,6-glucosidase (strch2 ->strch3), extracellular	[e] : h2o + strch2 --> glc-D + malt	3.2.1.10	Starch and Sucrose Metabolism	6476.1
O2St	superoxide anion transport via diffusion (extracellular)	o2s[c] <==> o2s[e]		Transport, Extracellular	
O2Stm	superoxide anion transport via diffusion (mitochondria)	o2s[c] <==> o2s[m]		Transport, Mitochondrial	
O2Stn	superoxide anion transport via diffusion (nucleus)	o2s[c] <==> o2s[n]		Transport, Nuclear	
O2Stx	superoxide anion transport via diffusion (peroxisome)	o2s[c] <==> o2s[x]		Transport, Peroxisomal	
O2t	o2 transport (diffusion)	o2[e] <==> o2[c]		Transport, Extracellular	
O2ter	O2 transport, endoplasmic reticulum	o2[c] <==> o2[r]		Transport, Endoplasmic Reticular	
O2tm	O2 transport (diffusion)	o2[c] <==> o2[m]		Transport, Mitochondrial	
O2tn	O2 nuclear transport	o2[c] <==> o2[n]		Transport, Nuclear	
O2tp	O2 transport, peroxisomal	o2[c] <==> o2[x]		Transport, Peroxisomal	
OAGD3te	oagd3_hs transport	oagd3_hs[c] <==> oagd3_hs[e]		Transport, Extracellular	
OAGD3tg	oagd3_hs intracellular transport	oagd3_hs[c] <==> oagd3_hs[g]		Transport, Golgi Apparatus	
OAGT3te	oagt3_hs transport	oagt3_hs[c] <==> oagt3_hs[e]		Transport, Extracellular	
OAGT3tg	oagt3_hs intracellular transport	oagt3_hs[c] <==> oagt3_hs[g]		Transport, Golgi Apparatus	
OBDHc	2-Oxobutanoate dehydrogenase, cytosolic	[c] : 2obut + coa + nad --> co2 + nadh + ppcoa	1.2.7.2	Glycine, Serine, and Threonine Metabolism	
OCBTm	ornithine carbamoyltransferase, irreversible	[m] : cbp + orn --> citr-L + h + pi	2.1.3.3	Urea cycle/amino group metabolism	5009.1
OCCOAtm	Octanoyl-CoA transport, diffusion	occoa[c] --> occoa[m]		Transport, Mitochondrial	
OCCOAtx	fatty acid intracellular transport	occoa[c] <==> occoa[x]		Transport, Peroxisomal	
OCDCAtr	fatty acid transport via diffusion	ocdca[e] <==> ocdca[c]		Transport, Extracellular	
OCDCEAtr	fatty acid transport via diffusion	ocdcea[e] <==> ocdcea[c]		Transport, Extracellular	
OCOAT1m	3-oxoacid CoA-transferase	[m] : acac + succoa <==> aacoa + succ	2.8.3.5	Valine, Leucine, and Isoleucine Metabolism	(5019.1 or 64064.1)
OCTAt	Octanoate transport via diffusion	octa[e] <==> octa[c]		Transport, Extracellular	
ODECOAtx	fatty acid intracellular transport	odecoa[c] <==> odecoa[x]		Transport, Peroxisomal	
OIVD1m	2-oxoisovalerate dehydrogenase (acylating; 4-methyl-2-oxopentaoate), mitochondrial	[m] : 4mop + coa + nad --> co2 + ivcoa + nadh	1.2.1.25	Valine, Leucine, and Isoleucine Metabolism	(((594.1 and 593.1) and 1738.1 and 1629.1) or (1738.1 and 1629.1 and (593.1 and 594.2)))
OIVD2m	2-oxoisovalerate dehydrogenase (acylating; 3-methyl-2-oxobutanoate), mitochondrial	[m] : 3mob + coa + nad --> co2 + ibcoa + nadh	1.2.1.25	Valine, Leucine, and Isoleucine Metabolism	((1738.1 and 1629.1 and (594.1 and 593.1)) or (1629.1 and (593.1 and 594.2) and 1738.1))
OIVD3m	2-oxoisovalerate dehydrogenase (acylating; 3-methyl-2-oxopentanoate), mitochondrial	[m] : 3mop + coa + nad --> 2mbcoa + co2 + nadh	1.2.1.25	Valine, Leucine, and Isoleucine Metabolism	(((594.1 and 593.1) and 1629.1 and 1738.1) or ((593.1 and 594.2) and 1738.1 and 1629.1))
OMEPRAZOLEte	xenobiotic transport	omeprazole[e] <==> omeprazole[c]		Transport, Extracellular	
OMPDC	orotidine-5'-phosphate decarboxylase	[c] : h + orot5p --> co2 + ump	4.1.1.23	Pyrimidine Biosynthesis	7372.1
ONPTHLte	xenobiotic transport	onpthl[e] <==> onpthl[c]		Transport, Extracellular	
OPAHir	5-Oxoproline amidohydrolase (ATP-hydrolysing) (ir)	[c] : 5oxpro + atp + (2) h2o --> adp + glu-L + h + pi	3.5.2.9	Glutathione Metabolism	26873.1
ORETNF	4-oxo-retinoic acid formation (oxidation)	[c] : o2 + (2) retn --> (2) oretn		Vitamin A Metabolism	
ORETNF2	13-cis-4-oxo-retinoic acid formation (oxidation)	[c] : (2) 13-cis-retn + o2 --> (2) 13-cis-oretn		Vitamin A Metabolism	
ORETNtn	4-oxo-retinoic acid transport, Nuclear	oretn[c] <==> oretn[n]		Transport, Nuclear	
ORETNtn2	13-cis-4-oxo-retinoic acid transport, Nuclear	13-cis-oretn[c] <==> 13-cis-oretn[n]		Transport, Nuclear	
ORNDC	Ornithine Decarboxylase	[c] : h + orn --> co2 + ptrc	4.1.1.17	Urea cycle/amino group metabolism	4953.1
ORNt3m	ornithine mitochondrial transport via proton antiport	h[c] + orn[m] <==> h[m] + orn[c]		Transport, Mitochondrial	(83884.1 or 10166.1)
ORNt4m	ornithine mitochondrial transport exchange with citruline	citr-L[c] + h[c] + orn[m] <==> citr-L[m] + h[m] + orn[c]		Transport, Mitochondrial	(10166.1 or 83884.1)
ORNTArm	ornithine transaminase reversible (m)	[m] : akg + orn <==> glu-L + glu5sa	2.6.1.13	Urea cycle/amino group metabolism	4942.1
ORNtiDF	ornithine transport via diffusion (extracellular to cytosol)	orn[e] --> orn[c]		Transport, Extracellular	(6541.1 or 6542.1 or 84889.1)
ORPT	orotate phosphoribosyltransferase	[c] : orot5p + ppi <==> orot + prpp	2.4.2.10	Pyrimidine Biosynthesis	7372.1
OXAHCOtex	oxalate transport via bicarbonate countertransport	(2) hco3[c] + oxa[e] --> (2) hco3[e] + oxa[c]		Transport, Extracellular	(10861.1 or 10861.2 or 10861.3 or 1836.1 or 1811.1)
OXAtp	oxalate transport out of peroxisome	oxa[x] --> oxa[c]		Transport, Peroxisomal	
P45011A1m	Cytochrome P450 11A1, mitochondrial [Precursor]	[m] : chsterol + h + nadph + (2) o2 --> 4mptnl + (2) h2o + nadp + prgnlone	1.14.15.6	Steroid Metabolism	1583.1
P45011B11m	Steroid 11-beta-hydroxylase	[m] : 11docrtstrm + h + nadph + o2 --> crtstrn + h2o + nadp	1.14.15.4	Steroid Metabolism	1584.1
P45011B12m	Steroid 11-beta-hydroxylase	[m] : 11docrtsl + h + nadph + o2 --> crtsl + h2o + nadp	1.14.15.4	Steroid Metabolism	1584.1
P45011B21m	Steroid 11-beta-hydroxylase	[m] : 11docrtstrm + h + nadph + (2) o2 --> aldstrm + (2) h2o + nadp	1.14.15.4	Steroid Metabolism	1585.1
P45017A1r	Cytochrome P450 17A1	[r] : h + nadph + o2 + prgnlone --> 17ahprgnlone + h2o + nadp	1.14.99.9	Steroid Metabolism	1586.1
P45017A2r	Cytochrome P450 17A1	[r] : 17ahprgnlone + h + nadph + (0.5) o2 --> acald + dhea + h2o + nadp	1.14.99.9	Steroid Metabolism	1586.1
P45017A3r	Cytochrome P450 17A1	[r] : h + nadph + o2 + prgstrn --> 17ahprgstrn + h2o + nadp	1.14.99.9	Steroid Metabolism	1586.1
P45017A4r	Cytochrome P450 17A1	[r] : 17ahprgstrn + h + nadph + (0.5) o2 --> acald + andrstndn + h2o + nadp	1.14.99.9	Steroid Metabolism	1586.1
P45019A1r	aromatase	[r] : andrstndn + nadph + (2) o2 --> estrone + for + (2) h2o + nadp	1.14.14.1	Steroid Metabolism	(1588.1 or 1588.2)
P45019A2r	aromatase	[r] : nadph + (2) o2 + tststerone --> estradiol + for + (2) h2o + nadp	1.14.14.1	Steroid Metabolism	(1588.1 or 1588.2)
P4501B1r	cytochrome P450 1B1	[r] : estradiol + h + nadph + o2 --> h2o + hestratriol + nadp	1.14.14.1	Steroid Metabolism	1545.1

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
P45021A1r	Steroid 21-hydroxylase	[r] : h + nadph + o2 + prgstrn --> 11docrtstrn + h2o + nadp	1.14.99.10	Steroid Metabolism	1589.1
P45021A2r	Steroid 21-hydroxylase	[r] : 17ahprgstrn + h + nadph + o2 --> 11docrtsl + h2o + nadp	1.14.99.10	Steroid Metabolism	1589.1
P45027A11m	5-beta-cholestane-3-alpha,7-alpha,12-alpha-triol 27-hydroxylase	[m] : h + nadph + o2 + xoltriol --> h2o + nadp + xoltetrol	1.14.13.15	Bile Acid Biosynthesis	1593.1
P45027A12m	5-beta-cholestane-3-alpha,7-alpha,12-alpha-triol 27-hydroxylase	[m] : nadp + xoltetrol --> h + nadph + thcholst	1.14.13.15	Bile Acid Biosynthesis	1593.1
P45027A13m	5-beta-cholestane-3-alpha,7-alpha,12-alpha-triol 27-hydroxylase	[m] : nadph + o2 + thcholst --> h2o + nadp + thcholstoic	1.14.13.15	Bile Acid Biosynthesis	1593.1
P45027A14m	5-beta-cytochrome P450, family 27, subfamily A, polypeptide 1	[m] : h + nadph + o2 + xol7ah2 --> h2o + nadp + xol7ah3	1.14.13.15	Bile Acid Biosynthesis	1593.1
P45027A15m	5-beta-cytochrome P450, family 27, subfamily A, polypeptide 1	[m] : h + nadph + o2 + xol7ah3 --> (2) h2o + nadp + xol7ah2al	1.14.13.15	Bile Acid Biosynthesis	1593.1
P45027A16m	Cytochrome P450 27	[m] : nadph + o2 + xol7ah2al --> dhcholestanate + h2o + nadp	1.14.13.15	Bile Acid Biosynthesis	1593.1
P45027A1m	Cytochrome P450 27	[m] : chsterol + h + nadph + o2 --> h2o + nadp + xol27oh		Bile Acid Biosynthesis	1593.1
P4502A6	cytochrome P450 2A6	[c] : coumarin + h + nadph + o2 --> h2o + hcoumarin + nadp		CYP Metabolism	(1553.1 or 1548.1)
P4502C18	cytochrome P450 2C18	[c] : antipyrene + h + nadph + (0.5) o2 --> dmantipyrine + meoh + nadp		CYP Metabolism	1562.1
P4502C19	cytochrome P450 2C19	[c] : h + nadph + o2 + omeprazole --> 5homeprazole + h2o + nadp		CYP Metabolism	1557.1
P4502C8	cytochrome P450 2C8	[c] : h + nadph + o2 + taxol --> h2o + htaxol + nadp		CYP Metabolism	(1558.1 or 1558.2)
P4502C9	cytochrome P450 2C9	[c] : h + nadph + o2 + tolbutamide --> 4mtolbutamide + h2o + nadp		CYP Metabolism	1559.1
P4502C92	cytochrome P450 2C9	[c] : h + limnen + nadph + o2 --> carveol + h2o + nadp		Limonene and pinene degradation	(1559.1 or 1557.1)
P4502C93	cytochrome P450 2C9	[c] : h + limnen + nadph + o2 --> h2o + nadp + perillyl		Limonene and pinene degradation	(1559.1 or 1557.1)
P4502C94	cytochrome P450 2C9	[c] : appnn + h + nadph + o2 --> apnnox + h2o + nadp		Limonene and pinene degradation	(1559.1 or 1557.1)
P4502D6	cytochrome P450 2D6	[c] : debrisoquine + h + nadph + o2 --> 4hdebrisoquine + h2o + nadp		CYP Metabolism	1565.1
P4502E1	cytochrome P450 2E1	[c] : 4nph + h + nadph + o2 --> 24nph + h2o + nadp		CYP Metabolism	1571.1
P4502F1	cytochrome P450 2F1	[c] : h + nadph + npthl + o2 --> h2o + nadp + onpthl		CYP Metabolism	1572.1
P45039A1r	oxysterol 7-alpha-hydroxylase	[r] : h + nadph + o2 + xol24oh --> h2o + nadp + xoltri24		Bile Acid Biosynthesis	51302.1
P4503A4	cytochrome P450 3A4	[c] : h + nadph + nifedipine + o2 --> h2o + hnifedipine + nadp		CYP Metabolism	1576.1
P4503A43r	cytochrome p450 P450 3A43	[r] : h + nadph + o2 + tststerone --> h2o + nadp + whtststerone		Steroid Metabolism	(64816.1 or 64816.2 or 64816.3)
P4503A5	cytochrome P450 3A5	[c] : aflatoxin + h + nadph + o2 --> eaflatoxin + h2o + nadp		CYP Metabolism	1577.1
P4503A7r	cytochrome p450 P450 3A7	[r] : h + nadph + o2 + tststerone --> 6htststerone + h2o + nadp		Steroid Metabolism	1551.1
P45046A1r	cytochrome P450, family 46, subfamily A, polypeptide 1	[r] : chsterol + h + nadph + o2 --> h2o + nadp + xol24oh		Bile Acid Biosynthesis	10858.1
P4504B1r	cytochrome P450 4B1	[r] : arachd + h + nadph + o2 --> 12harachd + h2o + nadp	1.14.14.1	Eicosanoid Metabolism	1572.1
P4504F121r	cytochrome p450 4F12/4F2	[r] : arachd + h + nadph + o2 --> h2o + nadp + wharachd		Eicosanoid Metabolism	66002.1
P4504F122r	cytochrome p450 4F12/4F2	[r] : h + leuktrB4 + nadph + o2 --> h2o + leuktrB4woh + nadp		Eicosanoid Metabolism	(4051.1 or 66002.1 or 8529.1)
P4504F123r	cytochrome p450 4F12/4F2	[r] : ebastine + h + nadph + o2 --> ebastineoh + h2o + nadp		CYP Metabolism	66002.1
P4504F81r	cytochrome p450 4F8	[r] : arachd + h + nadph + o2 --> 18harachd + h2o + nadp		Eicosanoid Metabolism	11283.1
P4507A1r	cytochrome P450, family 7, subfamily A, polypeptide 1	[r] : chsterol + h + nadph + o2 --> h2o + nadp + xol7a	1.14.13.17	Bile Acid Biosynthesis	1581.1
P4507B11r	oxysterol 7alpha-hydroxylase	[r] : h + nadph + o2 + xol25oh --> h2o + nadp + xoltri25		Bile Acid Biosynthesis	9420.1
P4507B12r	oxysterol 7alpha-hydroxylase	[r] : h + nadph + o2 + xol27oh --> h2o + nadp + xoltri27		Bile Acid Biosynthesis	9420.1
P4508B11r	sterol 12-alpha-hydroxylase	[r] : h + nadph + o2 + xol7aone --> h2o + nadp + xoldiolone		Bile Acid Biosynthesis	1582.1
P4508B13r	sterol 12-alpha-hydroxylase (nadh)	[r] : h + nadh + o2 + xol7aone --> h2o + nad + xoldiolone		Bile Acid Biosynthesis	1582.1
P450LTB4r	cytochrome p450 leukotriene B4	[r] : leuktrB4woh + nadph + (1.5) o2 --> (2) h2o + leuktrB4wcooh + nadp		Eicosanoid Metabolism	
P450SCC1m	cholesterol monooxygenase	[m] : chsterol + h + nadph + o2 <==> 20ahchsterol + h2o + nadp		Cholesterol Metabolism	
P5CDm	1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	[m] : 1pyr5c + (2) h2o + nad --> glu-L + h + nadh		Glutamate metabolism	(8659.1 or 8659.2)
P5CR	pyrroline-5-carboxylate reductase	[c] : 1pyr5c + (2) h + nadph --> nadp + pro-L	1.5.1.2	Urea cycle/amino group metabolism	(29920.1 or 65263.1)
P5CRm	pyrroline-5-carboxylate reductase (m)	[m] : 1pyr5c + (2) h + nadph --> nadp + pro-L	1.5.1.2	Arginine and Proline Metabolism	(5831.1 or 5831.2)
P5CRx	pyrroline-5-carboxylate reductase	[c] : 1pyr5c + (2) h + nadh --> nad + pro-L	1.5.1.2	Urea cycle/amino group metabolism	(29920.1 or 65263.1)
P5CRxm	pyrroline-5-carboxylate reductase (m)	[m] : 1pyr5c + (2) h + nadh --> nad + pro-L	1.5.1.2	Arginine and Proline Metabolism	(5831.1 or 5831.2)
PA_HSter	phosphatidate scramblase	pa_hs[c] <==> pa_hs[r]		Transport, Endoplasmic Reticular	
PA_HStg	phosphatidate scramblase	pa_hs[c] <==> pa_hs[g]		Transport, Golgi Apparatus	
PA_HStn	phosphatidate transport, nuclear	pa_hs[c] <==> pa_hs[n]		Transport, Nuclear	
PACCOAL	phenylacetate-CoA ligase	[c] : atp + coa + pac --> amp + phaccoa + ppi	6.2.1.30	Phenylalanine metabolism	
PAFH	Platelet-activating factor acetylhydrolase	[c] : h2o + paf_hs --> ac + ak2lgchol_hs + h	3.1.1.47	Glycerophospholipid Metabolism	(5051.1 or (5049.1 and 5050.1 and 5048.1) or (5049.1 and 5050.1))
PAFHe	Platelet-activating factor acetylhydrolase	[e] : h2o + paf_hs --> ac + ak2lgchol_hs + h	3.1.1.47	Glycerophospholipid Metabolism	7941.1
PAFS	alkyl glycerol phosphocholine acetyl transferase	[c] : accoa + ak2lgchol_hs --> coa + paf_hs		Glycerophospholipid Metabolism	
PAIL_HStn	phosphatidylinositol nuclear transport (diffusion)	pail_hs[c] <==> pail_hs[n]		Transport, Nuclear	
PAIL45P_HStn	phosphatidylinositol 4,5-bisphosphate nuclear transport (diffusion)	pail45p_hs[c] <==> pail45p_hs[n]		Transport, Nuclear	
PAIL4P_HStn	phosphatidylinositol 4-phosphate nuclear transport (diffusion)	pail4p_hs[c] <==> pail4p_hs[n]		Transport, Nuclear	
PAN4PP	phosphatase (pan4p)	[c] : h2o + pan4p --> pi + ptth		CoA Catabolism	
PAPStg	3'-Phosphoadenylyl sufate Golgi transport	paps[c] <==> paps[g]		Transport, Golgi Apparatus	347734.1
PAPtg	adenosine 3',5'-bisphosphate Golgi transport	pap[g] --> pap[c]		Transport, Golgi Apparatus	
PCFLOPm	phosphatidylcholine flippase	atp[c] + h2o[c] + pchol_hs[m] --> adp[c] + h[c] + pchol_hs[c] + pi[c]		Transport, Mitochondrial	57194.1
PCHOL_HSter	phosphatidylcholine scramblase	pchol_hs[c] <==> pchol_hs[r]		Transport, Endoplasmic Reticular	

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
PCHOL_HStg	phosphatidylcholine scramblase	pchol_hs[c] <==> pchol_hs[g]		Transport, Golgi Apparatus	
PCHOLP_hs	choline phosphatase	[c] : h2o + pchol_hs --> chol + h + pa_hs	3.1.4.4	Glycerophospholipid Metabolism	5338.1
PCHOLPg_hs	choline phosphatase	[g] : h2o + pchol_hs --> chol + h + pa_hs	3.1.4.4	Glycerophospholipid Metabolism	5337.1
PCHOLPm_hs	choline phosphatase	[m] : h2o + pchol_hs --> chol + h + pa_hs	3.1.4.4	Glycerophospholipid Metabolism	5337.1
PCHOLPr_hs	choline phosphatase	[r] : h2o + pchol_hs --> chol + h + pa_hs	3.1.4.4	Glycerophospholipid Metabolism	5337.1
PCLAD	picolinic acid decarboxylase	[c] : cmusa + h --> am6sa + co2	4.1.1.45	Tryptophan metabolism	130013.1
PCLYSOX	Procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase	[c] : akg + o2 + pcollglys --> co2 + pcollg5hlys + succ	1.14.11.4	Lysine Metabolism	(5352.2 or 5351.1 or 5352.1 or 8985.1)
PCm	pyruvate carboxylase	[m] : atp + hco3 + pyr --> adp + h + oaa + pi	6.4.1.1	Pyruvate Metabolism	(5091.1 or 5091.2)
PCREATtmdiffir	Phosphocreatine transport to/from mitochondria via diffusion	pcreat[m] --> pcreat[c]		Urea cycle/amino group metabolism	
PCRNtc	transport into the cytosol from peroxisome (carnitine)	pcrn[x] --> pcrn[c]		Carnitine shuttle	
PCRNtm	transport into the mitochondria from cytosol (carnitine)	pcrn[c] --> pcrn[m]		Carnitine shuttle	
PCt	phosphatidylcholine transporter	atp[c] + h2o[c] + pchol_hs[c] <==> adp[c] + h[c] + pchol_hs[e] + pi[c]		Transport, Extracellular	(5244.1 or 5244.2 or 5244.3)
PDE1	3',5'-cyclic-nucleotide phosphodiesterase	[c] : camp + h2o --> amp + h	3.1.4.17	Nucleotides	(5150.1 or 5150.2 or 10846.1 or 5139.1 or 5140.1 or 5140.2 or 5138.1 or 5136.1 or 5136.2 or 5153.1 or 5137.1 or 27115.1 or 5151.1 or 8622.1 or 5151.2 or 5151.3 or 5151.4 or 5151.5 or 50940.1 or 5141.1 or 5142.1 or 5143.1 or 5144.1)
PDE1g	3',5'-cyclic-nucleotide phosphodiesterase,Golgi	[g] : camp + h2o --> amp + h	3.1.4.17	Nucleotides	10846.1
PDE4	3',5'-cyclic-nucleotide phosphodiesterase	[c] : 35cgmp + h2o --> gmp + h	3.1.4.17	Nucleotides	(10846.1 or 5140.1 or 5140.2 or 5138.1 or 5136.1 or 5136.2 or 5153.1 or 5137.1 or 5152.2 or 5152.20 or 5152.3 or 5152.4 or 5152.5 or 5152.6 or 5152.7 or 5152.19 or 5152.18 or 5152.17 or 5152.16 or 5152.15 or 5152.14 or 5152.13 or 5152.12 or 5152.11 or 5152.10 or 50940.1 or 8654.2 or 8654.1 or 8654.3 or (5158.1 and 5149.1 and 5145.1) or (5146.1 and 5148.1 and 5145.1 and 5158.1 and 5147.1) or 5146.1 or 5139.1)
PDE4g	3',5'-cyclic-nucleotide phosphodiesterase, Golgi	[g] : 35cgmp + h2o --> gmp + h	3.1.4.17	Nucleotides	10846.1
PDE4n	3',5'-cyclic-nucleotide phosphodiesterase, Nucleus	[n] : 35cgmp + h2o --> gmp + h	3.1.4.17	Nucleotides	5152.1
PDHm	pyruvate dehydrogenase	[m] : coa + nad + pyr --> accoa + co2 + nadh	1.2.4.1	Glycolysis/Gluconeogenesis	((1737.1 and (8050.1 and 1738.1) and (5162.1 and 5161.1)) or (1737.1 and (5160.1 and 5162.1) and (8050.1 and 1738.1)))
PDX5PO	pyridoxine 5'-phosphate oxidase	[c] : o2 + pdx5p <==> h2o2 + pydx5p	1.4.3.5	Vitamin B6 Metabolism	55163.1
PDXPP	Pyridoxine 5-phosphate phosphatase	[c] : h2o + pdx5p --> pi + pydxn		Vitamin B6 Metabolism	57026.1
PE_HSter	phosphatidylethanolamine scramblase	pe_hs[c] <==> pe_hs[r]		Transport, Endoplasmic Reticular	
PE_HStg	phosphatidylethanolamine scramblase	pe_hs[c] <==> pe_hs[g]		Transport, Golgi Apparatus	
PE_HStm	phosphatidylethanolamine scramblase	pe_hs[c] <==> pe_hs[m]		Transport, Mitochondrial	
PEAMNO	Phenethylamine oxidase	[c] : h2o + o2 + peamn --> h2o2 + nh4 + pacald	1.4.3.6	Phenylalanine metabolism	(26.1 or 314.1 or 4128.1 or 4129.1 or 314.2)
PECGONCOATr	Pseudoecgonine CoA transferase (ER)	[r] : atp + coa + h + pecgon --> amp + pecgoncoa + ppi		Alkaloid biosynthesis II	
PEFLIP	phosphatidylethanolamine flippase	atp[c] + h2o[c] + pe_hs[e] --> adp[c] + h[c] + pe_hs[c] + pi[c]		Transport, Extracellular	(10396.1 or 57194.1)
PEFLIPm	phosphatidylethanolamine flippase	atp[c] + h2o[c] + pe_hs[c] --> adp[c] + h[c] + pe_hs[m] + pi[c]		Transport, Mitochondrial	(10396.1 or 57194.1)
PEPCK	Phosphoenolpyruvate carboxykinase (GTP)	[c] : gtp + oaa --> co2 + gdp + pep	4.1.1.32	Glycolysis/Gluconeogenesis	5105.1
PEPCKm	Phosphoenolpyruvate carboxykinase (GTP)	[m] : gtp + oaa --> co2 + gdp + pep	4.1.1.32	Glycolysis/Gluconeogenesis	5106.1
PEPLYStn	peptide (lysine) nuclear transport via diffusion	peplys[e] <==> peplys[n]		Transport, Nuclear	
PERILLYLte	xenobiotic transport	perillyl[e] <==> perillyl[c]		Transport, Extracellular	
PEROXx	peroxisomal lumped long chain fatty acid oxidation	[x] : (3) coa + (3) h2o + (3) nad + (2) o2 + pristcoa --> accoa + dmnoncoa + (3) h + (2) h2o2 + (3) nadh + (2) ppcoa		Fatty acid oxidation, peroxisome	(30.1 and 8310.1 and 3295.1 and 1962.1)
PETHCT	phosphoethanolamine cytidyltransferase	[c] : ctp + ethamp + h --> cdpea + ppi	2.7.7.14	Glycerophospholipid Metabolism	5833.1
PETOHMm_hs	phosphatidylethanolamine N-methyltransferase	[m] : (3) amet + pe_hs --> (3) ahcys + (3) h + pchol_hs	2.1.1.17	Glycerophospholipid Metabolism	(10400.2 or 10400.3 or 10400.1)
PETOHMr_hs	phosphatidylethanolamine N-methyltransferase	[r] : (3) amet + pe_hs --> (3) ahcys + (3) h + pchol_hs	2.1.1.17	Glycerophospholipid Metabolism	(10400.2 or 10400.3 or 10400.1)
PFK	phosphofructokinase	[c] : atp + f6p --> adp + fdp + h	2.7.1.11	Glycolysis/Gluconeogenesis	(5211.1 or 5213.1 or 5211.2 or (5211.1 and 5213.1) or (5211.2 and 5213.1) or 5214.1 or (5214.1 and 5211.1) or (5214.1 and 5211.2) or (5213.1 and 5214.1))

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
PFK26	6-phosphofructo-2-kinase	[c] : atp + f6p --> adp + f26bp + h	2.7.1.105	Fructose and Mannose Metabolism	(5207.1 or 5208.1 or 5209.1 or 5210.1)
PGCD	phosphoglycerate dehydrogenase	[c] : 3pg + nad --> 3php + h + nadh	1.1.1.95	Glycine, Serine, and Threonine Metabolism	26227.1
PGDI	Prostaglandin-H2 D-isomerase [Precursor]	[c] : prostgh2 <==> prostgd2	5.3.99.2	Eicosanoid Metabolism	(5730.1 or 27306.1)
PGDIr	Prostaglandin-H2 D-isomerase [Precursor]	[r] : prostgh2 <==> prostgd2	5.3.99.2	Eicosanoid Metabolism	(5730.1 or 27306.1)
PGESr	Prostaglandin E synthase	[r] : prostgh2 <==> prostge2	5.3.99.3	Eicosanoid Metabolism	(9536.1 or 9536.2 or 80142.1 or 80142.2 or 80142.3 or 80142.4)
PGI	glucose-6-phosphate isomerase	[c] : g6p <==> f6p	5.3.1.9	Glycolysis/Gluconeogenesis	2821.1
PGISr	Prostaglandin I2 synthase	[r] : prostgh2 <==> prostgi2	5.3.99.4	Eicosanoid Metabolism	5740.1
PGK	phosphoglycerate kinase	[c] : 3pg + atp <==> 13dpg + adp	2.7.2.3	Glycolysis/Gluconeogenesis	(5230.1 or 5232.1 or 348477.1)
PGL	6-phosphogluconolactonase	[c] : 6pgl + h2o --> 6pgc + h	3.1.1.31	Pentose Phosphate Pathway	25796.1
PGLer	6-phosphogluconolactonase, endoplasmic reticulum	[r] : 6pgl + h2o --> 6pgc + h	3.1.1.31	Pentose Phosphate Pathway	9563.1
PGLYCP	Phosphoglycolate phosphatase	[c] : 2pglyc + h2o --> glyclt + pi	3.1.3.18	Glyoxylate and Dicarboxylate Metabolism	5240.1
PGM	phosphoglycerate mutase	[c] : 2pg <==> 3pg	5.4.2.1	Glycolysis/Gluconeogenesis	(5223.1 or 5224.1 or 5224.2 or 669.1 or 669.2)
PGMT	phosphoglucomutase	[c] : g1p <==> g6p	5.4.2.2	Glycolysis/Gluconeogenesis	(5236.1 or 55276.1)
PGPP_hs	Phosphatidylglycerol phosphate phosphatase (homo sapiens)	[c] : h2o + pgp_hs --> pglyc_hs + pi	3.1.3.27	Glycerophospholipid Metabolism	
PGPPT	phosphatidyl-CMP: glycerophosphate phosphatidyltransferase	[c] : cdpdag_hs + glyc3p --> cmp + h + pgp_hs	2.7.8.11	Glycerophospholipid Metabolism	9489.1
PGS	Prostaglandin G/H synthase	[c] : arachd + h + nadph + (2) o2 --> h2o + nadp + prostgh2	1.14.99.1	Eicosanoid Metabolism	(5743.1 or 5742.1)
PGSr	Prostaglandin G/H synthase	[r] : arachd + h + nadph + (2) o2 --> h2o + nadp + prostgh2	1.14.99.1	Eicosanoid Metabolism	(5743.1 or 5742.1)
PHACCOAGLNAC	Phenylacetyl-CoA:L-glutamine alpha-N-phenylacetyltransferase	[c] : gln-L + phaccoa --> coa + pheacgln	2.3.1.14	Phenylalanine metabolism	
PHCDm	L-1-pyrroline-3-hydroxy-5-carboxylate dehydrogenase	[m] : 1p3h5c + (2) h2o + nad --> e4hglu + h + nadh	1.5.1.12	Arginine and Proline Metabolism	(8659.1 or 8659.2)
PHCHGSm	L-1-Pyrroline-3-hydroxy-5-carboxylate spontaneous conversion to L-4-Hydroxyglutamate semialdehyde, mitochondrial	[m] : 1p3h5c + h + h2o <==> 4hglusa		Arginine and Proline Metabolism	
PHEACGLNt	PHEACGLN extracellular transport via diffusion	pheacgln[c] <==> pheacgln[e]		Transport, Extracellular	
PHEMEt	heme transport	pheme[e] --> pheme[c]		Transport, Extracellular	113235.1
PHEMEtm	Heme transport to cytosol	pheme[m] <==> pheme[c]		Transport, Mitochondrial	
PHEt4	L-phenylalanine transport in via sodium symport	na1[e] + phe-L[e] --> na1[c] + phe-L[c]		Transport, Extracellular	(11254.1 or 55089.1 or 54407.1 or 81539.1 or 6541.1 or 6542.1 or 84889.1)
PHETA1	phenylalanine transaminase	[c] : akg + phe-L <==> glu-L + phpyr	2.6.1.58	Phenylalanine metabolism	2805.1
PHETA1m	phenylalanine transaminase (m)	[m] : akg + phe-L <==> glu-L + phpyr	2.6.1.58	Phenylalanine metabolism	(2806.1 or 6898.1)
PHEtec	L-phenylalanine transport via diffusion (extracellular to cytosol)	phe-L[e] <==> phe-L[c]		Transport, Extracellular	(124935.1 or 117247.1)
PHETHPTOX2	L-Phenylalanine,tetrahydrobiopterin:oxygen oxidoreductase (4-hydroxylating)	[c] : o2 + phe-L + thbpt --> thbpt4acam + tyr-L	1.14.16.1	Tyr, Phe, Trp Biosynthesis	5053.1
PHYCBOXL	L-Phenylalanine carboxy-lyase	[c] : h + phe-L --> co2 + peamn	4.1.1.28	Phenylalanine metabolism	1644.1
PHYHx	Phytanoyl-CoA dioxygenase, peroxisomal	[x] : akg + o2 + phytcoa --> co2 + phyt2ohcoa + succ	1.14.11.18	Fatty acid oxidation, peroxisome	5264.1
PHYQt	Phylloquinone transport	atp[c] + h2o[c] + phyQ[e] --> adp[c] + h[c] + phyQ[c] + pi[c]		Transport, Extracellular	
PHYTt	fatty acid transport via diffusion	phyt[e] <==> phyt[c]		Transport, Extracellular	
PI345P3P	phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase	[c] : h2o + pail345p_hs --> pail45p_hs + pi	3.1.3.67	Inositol Phosphate Metabolism	5728.1
PI345P3Pn	phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase, nuclear	[n] : h2o + pail345p_hs --> pail45p_hs + pi	3.1.3.67	Inositol Phosphate Metabolism	5728.1
PI345P5P	phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase	[c] : h2o + pail345p_hs --> pail34p_hs + pi		Inositol Phosphate Metabolism	(8867.2 or 8871.1 or 27124.1 or 27124.2 or 3632.1 or 3633.1 or 3635.1 or 56623.1 or 3636.1 or 8867.1)
PI345P5Pn	phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase, nuclear	[n] : h2o + pail345p_hs --> pail34p_hs + pi		Inositol Phosphate Metabolism	
PI34P3Pn	phosphatidylinositol-3,4-bisphosphate 3-phosphatase, nuclear	[n] : h2o + pail34p_hs --> pail4p_hs + pi		Inositol Phosphate Metabolism	
PI34P4Pn	phosphatidylinositol-3,4-bisphosphate 4-phosphatase, nuclear	[n] : h2o + pail34p_hs --> pail3p_hs + pi		Inositol Phosphate Metabolism	
PI34P5K	phosphatidylinositol 3,4-bisphosphate 5-kinase	[c] : atp + pail34p_hs --> adp + h + pail345p_hs		Inositol Phosphate Metabolism	(8394.1 or 8395.1 or 23396.1)
PI34P5Kn	phosphatidylinositol 3,4-bisphosphate 5-kinase, nuclear	[n] : atp + pail34p_hs --> adp + h + pail345p_hs		Inositol Phosphate Metabolism	
PI35P3P	phosphatidylinositol-3,5-bisphosphate 3-phosphatase	[c] : h2o + pail35p_hs --> pail5p_hs + pi		Inositol Phosphate Metabolism	(8897.1 or 8897.2 or 8897.3)
PI3P3Pn	phosphatidylinositol-3-phosphate 3-phosphatase, nuclear	[n] : h2o + pail3p_hs --> pail_hs + pi		Inositol Phosphate Metabolism	
PI3P4K	phosphatidylinositol 3-phosphate 4-kinase	[c] : atp + pail3p_hs --> adp + h + pail34p_hs		Inositol Phosphate Metabolism	(8394.1 or 8395.1 or 23396.1 or 5297.1 or 5298.1 or 55361.1)
PI3P4Kn	phosphatidylinositol 3-phosphate 4-kinase, nuclear	[n] : atp + pail3p_hs --> adp + h + pail34p_hs		Inositol Phosphate Metabolism	
PI3P5K	phosphatidylinositol 3-phosphate 5-kinase	[c] : atp + pail3p_hs --> adp + h + pail35p_hs		Inositol Phosphate Metabolism	(8394.1 or 8395.1 or 23396.1)
PI3PP	phosphatidylinositol-3-phosphate 3-phosphatase	[c] : h2o + pail3p_hs --> pail_hs + pi		Inositol Phosphate Metabolism	(8897.2 or 8897.1 or 8897.3)

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
PI45P3K	phosphatidylinositol 4,5-bisphosphate 3-kinase	[c] : atp + pail45p_hs --> adp + h + pail345p_hs	2.7.1.153	Inositol Phosphate Metabolism	((5290.1 and 5295.3) or (5295.1 and 5291.1) or (5290.1 and 5295.1) or (5290.1 and 5295.2) or (5290.1 and 5296.1) or (5290.1 and 8503.1) or (5295.2 and 5291.1) or (5295.3 and 5291.1) or (5295.1 and 5293.1) or (5295.2 and 5293.1) or (5295.3 and 5293.1) or (5293.1 and 5296.1) or (8503.1 and 5293.1) or (5291.1 and 5296.1) or (5291.1 and 8503.1) or (23533.1 and 5294.1) or (5294.1 and 10870.1))
PI45P3Kn	phosphatidylinositol 4,5-bisphosphate 3-kinase, nuclear	[n] : atp + pail45p_hs --> adp + h + pail345p_hs	2.7.1.153	Inositol Phosphate Metabolism	
PI45P4P	phosphatidylinositol-4,5-bisphosphate 4-phosphatase	[c] : h2o + pail45p_hs --> pail5p_hs + pi		Inositol Phosphate Metabolism	
PI45P5P	phosphatidylinositol-4,5-bisphosphate 5-phosphatase	[c] : h2o + pail45p_hs --> pail4p_hs + pi	3.1.3.36	Inositol Phosphate Metabolism	(4952.1 or 4952.2 or 8871.1 or 56623.1 or 3633.1 or 8867.1 or 8867.2)
PI45P5Pn	phosphatidylinositol-4,5-bisphosphate 5-phosphatase, nuclear	[n] : h2o + pail45p_hs --> pail4p_hs + pi	3.1.3.36	Inositol Phosphate Metabolism	
PI45PLC	phosphatidylinositol 4,5-bisphosphate phospholipase C	[c] : h2o + pail45p_hs --> dag_hs + h + mi145p	3.1.4.11	Inositol Phosphate Metabolism	(89869.1 or 113026.1 or 257068.1 or 23007.1 or 51196.1 or 5336.1 or 5332.1 or 5332.2 or 23236.1 or 23236.2 or 5331.1 or 5335.1 or 5335.2 or 5334.1 or 84812.1 or 5330.1 or 9651.1 or 5333.1)
PI45PLCn	phosphatidylinositol 4,5-bisphosphate phospholipase C, nucleus	[n] : h2o + pail45p_hs --> dag_hs + h + mi145p	3.1.4.11	Inositol Phosphate Metabolism	(23236.1 or 23236.2)
PI4P3K	phosphatidylinositol 4-phosphate 3-kinase	[c] : atp + pail4p_hs --> adp + h + pail34p_hs		Inositol Phosphate Metabolism	(5286.1 or 5287.1 or 5288.1 or (5290.1 and 5295.3) or (5290.1 and 5295.1) or (5290.1 and 5295.2) or (5290.1 and 5296.1) or (5290.1 and 8503.1) or (5295.1 and 5291.1) or (5295.2 and 5291.1) or (5295.3 and 5291.1) or (5291.1 and 5296.1) or (5291.1 and 8503.1) or (5295.1 and 5293.1) or (5295.2 and 5293.1) or (5295.3 and 5293.1) or (5293.1 and 5296.1) or (8503.1 and 5293.1) or (5294.1 and 10870.1) or (23533.1 and 5294.1))
PI4P3Ker	phosphatidylinositol 4-phosphate 3-kinase, endoplasmic reticulum	[r] : atp + pail4p_hs --> adp + h + pail34p_hs		Inositol Phosphate Metabolism	5287.1
PI4P3Kn	phosphatidylinositol 4-phosphate 3-kinase, nuclear	[n] : atp + pail4p_hs --> adp + h + pail34p_hs		Inositol Phosphate Metabolism	
PI4P4Pn	phosphatidylinositol-4-phosphate 4-phosphatase, nuclear	[n] : h2o + pail4p_hs --> pail_hs + pi		Inositol Phosphate Metabolism	
PI4P5K	phosphatidylinositol 4-phosphate 5-kinase	[c] : atp + pail4p_hs --> adp + h + pail45p_hs	2.7.1.68	Glycerophospholipid Metabolism	(200576.1 or 200576.2 or 200576.3 or 23396.1 or 79837.1 or 5305.1 or 8395.1 or 8394.1 or 8396.1 or 8396.2)
PI4P5Kn	phosphatidylinositol 4-phosphate 5-kinase, nuclear	[n] : atp + pail4p_hs --> adp + h + pail45p_hs	2.7.1.68	Inositol Phosphate Metabolism	
PI4PLC	phosphatidylinositol 4-phosphate phospholipase C	[c] : h2o + pail4p_hs --> dag_hs + h + mi14p		Inositol Phosphate Metabolism	(89869.1 or 113026.1 or 257068.1 or 5333.1 or 51196.1 or 5336.1 or 5332.1 or 5332.2 or 23236.1 or 23236.2 or 5331.1 or 5335.1 or 5335.2 or 5334.1 or 5330.1 or 9651.1 or 23007.1 or 84812.1)
PI4PLCn	phosphatidylinositol 4-phosphate phospholipase C, nucleus	[n] : h2o + pail4p_hs --> dag_hs + h + mi14p		Inositol Phosphate Metabolism	(23236.2 or 23236.1)
PI4PP	phosphatidylinositol-4-phosphate 4-phosphatase	[c] : h2o + pail4p_hs --> pail_hs + pi		Inositol Phosphate Metabolism	

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
PI5P3K	phosphatidylinositol-5-phosphate 3-kinase	[c] : atp + pail5p_hs --> adp + h + pail35p_hs		Inositol Phosphate Metabolism	(5287.1 or 5288.1 or 5289.1 or (5290.1 and 5295.3) or (5290.1 and 5295.1) or (5290.1 and 5295.2) or (5290.1 and 5296.1) or (5290.1 and 8503.1) or (5295.1 and 5291.1) or (5295.2 and 5291.1) or (5295.3 and 5291.1) or (5291.1 and 5296.1) or (5291.1 and 8503.1) or (5295.1 and 5293.1) or (5295.2 and 5293.1) or (5295.3 and 5293.1) or (5293.1 and 5296.1) or (8503.1 and 5293.1) or (5294.1 and 10870.1) or (23533.1 and 5294.1) or 5286.1)
PI5P3Ker	phosphatidylinositol-5-phosphate 3-kinase, endoplasmic reticulum	[r] : atp + pail5p_hs --> adp + h + pail35p_hs		Inositol Phosphate Metabolism	5287.1
PI5P4K	phosphatidylinositol-5-phosphate 4-kinase	[c] : atp + pail5p_hs --> adp + h + pail45p_hs	2.7.1.149	Inositol Phosphate Metabolism	(5297.1 or 5298.1 or 55361.1)
PI5P4Kn	phosphatidylinositol-5-phosphate 4-kinase, nuclear	[n] : atp + pail5p_hs --> adp + h + pail45p_hs	2.7.1.149	Inositol Phosphate Metabolism	
PIACGT	phosphatidylinositol N-acetylglucosaminyltransferase	[c] : pail_hs + uacgam --> acgpail_hs + h + udp	2.4.1.198	Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	(9091.1 and 8818.1 and 51227.1 and 5277.1 and 5279.1 and 5283.1) or (5277.1 and 5279.1 and 8818.2 and 51227.1 and 5283.1 and 9091.1) or (8818.1 and 5283.1 and 5279.1 and 5277.1 and 9091.2 and 51227.1) or (8818.2 and 9091.2 and 5277.1 and 5283.1 and 5279.1 and 51227.1) or (5283.1 and 9091.1 and 5277.1 and 5279.1 and 8818.1 and 51227.2) or (5283.1 and 5277.1 and 5279.1 and 8818.2 and 9091.1 and 51227.2) or (9091.2 and 51227.2 and 5277.1 and 5279.1 and 5283.1 and 8818.1) or (5277.1 and 5279.1 and 51227.2 and 5283.1 and 9091.2 and 8818.2) or (9091.1 and 5283.1 and 51227.3 and 5279.1 and 8818.1 and 5277.1) or (9091.1 and 51227.3 and 5279.1 and 8818.2 and 5283.1 and 5277.1) or (8818.1 and 51227.3 and 5277.1 and 9091.2 and 5279.1 and 5283.1) or (51227.3 and 5277.1 and 5279.1 and 8818.2 and 9091.2 and 5283.1) or (9091.1 and 5277.1 and 8818.1 and 51227.1 and
PIK3	phosphatidylinositol 3-kinase	[c] : atp + pail_hs --> adp + h + pail3p_hs	2.7.1.137	Inositol Phosphate Metabolism	(5286.1 or 5287.1 or 5288.1 or 5289.1 or (5290.1 and 5295.2) or (5290.1 and 5295.3) or (5290.1 and 5295.1) or (5290.1 and 5296.1) or (5290.1 and 8503.1) or (5295.1 and 5291.1) or (5295.2 and 5291.1) or (5295.3 and 5291.1) or (5291.1 and 5296.1) or (5291.1 and 8503.1) or (5295.1 and 5293.1) or (5295.2 and 5293.1) or (5295.3 and 5293.1) or (5293.1 and 5296.1) or (8503.1 and 5293.1) or (5294.1 and 10870.1) or (23533.1 and 5294.1))
PIK3er	phosphatidylinositol 3-kinase, endoplasmic reticulum	[r] : atp + pail_hs --> adp + h + pail3p_hs	2.7.1.137	Inositol Phosphate Metabolism	5287.1
PIK3n	phosphatidylinositol 3-kinase, nuclear	[n] : atp + pail_hs --> adp + h + pail3p_hs	2.7.1.137	Inositol Phosphate Metabolism	
PIK4	phosphatidylinositol 4-kinase	[c] : atp + pail_hs --> adp + h + pail4p_hs	2.7.1.67	Glycerophospholipid Metabolism	(5298.1 or 5297.1 or 55361.1)
PIK4n	phosphatidylinositol 4-kinase, nuclear	[n] : atp + pail_hs --> adp + h + pail4p_hs	2.7.1.67	Inositol Phosphate Metabolism	
PIK5	phosphatidylinositol 5-kinase	[c] : atp + pail_hs --> adp + h + pail5p_hs		Inositol Phosphate Metabolism	(8394.1 or 8395.1 or 23396.1)
PIK5n	phosphatidylinositol 5-kinase, nuclear	[n] : atp + pail_hs --> adp + h + pail5p_hs		Inositol Phosphate Metabolism	

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
PIPLC	phosphatidylinositol phospholipase C	[c] : h2o + pail_hs --> dag_hs + h + mi1p-D	3.1.4.3	Inositol Phosphate Metabolism	(89869.1 or 113026.1 or 257068.1 or 5333.1 or 51196.1 or 5336.1 or 5332.1 or 5332.2 or 23236.1 or 23236.2 or 5331.1 or 5335.1 or 5335.2 or 5334.1 or 84812.1 or 5330.1 or 9651.1 or 23007.1)
PIPLCn	phosphatidylinositol phospholipase C, nucleus	[n] : h2o + pail_hs --> dag_hs + h + mi1p-D	3.1.4.3	Inositol Phosphate Metabolism	(23236.2 or 23236.1)
PIt2m	phosphate transporter, mitochondrial	h[c] + pi[c] <==> h[m] + pi[m]		Transport, Mitochondrial	(5250.1 or 5250.2 or 5250.3 or 5250.4)
PIt7	phosphate transport in/out via three Na+ symporter	(3) na1[e] + pi[e] <==> (3) na1[c] + pi[c]		Transport, Extracellular	(6569.1 or 10568.1)
PIt7ir	phosphate transport in/out via three Na+ symporter (irreversible)	(3) na1[e] + pi[e] --> (3) na1[c] + pi[c]		Transport, Extracellular	(10786.1 or 6568.1 or 10246.1 or 10050.1)
PIt8	phosphate transport in/out via Na+ symporter	(1.5) na1[e] + pi[e] <==> (1.5) na1[c] + pi[c]		Transport, Extracellular	(6574.1 or 6575.1)
PIt9	phosphate transport in/out via two Na+ symporter	(2) na1[e] + pi[e] <==> (2) na1[c] + pi[c]		Transport, Extracellular	142680.1
PIter	phosphate transport, endoplasmic reticulum	pi[r] <==> pi[c]		Transport, Endoplasmic Reticular	2544.1
PItg	phosphate transport, Golgi apparatus	pi[g] --> pi[c]		Transport, Golgi Apparatus	
PItn	phosphate transport, nuclear	pi[n] <==> pi[c]		Transport, Nuclear	
PItx	Phosphate transporter, peroxisome	pi[c] <==> pi[x]		Transport, Peroxisomal	
PLA2	phospholipase A2	[c] : ak2gchol_hs + h2o --> Rtotal2 + ak2lgchol_hs + h		Glycerophospholipid Metabolism	
PLA2_2	phospholipase A2	[c] : h2o + pchol_hs --> Rtotal2 + h + lpchol_hs	3.1.1.4	Glycerophospholipid Metabolism	(8398.1 or 8398.2 or 5320.1)
PLA2_2e	phospholipase A2	[e] : h2o + pchol_hs --> Rtotal2 + h + lpchol_hs	3.1.1.4	Glycerophospholipid Metabolism	(64600.1 or 8399.1 or 26279.1 or 5319.1 or 81579.1 or 30814.1 or 5320.1 or 5322.1)
PLYSPSer	protein lysine peptidase (endoplasmic reticulum)	[r] : Ntmelys + h2o --> pepslys + tmlys		Lysine Metabolism	(28972.1 and 23478.1 and 60559.1 and 90701.1 and 9789.1)
PMANM	phosphomannomutase	[c] : man1p <==> man6p	5.4.2.8	Fructose and Mannose Metabolism	(5372.1 or 5373.1 or 55276.1)
PMEVKx	phosphomevalonate kinase	[x] : 5pmev + atp --> 5dpmev + adp	2.7.4.2	Cholesterol Metabolism	10654.1
PMI12346PH	5-diphosphoinositol-1,2,3,4,6-pentakisphosphate diphosphohydrolase	[c] : h2o + ppmi12346p --> h + minohp + pi	3.6.1.52	Inositol Phosphate Metabolism	(117283.1 or 9807.1 or 9807.2)
PMI12346PHn	5-diphosphoinositol-1,2,3,4,6-pentakisphosphate diphosphohydrolase, nuclear	[n] : h2o + ppmi12346p --> h + minohp + pi	3.6.1.52	Inositol Phosphate Metabolism	(117283.1 or 9807.1 or 9807.2 or 51447.1 or 51447.2 or 51447.3 or 51447.4 or 51447.5 or 51447.6)
PMI1346PH	diphosphoinositol-1,3,4,6-tetrakisphosphate diphosphohydrolase	[c] : h2o + ppmi1346p --> h + mi13456p + pi		Inositol Phosphate Metabolism	(117283.1 or 9807.1 or 9807.2)
PMI1346PHn	diphosphoinositol-1,3,4,6-tetrakisphosphate diphosphohydrolase, nucleus	[n] : h2o + ppmi1346p --> h + mi13456p + pi		Inositol Phosphate Metabolism	(51447.2 or 51447.3 or 51447.4 or 51447.5 or 51447.6 or 117283.1 or 9807.1 or 9807.2 or 51447.1)
PMTCOAtx	fatty acid intracellular transport	pmtcoa[c] <==> pmtcoa[x]		Transport, Peroxisomal	
PNP	purine-nucleoside phosphorylase	[c] : pi + mam <==> h + ncam + r1p	2.4.2.1	NAD Metabolism	4860.1
PNTEH	Hydrolase Class (RXN R02973)	[c] : h2o + ptth --> cysam + pnto-R		CoA Catabolism	((55350.1 and 8875.1 and 8876.1) or (8876.1 and 8875.2 and 55350.1) or (8876.1 and 55350.2 and 8875.1) or (8875.2 and 55350.2 and 8876.1) or (8875.1 and 8876.1 and 55350.3) or (8875.2 and 55350.3 and 8876.1))
PNTK	pantothenate kinase	[c] : atp + pnto-R --> 4ppan + adp + h	2.7.1.33	CoA Biosynthesis	(80025.3 or 80025.1 or 80025.2 or 80025.4 or 55229.1 or 79646.1 or 53354.1 or 53354.2 or 53354.3)
PNTKm	pantothenate kinase (mitochondrial)	[m] : atp + pnto-R --> 4ppan + adp + h	2.7.1.33	CoA Biosynthesis	80025.5
PNTOt5	Pantothenate sodium symporter II	atp[c] + h2o[c] + (2) na1[e] + pnto-R[e] --> adp[c] + h[c] + (2) na1[c] + pi[c] + pnto-R[c]		Transport, Extracellular	8884.1
PPA	inorganic diphosphatase	[c] : h2o + ppi --> h + (2) pi	3.6.1.1	Oxidative Phosphorylation	5464.1
PPA2	inorganic triphosphatase	[c] : h2o + pppi --> h + pi + ppi	3.6.1.1	Others	
PPA2m	inorganic triphosphatase, mitochondrial	[m] : h2o + pppi --> h + pi + ppi	3.6.1.1	Others	
PPAer	inorganic diphosphatase, endoplasmic reticulum	[r] : h2o + ppi --> h + (2) pi	3.6.1.1	Miscellaneous	(2538.1 or 57818.1 or 92579.1)
PPAm	inorganic diphosphatase	[m] : h2o + ppi --> h + (2) pi	3.6.1.1	Oxidative Phosphorylation	(27068.1 or 27068.2 or 27068.3 or 27068.4)
PPAn	inorganic diphosphatase, nuclear	[n] : h2o + ppi --> h + (2) pi	3.6.1.1	Miscellaneous	
PPAP	phosphatidic acid phosphatase	[c] : h2o + pa_hs --> dag_hs + pi	3.1.3.4	Triacylglycerol Synthesis	(8611.1 or 8611.2 or 8613.1 or 8612.1)
PPAt	Propionate transport, diffusion	ppa[e] --> ppa[c]		Transport, Extracellular	
PPAtm	Propionate transport, diffusion	ppa[c] --> ppa[m]		Transport, Mitochondrial	
PPBNGS	porphobilinogen synthase	[c] : (2) 5aop --> h + (2) h2o + ppbng	4.2.1.24	Heme Biosynthesis	(210.1 or 210.2)
PPCDC	phosphopantothenoylcysteine decarboxylase	[c] : 4ppcys + h --> co2 + pan4p	4.1.1.36	CoA Biosynthesis	60490.1
PPCOACm	Propionyl-CoA carboxylase, mitochondrial	[m] : atp + hco3 + ppcoa --> adp + h + mmcoa-S + pi	6.4.1.3	Valine, Leucine, and Isoleucine Metabolism	(5095.1 and 5096.1)

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
PPCOAOm	Propanoyl-CoA:FAD 2,3-oxidoreductase, mitochondrial	[m] : fad + ppcoa --> fadh2 + prpncoa	1.3.99.3	Propanoate Metabolism	(36.1 or 34.1 or 35.1 or 27034.1 or 28976.1 or 80724.1 or 84129.1)
PPD2CSPp	PPD2CSPp	[x] : 6a2ohxnt --> 1pipdn2c + h2o		Lysine Metabolism	
PPDOx	Propane-1,2-diol:NAD+ 1-oxidoreductase	[c] : h + lald-D + nadh --> 12ppd-R + nad	1.1.1.21	Pyruvate Metabolism	8574.1
PPDOy	Propane-1,2-diol:NADP+ 1-oxidoreductase	[c] : h + lald-D + nadph --> 12ppd-R + nadp	1.1.1.21	Pyruvate Metabolism	(231.1 or 10327.1 or 10327.2 or 8574.1)
PPItr	Diphosphate transporter, endoplasmic reticulum	ppi[c] <==> ppi[r]		Transport, Endoplasmic Reticular	
PPItx	Diphosphate transporter, peroxisome	ppi[c] <==> ppi[x]		Transport, Peroxisomal	
PPM	phosphopentomutase	[c] : r1p <==> r5p	5.4.2.7	Pentose Phosphate Pathway	5236.1
PPMI12346Ptn	5-diphosphatidylinositol pentakisphosphate nuclear transport (diffusion)	ppmi12346p[c] <==> ppmi12346p[n]		Transport, Nuclear	
PPMI1346Ptn	diphosphatidylinositol tetrakisphosphate nuclear transport (diffusion)	ppmi1346p[c] <==> ppmi1346p[n]		Transport, Nuclear	
PPNCL3	phosphopantothenate-cysteine ligase	[c] : 4ppan + atp + cys-L --> 4ppcys + amp + h + ppi	6.3.2.5	CoA Biosynthesis	79717.1
PPOR	Phenylpyruvate:oxygen oxidoreductase (hydroxylating,decarboxylating)	[c] : o2 + phpyr --> 2hyoxplac + co2	1.13.11.27	Phenylalanine metabolism	3242.1
PPPG9tm	protoporphyrinogen IX mitochondrial transport	pppg9[c] <==> pppg9[m]		Heme Biosynthesis	
PPPGOm	protoporphyrinogen oxidase, mitochondrial	[m] : (3) o2 + (2) pppg9 --> (6) h2o + (2) ppp9	1.3.3.4	Heme Biosynthesis	5498.1
PPPItn	Inorganic triphosphate transport through nuclear pore	pppi[c] <==> pppi[n]		Transport, Nuclear	
PRAGSr	phosphoribosylglycinamide synthase	[c] : atp + gly + pram <==> adp + gar + h + pi	6.3.4.13	IMP Biosynthesis	(2618.1 or 2618.2)
PRAIS	phosphoribosylaminoimidazole synthase	[c] : atp + fpram --> adp + air + (2) h + pi	6.3.3.1	IMP Biosynthesis	(2618.1 or 2618.2)
PRASCS	phosphoribosylaminoimidazolesuccinocarboxamide synthase	[c] : 5aizc + asp-L + atp <==> 25aics + adp + h + pi	6.3.2.6	IMP Biosynthesis	10606.1
PRDX	Peroxidase (multiple substrates)	[c] : h2o2 + meoh --> fald + (2) h2o	1.11.1.7	Miscellaneous	8288.1
PRDXl	Peroxidase (multiple substrates)	[l] : h2o2 + meoh --> fald + (2) h2o	1.11.1.7	Miscellaneous	4353.1
PRFGS	phosphoribosylformylglycinamidine synthase	[c] : atp + fgam + gln-L + h2o --> adp + fpram + glu-L + h + pi	6.3.5.3	IMP Biosynthesis	5198.1
PRGNLONESULT	steroid sulfotransferase	[c] : paps + prgnlone --> h + pap + prgnlones	2.8.2.2	Steroid Metabolism	(6822.1 or 6820.2)
PRGNLONEtm	pregnenolone intracellular transport	prgnlone[c] <==> prgnlone[m]		Transport, Mitochondrial	
PRGNLONEtr	pregnenolone intracellular transport	prgnlone[c] <==> prgnlone[r]		Transport, Endoplasmic Reticular	
PRISTANALtx	pristanal peroxisomal transport	pristanal[x] <==> pristanal[c]		Transport, Peroxisomal	
PRISTCOAtx	pristcoa peroxisomal transport	pristcoa[x] <==> pristcoa[c]		Transport, Peroxisomal	
PRISTtx	prist peroxisomal transport	prist[x] <==> prist[c]		Transport, Peroxisomal	
PRO1x	proline oxidase (L-proline, NAD)	[c] : nad + pro-L --> 1pyr5c + (2) h + nadh	1.5.1.2	Arginine and Proline Metabolism	58510.1
PRO1xm	proline oxidase (NAD), mitochondrial	[m] : nad + pro-L --> 1pyr5c + (2) h + nadh		Arginine and Proline Metabolism	5625.1
PROAKGOX1r	L-Proline,2-oxoglutarate:oxygen oxidoreductase (4-hydroxylating) (ER)	[r] : akg + o2 + pro-L --> 4hpro-LT + co2 + succ	1.14.11.2	Arginine and Proline Metabolism	((5033.1 and 5034.1) or (8974.1 and 5034.1))
PROD2	Proline dehydrogenase	[c] : fad + pro-L --> 1pyr5c + fadh2 + h	1.5.99.8	Arginine and Proline Metabolism	58510.1
PROD2m	Proline dehydrogenase (m)	[m] : fad + pro-L --> 1pyr5c + fadh2 + h	1.5.99.8	Arginine and Proline Metabolism	5625.1
PRODt2r	D-proline reversible transport via proton symport	h[e] + pro-D[e] <==> h[c] + pro-D[c]		Transport, Extracellular	206358.1
PRODt2rL	D-proline reversible transport via proton symport (lysosome)	h[l] + pro-D[l] <==> h[c] + pro-D[c]		Transport, Lysosomal	206358.1
PROSTGD2t	prostaglandin transport via bicarbonate countertransport	hco3[c] + prostgd2[e] <==> hco3[e] + prostgd2[c]		Transport, Extracellular	6578.1
PROSTGE1t	prostaglandin transport via bicarbonate countertransport	hco3[c] + prostge1[e] <==> hco3[e] + prostge1[c]		Transport, Extracellular	6578.1
PROSTGE1t3	prostaglandine E1 transport (ATP-dependent)	atp[c] + h2o[c] + prostge1[c] --> adp[c] + h[c] + pi[c] + prostge1[e]		Transport, Extracellular	10257.1
PROSTGE2t	prostaglandin transport via bicarbonate countertransport	hco3[c] + prostge2[e] <==> hco3[e] + prostge2[c]		Transport, Extracellular	(6578.1 or 6579.1 or 28232.1 or 28231.1)
PROSTGE2t2	prostaglandin uniport	prostge2[e] <==> prostge2[c]		Transport, Extracellular	(6582.2 or 6580.1 or 6582.1)
PROSTGE2t3	prostaglandine E2 transport (ATP-dependent)	atp[c] + h2o[c] + prostge2[c] --> adp[c] + h[c] + pi[c] + prostge2[e]		Transport, Extracellular	10257.1
PROSTGF2t	prostaglandin uniport	prostgf2[e] <==> prostgf2[c]		Transport, Extracellular	(6582.2 or 6580.1 or 6582.1)
PROt2r	L-proline reversible transport via proton symport	h[e] + pro-L[e] <==> h[c] + pro-L[c]		Transport, Extracellular	206358.1
PROt2rL	L-proline reversible transport via proton symport (lysosome)	h[l] + pro-L[l] <==> h[c] + pro-L[c]		Transport, Lysosomal	206358.1
PROt4	Na+/Proline-L symporter	na1[e] + pro-L[e] --> na1[c] + pro-L[c]		Transport, Extracellular	(55089.1 or 54407.1 or 81539.1)
PROt4(2)r	Proline transport (sodium symport) (2:1)	(2) na1[e] + pro-L[e] <==> (2) na1[c] + pro-L[c]		Transport, Extracellular	6534.1
PROtm	L-proline transport, mitochondrial	pro-L[c] <==> pro-L[m]		Transport, Mitochondrial	
PRPNCOAHYDm	Propenoyl-CoA hydrolase (m)	[m] : h2o + prpncoa --> 3hpcoa	4.2.1.17	beta-Alanine metabolism	(1892.1 or 549.1 or (3032.1 and 3030.1))
PRPNCOAHYDx	Propenoyl-CoA hydrolase (x)	[x] : h2o + prpncoa --> 3hpcoa	4.2.1.17	beta-Alanine metabolism	1962.1
PRPPS	phosphoribosylpyrophosphate synthetase	[c] : atp + r5p <==> amp + h + prpp	2.7.6.1	Pentose Phosphate Pathway	(5631.1 or 5634.1 or 221823.1 or 221823.2)
PS_HSter	phosphatidylserine scramblase	ps_hs[c] <==> ps_hs[r]		Transport, Endoplasmic Reticular	
PS_HStg	phosphatidylserine scramblase	ps_hs[c] <==> ps_hs[g]		Transport, Golgi Apparatus	
PSDm_hs	Phosphatidylserine decarboxylase	[m] : h + ps_hs --> co2 + pe_hs	4.1.1.65	Glycerophospholipid Metabolism	23761.1
PSERT	phosphoserine transaminase	[c] : 3php + glu-L --> akg + pser-L	2.6.1.52	Glycine, Serine, and Threonine Metabolism	(29968.1 or 29968.2)
PSFLIP	phosphatidylserine flippase	atp[c] + h2o[c] + ps_hs[e] --> adp[c] + h[c] + pi[c] + ps_hs[c]		Transport, Extracellular	(10396.1 or 57194.1)
PSFLIPm	phosphatidylserine flippase	atp[c] + h2o[c] + ps_hs[c] --> adp[c] + h[c] + pi[c] + ps_hs[m]		Transport, Mitochondrial	(10396.1 or 57194.1)
PSP_L	phosphoserine phosphatase (L-serine)	[c] : h2o + pser-L --> pi + ser-L	3.1.3.3	Glycine, Serine, and Threonine Metabolism	(5723.1 or 8781.1)
PSSA1_hs	Phosphatidylserine synthase homo sapiens	[c] : pchol_hs + ser-L <==> chol + ps_hs	2.7.8.8	Glycerophospholipid Metabolism	9791.1
PSSA2_hs	Phosphatidylserine synthase homo sapiens	[c] : pe_hs + ser-L <==> etha + ps_hs	2.7.8.8	Glycerophospholipid Metabolism	81490.1
PTDCACRNCPT1	carnitine fatty-acyl transferase	[c] : crn + ptdcacoa --> coa + ptdcacrn	2.3.1.21	Carnitine shuttle	(1375.3 or 126129.1 or 1374.1 or 1375.4 or 1375.2 or 1375.1)
PTDCACRNCPT2	pentadecanoate transport into the mitochondria	[m] : coa + ptdcacrn --> crn + ptdcacoa		Carnitine shuttle	1376.1
PTDCACRNt	pentadecanoate transport into the mitochondria	ptdcacrn[c] --> ptdcacrn[m]		Carnitine shuttle	788.1
PTDCAt	fatty acid transport via diffusion	ptdca[e] <==> ptdca[c]		Transport, Extracellular	

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
PTE2x	peroxisomal acyl-CoA thioesterase	[x] : h2o + pmtcoa --> coa + h + hdca		Fatty Acid Metabolism	(10005.1 or 10005.2 or 10005.3 or 10965.1)
PTE3x	peroxisomal acyl-CoA thioesterase	[x] : h2o + pristcoa --> coa + h + prist		Fatty Acid Metabolism	10965.1
PTE4x	peroxisomal acyl-CoA thioesterase	[x] : h2o + phytcoa --> coa + h + phyt		Fatty Acid Metabolism	10965.1
PTE5x	peroxisomal acyl-CoA thioesterase	[x] : admcoa + h2o --> adm + coa + h		Fatty Acid Metabolism	10965.1
PTHPS	6-pyruvoyltetrahydropterin synthase	[c] : ahdt --> 6pthp + pppi	4.2.3.12	Tetrahydrobiopterin	5805.1
PTHPSn	6-pyruvoyltetrahydropterin synthase, nuclear	[n] : ahdt --> 6pthp + pppi	4.2.3.12	Tetrahydrobiopterin	5805.1
PTPAT	pantetheine-phosphate adenylyltransferase	[c] : atp + h + pan4p <==> dpcoa + ppi	2.7.7.3	CoA Biosynthesis	80347.1
PTRCAT1	Putrescine acetyltransferase	[c] : accoa + ptrc --> aprut + coa + h	2.3.1.57	Arginine and Proline Metabolism	(6303.1 or 112483.1)
PTRCOX1	Putrescine:oxygen oxidoreductase (deaminating)	[c] : h2o + o2 + ptrc --> 4abutn + h2o2 + nh4	1.4.3.6	Arginine and Proline Metabolism	(314.1 or 314.2 or 8639.1 or 26.1)
PUNP1	purine-nucleoside phosphorylase (Adenosine)	[c] : adn + pi <==> ade + r1p	2.4.2.1	Nucleotides	4860.1
PUNP2	purine-nucleoside phosphorylase (Deoxyadenosine)	[c] : dad-2 + pi <==> 2dr1p + ade	2.4.2.1	Purine Catabolism	4860.1
PUNP3	purine-nucleoside phosphorylase (Guanosine)	[c] : gsn + pi <==> gua + r1p	2.4.2.1	Purine Catabolism	4860.1
PUNP4	purine-nucleoside phosphorylase (Deoxyguanosine)	[c] : dgsn + pi <==> 2dr1p + gua	2.4.2.1	Purine Catabolism	4860.1
PUNP5	purine-nucleoside phosphorylase (Inosine)	[c] : ins + pi <==> hxan + r1p	2.4.2.1	Purine Catabolism	4860.1
PUNP6	purine-nucleoside phosphorylase (Deoxyinosine)	[c] : din + pi <==> 2dr1p + hxan	2.4.2.1	Purine Catabolism	4860.1
PUNP7	purine-nucleoside phosphorylase (Xanthosine)	[c] : pi + xtsn <==> r1p + xan	2.4.2.1	Nucleotides	4860.1
PVD3	Previtamin D3 formation	[c] : 7dhchsterol <==> pd3		Vitamin D	
PYAM5POr	pyridoxamine 5'-phosphate oxidase	[c] : h2o + o2 + pyam5p <==> h2o2 + nh4 + pydx5p	1.4.3.5	Vitamin B6 Metabolism	55163.1
PYAM5Ptm	Pyridoxamine 5'-phosphate transport via diffusion, mitochondrial	pyam5p[c] <==> pyam5p[m]		Transport, Mitochondrial	
PYDAMK	pyridoxamine kinase	[c] : atp + pydam --> adp + h + pyam5p	2.7.1.35	Vitamin B6 Metabolism	8566.1
PYDAMtr	pyridoxamine transport via diffusion	pydam[e] <==> pydam[c]		Transport, Extracellular	
PYDX5Ptm	Pyridoxal 5'-phosphate transport via diffusion, mitochondrial	pydx5p[c] <==> pydx5p[m]		Transport, Mitochondrial	
PYDXDH	pyridoxal dehydrogenase	[c] : h2o + o2 + pydx --> 4pyrdx + h2o2	1.2.3.1	Vitamin B6 Metabolism	316.1
PYDXK	pyridoxal kinase	[c] : atp + pydx --> adp + h + pydx5p	2.7.1.35	Vitamin B6 Metabolism	8566.1
PYDXNK	pyridoxine kinase	[c] : atp + pydxn --> adp + h + pdx5p	2.7.1.35	Vitamin B6 Metabolism	8566.1
PYDXNtr	pyridoxine transport via diffusion	pydxn[e] <==> pydxn[c]		Transport, Extracellular	
PYDXPP	Pyridoxal 5-phosphate phosphatase	[c] : h2o + pydx5p --> pi + pydx		Vitamin B6 Metabolism	57026.1
PYDXtr	pyridoxal transport via diffusion	pydx[e] <==> pydx[c]		Transport, Extracellular	
PYK	pyruvate kinase	[c] : adp + h + pep --> atp + pyr	2.7.1.40	Glycolysis/Gluconeogenesis	(5313.1 or 5313.2 or 5315.1 or 5315.2 or 5315.3 or 113452.1)
PYLALDOX	Perillyl aldehyde:NAD+ oxidoreductase	[c] : h2o + nad + pylald --> (2) h + nadh + peracd	1.2.1.3	Limonene and pinene degradation	(216.1 or 223.1 or 224.1 or 501.1 or 8854.1 or 8854.2 or 8854.3)
PYLALDOXm	Perillyl aldehyde:NAD+ oxidoreductase (m)	[m] : h2o + nad + pylald --> (2) h + nadh + peracd	1.2.1.3	Limonene and pinene degradation	(217.1 or 219.1 or 8659.1 or 8659.2)
PYNP2r	pyrimidine-nucleoside phosphorylase (uracil)	[c] : pi + uri <==> r1p + ura	2.4.2.2	Pyrimidine Catabolism	(7378.2 or 7378.1 or 151531.1)
PYRt2m	pyruvate mitochondrial transport via proton symport	h[c] + pyr[c] <==> h[m] + pyr[m]		Transport, Mitochondrial	6566.1
PYRt2p	pyruvate peroxisomal transport via proton symport	h[c] + pyr[c] <==> h[x] + pyr[x]		D-alanine metabolism	(6566.1 or 9194.1)
PYRt2r	pyruvate reversible transport via proton symport	h[e] + pyr[e] <==> h[c] + pyr[c]		Transport, Extracellular	(6566.1 or 9194.1 or 9123.1)
QUILSYN	Quinolinate Synthase (Eukaryotic)	[c] : cmusa --> h + h2o + quln		Tryptophan metabolism	
RADH	retinal dehydrogenase	[c] : h2o + nad + retinal <==> (2) h + nadh + retn		Vitamin A Metabolism	
RADH2	retinal dehydrogenase (NADPH)	[c] : h2o + nadp + retinal <==> (2) h + nadph + retn		Vitamin A Metabolism	
RADH3	retinal dehydrogenase	[c] : h2o + nad + retinal-cis-13 <==> 13-cis-retn + (2) h + nadh		Vitamin A Metabolism	
RADH4	retinal dehydrogenase (NADPH)	[c] : h2o + nadp + retinal-cis-13 <==> 13-cis-retn + (2) h + nadph		Vitamin A Metabolism	
RAHY	retinoic acid hydroxylation (P450)	[c] : h + nadph + o2 + retn --> h2o + hretn + nadp		Vitamin A Metabolism	
RAI1	retinal isomerase (11-cis)	[c] : retinal <==> retinal-11-cis	5.2.1.3	Vitamin A Metabolism	
RAI2	retinal isomerase (9-cis)	[c] : retinal <==> retinal-cis-9	5.2.1.3	Vitamin A Metabolism	
RAI3	13-cis-retinoic acid isomerase	[c] : retn <==> 13-cis-retn		Vitamin A Metabolism	(2944.1 or 2944.2)
RAI4	13-cis-4-oxo-retinoic acid isomerase	[c] : oretn <==> 13-cis-oretn		Vitamin A Metabolism	
RAtn	Retinoate transport, nuclear	retn[c] <==> retn[n]		Transport, Nuclear	
RAtn3	13-cis-retinoic acid transport, nuclear	13-cis-retn[c] <==> 13-cis-retn[n]		Transport, Nuclear	
RBFK	riboflavin kinase	[c] : atp + ribflv --> adp + fmn + h	2.7.1.26	Riboflavin Metabolism	55312.1
RBK	ribokinase	[c] : atp + rib-D --> adp + h + r5p	2.7.1.15	Pentose Phosphate Pathway	64080.1
RBK_D	D-ribulokinase	[c] : atp + rbl-D --> adp + h + ru5p-D	2.7.1.47	Pentose and Glucuronate Interconversions	
RBTt	ribitol transport via passive diffusion	rbt[c] --> rbt[e]		Transport, Extracellular	
RDH1	retinol dehydrogenase (all-trans)	[c] : nad + retinol <==> h + nadh + retinal	1.1.1.105	Vitamin A Metabolism	(8608.1 or 5959.1)
RDH1a	retinol dehydrogenase (all-trans,NADPH)	[c] : nadp + retinol <==> h + nadph + retinal	1.1.1.105	Vitamin A Metabolism	(145226.1 or 57665.1 or 51109.1 or 112724.1 or 50700.1 or 157506.1 or 195814.1)
RDH2	retinol dehydrogenase (9-cis,NADH)	[c] : nad + retinol-9-cis <==> h + nadh + retinal-cis-9	1.1.1.105	Vitamin A Metabolism	5959.1
RDH2a	retinol dehydrogenase (9-cis,NADPH)	[c] : nadp + retinol-9-cis <==> h + nadph + retinal-cis-9	1.1.1.105	Vitamin A Metabolism	(145226.1 or 57665.1 or 51109.1 or 112724.1 or 50700.1 or 195814.1)
RDH3	retinol dehydrogenase (11-cis,NADH)	[c] : nad + retinol-cis-11 <==> h + nadh + retinal-11-cis	1.1.1.105	Vitamin A Metabolism	5959.1
RDH3a	retinol dehydrogenase (11-cis,NADPH)	[c] : nadp + retinol-cis-11 <==> h + nadph + retinal-11-cis	1.1.1.105	Vitamin A Metabolism	(145226.1 or 57665.1 or 51109.1 or 112724.1 or 195814.1)
RDH4	retinol dehydrogenase (13-cis,NADH)	[c] : nad + retinol-cis-13 <==> h + nadh + retinal-cis-13	1.1.1.105	Vitamin A Metabolism	5959.1
RETFA	retinol acyltransferase	[c] : Rtotal2coa + retinol --> coa + retfa	2.3.1.76	Vitamin A Metabolism	
RETFAt	fatty acid retinol efflux	retfa[c] --> retfa[e]		Transport, Extracellular	

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
RETFAt1	fatty acid retinol efflux (9-cis)	9-cis-retfa[c] --> 9-cis-retfa[e]		Transport, Extracellular	
RETFAt2	fatty acid retinol efflux (11-cis)	11-cis-retfa[c] --> 11-cis-retfa[e]		Transport, Extracellular	
RETH	retinyl ester hydrolase	[c] : h2o + retfa --> Rtotal2 + h + retinol		Vitamin A Metabolism	8228.1
RETH1	retinyl ester hydrolase (9-cis)	[c] : 9-cis-retfa + h2o --> Rtotal2 + h + retinol-9-cis		Vitamin A Metabolism	
RETH1e	retinyl ester hydrolase (9-cis), extracellular	[e] : 9-cis-retfa + h2o --> Rtotal2 + h + retinol-9-cis		Vitamin A Metabolism	
RETH2	retinyl ester hydrolase (11-cis)	[c] : 11-cis-retfa + h2o --> Rtotal2 + h + retinol-cis-11		Vitamin A Metabolism	
RETH2e	retinyl ester hydrolase (11-cis), extracellular	[e] : 11-cis-retfa + h2o --> Rtotal2 + h + retinol-cis-11		Vitamin A Metabolism	
RETHe	retinyl ester hydrolase, extracellular	[e] : h2o + retfa --> Rtotal2 + h + retinol		Vitamin A Metabolism	
RETI1	retinol isomerase (11-cis)	[c] : retinol <==> retinol-cis-11	5.2.1.7	Vitamin A Metabolism	
RETI2	retinol isomerase (9-cis)	[c] : retinol <==> retinol-9-cis	5.2.1.7	Vitamin A Metabolism	
RETI3	retinol isomerase (13-cis)	[c] : retinol <==> retinol-cis-13	5.2.1.7	Vitamin A Metabolism	
RETNCOA	Retinoyl CoA formation	[c] : atp + coa + retn --> amp + ppi + retncoa		Vitamin A Metabolism	
RETNGLCt	retinoyl glucuronide efflux	retnglc[c] --> retnglc[e]		Transport, Extracellular	
RETNGLCt2	retinoyl glucuronide efflux (13-cis)	13-cis-retnglc[c] --> 13-cis-retnglc[e]		Transport, Endoplasmic Reticular	
RETNGLCt2r	retinoyl glucuronide efflux (13-cis) from ER	13-cis-retnglc[r] --> 13-cis-retnglc[c]		Transport, Endoplasmic Reticular	
RETNGLCtr	retinoyl glucuronide efflux from ER	retnglc[r] --> retnglc[c]		Transport, Endoplasmic Reticular	
RETNt	retinoic acid transport	retn[c] <==> retn[e]		Transport, Extracellular	
RETNtr	retinoic acid transport in ER	retn[c] --> retn[r]		Transport, Endoplasmic Reticular	
RETNtr2	retinoic acid transport in ER (13-cis)	13-cis-retn[c] --> 13-cis-retn[r]		Transport, Endoplasmic Reticular	
RETt	Retinol transport via faciliated diffusion	retinol[e] --> retinol[c]		Transport, Extracellular	
RIBFLVt3	riboflavin transport (ATP dependent)	atp[c] + h2o[c] + ribflv[e] --> adp[c] + h[c] + pi[c] + ribflv[c]		Transport, Extracellular	
RIBt	ribose transport via diffusion	rib-D[e] <==> rib-D[c]		Transport, Extracellular	
RIBt2	ribose transport in via proton symporter	h[e] + rib-D[e] --> h[c] + rib-D[c]		Transport, Extracellular	
RNDR1	ribonucleoside-diphosphate reductase (ADP)	[c] : adp + trdrd --> dadp + h2o + trdox	1.17.4.1	Nucleotides	(6240.1 and 6241.1)
RNDR2	ribonucleoside-diphosphate reductase (GDP)	[c] : gdp + trdrd --> dgdp + h2o + trdox	1.17.4.1	Nucleotides	(6240.1 and 6241.1)
RNDR3	ribonucleoside-diphosphate reductase (CDP)	[c] : cdp + trdrd --> dcdp + h2o + trdox	1.17.4.1	Nucleotides	(6240.1 and 6241.1)
RNDR4	ribonucleoside-diphosphate reductase (UDP)	[c] : trdrd + udp --> dudp + h2o + trdox	1.17.4.1	Nucleotides	(6240.1 and 6241.1)
RNMK	ribosylnicotinamide kinase	[c] : atp + rnam --> adp + h + nmn	2.7.1.22	NAD Metabolism	54981.1
RPE	ribulose 5-phosphate 3-epimerase	[c] : ru5p-D <==> xu5p-D	5.1.3.1	Pentose Phosphate Pathway	(6120.1 or 6120.2)
RPI	ribose-5-phosphate isomerase	[c] : r5p <==> ru5p-D	5.3.1.6	Pentose Phosphate Pathway	22934.1
RTOT_2	R total flux 2 position	[c] : R2coa_hs + R4coa_hs --> (2) Rtotal2coa		R Group Synthesis	
RTOT_3	R total flux 3 position	[c] : R1coa_hs + R2coa_hs --> (2) Rtotal3coa		R Group Synthesis	
RTOT1	R total flux	[c] : R1coa_hs --> Rtotalcoa		R Group Synthesis	
RTOT2	R total flux	[c] : R2coa_hs --> Rtotalcoa		R Group Synthesis	
RTOT3	R total flux	[c] : R3coa_hs --> Rtotalcoa		R Group Synthesis	
RTOT4	R total flux	[c] : R4coa_hs --> Rtotalcoa		R Group Synthesis	
RTOT5	R total flux	[c] : R5coa_hs --> Rtotalcoa		R Group Synthesis	
RTOT6	R total flux	[c] : R6coa_hs --> Rtotalcoa		R Group Synthesis	
RTOTAL2CRNCPT1	carnitine fatty-acyl transferase	[c] : Rtotal2coa + crn --> Rtotal2crn + coa	2.3.1.21	Carnitine shuttle	(1375.3 or 126129.1 or 1374.1 or 1375.4 or 1375.2 or 1375.1)
RTOTAL2CRNCPT2	R group transport into the mitochondria	[m] : Rtotal2crn + coa --> Rtotal2coa + crn		Carnitine shuttle	1376.1
RTOTAL2CRNt	R group transport into the mitochondria	Rtotal2crn[c] --> Rtotal2crn[m]		Carnitine shuttle	788.1
RTOTAL3CRNCPT1	carnitine fatty-acyl transferase	[c] : Rtotal3coa + crn --> Rtotal3crn + coa	2.3.1.21	Carnitine shuttle	(1375.1 or 126129.1 or 1374.1 or 1375.4 or 1375.2 or 1375.1)
RTOTAL3CRNCPT2	R group transport into the mitochondria	[m] : Rtotal3crn + coa --> Rtotal3coa + crn		Carnitine shuttle	1376.1
RTOTAL3CRNt	R group transport into the mitochondria	Rtotal3crn[c] --> Rtotal3crn[m]		Carnitine shuttle	788.1
RTOTALCRNCPT1	carnitine fatty-acyl transferase	[c] : Rtotalcoa + crn --> Rtotalcrn + coa	2.3.1.21	Carnitine shuttle	(1375.3 or 126129.1 or 1374.1 or 1375.4 or 1375.2 or 1375.1)
RTOTALCRNCPT2	R group transport into the mitochondria	[m] : Rtotalcrn + coa --> Rtotalcoa + crn		Carnitine shuttle	1376.1
RTOTALCRNt	R group transport into the mitochondria	Rtotalcrn[c] --> Rtotalcrn[m]		Carnitine shuttle	788.1
Rtotaltl	fatty acid intracellular transport	Rtotal[c] <==> Rtotal[l]		Transport, Lysosomal	
Rtotaltp	fatty acid intracellular transport	Rtotal[c] <==> Rtotal[x]		Transport, Peroxisomal	
S23T2g	beta-galactoside alpha-2,3-sialyltransferase (core 2)	[g] : cmpacna + core2 --> cmp + h + ksii_core2_pre1	2.4.99.4	Keratan sulfate biosynthesis	(6482.1 or 6482.2 or 6483.1 or 6484.1)
S23T3g	beta-galactoside alpha-2,3-sialyltransferase (complex N-glycan)	[g] : cmpacna + l2fn2m2masn --> cmp + h + ksi_pre1	2.4.99.6	Keratan sulfate biosynthesis	(6487.1 or 6487.10 or 6487.11 or 6487.2 or 6487.3 or 6487.4 or 6487.6 or 6487.5 or 6487.7 or 6487.8 or 6487.9)
S23T4g	beta-galactoside alpha-2,3-sialyltransferase	[g] : cmpacna + ksii_core4_pre1 --> cmp + h + ksii_core4_pre2	2.4.99.4	Keratan sulfate biosynthesis	(6482.1 or 6482.2 or 6483.1 or 6484.1)
S23Tg	beta-galactoside alpha-2,3-sialyltransferase (T antigen)	[g] : T_antigen + cmpacna --> cmp + h + sT_antigen	2.4.99.4	O-Glycan Biosynthesis	(6482.2 or 6482.1)
S26Tg	beta-galactoside alpha-2,6-sialyltransferase	[g] : (2) cmpacna + l2fn2m2masn --> (2) cmp + (2) h + s2l2fn2m2masn	2.4.99.1	N-Glycan Biosynthesis	(6480.1 or 6480.2 or 6480.3)
S2L2FN2M2MASNt	s2l2fn2m2masn transport, Golgi to extracellular	s2l2fn2m2masn[g] --> s2l2fn2m2masn[e]		Transport, Extracellular	
S2L2FN2M2MASNtly	s2l2fn2m2masn transport, extracellular to lysosome	s2l2fn2m2masn[e] --> s2l2fn2m2masn[l]		Transport, Lysosomal	
S2L2N2M2MASNtly	s2l2n2m2masn transport, extracellular to lysosome	s2l2n2m2masn[e] --> s2l2n2m2masn[l]		Transport, Lysosomal	
S2T1g	chondroitin 2-sulfotransferase, Golgi	[g] : cs_c,d,e_pre1 + paps --> cs_d_pre2 + h + pap		Chondroitin / heparan sulfate biosynthesis	10090.1
S2T2g	chondroitin 2-sulfotransferase, Golgi	[g] : cs_d_pre5 + paps --> cspg_d + h + pap		Chondroitin / heparan sulfate biosynthesis	10090.1
S2T3g	uronyl 2-sulfotransferase, Golgi	[g] : cs_b_pre5 + paps --> cspg_b + h + pap		Chondroitin / heparan sulfate biosynthesis	10090.1
S2T4g	uronyl 2-sulfotransferase, Golgi	[g] : hs_pre11 + (2) paps --> (2) h + hs_pre12 + (2) pap		Chondroitin / heparan sulfate biosynthesis	9653.1
S2TASE1ly	iduronate-2-sulfatase, lysosomal	[l] : h2o + hs_deg15 --> h + hs_deg16 + so4	3.1.6.13	Heparan sulfate degradation	(3423.1 or 3423.2)
S2TASE2ly	iduronate-2-sulfatase, lysosomal	[l] : h2o + hs_deg21 --> h + hs_deg22 + so4	3.1.6.13	Heparan sulfate degradation	(3423.1 or 3423.2)
S2TASE3ly	iduronate-2-sulfatase, lysosomal	[l] : cs_b_deg2 + h2o --> cs_b_deg3 + h + so4	3.1.6.13	Chondroitin sulfate degradation	(3423.2 or 3423.1)
S2TASE4ly	glucuronate-2-sulfatase, lysosomal	[l] : cs_d_deg2 + h2o --> cs_d_deg3 + h + so4	3.1.6.18	Chondroitin sulfate degradation	
S2TASE5ly	glucuronate-2-sulfatase, lysosomal	[l] : cs_d_deg6 + h2o --> cs_c_deg5 + h + so4	3.1.6.18	Chondroitin sulfate degradation	
S3T1g	heparin-glucosamine 3-O-sulfotransferase	[g] : hs_pre13 + paps --> h + hs_pre14 + pap	2.8.2.23	Chondroitin / heparan sulfate biosynthesis	(9957.1 or 222537.1 or 9951.1)
S3T2g	heparin-glucosamine 3-O-sulfotransferase	[g] : hs_pre14 + paps --> h + hs_pre15 + pap	2.8.2.23	Chondroitin / heparan sulfate biosynthesis	(9956.1 or 222537.1 or 9951.1)
S3T3g	heparin-glucosamine 3-O-sulfotransferase	[g] : hs_pre15 + paps --> h + hspg + pap	2.8.2.23	Chondroitin / heparan sulfate biosynthesis	(9955.1 or 9954.1 or 9953.1 or 9952.1 or 64711.1 or 9951.1)

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
S3TASE1ly	N-acetylglucosamine-3-sulfatase, lysosomal	[l] : h2o + hs_deg10 <==> h + hs_deg11 + so4	3.1.6.15	Heparan sulfate degradation	
S3TASE2ly	N-acetylglucosamine-3-sulfatase, lysosomal	[l] : h2o + hs_deg17 <==> h + hs_deg18 + so4	3.1.6.15	Heparan sulfate degradation	
S3TASE3ly	N-acetylglucosamine-3-sulfatase, lysosomal	[l] : h2o + hs_deg23 <==> h + hs_deg24 + so4	3.1.6.15	Heparan sulfate degradation	
S4T1g	chondroitin 4-sulfotransferase, Golgi apparatus	[g] : cs_pre + (2) paps --> cs_a,b,e_pre1 + (2) h + (2) pap	2.8.2.5	Chondroitin / heparan sulfate biosynthesis	(166012.1 or 113189.1 or 50515.1 or 55501.1)
S4T2g	chondroitin 4-sulfotransferase, Golgi apparatus	[g] : cs_a,b_pre3 + paps --> cspg_a + h + pap	2.8.2.5	Chondroitin / heparan sulfate biosynthesis	(166012.1 or 113189.1 or 50515.1 or 55501.1)
S4T3g	chondroitin 4-sulfotransferase, Golgi apparatus	[g] : cs_e_pre4 + paps --> cs_e_pre5a + h + pap	2.8.2.5	Chondroitin / heparan sulfate biosynthesis	(166012.1 or 113189.1 or 50515.1 or 55501.1)
S4T4g	chondroitin 4-sulfotransferase, Golgi apparatus	[g] : cs_c,d,e_pre1 + (2) paps --> cs_e_pre2 + (2) h + (2) pap	2.8.2.5	Chondroitin / heparan sulfate biosynthesis	
S4T5g	chondroitin 4-sulfotransferase, Golgi apparatus	[g] : cs_e_pre5b + paps --> cspg_e + h + pap	2.8.2.5	Chondroitin / heparan sulfate biosynthesis	
S4T6g	chondroitin 4-sulfotransferase, Golgi apparatus	[g] : cs_b_pre4 + paps --> cs_b_pre5 + h + pap	2.8.2.5	Chondroitin / heparan sulfate biosynthesis	(113189.1 or 55501.1 or 50515.1 or 166012.1)
S4TASE1ly	N-acetylgalactosamine-4-sulfatase, lysosomal	[l] : cs_a + h2o <==> cs_a_deg1 + h + so4	3.1.6.12	Chondroitin sulfate degradation	(411.1 or 411.2)
S4TASE2ly	N-acetylgalactosamine-4-sulfatase, lysosomal	[l] : cs_a_deg3 + h2o <==> cs_a_deg4 + h + so4	3.1.6.12	Chondroitin sulfate degradation	(411.2 or 411.1)
S4TASE3ly	N-acetylgalactosamine-4-sulfatase, lysosomal	[l] : cs_b + h2o <==> cs_b_deg1 + h + so4	3.1.6.12	Chondroitin sulfate degradation	(411.1 or 411.2)
S4TASE4ly	N-acetylgalactosamine-4-sulfatase, lysosomal	[l] : cs_e + h2o <==> cs_e_deg1 + h + so4	3.1.6.12	Chondroitin sulfate degradation	(411.1 or 411.2)
S4TASE5ly	N-acetylgalactosamine-4-sulfatase, lysosomal	[l] : cs_e_deg4 + h2o <==> cs_e_deg5 + h + so4	3.1.6.12	Chondroitin sulfate degradation	(411.1 or 411.2)
S6T10g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	[g] : ksi_pre22 + paps --> h + ksi_pre23 + pap		Keratan sulfate biosynthesis	(9435.1 or 10164.1 or 23563.1 or 23563.2 or 4166.1)
S6T11g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	[g] : ksi_pre25 + paps --> h + ksi_pre26 + pap		Keratan sulfate biosynthesis	(9435.1 or 10164.1 or 23563.1 or 23563.2 or 4166.1)
S6T12g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	[g] : ksi_pre28 + paps --> h + ksi_pre29 + pap		Keratan sulfate biosynthesis	(9435.1 or 4166.1 or 10164.1 or 23563.1 or 23563.2)
S6T13g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	[g] : ksi_pre31 + paps --> h + ksi_pre32 + pap		Keratan sulfate biosynthesis	(10164.1 or 23563.1 or 23563.2 or 4166.1 or 9435.1)
S6T14g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	[g] : ksi_pre34 + paps --> h + ksi_pre35 + pap		Keratan sulfate biosynthesis	(9435.1 or 10164.1 or 23563.1 or 23563.2 or 4166.1)
S6T15g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	[g] : ksi_pre36 + paps --> h + ksi + pap		Keratan sulfate biosynthesis	(8534.1 or 9469.1)
S6T16g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	[g] : ksii_core4_pre5 + paps --> h + ksii_core4_pre6 + pap		Keratan sulfate biosynthesis	(9435.1 or 10164.1 or 23563.1 or 23563.2 or 4166.1)
S6T17g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	[g] : ksii_core4_pre8 + paps --> h + ksii_core4_pre9 + pap		Keratan sulfate biosynthesis	(9435.1 or 10164.1 or 23563.1 or 23563.2 or 4166.1)
S6T18g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	[g] : ksii_core4_pre10 + paps --> h + ksii_core4 + pap		Keratan sulfate biosynthesis	(8534.1 or 9469.1)
S6T19g	chondroitin 6-sulfotransferase, Golgi apparatus	[g] : cs_pre + (2) paps --> cs_c,d,e_pre1 + (2) h + (2) pap	2.8.2.17	Chondroitin / heparan sulfate biosynthesis	(9469.1 or 56548.1)
S6T1g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	[g] : ksii_core2_pre5 + paps --> h + ksii_core2_pre6 + pap		Keratan sulfate biosynthesis	(9435.1 or 10164.1 or 23563.1 or 23563.2 or 4166.1)
S6T20g	chondroitin 6-sulfotransferase, Golgi apparatus	[g] : cs_c_pre3 + paps --> cspg_c + h + pap	2.8.2.17	Chondroitin / heparan sulfate biosynthesis	(9469.1 or 56548.1)
S6T21g	chondroitin 6-sulfotransferase, Golgi apparatus	[g] : cs_d_pre4 + paps --> cs_d_pre5 + h + pap	2.8.2.17	Chondroitin / heparan sulfate biosynthesis	(9469.1 or 56548.1)
S6T22g	chondroitin 6-sulfotransferase, Golgi apparatus	[g] : cs_a,b,e_pre1 + (2) paps --> cs_e_pre2 + (2) h + (2) pap	2.8.2.17	Chondroitin / heparan sulfate biosynthesis	56548.1
S6T23g	chondroitin 6-sulfotransferase, Golgi apparatus	[g] : cs_e_pre5a + paps --> cspg_e + h + pap	2.8.2.17	Chondroitin / heparan sulfate biosynthesis	56548.1
S6T24g	chondroitin 6-sulfotransferase, Golgi apparatus	[g] : cs_e_pre4 + paps --> cs_e_pre5b + h + pap	2.8.2.17	Chondroitin / heparan sulfate biosynthesis	(9469.1 or 56548.1)
S6T25g	heparan sulfate 6-sulfotransferase, Golgi apparatus	[g] : hs_pre12 + (3) paps --> (3) h + hs_pre13 + (3) pap		Chondroitin / heparan sulfate biosynthesis	(9394.1 or 90161.1 or 90161.2 or 266722.1)
S6T2g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	[g] : ksii_core2_pre8 + paps --> h + ksii_core2_pre9 + pap		Keratan sulfate biosynthesis	(9435.1 or 10164.1 or 23563.1 or 23563.2 or 4166.1)
S6T3g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	[g] : ksii_core2_pre10 + paps --> h + ksii_core2 + pap		Keratan sulfate biosynthesis	(8534.1 or 9469.1)
S6T4g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	[g] : ksi_pre4 + paps --> h + ksi_pre5 + pap		Keratan sulfate biosynthesis	(9435.1 or 10164.1 or 23563.1 or 23563.2 or 4166.1)
S6T5g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	[g] : ksi_pre7 + paps --> h + ksi_pre8 + pap		Keratan sulfate biosynthesis	(9435.1 or 10164.1 or 23563.1 or 23563.2 or 4166.1)
S6T6g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	[g] : ksi_pre10 + paps --> h + ksi_pre11 + pap		Keratan sulfate biosynthesis	(9435.1 or 10164.1 or 23563.1 or 23563.2 or 4166.1)
S6T7g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	[g] : ksi_pre13 + paps --> h + ksi_pre14 + pap		Keratan sulfate biosynthesis	(9435.1 or 10164.1 or 23563.1 or 23563.2 or 4166.1)
S6T8g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	[g] : ksi_pre16 + paps --> h + ksi_pre17 + pap		Keratan sulfate biosynthesis	(9435.1 or 10164.1 or 23563.1 or 23563.2 or 4166.1)
S6T9g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	[g] : ksi_pre19 + paps --> h + ksi_pre20 + pap		Keratan sulfate biosynthesis	(9435.1 or 10164.1 or 23563.1 or 23563.2 or 4166.1)
S6TASE10ly	galactose-6-sulfate sulfatase, lysosomal	[l] : h2o + ksi_deg4 <==> h + ksi_deg5 + so4	3.1.6.4	Keratan sulfate degradation	(2720.1 and 4758.1 and 2588.1 and 5476.1)
S6TASE11ly	N-acetylglucosamine-6-sulfatase, lysosomal	[l] : h2o + ksi_deg6 <==> h + ksi_deg7 + so4	3.1.6.14	Keratan sulfate degradation	2799.1
S6TASE12ly	N-acetylglucosamine-6-sulfatase, lysosomal	[l] : h2o + ksi_deg9 <==> h + ksi_deg10 + so4	3.1.6.14	Keratan sulfate degradation	2799.1
S6TASE13ly	N-acetylglucosamine-6-sulfatase, lysosomal	[l] : h2o + ksi_deg12 <==> h + ksi_deg13 + so4	3.1.6.14	Keratan sulfate degradation	2799.1
S6TASE14ly	N-acetylglucosamine-6-sulfatase, lysosomal	[l] : h2o + ksi_deg15 <==> h + ksi_deg16 + so4	3.1.6.14	Keratan sulfate degradation	2799.1

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
S6TASE15ly	N-acetylglucosamine-6-sulfatase, lysosomal	[l] : h2o + ksi_deg18 <==> h + ksi_deg19 + so4	3.1.6.14	Keratan sulfate degradation	2799.1
S6TASE16ly	N-acetylglucosamine-6-sulfatase, lysosomal	[l] : h2o + ksi_deg21 <==> h + ksi_deg22 + so4	3.1.6.14	Keratan sulfate degradation	2799.1
S6TASE17ly	N-acetylglucosamine-6-sulfatase, lysosomal	[l] : h2o + ksi_deg24 <==> h + ksi_deg25 + so4	3.1.6.14	Keratan sulfate degradation	2799.1
S6TASE18ly	N-acetylglucosamine-6-sulfatase, lysosomal	[l] : h2o + ksi_deg27 <==> h + ksi_deg28 + so4	3.1.6.14	Keratan sulfate degradation	2799.1
S6TASE19ly	N-acetylglucosamine-6-sulfatase, lysosomal	[l] : h2o + ksi_deg30 <==> h + ksi_deg31 + so4	3.1.6.14	Keratan sulfate degradation	2799.1
S6TASE1ly	N-acetylglucosamine-6-sulfatase, lysosomal	[l] : h2o + hs <==> h + hs_deg1 + so4	3.1.6.14	Heparan sulfate degradation	2799.1
S6TASE20ly	N-acetylglucosamine-6-sulfatase, lysosomal	[l] : h2o + ksi_deg33 <==> h + ksi_deg34 + so4	3.1.6.14	Keratan sulfate degradation	2799.1
S6TASE21ly	N-acetylglucosamine-6-sulfatase, lysosomal	[l] : h2o + ksi_deg36 <==> h + ksi_deg37 + so4	3.1.6.14	Keratan sulfate degradation	2799.1
S6TASE22ly	galactose-6-sulfate sulfatase, lysosomal	[l] : h2o + ksii_core2_deg1 <==> h + ksii_core2_deg2 + so4	3.1.6.4	Keratan sulfate degradation	(2720.1 and 2588.1 and 4758.1 and 5476.1)
S6TASE23ly	N-acetylglucosamine-6-sulfatase, lysosomal	[l] : h2o + ksii_core2_deg3 <==> h + ksii_core2_deg4 + so4	3.1.6.14	Keratan sulfate degradation	2799.1
S6TASE24ly	N-acetylglucosamine-6-sulfatase, lysosomal	[l] : h2o + ksii_core2_deg6 <==> h + ksii_core2_deg7 + so4	3.1.6.14	Keratan sulfate degradation	2799.1
S6TASE25ly	galactose-6-sulfate sulfatase, lysosomal	[l] : h2o + ksii_core4_deg1 <==> h + ksii_core4_deg2 + so4	3.1.6.4	Keratan sulfate degradation	(2720.1 and 2588.1 and 4758.1 and 5476.1)
S6TASE26ly	N-acetylglucosamine-6-sulfatase, lysosomal	[l] : h2o + ksii_core4_deg3 <==> h + ksii_core4_deg4 + so4	3.1.6.14	Keratan sulfate degradation	2799.1
S6TASE2ly	N-acetylglucosamine-6-sulfatase, lysosomal	[l] : h2o + hs_deg5 <==> h + hs_deg6 + so4	3.1.6.14	Heparan sulfate degradation	2799.1
S6TASE3ly	N-acetylglucosamine-6-sulfatase, lysosomal	[l] : h2o + hs_deg11 <==> h + hs_deg12 + so4	3.1.6.14	Heparan sulfate degradation	2799.1
S6TASE4ly	N-acetylgalactosamine-6-sulfatase, lysosomal	[l] : cs_c + h2o <==> cs_c_deg1 + h + so4	3.1.6.4	Chondroitin sulfate degradation	(2720.1 and 2588.1 and 4758.1 and 5476.1)
S6TASE5ly	N-acetylgalactosamine-6-sulfatase, lysosomal	[l] : cs_c_deg3 + h2o <==> cs_c_deg4 + h + so4	3.1.6.4	Chondroitin sulfate degradation	(4758.1 and 2588.1 and 2720.1 and 5476.1)
S6TASE6ly	N-acetylgalactosamine-6-sulfatase, lysosomal	[l] : cs_d + h2o <==> cs_d_deg1 + h + so4	3.1.6.4	Chondroitin sulfate degradation	(2588.1 and 4758.1 and 5476.1 and 2720.1)
S6TASE7ly	N-acetylgalactosamine-6-sulfatase, lysosomal	[l] : cs_d_deg4 + h2o <==> cs_d_deg5 + h + so4	3.1.6.4	Chondroitin sulfate degradation	(4758.1 and 2720.1 and 2588.1 and 5476.1)
S6TASE8ly	N-acetylgalactosamine-6-sulfatase, lysosomal	[l] : cs_e_deg1 + h2o <==> cs_e_deg2 + h + so4	3.1.6.4	Chondroitin sulfate degradation	(2720.1 and 4758.1 and 2588.1 and 5476.1)
S6TASE9ly	N-acetylgalactosamine-6-sulfatase, lysosomal	[l] : cs_e_deg5 + h2o <==> cs_e_deg6 + h + so4	3.1.6.4	Chondroitin sulfate degradation	(5476.1 and 2588.1 and 4758.1 and 2720.1)
SACCD3m	saccharopine dehydrogenase (NADP, L-lysine forming), mitochondrial	[m] : akg + h + lys-L + nadph --> h2o + nadp + saccrp-L	1.5.1.8	Lysine Metabolism	10157.1
SACCD4m	saccharopine dehydrogenase (NAD, L-glutamate forming), mitochondrial	[m] : h2o + nadp + saccrp-L --> L2aadp6sa + glu-L + h + nadph	1.5.1.10	Lysine Metabolism	10157.1
SADT	sulfate adenylyltransferase	[c] : atp + h + so4 --> aps + ppi	2.7.7.4	Nucleotides	(9060.1 or 9061.1)
SALMCOM	S-Adenosyl-L-methionine:catechol O-methyltransferase	[c] : amet + nrpphr --> ahcys + h + normete-L	2.1.1.6	Tyrosine metabolism	(1312.1 or 1312.2 or 118881.1)
SALMCOM2	S-Adenosyl-L-methionine:catechol O-methyltransferase	[c] : adml + amet --> ahcys + h + mepi	2.1.1.6	Tyrosine metabolism	118881.1
SAMHISTA	S-Adenosyl-L-methionine:histamine N-tele-methyltransferase	[c] : amet + hista --> ahcys + h + mhista	2.1.1.8	Histidine Metabolism	3176.1
SARCOXp	sarcosine oxidase, peroxisomal	[x] : h2o + o2 + sarcs --> fald + gly + h2o2	1.5.3.1	Glycine, Serine, and Threonine Metabolism	51268.1
SARCStex	Sarcosine transport (extracellular to cytosol)	sarcs[e] --> sarcs[c]		Transport, Extracellular	
SARCStm	Sarcosine transport (mitochondrial)	sarcs[c] --> sarcs[m]		Transport, Mitochondrial	
SARCStp	Sarcosine transport (peroxisomal)	sarcs[c] --> sarcs[x]		Transport, Peroxisomal	
SARDHm	Sarcosine dehydrogenase (m)	[m] : fad + sarcs + thf --> fadh2 + gly + mlthf	1.5.99.1	Urea cycle/amino group metabolism	1757.1
SBPP1er	sphingoid base-phosphate phosphatase (sphinganine 1-phosphatase), endoplasmic reticulum	[r] : h2o + sph1p --> pi + sphgn		Sphingolipid Metabolism	81537.1
SBPP3er	sphingoid base-phosphate phosphatase (sphinganine 1-phosphatase), endoplasmic reticulum	[r] : h2o + sphs1p --> pi + sphings		Sphingolipid Metabolism	81537.1
SBTD_D2	D-sorbitol dehydrogenase (D-fructose producing)	[c] : nad + sbt-D --> fru + h + nadh	1.1.1.14	Fructose and Mannose Metabolism	6652.1
SBTR	D-sorbitol reductase	[c] : glc-D + h + nadph --> nadp + sbt-D	1.1.1.21	Fructose and Mannose Metabolism	(231.1 or 10327.1 or 10327.2 or 8574.1)
SCP21x	Sterol carrier protein 2	phytcoa[c] <==> phytcoa[x]		Transport, Peroxisomal	6342.1
SCP22x	Sterol carrier protein 2	dmnoncoa[c] <==> dmnoncoa[x]		Transport, Peroxisomal	6342.1
SCP2x	peroxisomal thiolase 2	[x] : coa + dhocholoylcoa --> dgcholcoa + ppcoa		Bile Acid Biosynthesis	6342.1
SCP3x	peroxisomal thiolase 2	[x] : coa + dhcholestancoa + o2 --> dcholcoa + h2o + ppcoa		Bile Acid Biosynthesis	6342.1
SCPx	peroxisomal thiolase 2	[x] : cholcoaone + coa --> cholcoa + ppcoa		Bile Acid Biosynthesis	6342.1
SEAHCYSHYD	Se-Adenosylselenohomocysteine hydrolase	[c] : h2o + seahcys --> adn + selhcys	3.3.1.1	Selenoamino acid metabolism	(191.1 or 10768.2 or 10768.1 or 23382.1)
SEAHCYStn	Se-adenosyl-seleno-L-homocysteine nuclear transport	seahcys[c] <==> seahcys[n]		Selenoamino acid metabolism	
SEASMETtn	Se-adenosyl-seleno-L-methionine nuclear transport	seasmet[c] <==> seasmet[n]		Selenoamino acid metabolism	
SELADT	selenate adenylyltransferase	[c] : atp + h + sel --> adsel + ppi	2.7.7.4	Selenoamino acid metabolism	(9061.1 or 9060.1)
SELCYSLY	selenocysteine lyase	[c] : dtt + selcys --> ala-L + dttOX + h + seln	4.4.1.16	Selenoamino acid metabolism	51540.1
SELCYSLY2	selenocysteine lyase	[c] : pdx5p + selcys --> ala-L + h + pydx5p + seln		Selenoamino acid metabolism	51540.1
SELCYSTGL	selanocystathionine g-lyase	[c] : h2o + selcyst --> 2obut + nh4 + selcys	4.4.1.1	Selenoamino acid metabolism	(1491.1 or 1491.2)
SELCYSTS	selanocystathionine beta-synthase	[c] : selhcys + ser-L --> h2o + selcyst	4.2.1.22	Selenoamino acid metabolism	875.1
SELMETAT	selenomethionine adenosyltransferase	[c] : atp + h2o + selmeth --> pi + ppi + seasmet	2.5.1.6	Selenoamino acid metabolism	(4143.1 or (27430.1 and 4144.1) or (27430.2 and 4144.1))
SELNPS	Selenophosphate synthase	[c] : atp + h2o + seln --> amp + pi + selnp	2.7.9.3	Selenoamino acid metabolism	(22929.1 or 22928.1)
SELt4_3	selenate transport via sodium symport	(3) na1[e] + sel[e] <==> (3) na1[c] + sel[c]		Transport, Extracellular	6561.1
SERALANaEx	L-alanine/L-serine Na-dependent exchange (Ser-L in)	ala-L[c] + na1[e] + ser-L[e] --> ala-L[e] + na1[c] + ser-L[c]		Transport, Extracellular	(6509.1 or 6510.1)
SERASNNaEx	L-serine/L-asparagine Na-dependent exchange (Ser-L in)	asn-L[c] + na1[e] + ser-L[e] --> asn-L[e] + na1[c] + ser-L[c]		Transport, Extracellular	6510.1
SERCYSNaEx	L-serine/L-cysteine Na-dependent exchange (Ser-L in)	cys-L[c] + na1[e] + ser-L[e] --> cys-L[e] + na1[c] + ser-L[c]		Transport, Extracellular	(6509.1 or 6510.1)
SERDGLNexR	D-Serine/Glutamine reversible exchange	gln-L[c] + ser-D[e] <==> gln-L[e] + ser-D[c]		Transport, Extracellular	(6520.1 and 56301.1)

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
SERDGLYexR	D-Serine/Glycine reversible exchange	gly[c] + ser-D[e] <==> gly[e] + ser-D[c]		Transport, Extracellular	(6520.1 and 56301.1)
SERGLNexR	L-Serine/Glutamine reversible exchange	gln-L[c] + ser-L[e] <==> gln-L[e] + ser-L[c]		Transport, Extracellular	(6520.1 and 56301.1)
SERGLNNaEx	L-serine/L-glutamine Na-dependent exchange (Ser-L in)	gln-L[c] + na1[e] + ser-L[e] --> gln-L[e] + na1[c] + ser-L[c]		Transport, Extracellular	6510.1
SERGLYexR	L-Serine/Glycine reversible exchange	gly[c] + ser-L[e] <==> gly[e] + ser-L[c]		Transport, Extracellular	(6520.1 and 56301.1)
SERHL	L-Serine hydro-lyase	[c] : ser-L --> 2amac + h2o		Glycine, Serine, and Threonine Metabolism	10993.1
SERLYSNaex	Serine/Lysine Na-dependent exchange (Ser in)	lys-L[c] + na1[e] + ser-L[e] --> lys-L[e] + na1[c] + ser-L[c]		Transport, Extracellular	(9056.1 and 6519.1)
SERPT	serine C-palmitoyltransferase	[c] : h + pmtcoa + ser-L --> 3dsphgn + co2 + coa	2.3.1.50	Sphingolipid Metabolism	(9517.1 and 10558.1)
SERt4	L-serine via sodium symport	na1[e] + ser-L[e] --> na1[c] + ser-L[c]		Transport, Extracellular	(11254.1 or 55089.1 or 54407.1 or 81539.1)
SERTHRNaEx	L-serine/L-threonine Na-dependent exchange (Ser-L in)	na1[e] + ser-L[e] + thr-L[c] --> na1[c] + ser-L[c] + thr-L[e]		Transport, Extracellular	(6509.1 or 6510.1)
SERtN1	Serine transport (Na, H coupled)	h[c] + (2) na1[e] + ser-L[e] <==> h[e] + (2) na1[c] + ser-L[c]		Transport, Extracellular	92745.1
SERtp	L-serine transport, peroxisomal	ser-L[c] <==> ser-L[x]		Transport, Peroxisomal	
SFGTH	S-Formylglutathione hydralase	[c] : Sfglutth + h2o <==> for + gthrd + h	3.1.2.12	Tyrosine metabolism	2098.1
SGALSIDEtg	sgalside_hs intracellular transport	sgalside_hs[c] <==> sgalside_hs[g]		Transport, Golgi Apparatus	
SGALSIDEtl	sgalside_hs intracellular transport	sgalside_hs[c] <==> sgalside_hs[l]		Transport, Lysosomal	
SGPL11r	Sphingosine-1-phosphate lyase 1	[r] : sph1p --> ethamp + hxdcal	4.1.2.27	Sphingolipid Metabolism	8879.1
SGPL12r	Sphingosine-1-phosphate lyase	[r] : h2o + sphs1p --> ethamp + h + hdca	4.1.2.27	Sphingolipid Metabolism	8879.1
SIAASE	sialidase	[c] : (2) h2o + s2l2n2m2mn --> (2) acnam + l2n2m2mn	3.2.1.18	N-Glycan Degradation	(4759.1 or 129807.1)
SIAASE2ly	sialidase, lysosomal	[l] : h2o + ksi_deg3 --> acnam + ksi_deg4	3.2.1.18	Keratan sulfate degradation	(2720.1 and 2588.1 and 4758.1 and 5476.1)
SIAASE3ly	sialidase, lysosomal	[l] : h2o + ksii_core2 --> acnam + ksii_core2_deg1	3.2.1.18	Keratan sulfate degradation	(2720.1 and 2588.1 and 5476.1 and 4758.1)
SIAASE4ly	sialidase, lysosomal	[l] : h2o + ksii_core4 --> acnam + ksii_core4_deg1	3.2.1.18	Keratan sulfate degradation	(2720.1 and 2588.1 and 4758.1 and 5476.1)
SIAASEly	sialidase, lysosomal	[l] : (2) h2o + s2l2n2m2mn --> (2) acnam + l2n2m2mn	3.2.1.18	N-Glycan Degradation	(2588.1 and 2720.1 and 5476.1 and 4758.1)
SIAT4Bg	Beta-galactoside alpha-2,3-sialyltransferase, Golgi apparatus	[g] : cmpacna + galgbside_hs --> acngalgbside_hs + cmp + h		Sphingolipid Metabolism	6483.1
SIAT9g	Lactosylceramide alpha-2,3-sialyltransferase, Golgi apparatus	[g] : cmpacna + galgluside_hs --> cmp + gm3_hs + h	2.4.99.9	Sphingolipid Metabolism	8869.1
SLCBK1	sphingolipid long chain base kinase (sphinganine)	[c] : atp + sphgn --> adp + h + sph1p		Sphingolipid Metabolism	56848.1
SLDt	L-sulfolactate transport (cytosol to extracellular)	sl-L[c] --> sl-L[e]		Cysteine Metabolism	
SLDx	L-sulfolactate dehydrogenase (NAD+)	[c] : nad + sl-L <==> 3spyr + h + nadh	1.1.1.272	Cysteine Metabolism	(4190.1 or 130752.1)
SLDxm	L-sulfolactate dehydrogenase (NAD+), mitochondrial	[m] : nad + sl-L <==> 3spyr + h + nadh	1.1.1.272	Cysteine Metabolism	4191.1
SMPD3g	sphingomyelin phosphodiesterase 3, neutral membran (neutral sphingomyelinase II)	[g] : h2o + sphmyln_hs --> cholp + crm_hs + h		Sphingolipid Metabolism	(55512.1 or 55512.2)
SMPD3l	sphingomyelin phosphodiesterase 3, neutral membran (neutral sphingomyelinase II)	[l] : h2o + sphmyln_hs --> cholp + crm_hs + h		Sphingolipid Metabolism	(55512.1 or 55512.2)
SMPD4	sphingomyelinase	[c] : h2o + spc_hs --> cholp + h + sphings		Sphingolipid Metabolism	
SMS	Sphingomyelin synthase (homo sapiens)	[c] : crm_hs + pchol_hs --> dag_hs + sphmyln_hs		Sphingolipid Metabolism	259230.1
SO4CLtex2	sulfate transport via chloride countertransport (2:1)	cl[c] + (2) so4[e] --> cl[e] + (2) so4[c]		Transport, Extracellular	(65010.1 or 65010.2 or 65010.3)
SO4HCOtex	sulfate transport via bicarbonate countertransport	(2) hco3[c] + so4[e] --> (2) hco3[e] + so4[c]		Transport, Extracellular	(10861.1 or 10861.2 or 1836.1 or 10861.3 or 1811.1 or 115111.1 or 115111.2 or 116369.1 or 116369.2 or 115019.1 or 115019.2 or 284129.1)
SO4OXAtex2	sulfate transport via oxalate countertransport (2:1)	oxa[c] + (2) so4[e] --> oxa[e] + (2) so4[c]		Transport, Extracellular	(65010.1 or 65010.2 or 65010.3)
SO4t4_2	sulfate transport via sodium symport	(2) na1[e] + so4[e] <==> (2) na1[c] + so4[c]		Transport, Extracellular	26266.1
SO4t4_3	sulfate transport via sodium symport	(3) na1[e] + so4[e] <==> (3) na1[c] + so4[c]		Transport, Extracellular	6561.1
SOAT11	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1	[c] : R1coa_hs + chsterol --> coa + xolest_hs		Cholesterol Metabolism	6646.1
SOAT11r	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1	[r] : R1coa_hs + chsterol --> coa + xolest_hs		Cholesterol Metabolism	6646.1
SOAT12	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1	[c] : R2coa_hs + chsterol --> coa + xolest_hs		Cholesterol Metabolism	6646.1
SOAT12r	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1	[r] : R2coa_hs + chsterol --> coa + xolest_hs		Cholesterol Metabolism	6646.1
SPC_HSt	sphingosylphosphorylcholine transport (diffusion)	spc_hs[c] <==> spc_hs[e]		Transport, Extracellular	
SPH1Pte	sph1p transport	sph1p[c] <==> sph1p[e]		Transport, Extracellular	
SPH1Ptr	sph1p intracellular transport	sph1p[c] <==> sph1p[r]		Transport, Endoplasmic Reticular	
SPHGNtr	sphinganine intracellular transport	sphgn[r] <==> sphgn[c]		Transport, Endoplasmic Reticular	
SPHINGStl	sphingosine intracellular transport	sphings[c] <==> sphings[l]		Transport, Lysosomal	
SPHINGStr	sphingosine intracellular transport	sphings[c] <==> sphings[r]		Transport, Endoplasmic Reticular	
SPHK21c	sphingosine kinase 2	[c] : atp + sphings --> adp + h + sphs1p		Sphingolipid Metabolism	56848.1
SPHMDAc	sphingomyelin deacylase	[c] : h2o + sphmyln_hs --> Rtotal + spc_hs		Sphingolipid Metabolism	
SPHMYLNtg	sphingomyelin intracellular transport	sphmyln_hs[c] <==> sphmyln_hs[g]		Transport, Golgi Apparatus	
SPHMYLNtl	sphingomyelin intracellular transport	sphmyln_hs[c] <==> sphmyln_hs[l]		Transport, Lysosomal	
SPHS1Pte	sphingosine-1-phosphate transport	sphs1p[c] <==> sphs1p[e]		Transport, Extracellular	
SPHS1Ptr	sphingosine-1-phosphate transport	sphs1p[c] <==> sphs1p[r]		Transport, Endoplasmic Reticular	
SPMDOX	Spermidine:(acceptor) oxidoreductase	[c] : h2o + o2 + spmd --> 13dampp + 4abutn + h2o2	1.5.99.6	beta-Alanine metabolism	
SPMS	spermidine synthase	[c] : ametam + ptrc --> 5mta + h + spmd	2.5.1.16	Urea cycle/amino group metabolism	6723.1
SPODM	superoxide dismutase	[c] : (2) h + (2) o2s --> h2o2 + o2	1.15.1.1	ROS Detoxification	6647.1
SPODMe	superoxide dismutase, extracellular	[e] : (2) h + (2) o2s --> h2o2 + o2	1.15.1.1	ROS Detoxification	6649.1

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
SPODMm	superoxide dismutase	[m] : (2) h + (2) o2s --> h2o2 + o2	1.15.1.1	ROS Detoxification	6648.1
SPODMn	superoxide dismutase, nuclear	[n] : (2) h + (2) o2s --> h2o2 + o2	1.15.1.1	ROS Detoxification	6647.1
SPODMx	superoxide dismutase, peroxisome	[x] : (2) h + (2) o2s --> h2o2 + o2	1.15.1.1	ROS Detoxification	6647.1
SPR	sepiapterin reductase	[c] : 6pthp + (2) h + (2) nadph --> (2) nadp + thbpt	1.1.1.153	Tetrahydrobiopterin	6697.1
SPRMS	spermine synthase	[c] : ametam + spmd --> 5mta + h + sprm	2.5.1.22	Urea cycle/amino group metabolism	6611.1
SPRn	sepiapterin reductase, nuclear	[n] : 6pthp + (2) h + (2) nadph --> (2) nadp + thbpt	1.1.1.153	Tetrahydrobiopterin	6697.1
SPTix	serine-pyruvate aminotransferase (irreversible), peroxisomal	[x] : pyr + ser-L --> ala-L + hpyr		Glycine, Serine, and Threonine Metabolism	189.1
SQLEr	Squalene epoxidase, endoplasmic reticular (NADP)	[r] : h + nadph + o2 + sql --> Ssq23epx + h2o + nadp	1.14.99.7	Cholesterol Metabolism	6713.1
SQLSr	Squalene synthase	[r] : (2) frdp + h + nadph --> nadp + (2) ppi + sql	2.5.1.21	Cholesterol Metabolism	2222.1
SR5AR2r	3-oxo-5-alpha-steroid 4-dehydrogenase	[r] : andrstndn + h + nadph --> andrstandn + nadp	1.3.99.5	Steroid Metabolism	(6715.1 or 6716.1)
SR5ARr	3-oxo-5-alpha-steroid 4-dehydrogenase	[r] : h + nadph + tststerone --> 5adtststerone + nadp	1.3.99.5	Steroid Metabolism	(6716.1 or 6715.1)
SRTN23OX	5-Hydroxytryptamine:oxygen 2,3-dioxygenase (indole-decyclizing)	[c] : o2 + srtn --> f5hoxkyn	1.13.11.42	Tryptophan metabolism	3620.1
SRTNACT	Acetyl-CoA:aralkylamine N-acetyltransferase	[c] : accoa + srtn --> Nacsertn + coa + h	2.3.1.87	Tryptophan metabolism	15.1
SRTNMTX	S-Adenosyl-L-methionine:amine N-methyltransferase (srtn)	[c] : amet + srtn --> ahcys + h + nmthsrtn	2.1.1.49	Tryptophan metabolism	11185.1
SRTNt6(2)r	Seratonin reversible transport in via sodium symport/potassium antiport (1:2)	(2) k[c] + (2) na1[e] + srtn[e] <==> (2) k[e] + (2) na1[c] + srtn[c]		Transport, Extracellular	6532.1
SRTNtu	Serotonin uniport	srtn[e] <==> srtn[c]		Transport, Extracellular	(6580.1 or 6582.1 or 6582.2)
SSALxm	succinate-semialdehyde dehydrogenase (NAD) reversible (mitochondrial)	[m] : h2o + nad + sucsal --> (2) h + nadh + succ	1.2.1.16	Glutamate metabolism	(7915.1 or 7915.2)
ST3GAL21g	CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransferase, Golgi apparatus	[g] : cmpacna + ga1_hs --> cmp + gm1b_hs + h		Sphingolipid Metabolism	6483.1
ST3GAL22g	CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransferase, Golgi apparatus	[g] : cmpacna + gm1_hs --> cmp + gd1a_hs + h		Sphingolipid Metabolism	6483.1
ST3GAL23g	CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransferase, Golgi apparatus	[g] : cmpacna + gd1b_hs --> cmp + gt1b_hs + h		Sphingolipid Metabolism	6483.1
ST3GAL31g	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	[g] : cmpacna + galacglcgalgluside_hs --> acngalacglcgalgluside_hs + cmp + h	2.4.99.6	Blood Group Biosynthesis	(6487.4 or 6487.1 or 6487.5 or 6487.3 or 6487.2 or 6487.6 or 6487.7 or 6487.8 or 6487.9 or 6487.10 or 6487.11)
ST3GAL61g	Type 2 lactosamine alpha-2,3-sialyltransferase	[g] : cmpacna + gal14acglcgalgluside_hs --> acngal14acglcgalgluside_hs + cmp + h		Blood Group Biosynthesis	10402.1
ST3GAL62g	Type 2 lactosamine alpha-2,3-sialyltransferase	[g] : cmpacna + galacglcgal14acglcgalgluside_hs --> acngalacglcgal14acglcgalgluside_hs + cmp + h		Blood Group Biosynthesis	10402.1
ST6GALNAC21	Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	[g] : acngalgbside_hs + cmpacna --> acn13acngalgbside_hs + cmp + h		Sphingolipid Metabolism	10610.1
ST6GALNAC22	Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	[g] : acngalgbside_hs + cmpacna --> acn23acngalgbside_hs + cmp + h		Sphingolipid Metabolism	10610.1
ST6GALNAC23	Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	[g] : cmpacna + ga2_hs --> cmp + gm2a_hs + h		Sphingolipid Metabolism	10610.1
ST6GALNAC24	Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	[g] : cmpacna + gm1a_hs --> cmp + gd1b2_hs + h		Sphingolipid Metabolism	10610.1
ST6GALNAC25	Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	[g] : cmpacna + gd1alpha_hs --> cmp + gt1alpha_hs + h		Sphingolipid Metabolism	10610.1
ST6GALNAC26	Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	[g] : cmpacna + gt1alpha_hs --> cmp + gq1balpha_hs + h		Sphingolipid Metabolism	10610.1
ST6GALNAC27	Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	[g] : cmpacna + gt1c_hs --> cmp + gq1c_hs + h		Sphingolipid Metabolism	10610.1
ST6GALNAC28	Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	[g] : cmpacna + gq1c_hs --> cmp + gp1c_hs + h		Sphingolipid Metabolism	10610.1
ST6GALNAC31	Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 3	[g] : cmpacna + gm1b_hs --> cmp + gd1alpha_hs + h		Sphingolipid Metabolism	(256435.1 or 81849.1 or 30815.1)
ST6GALNAC61	sialytransferase 7 ((alpha-N-acetylneuraminyl 2,3-betagalactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialytransferase) F	[g] : cmpacna + gd1a_hs --> cmp + gt1alpha_hs + h		Sphingolipid Metabolism	30815.1
ST6GALNAC62	sialytransferase 7 ((alpha-N-acetylneuraminyl 2,3-betagalactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialytransferase) F	[g] : cmpacna + gt1b_hs --> cmp + gq1balpha_hs + h		Sphingolipid Metabolism	30815.1
ST8SIA11	Beta-galactoside alpha-2,3-sialyltransferase	[g] : acngalgbside_hs + cmpacna --> acnacngalgbside_hs + cmp + h	2.4.99.8	Sphingolipid Metabolism	6489.1
ST8SIA12	Beta-galactoside alpha-2,3-sialyltransferase	[g] : cmpacna + gm3_hs --> cmp + gd3_hs + h	2.4.99.8	Sphingolipid Metabolism	6489.1
ST8SIA51g	Beta-galactoside alpha-2,3-sialyltransferase	[g] : cmpacna + gd3_hs --> cmp + gt3_hs + h	2.4.99.8	Sphingolipid Metabolism	29906.1
ST8SIA52g	Beta-galactoside alpha-2,3-sialyltransferase	[g] : cmpacna + gt1b_hs --> cmp + gq1b_hs + h	2.4.99.8	Sphingolipid Metabolism	29906.1
ST8SIA53g	Beta-galactoside alpha-2,3-sialyltransferase	[g] : cmpacna + gd1a_hs --> cmp + gt1a_hs + h	2.4.99.8	Sphingolipid Metabolism	29906.1
ST8SIA54g	Beta-galactoside alpha-2,3-sialyltransferase	[g] : cmpacna + gm1b_hs --> cmp + gd1c_hs + h	2.4.99.8	Sphingolipid Metabolism	29906.1
ST8SIA55g	Beta-galactoside alpha-2,3-sialyltransferase	[g] : cmpacna + gq1c_hs --> cmp + gp1calpha_hs + h	2.4.99.8	Sphingolipid Metabolism	29906.1
ST8SIA56g	Alpha-2,8-sialyltransferase 8E	[g] : acngal14acglcgalgluside_hs + cmpacna --> acnacngal14acglcgalgluside_hs + cmp + h	2.4.99.8	Blood Group Biosynthesis	29906.1
STCOAtx	fatty acid intracellular transport	stcoa[c] <==> stcoa[x]		Transport, Peroxisomal	
STRDNCCPT1	carnitine O-palmitoyltransferase	[c] : crn + strdnccoa --> coa + strdnccrn	2.3.1.21	Carnitine shuttle	(1375.4 or 1374.1 or 126129.1 or 1375.3 or 1375.2 or 1375.1)
STRDNCCPT2	carnitine transferase	[m] : coa + strdnccrn --> crn + strdnccoa		Carnitine shuttle	1376.1
STRDNCCRNt	transport into the mitochondria (carnitine)	strdnccrn[c] --> strdnccrn[m]		Carnitine shuttle	788.1
STRDNCt	fatty acid transport via diffusion	strdnc[e] <==> strdnc[c]		Transport, Extracellular	
STS1	Steryl-sulfatase	[c] : dheas + h2o --> dhea + h + so4	3.1.6.2	Steroid Metabolism	412.1
STS1r	Steryl-sulfatase	[r] : dheas + h2o --> dhea + h + so4	3.1.6.2	Steroid Metabolism	412.1
STS2	Steryl-sulfatase	[c] : estrones + h2o --> estrone + h + so4	3.1.6.2	Steroid Metabolism	412.1
STS2r	Steryl-sulfatase	[r] : estrones + h2o --> estrone + h + so4	3.1.6.2	Steroid Metabolism	412.1
STS3	Steryl-sulfatase	[c] : chsterols + h2o --> chsterol + h + so4	3.1.6.2	Steroid Metabolism	412.1
STS3r	Steryl-sulfatase	[r] : chsterols + h2o --> chsterol + h + so4	3.1.6.2	Steroid Metabolism	412.1
STS4	Steryl-sulfatase	[c] : h2o + prgnlones --> h + prgnlone + so4	3.1.6.2	Steroid Metabolism	412.1
STS4r	Steryl-sulfatase	[r] : h2o + prgnlones --> h + prgnlone + so4	3.1.6.2	Steroid Metabolism	412.1
SUCCt2m	succinate transport, mitochondrial	pi[m] + succ[c] <==> pi[c] + succ[m]		Transport, Mitochondrial	1468.1
SUCCt4_2	succinate transport via sodium symport	(2) na1[e] + succ[e] <==> (2) na1[c] + succ[c]		Transport, Extracellular	9058.1
SUCCt4_3	succinate transport via sodium symport	(3) na1[e] + succ[e] <==> (3) na1[c] + succ[c]		Transport, Extracellular	(64849.1 or 64849.2)

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
SUCCtp	succinate transporter, peroxisome	succ[c] <==> succ[x]		Transport, Peroxisomal	
SUCD1m	succinate dehydrogenase	[m] : fad + succ <==> fadh2 + fum	1.3.99.1	Citric Acid Cycle	(6389.1 and 6391.1 and 6392.1 and 6390.1)
SUCOAS1m	Succinate--CoA ligase (GDP-forming)	[m] : coa + gtp + succ <==> gdp + pi + succoa	6.2.1.4	Citric Acid Cycle	(8802.1 and 8801.1)
SUCOASm	Succinate--CoA ligase (ADP-forming)	[m] : atp + coa + succ <==> adp + pi + succoa	6.2.1.5	Citric Acid Cycle	(8802.1 and 8803.1)
SUCRe	sucrose hydrolyzing enxyme, extracellular	[e] : h2o + sucr --> fru + glc-D	3.2.1.26	Galactose metabolism	(6476.1 or 8972.1)
SULFOX	sulfite oxidase	(2) ficytC[m] + h2o[c] + so3[c] --> (2) focytC[m] + (2) h[c] + so4[c]	1.8.3.1	Cysteine Metabolism	6821.1
T2M26DCOAHLm	trans-2-Methyl-5-isopropylhexa-2,5-dienoyl-CoA hydro-lyase (m)	[m] : h2o + t2m26dcoa <==> 3h26dm5coa	4.2.1.17	Limonene and pinene degradation	(549.1 or (3030.1 and 3032.1))
T2M26DCOAHLx	trans-2-Methyl-5-isopropylhexa-2,5-dienoyl-CoA hydro-lyase (x)	[x] : h2o + t2m26dcoa <==> 3h26dm5coa	4.2.1.17	Limonene and pinene degradation	(1891.1 or 1962.1)
T4HCINNMFM	4-hydroxycinnamate formation	[m] : 34hpl --> T4hcinnm + h2o		Ubiquinone Biosynthesis	
T4HCINNOX	4-Coumarate:oxygen oxidoreductase	[c] : (2) T4hcinnm + o2 --> (2) 34dhcinm	1.14.18.1	Stilbene, coumarine and lignin biosynthesis	7299.1
TAGAT-Dt	D-tagatose uptake via diffusion	tagat-D[e] --> tagat-D[c]		Transport, Extracellular	
TALA	transaldolase	[c] : g3p + s7p <==> e4p + f6p	2.2.1.2	Pentose Phosphate Pathway	6888.1
TAURt4(2)r	taurine transport (sodium symport) (2:1)	(2) na1[e] + taur[e] <==> (2) na1[c] + taur[c]		Transport, Extracellular	6533.1
TAURtcx	taurine transport (sodium symport) (cytosol to peroxisome)	na1[c] + taur[c] <==> na1[x] + taur[x]		Taurine and hypotaurine metabolism	6533.1
TAXOLte	xenobiotic transport	taxol[e] <==> taxol[c]		Transport, Extracellular	
TCHOLAt	taurocholate transport via bicarbonate countertranspo	hco3[c] + tchola[e] <==> hco3[e] + tchola[c]		Transport, Extracellular	(6579.1 or 10599.1 or 28234.1 or 28231.1)
TCHOLAt2	taurocholate transport via sodium cotransport	(2) na1[e] + tchola[e] --> (2) na1[c] + tchola[c]		Transport, Extracellular	(6554.1 or 6555.1)
TCHOLAt3	ABC bile acid transporter	atp[c] + h2o[c] + tchola[c] --> adp[c] + h[c] + pi[c] + tchola[e]		Transport, Extracellular	(8647.1 or 8714.1 or 8714.2 or 8714.3)
TCHOLAte	bile acid intracellular transport	tchola[e] <==> tchola[c]		Transport, Extracellular	
TCHOLAtx	bile acid intracellular transport	tchola[x] <==> tchola[c]		Transport, Peroxisomal	
TCYNTt	Thiocyanate transport via diffusion (cytosol to extracellular)	tcynt[c] --> tcynt[e]		Transport, Extracellular	
TCYNTtm	Thiocyanate transport via diffusion (mitochondrial)	tcynt[m] --> tcynt[c]		Transport, Mitochondrial	
TDCHOLAte	bile acid intracellular transport	tdchola[e] <==> tdchola[c]		Transport, Extracellular	
TDCHOLAtx	bile acid intracellular transport	tdchola[x] <==> tdchola[c]		Transport, Peroxisomal	
TDP	thiamine triphosphatase	[c] : h2o + thmpp --> h + pi + thmmp	3.6.1.15	Thiamine Metabolism	
TDPDRE	dTDP-4-dehydrorhamnose 3,5-epimerase	[c] : dtdp4d6dg --> dtdp4d6dm	5.1.3.13	Nucleotide Sugar Metabolism	
TDPDRR	dTDP-4-dehydrorhamnose reductase	[c] : dtdp4d6dm + h + nadph --> dtdprmn + nadp	1.1.1.133	Nucleotide Sugar Metabolism	
TDPGDH	dTDPglucose 4,6-dehydratase	[c] : dtdpglu --> dtdp4d6dg + h2o	4.2.1.46	Nucleotide Sugar Metabolism	23483.1
TDPm	thiamine triphosphatase, mitochondrial	[m] : h2o + thmpp --> h + pi + thmmp	3.6.1.15	Thiamine Metabolism	
TETHEX3COAtx	fatty acid intracellular transport	tethex3coa[c] <==> tethex3coa[x]		Transport, Peroxisomal	
TETHEX3t	fatty acid transport via diffusion	tethex3[e] <==> tethex3[c]		Transport, Extracellular	
TETPENT3COAtx	fatty acid intracellular transport	tetpent3coa[c] <==> tetpent3coa[x]		Transport, Peroxisomal	
TETPENT3CPT1	carnitine O-palmitoyltransferase	[c] : crn + tetpent3coa --> coa + tetpent3crn	2.3.1.21	Carnitine shuttle	(1375.4 or 1374.1 or 126129.1 or 1375.3 or 1375.2 or 1375.1)
TETPENT3CPT2	carnitine transferase	[m] : coa + tetpent3crn --> crn + tetpent3coa		Carnitine shuttle	1376.1
TETPENT3CRNt	transport into the mitochondria (carnitine)	tetpent3crn[c] --> tetpent3crn[m]		Carnitine shuttle	788.1
TETPENT3t	fatty acid transport via diffusion	tetpent3[e] <==> tetpent3[c]		Transport, Extracellular	
TETPENT6COAtx	fatty acid intracellular transport	tetpent6coa[c] <==> tetpent6coa[x]		Transport, Peroxisomal	
TETPENT6CPT1	carnitine O-palmitoyltransferase	[c] : crn + tetpent6coa --> coa + tetpent6crn	2.3.1.21	Carnitine shuttle	(1375.4 or 1374.1 or 126129.1 or 1375.3 or 1375.2 or 1375.1)
TETPENT6CPT2	carnitine transferase	[m] : coa + tetpent6crn --> crn + tetpent6coa		Carnitine shuttle	1376.1
TETPENT6CRNt	transport into the mitochondria (carnitine)	tetpent6crn[c] --> tetpent6crn[m]		Carnitine shuttle	788.1
TETPENT6t	fatty acid transport via diffusion	tetpent6[e] <==> tetpent6[c]		Transport, Extracellular	
TETTET6COAtx	fatty acid intracellular transport	tettet6coa[c] <==> tettet6coa[x]		Transport, Peroxisomal	
TETTET6CPT1	carnitine O-palmitoyltransferase	[c] : crn + tettet6coa --> coa + tettet6crn	2.3.1.21	Carnitine shuttle	(1375.4 or 1374.1 or 126129.1 or 1375.3 or 1375.2 or 1375.1)
TETTET6CPT2	carnitine transferase	[m] : coa + tettet6crn --> crn + tettet6coa		Carnitine shuttle	1376.1
TETTET6CRNt	transport into the mitochondria (carnitine)	tettet6crn[c] --> tettet6crn[m]		Carnitine shuttle	788.1
TETTET6t	fatty acid transport via diffusion	tettet6[e] <==> tettet6[c]		Transport, Extracellular	
THBPT4ACAMDASE	Tetrahydrobiopterin-4a-carbinolamine dehydratase	[c] : thbpt4acam --> dhbpt + h2o	4.2.1.96	Tetrahydrobiopterin	(5092.1 or 5092.2)
THCHOLSTOICtm	lipid, flip-flop intracellular transport	thcholstoic[m] <==> thcholstoic[x]		Transport, Peroxisomal	
THD1m	NAD(P) transhydrogenase	h[c] + nadh[m] + nadp[m] <==> h[m] + nad[m] + nadph[m]	1.6.1.1	NAD Metabolism	(23530.2 or 23530.1)
THFt2	tetrahydrofolate transport via anion exchange	oh1[c] + thf[e] <==> oh1[e] + thf[c]		Transport, Extracellular	(6573.1 or 6573.2)
THFtl	5,6,7,8-Tetrahydrofolate transport, diffusion, lysosomal	thf[c] <==> thf[l]		Transport, Lysosomal	
THFtm	5,6,7,8-Tetrahydrofolate transport, diffusion, mitochondrial	thf[c] <==> thf[m]		Transport, Mitochondrial	
THMDt4	thymidine transport in via sodium symport	na1[e] + thymd[e] --> na1[c] + thymd[c]		Transport, Extracellular	(9154.1 or 64078.1 or 9154.2)
THMDt5	thymidine transport (1:2 Na/Thymd cotransport)	(2) na1[e] + thymd[e] --> (2) na1[c] + thymd[c]		Transport, Extracellular	64078.1
THMMPt4	Thiamine monophosphate transport in via anion antiport	oh1[c] + thmmp[e] <==> oh1[e] + thmmp[c]		Transport, Extracellular	(6573.1 or 6573.2)
THMMPtm	Thiamine monophosphate transport, mitochondrial	oh1[m] + thmmp[c] <==> oh1[c] + thmmp[m]		Transport, Mitochondrial	
THMP	thiamin phosphatase	[c] : h2o + thmmp --> pi + thm		Thiamine Metabolism	
THMPPtm	Thiamine diphosphate transport in via anion antiport, mitochondria	(2) oh1[m] + thmpp[c] --> (2) oh1[c] + thmpp[m]		Transport, Mitochondrial	
THMt2m	Thiamine transport in via proton symport, mitochondrial	h[c] + thm[c] --> h[m] + thm[m]		Transport, Mitochondrial	
THMt3	Thiamine transport in via proton antiport	h[c] + thm[e] <==> h[e] + thm[c]		Transport, Extracellular	(80704.1 or 10560.1)
THMTP	thiamine-triphosphatase	[c] : h2o + thmtp --> h + pi + thmpp	3.6.1.28	Thiamine Metabolism	79178.1
THMTPt	Thiamine triphosphate transport in via anion antiport	(3) oh1[e] + thmtp[c] --> (3) oh1[c] + thmtp[e]		Transport, Extracellular	(6573.1 or 6573.2)
THP2Ctp	2,3,4,5-Tetrahydropyridine-2-carboxylate transport, peroxisomal	thp2c[c] <==> thp2c[x]		Transport, Peroxisomal	
THRALANaEx	L-alanine/L-threonine Na-dependent exchange (Thr-L in)	ala-L[c] + na1[e] + thr-L[e] --> ala-L[e] + na1[c] + thr-L[c]		Transport, Extracellular	(6509.1 or 6510.1)

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
THRASNNaEx	L-threonine/L-asparagine Na-dependent exchange (Thr-L in)	asn-L[c] + na1[e] + thr-L[e] --> asn-L[e] + na1[c] + thr-L[c]		Transport, Extracellular	6510.1
THRCYSNaEx	L-cysteine/L-threonine Na-dependent exchange (Thr-in)	cys-L[c] + na1[e] + thr-L[e] --> cys-L[e] + na1[c] + thr-L[c]		Transport, Extracellular	(6509.1 or 6510.1)
THRD_L	L-threonine deaminase	[c] : thr-L --> 2obut + nh4		Glycine, Serine, and Threonine Metabolism	10993.1
THRGLNexR	L-threonine/glycine reversible exchange	gln-L[c] + thr-L[e] <==> gln-L[e] + thr-L[c]		Transport, Extracellular	(6520.1 and 56301.1)
THRGLNNaEx	L-threonine/L-glutamine Na-dependent exchange (Thr-L in)	gln-L[c] + na1[e] + thr-L[e] --> gln-L[e] + na1[c] + thr-L[c]		Transport, Extracellular	6510.1
THRGLYexR	L-threonine/glycine reversible exchange	gly[c] + thr-L[e] <==> gly[e] + thr-L[c]		Transport, Extracellular	(6520.1 and 56301.1)
THRS	threonine synthase	[c] : h2o + phom --> pi + thr-L	4.2.3.1	Glycine, Serine, and Threonine Metabolism	79896.1
THRSERNaEx	L-serine/L-threonine Na-dependent exchange (Thr-L in)	na1[e] + ser-L[c] + thr-L[e] --> na1[c] + ser-L[e] + thr-L[c]		Transport, Extracellular	(6509.1 or 6510.1)
THRt4	L-threonine via sodium symport	na1[e] + thr-L[e] --> na1[c] + thr-L[c]		Transport, Extracellular	(11254.1 or 54407.1 or 81539.1)
THYMDt1	thymd transport	thymd[e] --> thymd[c]		Transport, Extracellular	(3177.1 or 2030.1)
THYMDtl	thymidine facilated transport from lysosome	thymd[l] <==> thymd[c]		Transport, Lysosomal	55315.1
THYMDtm	thymd transport	thymd[c] <==> thymd[m]		Transport, Mitochondrial	2030.1
THYMt	thymine reversible transport via facilated diffusion	thym[e] <==> thym[c]		Transport, Extracellular	3177.1
THYOXt	T4 transport via bicarbonate countertransport	hco3[c] + thyox-L[e] <==> hco3[e] + thyox-L[c]		Transport, Extracellular	(6579.1 or 10599.1 or 28231.1 or 53919.1)
THYOXt2	T4 transport via facilitated diffusion	thyox-L[e] <==> thyox-L[c]		Transport, Extracellular	6567.1
THYPX	thyroid peroxidase	[c] : (2) h + h2o2 + (2) i --> (2) h2o + iodine		Tyrosine metabolism	(7173.1 or 7173.2 or 7173.3 or 7173.4 or 7173.5)
TKT1	transketolase	[c] : r5p + xu5p-D <==> g3p + s7p	2.2.1.1	Pentose Phosphate Pathway	(7086.1 or 8277.1 or 84076.1)
TKT2	transketolase	[c] : e4p + xu5p-D <==> f6p + g3p	2.2.1.1	Pentose Phosphate Pathway	(7086.1 or 8277.1 or 84076.1)
TMABADH	4-trimethylaminobutyraldehyde dehydrogenase	[c] : 4tmeabut + h2o + nad --> 4tmeabutn + (2) h + nadh	1.2.1.47	Lysine Metabolism	223.1
TMDK1	thymidine kinase (ATP:thymidine)	[c] : atp + thymd --> adp + dtmp + h	2.7.1.21	Nucleotides	(7084.1 or 7083.1)
TMDK1m	thymidine kinase (ATP:thymidine)	[m] : atp + thymd --> adp + dtmp + h	2.7.1.21	Nucleotides	7084.1
TMDPK	thiamine diphosphokinase	[c] : atp + thm --> amp + h + thmpp	2.7.6.2	Thiamine Metabolism	27010.1
TMDPP	thymidine phosphorylase	[c] : pi + thymd <==> 2dr1p + thym	2.4.2.4	Pyrimidine Catabolism	1890.1
TMDPPK	thiamine-diphosphate kinase	[c] : atp + thmpp --> adp + thmtp	2.7.4.15	Thiamine Metabolism	
TMDS	thymidylate synthase	[c] : dump + mlthf --> dhf + dtmp	2.1.1.45	Nucleotides	7298.1
TMLYSOX	trimethyllysine dioxygenase	[c] : akg + o2 + tmlys --> 3htmelys + co2 + succ	1.14.11.8	Lysine Metabolism	55217.1
TMLYSter	trimethyl-L-lysine transport (ER to cytosol)	tmlys[r] --> tmlys[c]		Transport, Endoplasmic Reticular	
TMNDNCCOAtx	fatty acid intracellular transport	tmndnccoa[c] <==> tmndnccoa[x]		Transport, Peroxisomal	
TMNDNCCPT1	carnitine O-palmitoyltransferase	[c] : crn + tmndnccoa --> coa + tmndnccrn	2.3.1.21	Carnitine shuttle	(1375.4 or 1374.1 or 126129.1 or 1375.3 or 1375.2 or 1375.1)
TMNDNCCPT2	carnitine transferase	[m] : coa + tmndnccrn --> crn + tmndnccoa		Carnitine shuttle	1376.1
TMNDNCCRNt	transport into the mitochondria (carnitine)	tmndnccrn[c] --> tmndnccrn[m]		Carnitine shuttle	788.1
TMNDNCt	fatty acid transport via diffusion	tmndnc[e] <==> tmndnc[c]		Transport, Extracellular	
TOLBUTAMIDEte	xenobiotic transport	tolbutamide[e] <==> tolbutamide[c]		Transport, Extracellular	
TPI	triose-phosphate isomerase	[c] : dhap <==> g3p	5.3.1.1	Glycolysis/Gluconeogenesis	(7167.1 or 286016.1)
TRDR	thioredoxin reductase (NADPH)	[c] : h + nadph + trdox --> nadp + trdrd	1.8.1.9	Nucleotides	(7296.1 or 7296.2 or 7296.4 or 7296.3)
TRDR2	Thioredoxin (ubiquinone 10) reductase (NADPH)	[c] : h + nadph + q10 --> nadp + q10h2	1.8.1.9	Miscellaneous	(7296.4 or 7296.3 or 7296.2 or 7296.1)
TRDR3	Thioredoxin (ubiquinone 10) reductase (NADH)	[c] : h + nadh + q10 --> nad + q10h2	1.8.1.9	Miscellaneous	(7296.1 or 7296.2 or 7296.3 or 7296.4)
TRDRm	thioredoxin reductase (NADPH)	[m] : h + nadph + trdox --> nadp + trdrd	1.8.1.9	Nucleotides	(10587.1 or 10587.2 or 10587.3 or 114112.1)
TREH	alpha,alpha-trehalase	[c] : h2o + tre --> (2) glc-D	3.2.1.28	Starch and Sucrose Metabolism	80162.1
TREHe	alpha,alpha-trehalase	[e] : h2o + tre --> (2) glc-D	3.2.1.28	Starch and Sucrose Metabolism	11181.1
TRIODTHYSUFt	Triiodothyronine sulfate transport (diffusion)	triodthysuf[c] --> triodthysuf[e]		Transport, Extracellular	
TRIODTHYSULT	Triiodothyronine Sulfotransferase	[c] : paps + triodthy --> h + pap + triodthysuf	2.8.2.1	Tyrosine metabolism	(6817.1 or 6817.2 or 6817.3 or 6817.4 or 6817.5)
TRIODTHYt	T3 transport via bicarbonate countertransport	hco3[c] + triodthy[e] <==> hco3[e] + triodthy[c]		Transport, Extracellular	(28231.1 or 6579.1 or 10599.1 or 28234.1 or 53919.1)
TRIODTHYt2	T3 transport via facilitated diffusion	triodthy[e] <==> triodthy[c]		Transport, Extracellular	6567.1
TRIOK	triokinase	[c] : atp + glyald --> adp + g3p + h	2.7.1.28	Fructose and Mannose Metabolism	
TRPHYDRO2	L-Tryptophan,tetrahydrobiopterin:oxygen oxidoreductase (5-hydroxylating)	[c] : o2 + thbpt + trp-L --> 5htrp + thbpt4acam	1.14.16.4	Tryptophan metabolism	(7166.1 or 121278.1)
TRPO2	L-Tryptophan:oxygen 2,3-oxidoreductase (decyclizing)	[c] : o2 + trp-L --> L.fmkynr	1.13.11.11	Tryptophan metabolism	6999.1
TRPt	L-tryptophan transport	trp-L[e] <==> trp-L[c]		Transport, Extracellular	117247.1
TRPt4	L-tryptophan transport in via sodium symport	na1[e] + trp-L[e] --> na1[c] + trp-L[c]		Transport, Extracellular	11254.1
TRYPTAOX	Tryptamine:oxygen oxidoreductase(deaminating)(flavin-containing)	[c] : h2o + o2 + trypta --> h2o2 + id3acald + nh4	1.4.3.4	Tryptophan metabolism	(4128.1 or 4129.1 or 26.1 or 314.1 or 314.2)
TS3	Tachysterol 3 formation	[c] : pd3 <==> ts3		Vitamin D	
TSTSTERONEGLCte	glucuronidated compound transport	atp[c] + h2o[c] + tststeroneglc[c] --> adp[c] + h[c] + pi[c] + tststeroneglc[e]		Transport, Extracellular	4363.1
TSTSTERONEGLCtr	glucuronidated compound transport	tststeroneglc[c] <==> tststeroneglc[r]		Transport, Endoplasmic Reticular	
TSTSTERONESte	sulfonated testosterone transport	tststerones[c] <==> tststerones[e]		Transport, Extracellular	
TSTSTERONESULT	testosterone sulfotransferase	[c] : paps + tststerone --> h + pap + tststerones	2.8.2.2	Steroid Metabolism	(6822.1 or 6822.1)
TSTSTERONEtr	testosterone intracellular transport	tststerone[r] <==> tststerone[c]		Transport, Endoplasmic Reticular	
TSULt4_3	thiosulfate transport via sodium symport	(3) na1[e] + tsul[e] <==> (3) na1[c] + tsul[c]		Transport, Extracellular	6561.1
TTDCAt	Tetradecanoate (n-C14:0) transport in via uniport	ttdca[e] --> ttdca[c]		Transport, Extracellular	
TTDCPT1	carnitine O-palmitoyltransferase	[c] : crn + tdcoa --> coa + ttdcrn	2.3.1.21	Carnitine shuttle	(1374.1 or 126129.1 or 1375.2 or 1375.3 or 1375.4 or 1375.1)
TTDCPT2	carnitine transferase	[m] : coa + ttdcrn --> crn + tdcoa		Carnitine shuttle	1376.1

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
TTDCRNt	transport into the mitochondria (carnitine)	ttdcrn[c] --> ttdcrn[m]		Carnitine shuttle	788.1
TXA2te	thromboxane A2 transport	txa2[e] <==> txa2[c]		Transport, Extracellular	
TXA2tr	thromboxane A2 intracellular transport	txa2[c] <==> txa2[r]		Transport, Endoplasmic Reticular	
TXASr	Thromboxane-A synthase	[r] : prostgh2 --> txa2	5.3.99.5	Eicosanoid Metabolism	6916.1
TYMSFt	Tyramine O-sulfate transport (diffusion)	tymsf[c] --> tymsf[e]		Transport, Extracellular	
TYMSULT	Tyramine Sulfotransferase	[c] : paps + tym --> h + pap + tymsf	2.8.2.1	Tyrosine metabolism	(6817.1 or 6817.2 or 6817.3 or 6817.4 or 6817.5 or 6818.1 or 6818.2 or 6818.3)
TYR3MO2	tyrosine 3-monooxygenase	[c] : o2 + thbpt + tyr-L --> 34dhphe + thbpt4acam	1.14.16.2	Tyrosine metabolism	(7054.1 or 7054.2 or 7054.3)
TYRASE	Tyrosinase	[c] : 56dihindlcrbxlt --> melanin	1.14.18	Tyrosine metabolism	7306.1
TYRCBOX	L-Tyrosine carboxy-lyase	[c] : h + tyr-L --> co2 + tym	4.1.1.25	Tyrosine metabolism	1644.1
TYRDOPO	Tyrosine:dopa oxidase	[c] : o2 + (2) tyr-L --> (2) 34dhphe	1.14.18.1	Tyrosine metabolism	7299.1
TYRDOPO3	Tyrosine:dopa oxidase (dopaquinone producing 2)	[c] : (2) 34dhphe + o2 --> (2) dopaqn + (2) h2o	1.14.18.1	Tyrosine metabolism	7299.1
TYROXDAc	Tyramine:oxygen oxidoreductase(deaminating)(flavin-containing) (cytosol)	[c] : h2o + o2 + tym --> 4hoxpacd + h2o2 + nh4	1.4.3.6	Tyrosine metabolism	(4128.1 or 4129.1)
TYRt	L-tyrosine transport	tyr-L[e] <==> tyr-L[c]		Transport, Extracellular	117247.1
TYRt4	L-tyrosine transport in via sodium symport	na1[e] + tyr-L[e] --> na1[c] + tyr-L[c]		Transport, Extracellular	11254.1
TYRTA	tyrosine transaminase	[c] : akg + tyr-L <==> 34hpp + glu-L	2.6.1.5	Tyrosine metabolism	2805.1
TYRTAm	tyrosine transaminase, mitochondrial	[m] : akg + tyr-L <==> 34hpp + glu-L	2.6.1.5	Tyrosine metabolism	(6898.1 or 2806.1)
UAG2EMAi	UDP-N-acetyl-D-glucosamine 2-epimerase (Hydrolysis)	[c] : h2o + uacgam --> acmana + h + udp	5.1.3.14	Aminosugar Metabolism	10020.1
UAG4E	UDP-N-acetylglucosamine 4-epimerase	[c] : uacgam <==> udpacgal	5.1.3.7	Aminosugar Metabolism	(2582.1 or 2582.2)
UAGALDP	UDP-N-acetylgalactosamine diphosphorylase	[c] : acgal1p + h + utp --> ppi + udpacgal		Aminosugar Metabolism	
UAGDP	UDP-N-acetylglucosamine diphosphorylase	[c] : acgam1p + h + utp --> ppi + uacgam	2.7.7.23	Aminosugar Metabolism	(6675.1 or 91373.1)
UDPACGALtl	udpacgal intracellular transport	udpacgal[c] <==> udpacgal[l]		Transport, Lysosomal	
UDPDOLPT_L	UDPglucose:dolichyl-phosphate beta-D-glucosyltransferase (liver)	[c] : (0.1) dolp_L + udpg --> (0.1) dolglcp_L + udp	2.4.1.117	N-Glycan Biosynthesis	29880.1
UDPDOLPT_U	UDPglucose:dolichyl-phosphate beta-D-glucosyltransferase (uterus)	[c] : (0.1) dolp_U + udpg --> (0.1) dolglcp_U + udp	2.4.1.117	N-Glycan Biosynthesis	29880.1
UDPG1P	UDPglucuronate uridine-monophosphohydrolase	[c] : h2o + udpglcur --> glcur1p + (2) h + ump		Pentose and Glucuronate Interconversions	
UDPG4E	UDPglucose 4-epimerase	[c] : udpg <==> udpgal	5.1.3.2	Galactose metabolism	(2582.1 or 2582.2)
UDPGALtg	UDP-Gal Golgi transport via CMP antiport	udpgal[c] + ump[g] <==> udpgal[g] + ump[c]		Transport, Golgi Apparatus	7355.1
UDPGD	UDPglucose 6-dehydrogenase	[c] : h2o + (2) nad + udpg --> (3) h + (2) nadh + udpglcur	1.1.1.22	Starch and Sucrose Metabolism	7358.1
UDPGLCAter	UDPGlcA endoplasmic reticulum transport via UMP antiport	udpglcur[r] + ump[c] <==> udpglcur[c] + ump[r]		Transport, Endoplasmic Reticular	23169.1
UDPGLCAtg	UDPGlcA Golgi transport via UMP antiport	udpglcur[g] + ump[c] <==> udpglcur[c] + ump[g]		Transport, Golgi Apparatus	
UDPGLCter	UDP-Glc endoplasmic reticulum transport via CMP antiport	udpg[c] + ump[r] <==> udpg[r] + ump[c]		Transport, Endoplasmic Reticular	
UDPGLCtg	UDP-Glc Golgi transport via CMP antiport	udpg[c] + ump[g] <==> udpg[g] + ump[c]		Transport, Golgi Apparatus	(23443.1 or 11046.1 or 84912.1)
UDPGLDCg	UDP-D-glucuronate decarboxylase, Golgi apparatus	[g] : h + udpglcur --> co2 + udpxyl	4.1.1.35	Nucleotide Sugar Metabolism	80146.1
UDPGNP	UDPglucuronate uridine-diphosphohydrolase	[c] : h2o + udpglcur --> glcur + h + udp		Pentose and Glucuronate Interconversions	
UDPGP	UDPglucose pyrophosphohydrolase	[c] : h2o + udpg --> g1p + (2) h + ump	3.6.1.9	Starch and Sucrose Metabolism	(5167.1 or 5168.1 or 5169.1)
UDPtl	udp intracellular transport	udp[c] <==> udp[l]		Transport, Lysosomal	
UDPXYLter	UDP-Xyl endoplasmic reticular transport via CMP antiport	udpxyl[c] + ump[r] <==> udpxyl[r] + ump[c]		Transport, Endoplasmic Reticular	
UDPXYLtg	UDP-Xyl Golgi transport via CMP antiport	udpxyl[c] + ump[g] <==> udpxyl[g] + ump[c]		Transport, Golgi Apparatus	84912.1
UGALGTg	UDPgalactose:D-glucose 4-beta-D-galactosyltransferase, Golgi apparatus	[g] : glc-D + udpgal --> h + lcts + udp	2.4.1.22	Galactose metabolism	((3906.1 and 2683.1) or 8704.1 or 8704.2)
UGALNACter	UDP-GalNAc endoplasmic reticulum transport via CMP antiport	udpacgal[c] + ump[r] <==> udpacgal[r] + ump[c]		Transport, Endoplasmic Reticular	23169.1
UGALNACtg	UDP-GalNAc Golgi transport via CMP antiport	udpacgal[c] + ump[g] <==> udpacgal[g] + ump[c]		Transport, Golgi Apparatus	7355.1
UGCG	Ceramide glucosyltransferase	[r] : crm_hs + udpg --> gluside_hs + h + udp	2.4.1.80	Sphingolipid Metabolism	7357.1
UGLCNACtg	UDP-GlcNAc Golgi transport via CMP antiport	uacgam[c] + ump[g] <==> uacgam[g] + ump[c]		Transport, Golgi Apparatus	11046.1
UGLT	UDPglucose--hexose-1-phosphate uridylyltransferase	[c] : gal1p + udpg <==> g1p + udpgal	2.7.7.12	Galactose metabolism	(2592.1 or 2592.2 or 2592.3)
UGT1A10r	UDP-glucuronosyltransferase 1-10 precursor, microsomal	[r] : bilirub + (2) h + udpglcur <==> bilglcur + udp	2.4.1.17	Steroid Metabolism	54576.1
UGT1A1r	UDP-glucuronosyltransferase 1-10 precursor, microsomal	[r] : estrone + udpglcur --> estroneglc + udp	2.4.1.17	Steroid Metabolism	(54575.1 or 54576.1)
UGT1A2r	UDP-glucuronosyltransferase 1-10 precursor, microsomal	[r] : bilirub + (2) udpglcur --> bildglcur + (2) udp	2.4.1.17	Steroid Metabolism	(54575.1 or 54576.1)
UGT1A3r	UDP-glucuronosyltransferase 1-10 precursor, microsomal	[r] : andrstrn + udpglcur --> andrstrnglc + udp	2.4.1.17	Steroid Metabolism	(54575.1 or 54576.1 or 54490.1 or 7364.1 or 7367.1)
UGT1A4r	UDP-glucuronosyltransferase 1-10 precursor, microsomal	[r] : tststerone + udpglcur --> tststeroneglc + udp	2.4.1.17	Steroid Metabolism	(54575.1 or 54576.1 or 54490.1)
UGT1A5r	UDP-glucuronosyltransferase 1-10 precursor, microsomal	[r] : retn + udpglcur --> retnglc + udp	2.4.1.17	Vitamin A Metabolism	(54575.1 or 54576.1)
UGT1A5r2	UDP-glucuronosyltransferase 1-10 precursor, microsomal (13-cis)	[r] : 13-cis-retn + udpglcur --> 13-cis-retnglc + udp	2.4.1.17	Vitamin A Metabolism	(54576.1 or 54575.1)
UGT1A6r	UDP-glucuronosyltransferase 1-10 precursor, microsomal	[r] : estradiol + udpglcur --> estradiolglc + udp	2.4.1.17	Steroid Metabolism	(54575.1 or 54576.1)
UGT1A7r	UDP-glucuronosyltransferase 1-10 precursor, microsomal	[r] : ahandrostan + udpglcur --> ahandrostanglc + udp	2.4.1.17	Steroid Metabolism	(54575.1 or 54576.1)
UGT1A8r	UDP-glucuronosyltransferase 1-10 precursor, microsomal	[r] : estriol + udpglcur --> estriolglc + udp	2.4.1.17	Steroid Metabolism	(54575.1 or 54576.1 or 54490.1 or 7363.1)
UGT1A9r	UDP-glucuronosyltransferase 1-10 precursor, microsomal	[r] : 5adtststerone + udpglcur --> 5adtststeroneglc + udp	2.4.1.17	Steroid Metabolism	54490.1
UMPK	UMP kinase	[c] : atp + ump <==> adp + udp	2.7.4.14	Nucleotides	51727.1
UMPK2	UMP kinase (CTP)	[c] : ctp + ump <==> cdp + udp	2.7.4.14	Nucleotides	51727.1
UMPK2n	UMP kinase (CTP),nuclear	[n] : ctp + ump <==> cdp + udp	2.7.4.14	Nucleotides	51727.1
UMPK3	UMP kinase (UTP)	[c] : ump + utp <==> (2) udp	2.7.4.14	Nucleotides	51727.1
UMPK3n	UMP kinase (UTP),nuclear	[n] : ump + utp <==> (2) udp	2.7.4.14	Nucleotides	51727.1
UMPK4	UMP kinase (GTP)	[c] : gtp + ump <==> gdp + udp	2.7.4.14	Nucleotides	51727.1

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
UMPK4n	UMP kinase (GTP),nuclear	[n] : gtp + ump <==> gdp + udp	2.7.4.14	Nucleotides	51727.1
UMPK5	UMP kinase (dATP)	[c] : datp + ump <==> dadp + udp	2.7.4.14	Nucleotides	51727.1
UMPK5n	UMP kinase (dATP),nuclear	[n] : datp + ump <==> dadp + udp	2.7.4.14	Nucleotides	51727.1
UMPK6	UMP kinase (dCTP)	[c] : dctp + ump <==> dcdp + udp	2.7.4.14	Nucleotides	51727.1
UMPK6n	UMP kinase (dCTP),nuclear	[n] : dctp + ump <==> dcdp + udp	2.7.4.14	Nucleotides	51727.1
UMPK7	UMP kinase (dGTP)	[c] : dgtp + ump <==> dgdp + udp	2.7.4.14	Nucleotides	51727.1
UMPK7n	UMP kinase (dGTP),nuclear	[n] : dgtp + ump <==> dgdp + udp	2.7.4.14	Nucleotides	51727.1
UMPKm	UMP kinase (mitochondrial, ATP)	[m] : atp + ump <==> adp + udp	2.7.4.14	Nucleotides	
UMPKn	UMP kinase, nuclear	[n] : atp + ump <==> adp + udp		Nucleotides	51727.1
UNK2	2-keto-4-methylthiobutyrate transamination	[c] : 2kmb + gln-L + h --> glu-L + met-L		Arginine and Proline Metabolism	
UNK3	2-keto-4-methylthiobutyrate transamination	[c] : 2kmb + glu-L --> akg + met-L		Arginine and Proline Metabolism	
UPP3S	uroporphyrinogen-III synthase	[c] : hmbil --> h2o + uppg3	4.2.1.75	Heme Biosynthesis	7390.1
UPPDC1	uroporphyrinogen decarboxylase (uroporphyrinogen III)	[c] : (4) h + uppg3 --> (4) co2 + cpppg3	4.1.1.37	Heme Biosynthesis	7389.1
UPPN	b-ureidopropionase	[c] : cala + (2) h + h2o --> ala-B + co2 + nh4	3.5.1.6	Pyrimidine Catabolism	51733.1
URAt	uracil transport via facilated diffusion	ura[e] <==> ura[c]		Transport, Extracellular	3177.1
URATEt	urate export from cytosol	urate[c] --> urate[e]		Transport, Extracellular	
URATEtx	urate export from peroxisome	urate[x] --> urate[c]		Transport, Peroxisomal	
URCN	urocanase	[c] : h2o + urcan --> 4izp	4.2.1.49	Histidine Metabolism	131669.1
UREAt	Urea transport via facilitate diffusion	urea[e] <==> urea[c]		Transport, Extracellular	(6563.1 or 8170.1 or 6528.1 or 6523.1)
UREAt5	urea, water cotransport	h2o[e] + urea[e] <==> h2o[c] + urea[c]		Transport, Extracellular	6523.1
UREAtm	Urea transport via diffusion	urea[c] <==> urea[m]		Urea cycle/amino group metabolism	366.1
URIDK2m	uridylate kinase (dUMP), mitochondrial	[m] : atp + dump <==> adp + dudp		Nucleotides	
URIK1	uridine kinase (ATP:Uridine)	[c] : atp + uri --> adp + h + ump	2.7.1.48	Pyrimidine Biosynthesis	(7371.1 or 83549.1)
URIt	uridine facilated transport in cytosol	uri[e] <==> uri[c]		Transport, Extracellular	(3177.1 or 2030.1)
URIt4	uridine transport in via sodium symport	na1[e] + uri[e] --> na1[c] + uri[c]		Transport, Extracellular	(9154.1 or 9153.1 or 64078.1 or 9154.2)
URIt5	uridine transport in via sodium symport (1:2)	(2) na1[e] + uri[e] --> (2) na1[c] + uri[c]		Transport, Extracellular	64078.1
Uritl	uridine facilated transport from lysosome	uri[l] <==> uri[c]		Transport, Lysosomal	55315.1
Uritm	uridine facilated transport in mitochondria	uri[c] <==> uri[m]		Transport, Mitochondrial	2030.1
Uritn	uridine transport in nucleus	uri[c] <==> uri[n]		Transport, Nuclear	
UROLACer	uronolactonase, endoplasmic reticulum	[r] : glcur + h <==> glac + h2o	3.1.1.19	Ascorbate and Aldarate Metabolism	
UTPtn	UTP diffusion in nucleus	utp[c] <==> utp[n]		Transport, Nuclear	
VACCCPT1	carnitine O-palmitoyltransferase	[c] : crn + vacccoa --> coa + vacccrn	2.3.1.21	Carnitine shuttle	(1375.4 or 1374.1 or 126129.1 or 1375.3 or 1375.2 or 1375.1)
VACCCPT2	carnitine transferase	[m] : coa + vacccrn --> crn + vacccoa		Carnitine shuttle	1376.1
VACCCRNt	transport into the mitochondria (carnitine)	vacccrn[c] --> vacccrn[m]		Carnitine shuttle	788.1
VACCt	fatty acid transport via diffusion	vacc[e] <==> vacc[c]		Transport, Extracellular	
VALt4	L-valine transport in via sodium symport	na1[e] + val-L[e] --> na1[c] + val-L[c]		Transport, Extracellular	11254.1
VALt5m	Valine reversible mitochondrial transport	val-L[c] <==> val-L[m]		Transport, Mitochondrial	
VALTA	valine transaminase	[c] : akg + val-L <==> 3mob + glu-L	2.6.1.42	Valine, Leucine, and Isoleucine Metabolism	586.1
VALTAm	valine transaminase, mitochondiral	[m] : akg + val-L <==> 3mob + glu-L	2.6.1.42	Valine, Leucine, and Isoleucine Metabolism	587.1
VALtec	L-valine transport via diffusion (extracellular to cytosol)	val-L[e] <==> val-L[c]		Transport, Extracellular	(8501.1 or 124935.1)
VD3	Vitamin D3 formation	[c] : pd3 <==> vitd3		Vitamin D	
VITD2Hm	Vitamin D-25-hydroxylase (D2)	[m] : h + nadph + o2 + vitd2 --> 25hvitd2 + h2o + nadp		Vitamin D	1593.1
VITD2t	Vitamin D2 release	vitd2[c] --> vitd2[e]		Transport, Extracellular	
VITD2tm	Vitamin D2 transport from mitochondria	vitd2[m] <==> vitd2[c]		Transport, Mitochondrial	
VITD3Hm	Vitamin D-25-hydroxylase (D3)	[m] : h + nadph + o2 + vitd3 --> 25hvitd3 + h2o + nadp		Vitamin D	1593.1
VITD3t	Vitamin D3 release	vitd3[c] --> vitd3[e]		Transport, Extracellular	
VITD3t2	Vitamin D3 uptake	vitd3[e] --> vitd3[c]		Transport, Extracellular	
VITD3tm	Vitamin D3 transport from mitochondria	vitd3[m] --> vitd3[c]		Transport, Mitochondrial	
VITD3tm3	Vitamin D3 transport in mitochondria	vitd3[c] --> vitd3[m]		Transport, Mitochondrial	
VLCS2p	Very-long-chain-fatty-acid-CoA ligase	[x] : atp + coa + dhcholestanate --> amp + dhcholestancoa + ppi	6.2.1.7	Bile Acid Biosynthesis	11001.1
VLCS2r	Very-long-chain-fatty-acid-CoA ligase	[r] : atp + coa + dhcholestanate --> amp + dhcholestancoa + ppi	6.2.1.7	Bile Acid Biosynthesis	11001.1
VLCSp	Very-long-chain-fatty-acid-CoA ligase	[x] : atp + coa + thcholstoic --> amp + cholcoar + ppi	6.2.1.7	Bile Acid Biosynthesis	11001.1
VLCSr	Very-long-chain-fatty-acid-CoA ligase	[r] : atp + coa + thcholstoic --> amp + cholcoar + ppi	6.2.1.7	Bile Acid Biosynthesis	11001.1
WHDDCAte	xenobiotic transport	whddca[e] <==> whddca[c]		Transport, Extracellular	
WHHDCAte	xenobiotic transport	whhdca[e] <==> whhdca[c]		Transport, Extracellular	
WHTSTSTERONEte	omega hydroxy testosterone transport	whtststerone[c] <==> whtststerone[e]		Transport, Extracellular	
WHTTDCAte	xenobiotic transport	whttdca[e] <==> whttdca[c]		Transport, Extracellular	
XANDp	xanthine dehydrogenase, peroxisomal	[x] : h2o + nad + xan --> h + nadh + urate	1.1.1.204	Purine Catabolism	7498.1
XANtx	xanthine diffusion in peroxisome	xan[c] --> xan[x]		Transport, Peroxisomal	
XAO2x	xanthine oxidase	[x] : h2o + hxan + o2 --> h2o2 + xan		Purine Catabolism	7498.1
XAOx	xanthine oxidase,peroxisomal	[x] : h2o + o2 + xan --> h2o2 + urate		Purine Catabolism	7498.1
XOL27OHtm	27 hydroxy cholesterol transport	xol27oh[r] <==> xol27oh[m]		Transport, Mitochondrial	
XOL7AH2tm	lipid, flip-flop intracellular transport	xol7ah2[c] <==> xol7ah2[m]		Transport, Mitochondrial	
XOL7AH2tr	lipid, flip-flop intracellular transport	xol7ah2[c] <==> xol7ah2[r]		Transport, Endoplasmic Reticular	
XOL7AONEtr	lipid, flip-flop intracellular transport	xol7aone[c] <==> xol7aone[r]		Transport, Endoplasmic Reticular	
XOLDIOLONEt	lipid, flip-flop intracellular transport	xoldiolone[c] <==> xoldiolone[r]		Transport, Endoplasmic Reticular	
XOLDIOLONEtm	lipid, flip-flop intracellular transport	xoldiolone[m] <==> xoldiolone[r]		Transport, Endoplasmic Reticular	
XOLEST2te	cholesterol ester transporter	xolest2_hs[e] <==> xolest2_hs[c]		Transport, Extracellular	
XOLESTte	cholesterol ester transporter	xolest_hs[e] <==> xolest_hs[c]		Transport, Extracellular	
XOLTRI24tc	24 trihydroxy cholesterol transport	xoltri24[r] <==> xoltri24[c]		Transport, Endoplasmic Reticular	
XOLTRI24te	24 trihydroxy cholesterol transport	xoltri24[c] <==> xoltri24[e]		Transport, Extracellular	
XOLTRI25tc	25 trihydroxy cholesterol transport	xoltri25[r] <==> xoltri25[c]		Transport, Endoplasmic Reticular	
XOLTRI25te	25 trihydroxy cholesterol transport	xoltri25[c] <==> xoltri25[e]		Transport, Extracellular	
XOLTRI27tc	27 trihydroxy cholesterol transport	xoltri27[r] <==> xoltri27[c]		Transport, Endoplasmic Reticular	
XOLTRI27te	27 trihydroxy cholesterol transport	xoltri27[c] <==> xoltri27[e]		Transport, Extracellular	
XOLTRIOLtm	lipid, flip-flop intracellular transport	xoltriol[c] <==> xoltriol[m]		Transport, Mitochondrial	
XOLTRIOLtr	lipid, flip-flop intracellular transport	xoltriol[c] <==> xoltriol[r]		Transport, Endoplasmic Reticular	
XSERtg	Xyl-L-Ser (protein) transport from endoplasmic reticulum to Golgi apparatus	xser[r] --> xser[g]		Transport, Golgi Apparatus	

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
XYLK	xylulokinase	[c] : atp + xylu-D --> adp + h + xu5p-D	2.7.1.17	Pentose and Glucuronate Interconversions	9942.1
XYLt	D-xylose reversible transport	xyl-D[e] <==> xyl-D[c]		Transport, Extracellular	6515.1
XYLTD_Dr	xylitol dehydrogenase (D-xyulose-forming)	[c] : nad + xylt <==> h + nadh + xylu-D	1.1.1.9	Pentose and Glucuronate Interconversions	
XYLTer	UDP-xylose:protein xylosyltransferase, endoplasmic reticulum	[r] : Ser-Gly/Ala-X-Gly + udpxyl --> h + udp + xser	2.4.2.26	Chondroitin / heparan sulfate biosynthesis	(64131.1 or 64132.1)
XYLtly	Xylose efflux from lysosome	xyl-D[l] --> xyl-D[c]		Transport, Lysosomal	
XYLTt	Xylitol transport via passive diffusion	xylt[e] <==> xylt[c]		Transport, Extracellular	
XYLUR	xylulose reductase	[c] : h + nadph + xylu-L <==> nadp + xylt	1.1.1.10	Pentose and Glucuronate Interconversions	51181.1
YVITEt	gamma-Tocopherol (Vit. E) transport	yvite[e] --> yvite[c]		Transport, Extracellular	

Table 6: *H. sapiens* Recon 1 demand and exchange reactions. Demand reactions are intrasystem sources or sinks which allow unlimited production or consumption of a specified metabolite. Exchange reactions describe metabolite entry or exit across the system boundary (the interface between the extracellular compartment and cellular environment). Compartmentalization is denoted by the following abbreviations. All reactions occur entirely within one compartment.

Compartment Abbreviations

[c], cytoplasm	[m], mitochondrion
[e], extracellular	[n], nucleus
[g], Golgi appratus	[r], endoplasmic reticulum
[l], lysosome	[x], peroxisome

Abbreviation	Reaction Name	Reaction
DM_13-cis-oretn(n)	13-cis-oxo-retinoic acid demand	[n] : 13-cis-oretn -->
DM_13-cis-retn(n)	13-cis-retinoate demand	[n] : 13-cis-retn -->
DM_Asn-X-Ser/Thr(ly)	DM_Asn-X-Ser/Thr(ly)	[l] : Asn-X-Ser/Thr -->
DM_avite1(c)	alpha-Tocopherol demand	[c] : avite1 -->
DM_avite2(c)	alpha-Tocotrienol demand	[c] : avite2 -->
DM_bvite(c)	beta-tocopherol demand	[c] : bvite -->
DM_datp(m)	dATP demand	[m] : datp -->
DM_datp(n)	DM_datp(n)	[n] : datp -->
DM_dctp(m)	dCTP demand	[m] : dctp -->
DM_dctp(n)	DM_dctp(n)	[n] : dctp -->
DM_dgtp(m)	DM_dgtp(m)	[m] : dgtp -->
DM_dgtp(n)	DM_dgtp(n)	[n] : dgtp -->
DM_dsT_antigen(g)	DM_dsT_antigen(g)	[g] : dsT_antigen -->
DM_dttp(m)	dTTP demand	[m] : dttp -->
DM_dttp(n)	DM_dttp(n)	[n] : dttp -->
DM_ethamp(r)	Ethanolamine phosphate demand	[r] : ethamp -->
DM_gpi_sig(er)	DM_gpi_sig(er)	[r] : gpi_sig -->
DM_hretn(n)	4 hydroxy retinoic acid demand	[n] : hretn -->
DM_kdn(c)	DM_kdn(c)	[c] : kdn -->
DM_melanin(c)	DM_melanin(c)	[c] : melanin -->
DM_oretn(n)	4-oxo-retonoic acid demand	[n] : oretn -->
DM_Ser/Thr(ly)	DM_Ser/Thr(ly)	[l] : Ser/Thr -->
DM_Ser-Gly/Ala-X-Gly(ly)	DM_Ser-Gly/Ala-X-Gly(ly)	[l] : Ser-Gly/Ala-X-Gly -->
DM_sprm(c)	DM_sprm(c)	[c] : sprm -->
DM_sTn_antigen(g)	DM_sTn_antigen(g)	[g] : sTn_antigen -->
DM_yvite(c)	gamma-Tocopherol demand	[c] : yvite -->
EX_10fthf(e)	10-Formyltetrahydrofolate exchange	[e] : 10fthf <==>
EX_10fthf5glu(e)	10-formyltetrahydrofolate-[Glu](5) exchange	[e] : 10fthf5glu <==>
EX_10fthf6glu(e)	10-formyltetrahydrofolate-[Glu](6) exchange	[e] : 10fthf6glu <==>
EX_10fthf7glu(e)	10-formyltetrahydrofolate-[Glu](7) exchange	[e] : 10fthf7glu <==>
EX_11-cis-retfa(e)	fatty acid 11-cis-retinol exchange	[e] : 11-cis-retfa <==>
EX_13-cis-retnglc(e)	13-cis-retinoyl glucuronide exchange	[e] : 13-cis-retnglc <==>
EX_1glyc_hs(e)	1 acyl phosphoglycerol exchange	[e] : 1glyc_hs <==>
EX_1mncam(e)	1-Methylnicotinamide exchange	[e] : 1mncam <==>
EX_2425dhvitd2(e)	24R,25-Dihyoxyvitamin D2 exchange	[e] : 2425dhvitd2 <==>
EX_2425dhvitd3(e)	24R,25-Dihydroxyvitamin D3 exchange	[e] : 2425dhvitd3 <==>
EX_24nph(e)	2,4 dihydroxy nitrophenol exchange	[e] : 24nph <==>
EX_25hvitd2(e)	25-Hydroxyvitamin D2 exchange	[e] : 25hvitd2 <==>
EX_25hvitd3(e)	25-Hydroxyvitamin D3 exchange	[e] : 25hvitd3 <==>
EX_2hb(e)	2-Hydroxybutyrate exchange	[e] : 2hb <==>
EX_2mcit(e)	2-Methylcitrate exchange	[e] : 2mcit <==>
EX_34dhoxpeg(e)	3,4-Dihydroxyphenylethyleneglycol exchange	[e] : 34dhoxpeg <==>
EX_34dhphe(e)	3,4-Dihydroxy-L-phenylalanine exchange	[e] : 34dhphe <==>
EX_35cgmp(e)	3',5'-Cyclic GMP exchange	[e] : 35cgmp <==>
EX_3aib(e)	L-3-Amino-isobutanoate exchange	[e] : 3aib <==>
EX_3aib-D(e)	D-3-Amino-isobutanoate exchange	[e] : 3aib-D <==>
EX_3mlda(e)	3-Methylimidazoleacetic acid exchange	[e] : 3mlda <==>
EX_4abut(e)	4-Aminobutanoate exchange	[e] : 4abut <==>
EX_4hdebrisoquine(e)	4 hydroxy debrisoquine exchange	[e] : 4hdebrisoquine <==>
EX_4hphac(e)	4-Hydroxyphenylacetate exchange	[e] : 4hphac <==>
EX_4mtolbutamide(e)	4 hydroxy tolbutamide exchange	[e] : 4mtolbutamide <==>
EX_4nph(e)	4-Nitrophenol exchange	[e] : 4nph <==>
EX_4nphsf(e)	4-Nitrophenyl sulfate exchange	[e] : 4nphsf <==>
EX_4pyrdx(e)	4-Pyridoxate exchange	[e] : 4pyrdx <==>
EX_5adtststerone(e)	5alpha-Dihydrotestosterone exchange	[e] : 5adtststerone <==>
EX_5adtststeroneglc(e)	5alpha-Dihydrotestosterone glucuronide exchange	[e] : 5adtststeroneglc <==>
EX_5adtststerones(e)	5alpha-Dihydrotestosterone sulfate exchange	[e] : 5adtststerones <==>
EX_5dhf(e)	pentaglutamyl folate (DHF) exchange	[e] : 5dhf <==>

Abbreviation	Reaction Name	Reaction
EX_5fthf(e)	5-Formyltetrahydrofolate exchange	[e] : 5fthf <==>
EX_5homeprazole(e)	5 hydroxy omeprazole exchange	[e] : 5homeprazole <==>
EX_5htrp(e)	5-Hydroxy-L-tryptophan exchange	[e] : 5htrp <==>
EX_5mthf(e)	5-Methyltetrahydrofolate exchange	[e] : 5mthf <==>
EX_5thf(e)	pentaglutamyl folate (THF) exchange	[e] : 5thf <==>
EX_6dhf(e)	haxglutamyl folate (DHF) exchange	[e] : 6dhf <==>
EX_6htststerone(e)	6 beta hydroxy testosterone exchange	[e] : 6htststerone <==>
EX_6thf(e)	hexaglutamyl folate (THF) exchange	[e] : 6thf <==>
EX_7dhf(e)	heptaglutamyl folate (DHF) exchange	[e] : 7dhf <==>
EX_7thf(e)	heptaglutamyl folate (THF) exchange	[e] : 7thf <==>
EX_9-cis-retfa(e)	fatty acid 9-cis-retinol exchange	[e] : 9-cis-retfa <==>
EX_abt(e)	L-Arabinitol exchange	[e] : abt <==>
EX_ac(e)	Acetate exchange	[e] : ac <==>
EX_acac(e)	Acetoacetate exchange	[e] : acac <==>
EX_acald(e)	Acetaldehyde exchange	[e] : acald <==>
EX_acetone(e)	Acetone exchange	[e] : acetone <==>
EX_acgalfucgalacgalfuc12gal14acglcgalgluside_hs(e)	Type IIIA glycolipid exchange	[e] : acgalfucgalacgalfuc12gal14acglcgalgluside_hs <==>
EX_acgalfucgalacgalfucgalacglcgal14acglcgalgluside_hs(e)	Type IIIAb exchange	[e] : acgalfucgalacgalfucgalacglcgal14acglcgalgluside_hs <==>
EX_acgam(e)	N-Acetyl-D-glucosamine exchange	[e] : acgam <==>
EX_ach(e)	Acetylcholine exchange	[e] : ach <==>
EX_acn13acngalgbside_hs(e)	sialyl (1,3) sialyl (2,6) galactosylgloboside (homo sapiens) exchange	[e] : acn13acngalgbside_hs <==>
EX_acn23acngalgbside_hs(e)	sialyl (2,3) sialyl (2,6) galactosylgloboside (homo sapiens) exchange	[e] : acn23acngalgbside_hs <==>
EX_acnacngal14acglcgalgluside_hs(e)	3',8'-LD1 exchange	[e] : acnacngal14acglcgalgluside_hs <==>
EX_acnacngalgbside_hs(e)	disialyl galactosylgloboside (homo sapiens) exchange	[e] : acnacngalgbside_hs <==>
EX_acngalacglcgal14acglcgalgluside_hs(e)	VI3NeuAc-nLc6Cer exchange	[e] : acngalacglcgal14acglcgalgluside_hs <==>
EX_ade(e)	Adenine exchange	[e] : ade <==>
EX_adn(e)	Adenosine exchange	[e] : adn <==>
EX_adp	adp exchange	[e] : adp <==>
EX_adprbp(e)	ADPribose 2'-phosphate exchange	[e] : adprbp <==>
EX_adprib(e)	ADPribose exchange	[e] : adprib <==>
EX_adrn(e)	adrenic acid exchange	[e] : adrn <==>
EX_adrnl(e)	Adrenaline exchange	[e] : adrnl <==>
EX_aflatoxin(e)	aflatoxin B1 exchange	[e] : aflatoxin <==>
EX_ahandrostanglc(e)	Etiocholan-3alpha-ol-17-one 3-glucuronide exchange	[e] : ahandrostanglc <==>
EX_ak2lgchol_hs(e)	1-alkyl 2-lysoglycerol 3-phosphocholine exchange	[e] : ak2lgchol_hs <==>
EX_akg(e)	2-Oxoglutarate exchange	[e] : akg <==>
EX_ala-B(e)	beta-Alanine exchange	[e] : ala-B <==>
EX_ala-D(e)	D-Alanine exchange	[e] : ala-D <==>
EX_ala-L(e)	L-Alanine exchange	[e] : ala-L <==>
EX_aldstrn(e)	Aldosterone exchange	[e] : aldstrn <==>
EX_amp(e)	AMP exchange	[e] : amp <==>
EX_andrstrn(e)	Androsterone exchange	[e] : andrstrn <==>
EX_andrstrnglc(e)	androsterone glucuronide exchange	[e] : andrstrnglc <==>
EX_antipyrene(e)	antipyrene exchange	[e] : antipyrene <==>
EX_apnnox(e)	alpha-Pinene-oxide exchange	[e] : apnnox <==>
EX_appnn(e)	(+)-alpha-Pinene exchange	[e] : appnn <==>
EX_aprgstrn(e)	20alpha-Hydroxyprogesterone exchange	[e] : aprgstrn <==>
EX_aqcobal(e)	Aquacob(III)alamin exchange	[e] : aqcobal <==>
EX_arab-L(e)	L-Arabinose exchange	[e] : arab-L <==>
EX_arach(e)	Arachidic acid exchange	[e] : arach <==>
EX_arachd(e)	nC20:4 exchange	[e] : arachd <==>
EX_arg-L(e)	L-Arginine exchange	[e] : arg-L <==>
EX_ascb-L(e)	L-Ascorbate exchange	[e] : ascb-L <==>
EX_asn-L(e)	L-Asparagine exchange	[e] : asn-L <==>
EX_asp-D(e)	D-Aspartate exchange	[e] : asp-D <==>

Abbreviation	Reaction Name	Reaction
EX_asp-L(e)	L-Aspartate exchange	[e] : asp-L <==>
EX_atp(e)	ATP exchange	[e] : atp <==>
EX_avite1(e)	alpha-Tocopherol exchange	[e] : avite1 <==>
EX_avite2(e)	alpha-Tocotrienol exchange	[e] : avite2 <==>
EX_bhb(e)	(R)-3-Hydroxybutanoate transport via H+ symport	[e] : bhb <==>
EX_bildglcur(e)	Bilirubin beta-diglucuronide exchange	[e] : bildglcur <==>
EX_bilglcur(e)	Bilirubin monoglucuronide exchange	[e] : bilglcur <==>
EX_bilirub(e)	Bilirubin exchange	[e] : bilirub <==>
EX_biocyt(e)	Biocytin exchange	[e] : biocyt <==>
EX_btn(e)	Biotin exchange	[e] : btn <==>
EX_but(e)	Butyrate (n-C4:0) exchange	[e] : but <==>
EX_bvite(e)	beta-tocopherol exchange	[e] : bvite <==>
EX_bz(e)	Benzoate exchange	[e] : bz <==>
EX_ca2(e)	Calcium exchange	[e] : ca2 <==>
EX_camp(e)	cAMP exchange	[e] : camp <==>
EX_caro(e)	beta-Carotene exchange	[e] : caro <==>
EX_carveol(e)	(E)-carveol exchange	[e] : carveol <==>
EX_cca_d3(e)	Calcitroic acid (D3) exchange	[e] : cca_d3 <==>
EX_cgly(e)	Cys-Gly exchange	[e] : cgly <==>
EX_chol(e)	Choline exchange	[e] : chol <==>
EX_cholate(e)	Cholate exchange	[e] : cholate <==>
EX_chsterol(e)	Cholesterol exchange	[e] : chsterol <==>
EX_chtn(e)	chitin exchange	[e] : chtn <==>
EX_cit(e)	Citrate exchange	[e] : cit <==>
EX_cl(e)	Chloride exchange	[e] : cl <==>
EX_CLPND(e)	clupanodonic acid (docosapentaenoic (n-3)) exchange	[e] : clpnd <==>
EX_cmp(e)	CMP exchange	[e] : cmp <==>
EX_co(e)	Carbon monoxide exchange	[e] : co <==>
EX_co2(e)	CO2 exchange	[e] : co2 <==>
EX_coumarin(e)	coumarin exchange	[e] : coumarin <==>
EX_creat(e)	Creatine exchange	[e] : creat <==>
EX_crmp_hs(e)	Ceramide 1-phosphate exchange	[e] : crmp_hs <==>
EX_crn(e)	L-Carnitine exchange	[e] : crn <==>
EX_crvnc(e)	nC22:6 exchange	[e] : crvnc <==>
EX_csn(e)	Cytosine exchange	[e] : csn <==>
EX_cspg_a(e)	chondroitin sulfate A (GalNAc4S-GlcA) proteoglycan exchange	[e] : cspg_a <==>
EX_cspg_b(e)	chondroitin sulfate B / dermatan sulfate (IdoA2S-GalNAc4S) proteoglycan exchange	[e] : cspg_b <==>
EX_cspg_c(e)	chondroitin sulfate C (GalNAc6S-GlcA) proteoglycan exchange	[e] : cspg_c <==>
EX_cspg_d(e)	chondroitin sulfate D (GlcNAc6S-GlcA2S) proteoglycan exchange	[e] : cspg_d <==>
EX_cspg_e(e)	chondroitin sulfate E (GalNAc4,6diS-GlcA) proteoglycan exchange	[e] : cspg_e <==>
EX_cyan(e)	Hydrogen cyanide exchange	[e] : cyan <==>
EX_cys-L(e)	L-Cysteine exchange	[e] : cys-L <==>
EX_cytd(e)	Cytidine exchange	[e] : cytd <==>
EX_dad-2(e)	Deoxyadenosine exchange	[e] : dad-2 <==>
EX_dad-5(e)	5'-Deoxyadenosine exchange	[e] : dad-5 <==>
EX_dag_hs(e)	diacylglycerol (homo sapiens) exchange	[e] : dag_hs <==>
EX_dcsptn1(e)	docosa-4,7,10,13,16-pentaenoic acid (n-6) exchange	[e] : dcsptn1 <==>
EX_dcyt(e)	Deoxycytidine exchange	[e] : dcyt <==>
EX_debrisoquine(e)	debrisoquine exchange	[e] : debrisoquine <==>
EX_dgchol(e)	Chenodeoxyglycocholate exchange	[e] : dgchol <==>
EX_dgsn(e)	Deoxyguanosine exchange	[e] : dgsn <==>
EX_dhdascb(e)	Dehydroascorbate exchange	[e] : dhdascb <==>
EX_dheas(e)	Dehydroepiandrosterone sulfate exchange	[e] : dheas <==>
EX_dhf(e)	7,8-Dihydrofolate exchange	[e] : dhf <==>
EX_digalsgalside_hs(e)	Digalactosylceramidesulfate exchange	[e] : digalsgalside_hs <==>
EX_din(e)	Deoxyinosine exchange	[e] : din <==>
EX_dlnlcg(e)	dihomo-gamma-linolenic acid (n-6) exchange	[e] : dlnlcg <==>

Abbreviation	Reaction Name	Reaction
EX_dmantipyrine(e)	demethylated antipyrine exchange	[e] : dmantipyrine <==>
EX_dmhptcrn(e)	2,6 dimethylheptanoyl carnitine exchange	[e] : dmhptcrn <==>
EX_dopa(e)	Dopamine exchange	[e] : dopa <==>
EX_dopasf(e)	Dopamine 3-O-sulfate exchange	[e] : dopasf <==>
EX_drib(e)	Deoxyribose exchange	[e] : drib <==>
EX_duri(e)	Deoxyuridine exchange	[e] : duri <==>
EX_eaflatoxin(e)	8,9 epxoy aflatoxin B1 exchange	[e] : eaflatoxin <==>
EX_ebastine(e)	ebastine exchange	[e] : ebastine <==>
EX_ebastineoh(e)	hydroxylated ebastine exchange	[e] : ebastineoh <==>
EX_eicostet(e)	eicosatetranoic acid exchange	[e] : eicostet <==>
EX_elaid(e)	elaidic acid exchange	[e] : elaid <==>
EX_estradiolglc(e)	estradiol glucuronide exchange	[e] : estradiolglc <==>
EX_estriolglc(e)	16-Glucuronide-estriol exchange	[e] : estriolglc <==>
EX_estroneglc(e)	estrone glucuronide exchange	[e] : estroneglc <==>
EX_estrones(e)	Estrone 3-sulfate exchange	[e] : estrones <==>
EX_etoh(e)	Ethanol exchange	[e] : etoh <==>
EX_fe2(e)	Fe2+ exchange	[e] : fe2 <==>
EX_fe3(e)	Fe3+ exchange	[e] : fe3 <==>
EX_fol(e)	Folate exchange	[e] : fol <==>
EX_for(e)	Formate exchange	[e] : for <==>
EX_fru(e)	D-Fructose exchange	[e] : fru <==>
EX_fuc13galacglcgal14acglcgalgluside_hs(e)	III3Fuc-nLc6Cer exchange	[e] : fuc13galacglcgal14acglcgalgluside_hs <==>
EX_fuc14galacglcgalgluside_hs(e)	Lea glycolipid exchange	[e] : fuc14galacglcgalgluside_hs <==>
EX_fucacgalfucgalacglcgalgluside_hs(e)	(Gal)2 (GalNAc)1 (Glc)1 (GlcNAc)1 (LFuc)2 (Cer)1 exchange	[e] : fucacgalfucgalacglcgalgluside_hs <==>
EX_fucacngal14acglcgalgluside_hs(e)	IV3-a-NeuAc,III3-a-Fuc-nLc4Cer exchange	[e] : fucacngal14acglcgalgluside_hs <==>
EX_fucacngalacglcgalgluside_hs(e)	IV3-a-Neu5Ac,III4-a-Fuc-Lc4Cer exchange	[e] : fucacngalacglcgalgluside_hs <==>
EX_fucfuc12gal14acglcgalgluside_hs(e)	Ley glycolipid exchange	[e] : fucfuc12gal14acglcgalgluside_hs <==>
EX_fucfuc132galacglcgal14acglcgalgluside_hs(e)	V3Fuc,III3Fuc-nLc6Cer exchange	[e] : fucfuc132galacglcgal14acglcgalgluside_hs <==>
EX_fucfucfucgalacglc13galacglcgal14acglcgalgluside_hs(e)	(Gal)4 (Glc)1 (GlcNAc)3 (LFuc)3 (Cer)1 exchange	[e] : fucfucfucgalacglc13galacglcgal14acglcgalgluside_hs <==>
EX_fucfucfucgalacglcgal14acglcgalgluside_hs(e)	(Gal)3 (Glc)1 (GlcNAc)2 (LFuc)3 (Cer)1 exchange	[e] : fucfucfucgalacglcgal14acglcgalgluside_hs <==>
EX_fucfucgalacglcgalgluside_hs(e)	Leb glycolipid exchange	[e] : fucfucgalacglcgalgluside_hs <==>
EX_fucgal14acglcgalgluside_hs(e)	Lacto-N-fucopentaosyl III ceramide exchange	[e] : fucgal14acglcgalgluside_hs <==>
EX_fucgalfucgalacglcgalgluside_hs(e)	(Gal)3 (Glc)1 (GlcNAc)1 (LFuc)2 (Cer)1 exchange	[e] : fucgalfucgalacglcgalgluside_hs <==>
EX_fucgalgbside_hs(e)	fucosyl galactosylgloboside (homo sapiens) exchange	[e] : fucgalgbside_hs <==>
EX_fuc-L(e)	L-Fucose exchange	[e] : fuc-L <==>
EX_gal(e)	D-Galactose exchange	[e] : gal <==>
EX_galacglcgalgbside_hs(e)	Gal-GlcNAc-Gal globoside (homo sapiens) exchange	[e] : galacglcgalgbside_hs <==>
EX_galfuc12gal14acglcgalgluside_hs(e)	(Gal)3 (Glc)1 (GlcNAc)1 (LFuc)1 (Cer)1 exchange	[e] : galfuc12gal14acglcgalgluside_hs <==>
EX_galfucgalacglcgal14acglcgalgluside_hs(e)	(Gal)4 (Glc)1 (GlcNAc)2 (LFuc)1 (Cer)1 exchange	[e] : galfucgalacglcgal14acglcgalgluside_hs <==>
EX_galgalfucfucgalacglcgalacglcgal14acglcgalgluside_hs(e)	(Gal)6 (Glc)1 (GlcNAc)3 (LFuc)2 (Cer)1 exchange	[e] : galgalfucfucgalacglcgalacglcgal14acglcgalgluside_hs <==>
EX_galgalgalthcrm_hs(e)	Gal-Gal-Gal-Gal-Gal-Glc-Cer (homo sapiens) exchange	[e] : galgalgalthcrm_hs <==>
EX_gam(e)	D-Glucosamine exchange	[e] : gam <==>
EX_gbside_hs(e)	globoside (homo sapiens) exchange	[e] : gbside_hs <==>
EX_gchola(e)	glycocholate exchange	[e] : gchola <==>
EX_gd1b2_hs(e)	GD1beta (homo sapiens) exchange	[e] : gd1b2_hs <==>
EX_gd1c_hs(e)	GD1c (homo sapiens) exchange	[e] : gd1c_hs <==>
EX_gdchola(e)	glycochenodeoxycholate exchange	[e] : gdchola <==>
EX_gdp(e)	GDP exchange	[e] : gdp <==>

Abbreviation	Reaction Name	Reaction
EX_glc(e)	D-Glucose exchange	[e] : glc-D <==>
EX_gln-L(e)	L-Glutamine exchange	[e] : gln-L <==>
EX_gluala(e)	5-L-Glutamyl-L-alanine exchange	[e] : gluala <==>
EX_glu-L(e)	L-Glutamate exchange	[e] : glu-L <==>
EX_gly(e)	Glycine exchange	[e] : gly <==>
EX_glyb(e)	Glycine betaine exchange	[e] : glyb <==>
EX_glyc(e)	Glycerol exchange	[e] : glyc <==>
EX_glyc-S(e)	(S)-Glycerate exchange	[e] : glyc-S <==>
EX_glygn2(e)	glycogen, structure 2 (glycogenin-1,6-{7[1,4-Glc], 4[1,4-Glc]}) exchange	[e] : glygn2 <==>
EX_glygn4(e)	glycogen, structure 4 (glycogenin-1,6-{2[1,4-Glc], [1,4-Glc]}) exchange	[e] : glygn4 <==>
EX_glygn5(e)	glycogen, structure 5 (glycogenin-2[1,4-Glc]) exchange	[e] : glygn5 <==>
EX_gmp(e)	GMP exchange	[e] : gmp <==>
EX_gp1c_hs(e)	GP1c (homo sapiens) exchange	[e] : gp1c_hs <==>
EX_gp1calpha_hs(e)	GP1c alpha (homo sapiens) exchange	[e] : gp1calpha_hs <==>
EX_gq1b_hs(e)	GQ1b (homo sapiens) exchange	[e] : gq1b_hs <==>
EX_gq1balpha_hs(e)	GQ1balpha (homo sapiens) exchange	[e] : gq1balpha_hs <==>
EX_gsn(e)	Guanosine exchange	[e] : gsn <==>
EX_gt1a_hs(e)	GT1a (homo sapiens) exchange	[e] : gt1a_hs <==>
EX_gthox(e)	Oxidized glutathione exchange	[e] : gthox <==>
EX_gthrd(e)	Reduced glutathione exchange	[e] : gthrd <==>
EX_gtp(e)	GTP exchange	[e] : gtp <==>
EX_gua(e)	Guanine exchange	[e] : gua <==>
EX_h(e)	H+ exchange	[e] : h <==>
EX_h2o(e)	H2O exchange	[e] : h2o <==>
EX_h2o2(e)	Hydrogen peroxide exchange	[e] : h2o2 <==>
EX_ha(e)	hyaluronan exchange	[e] : ha <==>
EX_ha_pre1(e)	hyaluronan biosynthesis, precursor 1 exchange	[e] : ha_pre1 <==>
EX_hco3(e)	Bicarbonate exchange	[e] : hco3 <==>
EX_hcoumarin(e)	hydroxy coumarin exchange	[e] : hcoumarin <==>
EX_hdca(e)	Hexadecanoate (n-C16:0) exchange	[e] : hdca <==>
EX_hdcea(e)	hexadecenoate (n-C16:1) exchange	[e] : hdcea <==>
EX_hestratriol(e)	4,17 dihydroxy estradiol exchange	[e] : hestratriol <==>
EX_hexc(e)	hexacosanoate (n-C26:0) exchange	[e] : hexc <==>
EX_his-L(e)	L-Histidine exchange	[e] : his-L <==>
EX_hista(e)	Histamine exchange	[e] : hista <==>
EX_hom-L(e)	L-Homoserine exchange	[e] : hom-L <==>
EX_hpdca(e)	heptadecanoate exchange	[e] : hpdca <==>
EX_hspg(e)	heparan sulfate proteoglycan exchange	[e] : hspg <==>
EX_htaxol(e)	hydroxylated taxol exchange	[e] : htaxol <==>
EX_hxan(e)	Hypoxanthine exchange	[e] : hxan <==>
EX_i(e)	Iodide exchange	[e] : i <==>
EX_idp(e)	IDP exchange	[e] : idp <==>
EX_ile-L(e)	L-Isoleucine exchange	[e] : ile-L <==>
EX_imp(e)	IMP exchange	[e] : imp <==>
EX_inost(e)	myo-Inositol exchange	[e] : inost <==>
EX_ins(e)	Inosine exchange	[e] : ins <==>
EX_k(e)	K+ exchange	[e] : k <==>
EX_ksi(e)	keratan sulfate I exchange	[e] : ksi <==>
EX_ksi_deg1(e)	keratan sulfate I, degradation product 1 exchange	[e] : ksi_deg1 <==>
EX_ksii_core2(e)	keratan sulfate II (core 2-linked) exchange	[e] : ksii_core2 <==>
EX_ksii_core4(e)	keratan sulfate II (core 4-linked) exchange	[e] : ksii_core4 <==>
EX_lac-D(e)	D-lactate exchange	[e] : lac-D <==>
EX_lac-L(e)	L-Lactate exchange	[e] : lac-L <==>
EX_lcts(e)	Lactose exchange	[e] : lcts <==>
EX_Lcystin(e)	L-Cystine exchange	[e] : Lcystin <==>
EX_leuktrC4(e)	Leukotriene C4 exchange	[e] : leuktrC4 <==>
EX_leu-L(e)	L-Leucine exchange	[e] : leu-L <==>
EX_lgnc(e)	lignoceric acid exchange	[e] : lgnc <==>
EX_limnen(e)	Limonene exchange	[e] : limnen <==>
EX_lipoate(e)	Lipoate exchange	[e] : lipoate <==>

Abbreviation	Reaction Name	Reaction
EX_lneldc(e)	linoelaidic acid exchange	[e] : lneldc <==>
EX_lnlc(e)	linoleic acid (all cis C18:2) exchange	[e] : lnlc <==>
EX_lnlc(e) [deleted 08/16/2005 05:23:37 PM]	linoleic acid exchange	[e] : lnlc <==>
EX_lnlnca(e)	alpha-Linolenic acid exchange	[e] : lnlnca <==>
EX_lnlncg(e)	gamma-linolenic acid exchange	[e] : lnlncg <==>
EX_lpchol_hs(e)	lysophosphatidylcholine (homo sapiens) exchange	[e] : lpchol_hs <==>
EX_lys-L(e)	L-Lysine exchange	[e] : lys-L <==>
EX_mag_hs(e)	monoacylglycerol 2 (homo sapiens) exchange	[e] : mag_hs <==>
EX_malt(e)	Maltose exchange	[e] : malt <==>
EX_malttr(e)	Maltotriose exchange	[e] : malttr <==>
EX_man(e)	D-Mannose exchange	[e] : man <==>
EX_meoh(e)	methanol exchange	[e] : meoh <==>
EX_mepi(e)	Metanephrine exchange	[e] : mepi <==>
EX_mercplaccys(e)	3-mercaptolactate-cysteine disulfide exchange	[e] : mercplaccys <==>
EX_met-L(e)	L-Methionine exchange	[e] : met-L <==>
EX_mthgxl(e)	Methylglyoxal exchange	[e] : mthgxl <==>
EX_n2m2nmasn(e)	N-Acetyl-beta-D-glucosaminyl-1,2-alpha-D-mannosyl-1,3-(N-acetyl-beta-D-glucosaminyl-1,2-alpha-D-mannosyl-1,6)-(N-acetyl-beta-D-glucosaminyl-1,4)-beta-D-mannosyl-1,4-N-acetyl-beta-D-glucosaminyl-R exchange	[e] : n2m2nmasn <==>
EX_na1(e)	Sodium exchange	[e] : na1 <==>
EX_nac(e)	Nicotinate exchange	[e] : nac <==>
EX_nad(e)	Nicotinamide adenine dinucleotide exchange	[e] : nad <==>
EX_nadp(e)	Nicotinamide adenine dinucleotide phosphate exchange	[e] : nadp <==>
EX_ncam(e)	Nicotinamide exchange	[e] : ncam <==>
EX_nh4(e)	Ammonia exchange	[e] : nh4 <==>
EX_nifedipine(e)	nifedipine exchange	[e] : nifedipine <==>
EX_no(e)	Nitric oxide exchange	[e] : no <==>
EX_npthl(e)	Naphthalene exchange	[e] : npthl <==>
EX_nrpphr(e)	Norepinephrine exchange	[e] : nrpphr <==>
EX_nrpphrsf(e)	Sulfate derivative of norepinephrine exchange	[e] : nrpphrsf <==>
EX_nrvnc(e)	nervonic acid exchange	[e] : nrvnc <==>
EX_o2(e)	O2 exchange	[e] : o2 <==>
EX_o2s(e)	Superoxide anion exchange	[e] : o2s <==>
EX_oagd3_hs(e)	9-O-Acetylated GD3 (homo sapiens) exchange	[e] : oagd3_hs <==>
EX_oagt3_hs(e)	9-O-Acetylated GT3 (homo sapiens) exchange	[e] : oagt3_hs <==>
EX_ocdca(e)	octadecanoate (n-C18:0) exchange	[e] : ocdca <==>
EX_ocdcea(e)	octadecenoate (n-C18:1) exchange	[e] : ocdcea <==>
EX_octa(e)	octanoate (n-C8:0) exchange	[e] : octa <==>
EX_oh1	OH1 Exchange	[e] : oh1 <==>
EX_omeprazole(e)	omeprazole exchange	[e] : omeprazole <==>
EX_onpthl(e)	naphthalene epoxide exchange	[e] : onpthl <==>
EX_orn(e)	Ornithine exchange	[e] : orn <==>
EX_oxa(e)	Oxalate exchange	[e] : oxa <==>
EX_paf_hs(e)	1-alkyl 2-acteylglycerol 3-phosphocholine (homo sapiens) exchange	[e] : paf_hs <==>
EX_pchol_hs(e)	Phosphatidylcholine (homo sapiens) exchange	[e] : pchol_hs <==>
EX_pe_hs(e)	phosphatidylethanolamine (homo sapiens) exchange	[e] : pe_hs <==>
EX_peplys(e)	Peptidyl-L-lysine exchange	[e] : peplys <==>
EX_perillyl(e)	Perillyl alcohol exchange	[e] : perillyl <==>
EX_pglyc_hs(e)	phosphatidylglycerol (homo sapiens) exchange	[e] : pglyc_hs <==>
EX_pheacgln(e)	alpha-N-Phenylacetyl-L-glutamine exchange	[e] : pheacgln <==>

Abbreviation	Reaction Name	Reaction
EX_phe-L(e)	L-Phenylalanine exchange	[e] : phe-L <==>
EX_pheme(e)	Protoheme exchange	[e] : pheme <==>
EX_phyQ(e)	Phylloquinone exchange	[e] : phyQ <==>
EX_phyt(e)	phytanic acid exchange	[e] : phyt <==>
EX_pi(e)	Phosphate exchange	[e] : pi <==>
EX_pnto-R(e)	(R)-Pantothenate exchange	[e] : pnto-R <==>
EX_ppa(e)	Propionate exchange	[e] : ppa <==>
EX_pro-D(e)	D-Proline exchange	[e] : pro-D <==>
EX_pro-L(e)	L-Proline exchange	[e] : pro-L <==>
EX_prostgd2(e)	Prostaglandin D2 exchange	[e] : prostgd2 <==>
EX_prostge1(e)	Prostaglandin E1 exchange	[e] : prostge1 <==>
EX_prostge2(e)	Prostaglandin E2 exchange	[e] : prostge2 <==>
EX_prostgf2(e)	Prostaglandin F2alpha exchange	[e] : prostgf2 <==>
EX_ps_hs(e)	phosphatidylserine (homo sapiens) exchange	[e] : ps_hs <==>
EX_ptdca(e)	pentadecanoate exchange	[e] : ptdca <==>
EX_pydam(e)	Pyridoxamine exchange	[e] : pydam <==>
EX_pydx(e)	Pyridoxal exchange	[e] : pydx <==>
EX_pydxn(e)	Pyridoxine exchange	[e] : pydxn <==>
EX_pyr(e)	Pyruvate exchange	[e] : pyr <==>
EX_rbt(e)	Ribitol exchange	[e] : rbt <==>
EX_retfa(e)	fatty acid retinol exchange	[e] : retfa <==>
EX_retinol(e)	Retinol exchange	[e] : retinol <==>
EX_retinol-9-cis(e)	9-cis-retinol exchange	[e] : retinol-9-cis <==>
EX_retinol-cis-11(e)	cis-11-retinol exchange	[e] : retinol-cis-11 <==>
EX_retn(e)	Retinoate exchange	[e] : retn <==>
EX_retnglc(e)	retinoyl glucuronide exchange	[e] : retnglc <==>
EX_retpalm [deleted 10/09/2005 06:18:49 PM](e)	Retinyl palminate exchange	[e] : retpalm [deleted 10/09/2005 06:18:49 PM] <==>
EX_retpalm(e) [deleted 10/09/2005 06:38:54 PM]	Retinyl palminate exchange	[e] : retpalm [deleted 10/09/2005 06:18:49 PM] <==>
EX_rib-D(e)	D-Ribose exchange	[e] : rib-D <==>
EX_ribflv(e)	Riboflavin exchange	[e] : ribflv <==>
EX_Rtotal(e)	R total exchange	[e] : Rtotal <==>
EX_Rtotal2(e)	R total 2 position exchange	[e] : Rtotal2 <==>
EX_Rtotal3(e)	R total 3 position exchange	[e] : Rtotal3 <==>
EX_s2l2fn2m2masn(e)	PA6 exchange	[e] : s2l2fn2m2masn <==>
EX_s2l2n2m2masn(e)	de-Fuc form of PA6 exchange	[e] : s2l2n2m2masn <==>
EX_sarcs(e)	Sarcosine exchange	[e] : sarcs <==>
EX_sel(e)	Selenate exchange	[e] : sel <==>
EX_ser-D(e)	D-Serine exchange	[e] : ser-D <==>
EX_ser-L(e)	L-Serine exchange	[e] : ser-L <==>
EX_sl-L(e)	L-sulfolactate exchange	[e] : sl-L <==>
EX_so4(e)	Sulfate exchange	[e] : so4 <==>
EX_spc_hs(e)	sphingosylphosphorylcholine (homo sapiens) exchange	[e] : spc_hs <==>
EX_sph1p(e)	Sphinganine 1-phosphate exchange	[e] : sph1p <==>
EX_sphs1p(e)	Sphingosine 1-phosphate exchange	[e] : sphs1p <==>
EX_srtn(e)	Serotonin exchange	[e] : srtn <==>
EX_strch1(e)	starch, structure 1 (1,6-{7[1,4-Glc], 4[1,4-Glc]}) exchange	[e] : strch1 <==>
EX_strch2(e)	starch, structure 2 (1,6-{2[1,4-Glc], [1,4-Glc]}) exchange	[e] : strch2 <==>
EX_strdnc(e)	stearidonic acid exchange	[e] : strdnc <==>
EX_succ(e)	Succinate exchange	[e] : succ <==>
EX_sucr(e)	Sucrose exchange	[e] : sucr <==>
EX_tag_hs(e)	triacylglycerol (homo sapiens) exchange	[e] : tag_hs <==>
EX_tagat-D(e)	D-Tagatose exchange	[e] : tagat-D <==>
EX_taur(e)	Taurine exchange	[e] : taur <==>
EX_taxol(e)	paclitaxel exchange	[e] : taxol <==>
EX_tchola(e)	Taurocholic acid exchange	[e] : tchola <==>
EX_tcynt(e)	Thiocyanate exchange	[e] : tcynt <==>
EX_tdchola(e)	taurochenodeoxycholate exchange	[e] : tdchola <==>
EX_tethex3(e)	tetracosahexaenoic acid, n-3 exchange	[e] : tethex3 <==>

Abbreviation	Reaction Name	Reaction
EX_tetpent3(e)	tetracosapentaenoic acid, n-3 exchange	[e] : tetpent3 <==>
EX_tetpent6(e)	tetracosapentaenoic acid, n-6 exchange	[e] : tetpent6 <==>
EX_tettet6(e)	tetracosatetraenoic acid n-6 exchange	[e] : tettet6 <==>
EX_thf(e)	5,6,7,8-Tetrahydrofolate exchange	[e] : thf <==>
EX_thm(e)	Thiamin exchange	[e] : thm <==>
EX_thmmp(e)	Thiamin monophosphate exchange	[e] : thmmp <==>
EX_thmtp(e)	Thiamin triphosphate exchange	[e] : thmtp <==>
EX_thr-L(e)	L-Threonine exchange	[e] : thr-L <==>
EX_thym(e)	Thymine exchange	[e] : thym <==>
EX_thymd(e)	Thymidine exchange	[e] : thymd <==>
EX_thyox-L(e)	L-Thyroxine exchange	[e] : thyox-L <==>
EX_tmndnc(e)	timnodonic acid exchange	[e] : tmndnc <==>
EX_tolbutamide(e)	tolbutamide exchange	[e] : tolbutamide <==>
EX_tre(e)	Trehalose exchange	[e] : tre <==>
EX_triodthy(e)	Triiodothyronine exchange	[e] : triodthy <==>
EX_triodthysuf(e)	Triiodothyronine sulfate exchange	[e] : triodthysuf <==>
EX_trp-L(e)	L-Tryptophan exchange	[e] : trp-L <==>
EX_tststeroneglc(e)	testosterone glucuronide exchange	[e] : tststeroneglc <==>
EX_tststerones(e)	testosterone sulfate exchange	[e] : tststerones <==>
EX_tsul(e)	Thiosulfate exchange	[e] : tsul <==>
EX_ttdca(e)	tetradecanoate (n-C14:0) exchange	[e] : ttdca <==>
EX_txa2(e)	Thromboxane A2 exchange	[e] : txa2 <==>
EX_tymsf(e)	Tyramine O-sulfate exchange	[e] : tymsf <==>
EX_Tyr-ggn(e)	Tyr-194 of apo-glycogenin protein (primer for glycogen synthesis) exchange	[e] : Tyr-ggn <==>
EX_tyr-L(e)	L-Tyrosine exchange	[e] : tyr-L <==>
EX_udp(e)	UDP exchange	[e] : udp <==>
EX_ump(e)	UMP exchange	[e] : ump <==>
EX_ura(e)	Uracil exchange	[e] : ura <==>
EX_urate(e)	Urate exchange	[e] : urate <==>
EX_urea(e)	Urea exchange	[e] : urea <==>
EX_uri(e)	Uridine exchange	[e] : uri <==>
EX_utp(e)	UTP exchange	[e] : utp <==>
EX_vacc(e)	vaccenic acid exchange	[e] : vacc <==>
EX_val-L(e)	L-Valine exchange	[e] : val-L <==>
EX_vitd2(e)	Vitamin D2 exchange	[e] : vitd2 <==>
EX_vitd3(e)	Vitamin D3 exchange	[e] : vitd3 <==>
EX_whddca(e)	omega hydroxy dodecanoate (n-C12:0) exchange	[e] : whddca <==>
EX_whhdca(e)	omega hydroxy hexadecanoate (n-C16:0) exchange	[e] : whhdca <==>
EX_whtststerone(e)	w hydroxy testosterone exchange	[e] : whtststerone <==>
EX_whttdca(e)	omega hydroxy tetradecanoate (n-C14:0) exchange	[e] : whttdca <==>
EX_xolest_hs(e)	cholesterol ester exchange	[e] : xolest_hs <==>
EX_xolest2_hs(e)	cholesterol ester (from FULLR2) exchange	[e] : xolest2_hs <==>
EX_xoltri24(e)	7-alpha,24(S)-Dihydroxycholesterol exchange	[e] : xoltri24 <==>
EX_xoltri25(e)	7-alpha,25-Dihydroxycholesterol exchange	[e] : xoltri25 <==>
EX_xoltri27(e)	7-alpha,27-Dihydroxycholesterol exchange	[e] : xoltri27 <==>
EX_xyl-D(e)	D-Xylose exchange	[e] : xyl-D <==>
EX_xylt(e)	Xylitol exchange	[e] : xylt <==>
EX_yvite(e)	gamma-Tocopherol exchange	[e] : yvite <==>

Table 7: *H. sapiens* Recon 1 metabolites. Alphabetized list of compartment-specific metabolites. Metabolite formula and charge were determined based on ionization state at pH 7.2 (see text for details).

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
10fthf	10-Formyltetrahydrofolate	10-Formyl-THF	C20H21N7O7	-2	Cytosol
10fthf	10-Formyltetrahydrofolate	10-Formyl-THF	C20H21N7O7	-2	Extracellular
10fthf	10-Formyltetrahydrofolate	10-Formyl-THF	C20H21N7O7	-2	Lysosome
10fthf	10-Formyltetrahydrofolate	10-Formyl-THF	C20H21N7O7	-2	Mitochondria
10fthf5glu	10-formyltetrahydrofolate-[Glu](5)		C40H45N11O19	-6	Cytosol
10fthf5glu	10-formyltetrahydrofolate-[Glu](5)		C40H45N11O19	-6	Extracellular
10fthf5glu	10-formyltetrahydrofolate-[Glu](5)		C40H45N11O19	-6	Lysosome
10fthf5glu	10-formyltetrahydrofolate-[Glu](5)		C40H45N11O19	-6	Mitochondria
10fthf6glu	10-formyltetrahydrofolate-[Glu](6)		C45H51N12O22	-7	Cytosol
10fthf6glu	10-formyltetrahydrofolate-[Glu](6)		C45H51N12O22	-7	Extracellular
10fthf6glu	10-formyltetrahydrofolate-[Glu](6)		C45H51N12O22	-7	Lysosome
10fthf6glu	10-formyltetrahydrofolate-[Glu](6)		C45H51N12O22	-7	Mitochondria
10fthf7glu	10-formyltetrahydrofolate-[Glu](7)		C50H57N13O25	-8	Cytosol
10fthf7glu	10-formyltetrahydrofolate-[Glu](7)		C50H57N13O25	-8	Extracellular
10fthf7glu	10-formyltetrahydrofolate-[Glu](7)		C50H57N13O25	-8	Lysosome
10fthf7glu	10-formyltetrahydrofolate-[Glu](7)		C50H57N13O25	-8	Mitochondria
11-cis-retfa	fatty acid 11-cis-retinol		C20H29OFULLR2CO	0	Cytosol
11-cis-retfa	fatty acid 11-cis-retinol		C20H29OFULLR2CO	0	Extracellular
11docrtsl	11-Deoxycortisol	11-Deoxycortisol	C21H30O4	0	Cytosol
11docrtsl	11-Deoxycortisol	11-Deoxycortisol	C21H30O4	0	Mitochondria
11docrtsl	11-Deoxycortisol	11-Deoxycortisol	C21H30O4	0	Endoplasmic Reticulum
11docrtstrn	11-Deoxycorticosterone	11-Deoxycorticosterone, 21-Hydroxy-4-pregnene-3,20-dione, Cortexone, DOC, Deoxycorticosterone	C21H30O3	0	Cytosol
11docrtstrn	11-Deoxycorticosterone	11-Deoxycorticosterone, 21-Hydroxy-4-pregnene-3,20-dione, Cortexone, DOC, Deoxycorticosterone	C21H30O3	0	Mitochondria
11docrtstrn	11-Deoxycorticosterone	11-Deoxycorticosterone, 21-Hydroxy-4-pregnene-3,20-dione, Cortexone, DOC, Deoxycorticosterone	C21H30O3	0	Endoplasmic Reticulum
12harachd	12 hydroxy arachidonic acid		C20H31O3	-1	Endoplasmic Reticulum
12HPET	12-Hydroperoxyeicosa-5,8,10,14-tetraenoate	(5Z,8Z,10E,14Z)-(12S)-12-Hydroperoxyicosa-5,8,10,14-tetraenoic acid, 12-HPETE, 12-Hydroperoxyeicosatetraenoate, 12-Hydroperoxyeicosatetraenoic acid, 12-Hydroperoxyicosatetraenoate, 12-Hydroperoxyicosatetraenoic acid	C20H31O4	-1	Cytosol
12ppd-R	(R)-Propane-1,2-diol	(R)-1,2-Propanediol, (R)-Propylene glycol, D-1,2-propanediol	C3H8O2	0	Cytosol
12ppd-S	(S)-Propane-1,2-diol	(S)-1,2-Propanediol, (S)-Propylene glycol, L-1,2-propanediol	C3H8O2	0	Cytosol
12RHPET	12R-Hydroperoxyeicosatetraenoate	(5Z,8Z,10E,14Z)-(12R)-12-Hydroperoxyicosa-5,8,10,14-tetraenoic acid, 12-HPETE, 12-Hydroperoxyeicosatetraenoic acid, 12-Hydroperoxyicosatetraenoate, 12-Hydroperoxyicosatetraenoic acid	C20H31O4	-1	Cytosol
13-cis-oretn	13-cis-oxo-retinoic acid		C20H27O3	-1	Cytosol
13-cis-oretn	13-cis-oxo-retinoic acid		C20H27O3	-1	Nucleus
13-cis-retn	13-cis-retinoate		C20H27O2	-1	Cytosol
13-cis-retn	13-cis-retinoate		C20H27O2	-1	Nucleus
13-cis-retn	13-cis-retinoate		C20H27O2	-1	Endoplasmic Reticulum
13-cis-retnglc	13-cis-retinoyl glucuronide		C26H35O8	-1	Cytosol
13-cis-retnglc	13-cis-retinoyl glucuronide		C26H35O8	-1	Extracellular
13-cis-retnglc	13-cis-retinoyl glucuronide		C26H35O8	-1	Endoplasmic Reticulum
13dampp	1,3-Diaminopropane	1,3-Propanediamine, Propane-1,3-diamine, Trimethylenediamine	C3H12N2	2	Cytosol
13dpg	3-Phospho-D-glyceroyl phosphate	(R)-2-Hydroxy-3-(phosphonooxy)-1-monoanhydride with phosphoric propanoic acid, 1,3-bis-phosphoglycerate, 3-Phospho-D-glyceroyl phosphate	C3H4O10P2	-4	Cytosol
15HPET	15-Hydroperoxyeicosatetraenoic acid	(5Z,8Z,11Z,13E)-(15S)-15-Hydroperoxyicosa-5,8,11,13-tetraenoate, 15-HPETE, 15-Hydroperoxyeicosatetraenoate, 15-Hydroperoxyeicosatetraenoic acid, 15-Hydroperoxyicosatetraenoate, 15-Hydroperoxyicosatetraenoic acid	C20H31O4	-1	Cytosol
17ahprgnlone	17alpha-Hydroxypregnenolone	17alpha-Hydroxypregnenolone	C21H32O3	0	Cytosol
17ahprgnlone	17alpha-Hydroxypregnenolone	17alpha-Hydroxypregnenolone	C21H32O3	0	Endoplasmic Reticulum
17ahprgstrn	17alpha-Hydroxyprogesterone	17alpha-Hydroxy-4-pregnene-3,20-dione, 17alpha-Hydroxy-progesterone, 17alpha-Hydroxyprogesterone;, Pregn-4-ene-3,20-dione-17-ol	C21H30O3	0	Cytosol
17ahprgstrn	17alpha-Hydroxyprogesterone	17alpha-Hydroxy-4-pregnene-3,20-dione, 17alpha-Hydroxy-progesterone, 17alpha-Hydroxyprogesterone;, Pregn-4-ene-3,20-dione-17-ol	C21H30O3	0	Endoplasmic Reticulum
18harachd	18 hydroxy arachidonic acid		C20H31O3	-1	Endoplasmic Reticulum
1a2425thvitd2	1-alpha,24R,25-Trihydroxyvitamin D2		C28H44O4	0	Mitochondria
1a2425thvitd3	1-alpha,24R,25-Trihydroxyvitamin D3		C27H44O4	0	Mitochondria
1a25dhvitd2	1-alpha,25-Dihydroxyvitamin D2		C28H44O3	0	Mitochondria
1a25dhvitd3	1-alpha,25-Dihydroxyvitamin D3	Calcitriol;, Rocaltrol (TN)	C27H44O3	0	Mitochondria
1glyc_hs	1 acyl phosphoglycerol	glycerol phosphate, glycerolipid, phoso glycerol, phosphate glycerol	C6H13O7PFULLRCO2	-1	Extracellular
1mncam	1-Methylnicotinamide		C7H9N2O	1	Cytosol
1mncam	1-Methylnicotinamide		C7H9N2O	1	Extracellular
1mpyr	1-Methylpyrrolinium	1-Methylpyrrolinium	C5H10N	1	Cytosol

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
1p2cbxl	1-Pyrroline-2-carboxylate	1-Pyrroline-2-carboxylic acid	C5H6NO2	-1	Peroxisome
1p3h5c	L-1-Pyrroline-3-hydroxy-5-carboxylate	3-Hydroxy-L-1-pyrroline-5-carboxylate	C5H6NO3	-1	Mitochondria
1pipdn2c	delta1-Piperideine-2-carboxylate		C6H9NO2	0	Peroxisome
1pyr5c	1-Pyrroline-5-carboxylate	(S)-1-Pyrroline-5-carboxylate, 1-Pyrroline-5-carboxylic acid, L-1-Pyrroline-5-carboxylate	C5H6NO2	-1	Cytosol
1pyr5c	1-Pyrroline-5-carboxylate	(S)-1-Pyrroline-5-carboxylate, 1-Pyrroline-5-carboxylic acid, L-1-Pyrroline-5-carboxylate	C5H6NO2	-1	Mitochondria
20ahchsterol	20alpha-hydroxy cholesterol		C27H46O2	0	Mitochondria
23doguln	2,3-Dioxo-L-gulonate	2,3-diketo-gulonic acid, 2,3-diketogulonate, DKG, diketogulonate	C6H7O7	-1	Cytosol
23dpg	2,3-Disphospho-D-glycerate	2,3-Bisphospho-D-glycerate, 3-Phospho-D-glycero phosphate, D-Greenwald ester, DPG	C3H3O10P2	-5	Cytosol
2425dhvitd2	24R,25-Dihyoxyvitamin D2		C28H44O3	0	Cytosol
2425dhvitd2	24R,25-Dihyoxyvitamin D2		C28H44O3	0	Extracellular
2425dhvitd2	24R,25-Dihyoxyvitamin D2		C28H44O3	0	Mitochondria
2425dhvitd3	24R,25-Dihydroxyvitamin D3		C27H44O3	0	Cytosol
2425dhvitd3	24R,25-Dihydroxyvitamin D3		C27H44O3	0	Extracellular
2425dhvitd3	24R,25-Dihydroxyvitamin D3		C27H44O3	0	Mitochondria
24nph	2,4 dihydroxy nitrophenol	2 hydroxy 4 nitrophenol, 2 hydroxy, 4 hydroxy nitr benzene	C6H5NO4	0	Cytosol
24nph	2,4 dihydroxy nitrophenol	2 hydroxy 4 nitrophenol, 2 hydroxy, 4 hydroxy nitr benzene	C6H5NO4	0	Extracellular
25aics	(S)-2-[5-Amino-1-(5-phospho-D-ribosyl)imidazole-4-carboxamido]succinate	1-(5'-Phosphoribosyl)-4-(N-succinocarboxamide)-5-aminoimidazole, 1-(5'-Phosphoribosyl)-5-amino-4-(N-succinocarboxamide)-imidazole, 5'-Phosphoribosyl-4-(N-succinocarboxamide)-5-aminoimidazole	C13H15N4O12P	-4	Cytosol
25hvitd2	25-Hydroxyvitamin D2		C28H44O2	0	Cytosol
25hvitd2	25-Hydroxyvitamin D2		C28H44O2	0	Extracellular
25hvitd2	25-Hydroxyvitamin D2		C28H44O2	0	Mitochondria
25hvitd3	25-Hydroxyvitamin D3	Calcidiol;, Calcifediol anhydrous;, Calcifediol;, Calderol (TN)	C27H44O2	0	Cytosol
25hvitd3	25-Hydroxyvitamin D3	Calcidiol;, Calcifediol anhydrous;, Calcifediol;, Calderol (TN)	C27H44O2	0	Extracellular
25hvitd3	25-Hydroxyvitamin D3	Calcidiol;, Calcifediol anhydrous;, Calcifediol;, Calderol (TN)	C27H44O2	0	Mitochondria
2amac	2-Aminoacrylate	Dehydroalanine	C3H5NO2	0	Cytosol
2ameph	(2-Aminoethyl)phosphonate	2-Aminoethylphosphonate, Ciliatine	C2H7NO3P	-1	Cytosol
2aobut	L-2-Amino-3-oxobutanoate	L-2-Amino-acetoacetate	C4H7NO3	0	Mitochondria
2c23dh56dhoxin	2-Carboxy-2,3-dihydro-5,6-dihydroxyindole	2-Carboxy-2,3-dihydro-5,6-dihydroxyindole, Leucodopachrome	C9H8NO4	-1	Cytosol
2coum	cis-2-Hydroxy cinnamate	2-Coumarinate	C9H7O3	-1	Cytosol
2dp6mep	2-Decaprenyl-6-methoxyphenol		C57H88O2	0	Mitochondria
2dp6mobq	2-Decaprenyl-6-methoxy-1,4-benzoquinone		C57H86O3	0	Mitochondria
2dp6mobq_me	2-Decaprenyl-3-methyl-6-methoxy-1,4-benzoquinone		C58H88O3	0	Mitochondria
2dpmhobq	2-Decaprenyl-3-methyl-5-hydroxy-6-methoxy-1,4-benzoquinone		C58H88O4	0	Mitochondria
2dr1p	2-Deoxy-D-ribose 1-phosphate	Deoxy-ribose 1-phosphate	C5H9O7P	-2	Cytosol
2dr5p	2-Deoxy-D-ribose 5-phosphate		C5H9O7P	-2	Cytosol
2hb	2-Hydroxybutyrate	2-Hydroxybutyric acid	C4H7O3	-1	Cytosol
2hb	2-Hydroxybutyrate	2-Hydroxybutyric acid	C4H7O3	-1	Extracellular
2hyoxplac	2-Hydroxyphenylacetate	2-Hydroxyphenylacetate	C8H7O3	-1	Cytosol
2kmb	2-keto-4-methylthiobutyrate	2-oxo-4-(methylthio)butyrate, 4-methylthio-2-oxobutanoate	C5H7O3S	-1	Cytosol
2maacoa	2-Methyl-3-acetoacetyl-CoA	2-Methylacetoacetyl-CoA	C26H38N7O18P3S	-4	Mitochondria
2mb2coa	trans-2-Methylbut-2-enoyl-CoA	(E)-2-Methylcrotonoyl-CoA, 2-Methylbut-2-enoyl-CoA, Tiglyl-CoA, methylcrotonoyl-CoA, methylcrotonyl-CoA, tigloyl-CoA	C26H38N7O17P3S	-4	Mitochondria
2mbcoa	2-Methylbutanoyl-CoA	2-Methylbutyryl-CoA	C26H40N7O17P3S	-4	Mitochondria
2mcacn	cis-2-Methylaconitate	(Z)-But-2-ene-1,2,3-tricarboxylate, cis-2-Methylaconitate	C7H5O6	-3	Cytosol
2mcit	2-Methylcitrate		C7H7O7	-3	Cytosol
2mcit	2-Methylcitrate		C7H7O7	-3	Extracellular
2mop	2-Methyl-3-oxopropanoate	(S)-methylmalonate semialdehyde, 3-Oxo-2-methylpropanoate, Methylmalonate semialdehyde	C4H5O3	-1	Mitochondria
2mp2coa	2-Methylprop-2-enoyl-CoA	Methacrylyl-CoA, Methylacrylyl-CoA	C25H36N7O17P3S	-4	Mitochondria
2obut	2-Oxobutanoate	2-Ketobutyric acid, 2-Oxobutanoic acid, 2-Oxobutyrate, 2-Oxobutyric acid, alpha-Ketobutyrate	C4H5O3	-1	Cytosol
2oxoadp	2-Oxoadipate	2-Oxoadipic acid	C6H6O5	-2	Cytosol
2oxoadp	2-Oxoadipate	2-Oxoadipic acid	C6H6O5	-2	Mitochondria
2pg	D-Glycerate 2-phosphate	2-Phospho-D-glycerate, 2-phosphoglyceric acid	C3H4O7P	-3	Cytosol
2pglyc	2-Phosphoglycolate	2-phosphoglycolic acid, Phosphoglycolic acid	C2H2O6P	-3	Cytosol
34dhcinm	3,4-Dihydroxy-trans-cinnamate	trans-Caffeate	C9H7O4	-1	Cytosol
34dhmald	3,4-Dihydroxymandelaldehyde		C8H8O4	0	Cytosol
34dhoxmand	3,4-Dihydroxymandelate		C8H7O5	-1	Cytosol
34dhoxpeg	3,4-Dihydroxyphenylethyleneglycol	3,4-Dihydroxyphenylethyleneglycol	C8H10O4	0	Cytosol
34dhoxpeg	3,4-Dihydroxyphenylethyleneglycol	3,4-Dihydroxyphenylethyleneglycol	C8H10O4	0	Extracellular
34dhpac	3,4-Dihydroxyphenylacetaldehyde	3,4-Dihydroxyphenylacetaldehyde, Protocatechuatealdehyde	C8H8O3	0	Cytosol

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
34dhpha	3,4-Dihydroxyphenylacetate	3,4-Dihydroxyphenyl acetate, 3,4-Dihydroxyphenyl acetic acid, 3,4-Dihydroxyphenylacetic acid, Homoprotocatechuate	C8H7O4	-1	Cytosol
34dhphe	3,4-Dihydroxy-L-phenylalanine	3-Hydroxy-L-tyrosine, Dihydroxy-L-phenylalanine, Hydroxy-L-tyrosine, L-Dopa, L-beta-(3,4-Dihydroxyphenyl)alanine, Levodopa	C9H11NO4	0	Cytosol
34dhphe	3,4-Dihydroxy-L-phenylalanine	3-Hydroxy-L-tyrosine, Dihydroxy-L-phenylalanine, Hydroxy-L-tyrosine, L-Dopa, L-beta-(3,4-Dihydroxyphenyl)alanine, Levodopa	C9H11NO4	0	Extracellular
34hpl	3-(4-Hydroxyphenyl)lactate	4-Hydroxyphenyllactate, p-Hydroxyphenyllactate	C9H9O4	-1	Mitochondria
34hpp	3-(4-Hydroxyphenyl)pyruvate	4-Hydroxyphenylpyruvate, p-Hydroxyphenylpyruvic acid	C9H7O4	-1	Cytosol
34hpp	3-(4-Hydroxyphenyl)pyruvate	4-Hydroxyphenylpyruvate, p-Hydroxyphenylpyruvic acid	C9H7O4	-1	Mitochondria
35cgmp	3',5'-Cyclic GMP	Cyclic GMP, Guanosine 3',5'-cyclic monophosphate, Guanosine 3',5'-cyclic phosphate	C10H11N5O7P	-1	Cytosol
35cgmp	3',5'-Cyclic GMP	Cyclic GMP, Guanosine 3',5'-cyclic monophosphate, Guanosine 3',5'-cyclic phosphate	C10H11N5O7P	-1	Extracellular
35cgmp	3',5'-Cyclic GMP	Cyclic GMP, Guanosine 3',5'-cyclic monophosphate, Guanosine 3',5'-cyclic phosphate	C10H11N5O7P	-1	Golgi Apparatus
35cgmp	3',5'-Cyclic GMP	Cyclic GMP, Guanosine 3',5'-cyclic monophosphate, Guanosine 3',5'-cyclic phosphate	C10H11N5O7P	-1	Nucleus
35diotyr	3,5-Diiodo-L-tyrosine	3,5-Diiodotyrosine, L-Diiodotyrosine	C9H9I2NO3	0	Cytosol
3aib	L-3-Amino-isobutanoate	(S)-3-Amino-isobutanoate, (S)-3-Amino-isobutyrate, L-3-Amino-isobutyrate, b-Aminoisobutyrate	C4H9NO2	0	Cytosol
3aib	L-3-Amino-isobutanoate	(S)-3-Amino-isobutanoate, (S)-3-Amino-isobutyrate, L-3-Amino-isobutyrate, b-Aminoisobutyrate	C4H9NO2	0	Extracellular
3aib	L-3-Amino-isobutanoate	(S)-3-Amino-isobutanoate, (S)-3-Amino-isobutyrate, L-3-Amino-isobutyrate, b-Aminoisobutyrate	C4H9NO2	0	Mitochondria
3aib-D	D-3-Amino-isobutanoate	D-3-Amino-isobutanoate	C4H9NO2	0	Cytosol
3aib-D	D-3-Amino-isobutanoate	D-3-Amino-isobutanoate	C4H9NO2	0	Extracellular
3aib-D	D-3-Amino-isobutanoate	D-3-Amino-isobutanoate	C4H9NO2	0	Mitochondria
3amp	3'-AMP	3'-Adenosine monophosphate, 3'-Adenylic acid, AMP 3'-phosphate, Adenosine 3'-phosphate, Adenosine-3'-monophosphate	C10H12N5O7P	-2	Lysosome
3dhguln	3-Dehydro-L-gulonate	3-keto-L-gulonate	C6H9O7	-1	Cytosol
3dpdhb	3-Decaprenyl-4,5-dihdydroxybenzoate		C57H85O4	-1	Mitochondria
3dpdhb_me	3-Decaprenyl-4-hydroxy-5-methoxybenzoate		C58H87O4	-1	Mitochondria
3dphb	3-Decaprenyl-4-hydroxybenzoate		C57H85O3	-1	Mitochondria
3dsphgn	3-Dehydrosphinganine	3-Dehydro-D-sphinganine	C18H38NO2	1	Cytosol
3h26dm5coa	3-Hydroxy-2,6-dimethyl-5-methylene-heptanoyl-CoA		C31H48N7O18P3S	-4	Mitochondria
3h26dm5coa	3-Hydroxy-2,6-dimethyl-5-methylene-heptanoyl-CoA		C31H48N7O18P3S	-4	Peroxisome
3hanthrn	3-Hydroxyanthranilate	3-Hydroxyanthranilic acid	C7H7NO3	0	Cytosol
3hbcoa	(S)-3-Hydroxybutanoyl-CoA	(S)-3-Hydroxybutyryl-CoA	C25H38N7O18P3S	-4	Mitochondria
3hbcoa	(S)-3-Hydroxybutanoyl-CoA	(S)-3-Hydroxybutyryl-CoA	C25H38N7O18P3S	-4	Peroxisome
3hbcoa-R	(R)-3-Hydroxybutanoyl-CoA	(3R)-3-Hydroxybutanoyl-CoA	C25H38N7O18P3S	-4	Mitochondria
3hibutcoa	(S)-3-Hydroxyisobutyryl-CoA		C25H38N7O18P3S	-4	Mitochondria
3hmbcoa	(S)-3-Hydroxy-2-methylbutyryl-CoA	(2S,3S)-3-Hydroxy-2-methylbutanoyl-CoA	C26H40N7O18P3S	-4	Mitochondria
3hmp	3-Hydroxy-2-methylpropanoate	(S)-3-hydroxyisobutyrate, 3-Hydroxyisobutyrate, 3-Hydroxyisobutyric acid	C4H7O3	-1	Mitochondria
3hpcoa	3-Hydroxypropionyl-CoA	3-Hydroxyisobutyryl coemzyme A, 3-Hydroxyisobutyryl-CoA, 3-Hydroxypropanoyl coemzymeA, 3-Hydroxypropanoyl-CoA, 3-Hydroxypropionyl coemzyme A	C24H36N7O18P3S	-4	Cytosol
3hpcoa	3-Hydroxypropionyl-CoA	3-Hydroxyisobutyryl coemzyme A, 3-Hydroxyisobutyryl-CoA, 3-Hydroxypropanoyl coemzymeA, 3-Hydroxypropanoyl-CoA, 3-Hydroxypropionyl coemzyme A	C24H36N7O18P3S	-4	Mitochondria
3hpcoa	3-Hydroxypropionyl-CoA	3-Hydroxyisobutyryl coemzyme A, 3-Hydroxyisobutyryl-CoA, 3-Hydroxypropanoyl coemzymeA, 3-Hydroxypropanoyl-CoA, 3-Hydroxypropionyl coemzyme A	C24H36N7O18P3S	-4	Peroxisome
3hpp	3-Hydroxypropanoate	3-Hydropropionic acid, 3-Hydroxyisobutyrate, 3-Hydroxyisobutyric acid, 3-Hydroxypropanoic acid, 3-Hydroxypropenoate, 3-Hydroxypropionate, 3-Hydroxypropionic acid, Hydracrylic acid	C3H5O3	-1	Cytosol
3htmelys	3-Hydroxy-N6,N6,N6-trimethyl-L-lysine		C9H20N2O3	0	Cytosol
3htmelys	3-Hydroxy-N6,N6,N6-trimethyl-L-lysine		C9H20N2O3	0	Mitochondria
3hxkynam	3-Hydroxykynurenamine		C9H13N2O2	1	Cytosol
3ityr-L	3-Iodo-L-tyrosine	3-Iodo-L-tyrosine	C9H10INO3	0	Cytosol
3m4hpga	3-Methoxy-4-hydroxyphenylglycolaldehyde		C9H10O4	0	Cytosol

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
3mb2coa	3-Methylbut-2-enoyl-CoA	3-Methylcrotonoyl-CoA	C26H38N7O17P3S	-4	Mitochondria
3mgcoa	3-Methylglutaconyl-CoA	trans-3-Methylglutaconyl-CoA	C27H37N7O19P3S	-5	Mitochondria
3mlda	3-Methylimidazoleacetic acid	1-Methyl-4-imidazoleacetic acid, Tele-methylimidazoleacetic acid	C6H7N2O2	-1	Cytosol
3mlda	3-Methylimidazoleacetic acid	1-Methyl-4-imidazoleacetic acid, Tele-methylimidazoleacetic acid	C6H7N2O2	-1	Extracellular
3mldz	3-Methylimidazole acetaldehyde	1-Methylimidazole-4-acetaldehyde, Methylimidazoleacetaldehyde	C6H8N2O	0	Cytosol
3mob	3-Methyl-2-oxobutanoate	2-Keto-3-methylbutyric acid, 2-Ketovaline, 2-Oxo-methylbutanoate, 2-Oxoisopentanoate, 2-Oxoisovalerate, 3-Methyl-2-oxobutyric acid, alpha-Ketovaline	C5H7O3	-1	Cytosol
3mob	3-Methyl-2-oxobutanoate	2-Keto-3-methylbutyric acid, 2-Ketovaline, 2-Oxo-methylbutanoate, 2-Oxoisopentanoate, 2-Oxoisovalerate, 3-Methyl-2-oxobutyric acid, alpha-Ketovaline	C5H7O3	-1	Mitochondria
3mop	(S)-3-Methyl-2-oxopentanoate	(R)-2-oxo-3-methylpentanoate, (S)-2-oxo-3-methylpentanoate, 2-oxo-3-methylpentanoate, alph keto-beta-methylvalerate, alpha-oxo-beta-methylvalerate, ketoisoleucine	C6H9O3	-1	Cytosol
3mop	(S)-3-Methyl-2-oxopentanoate	(R)-2-oxo-3-methylpentanoate, (S)-2-oxo-3-methylpentanoate, 2-oxo-3-methylpentanoate, alph keto-beta-methylvalerate, alpha-oxo-beta-methylvalerate, ketoisoleucine	C6H9O3	-1	Mitochondria
3mox4hoxm	3-Methoxy-4-hydroxymandelate	Vanillylmandelic acid	C9H9O5	-1	Cytosol
3mox4hpac	3-Methoxy-4-hydroxyphenylacetaldehyde		C9H10O3	0	Cytosol
3moxtyr	3-Methoxytyramine		C9H14NO2	1	Cytosol
3odcoa	3-Oxodecanoyl-CoA		C31H48N7O18P3S	-4	Peroxisome
3oddcoa	3-Oxododecanoyl-CoA		C33H52N7O18P3S	-4	Peroxisome
3ohdcoa	3-Oxohexadecanoyl-CoA		C37H60N7O18P3S	-4	Peroxisome
3ohodcoa	3-Oxooctadecanoyl-CoA		C39H64N7O18P3S	-4	Peroxisome
3ohxccoa	3-Oxohexacosyl-CoA		C47H80N7O18P3S	-4	Peroxisome
3otdcoa	3-Oxotetradecanoyl-CoA		C35H56N7O18P3S	-4	Peroxisome
3padsel	3'-Phosphoadenylylselenate	3'-Phosphoadenosine-5'-phosphoselanate	C10H11N5O13P2Se	-4	Cytosol
3pg	3-Phospho-D-glycerate	3-Phosphoglycerate, 3-phosphoglyceric acid, D-Glycerate 3-phosphate	C3H4O7P	-3	Cytosol
3php	3-Phosphohydroxypyruvate	3-Phosphohydroxypyruvic acid, 3-Phosphonooxypyruvate, 3-Phosphonooxypyruvic acid	C3H2O7P	-3	Cytosol
3sala	3-Sulfino-L-alanine	3-Sulfinoalanine, 3-sulphino-L-alanine, L-Cysteine sulfinic acid, L-Cysteinesulfinic acid	C3H5NO4S	-2	Cytosol
3sala	3-Sulfino-L-alanine	3-Sulfinoalanine, 3-sulphino-L-alanine, L-Cysteine sulfinic acid, L-Cysteinesulfinic acid	C3H5NO4S	-2	Mitochondria
3snpyr	3-Sulfinopyruvate	3-Sulfinopyruvate, 3-Sulfinylpyruvate	C3H2O5S	-2	Cytosol
3snpyr	3-Sulfinopyruvate	3-Sulfinopyruvate, 3-Sulfinylpyruvate	C3H2O5S	-2	Mitochondria
3spyr	3-Sulfopyruvate		C3H2O6S	-2	Cytosol
3spyr	3-Sulfopyruvate		C3H2O6S	-2	Mitochondria
3uib	3-Ureidoisobutyrate		C5H9N2O3	-1	Cytosol
42A3HP24DB	4-(2-Amino-3-hydroxyphenyl)-2,4-dioxobutanoate		C10H8NO5	-1	Cytosol
44mctr	4,4-dimethylcholesta-8,14,24-trienol	4,4'-dimethyl cholesta-8,14,24-triene-3-beta-ol, delta-8-14-24-dimethylsterol	C29H46O	0	Cytosol
44mctr	4,4-dimethylcholesta-8,14,24-trienol	4,4'-dimethyl cholesta-8,14,24-triene-3-beta-ol, delta-8-14-24-dimethylsterol	C29H46O	0	Endoplasmic Reticulum
44mzym	4,4-dimethylzymosterol	14-Desmethyllanosterol, 4,4-dimethyl-5alpha-cholesta-8,14,24-trien-3beta-ol	C29H48O	0	Endoplasmic Reticulum
46dhoxquin	4,6-Dihydroxyquinoline	Quinoline-4,6-diol	C9H7NO2	0	Cytosol
48dhoxquin	4,8-Dihydroxyquinoline	Quinoline-4,8-diol	C9H7NO2	0	Cytosol
4aabutn	4-Acetamidobutanoate		C6H10NO3	-1	Cytosol
4aabutn	4-Acetamidobutanoate		C6H10NO3	-1	Mitochondria
4abut	4-Aminobutanoate	(4-Aminobutyl)guanidine, 4-Aminobutanoic acid, 4-Aminobutylate, 4-Aminobutyric acid, GABA, gamma-Aminobutyric acid	C4H9NO2	0	Cytosol
4abut	4-Aminobutanoate	(4-Aminobutyl)guanidine, 4-Aminobutanoic acid, 4-Aminobutylate, 4-Aminobutyric acid, GABA, gamma-Aminobutyric acid	C4H9NO2	0	Extracellular
4abut	4-Aminobutanoate	(4-Aminobutyl)guanidine, 4-Aminobutanoic acid, 4-Aminobutylate, 4-Aminobutyric acid, GABA, gamma-Aminobutyric acid	C4H9NO2	0	Lysosome
4abut	4-Aminobutanoate	(4-Aminobutyl)guanidine, 4-Aminobutanoic acid, 4-Aminobutylate, 4-Aminobutyric acid, GABA, gamma-Aminobutyric acid	C4H9NO2	0	Mitochondria
4abutn	4-Aminobutanal	4-Aminobutyraldehyde, 4-amino-Butyraldehyde, gamma-aminobutanal	C4H10NO	1	Cytosol
4aphdob	4-(2-Aminophenyl)-2,4-dioxobutanoate		C10H8NO4	-1	Cytosol
4fumacac	4-Fumarylacetoacetate	4-Fumarylacetoacetic acid, Fumarylacetoacetate	C8H6O6	-2	Cytosol
4h2oglt	4-Hydroxy-2-oxoglutarate	4-Hydroxy-2-oxoglutaric acid, D-4-Hydroxy-2-oxoglutarate	C5H4O6	-2	Cytosol
4h2oglt	4-Hydroxy-2-oxoglutarate	4-Hydroxy-2-oxoglutaric acid, D-4-Hydroxy-2-oxoglutarate	C5H4O6	-2	Mitochondria

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
4hbz	4-Hydroxybenzoate	4-Hydroxybenzoic acid, Hydroxybenzenecarboxylic acid, Hydroxybenzoic acid	C7H5O3	-1	Mitochondria
4hbzcoa	4-hydroxybenoyl-CoA		C28H36N7O18P3S	-4	Mitochondria
4hdebrisoquine	4 hydroxy debrisoquine		C10H14N3O	1	Cytosol
4hdebrisoquine	4 hydroxy debrisoquine		C10H14N3O	1	Extracellular
4hglusa	L-4-Hydroxyglutamate semialdehyde		C5H9NO4	0	Mitochondria
4hoxpacd	4-Hydroxyphenylacetaldehyde	2-(4-Hydroxyphenyl)acetaldehyde	C8H8O2	0	Cytosol
4hphac	4-Hydroxyphenylacetate	4-Hydroxyphenylacetic acid	C8H7O3	-1	Cytosol
4hphac	4-Hydroxyphenylacetate	4-Hydroxyphenylacetic acid	C8H7O3	-1	Extracellular
4hpro-LT	trans-4-Hydroxy-L-proline		C5H9NO3	0	Mitochondria
4hpro-LT	trans-4-Hydroxy-L-proline		C5H9NO3	0	Endoplasmic Reticulum
4izp	4-Imidazolone-5-propanoate	4,5-Dihydro-4-oxo-5-imidazolepropanoate, 4-Imidazolone-5-propionic acid	C6H7N2O3	-1	Cytosol
4mlacac	4-Maleylacetoacetate		C8H6O6	-2	Cytosol
4mop	4-Methyl-2-oxopentanoate	2-Oxoisocaproate, alpha-ketoisocaproate	C6H9O3	-1	Cytosol
4mop	4-Methyl-2-oxopentanoate	2-Oxoisocaproate, alpha-ketoisocaproate	C6H9O3	-1	Mitochondria
4mptnl	4-Methylpentanal	4-Methylpentanal	C6H12O	0	Mitochondria
4mtolbutamide	4 hydroxy tolbutamide	4 methyl hydroxy tolbutamide	C12H18N2O4S	0	Cytosol
4mtolbutamide	4 hydroxy tolbutamide	4 methyl hydroxy tolbutamide	C12H18N2O4S	0	Extracellular
4mzym_int1	4-Methylzymosterol intermediate 1		C29H46O3	0	Endoplasmic Reticulum
4mzym_int2	4-Methylzymosterol intermediate 2		C28H44O	0	Endoplasmic Reticulum
4nph	4-Nitrophenol	4-Hydroxynitrobenzene, Niphen, PNP, p-Nitrophenol	C6H5NO3	0	Cytosol
4nph	4-Nitrophenol	4-Hydroxynitrobenzene, Niphen, PNP, p-Nitrophenol	C6H5NO3	0	Extracellular
4nphsf	4-Nitrophenyl sulfate	IUPAC Name: 1-nitro-4-sulfooxy-benzene, Sulfuric acid mono(4-nitrophenyl) ester, p-Nitrophenol sulfate, p-Nitrophenyl sulfate	C6H4NO6S	-1	Cytosol
4nphsf	4-Nitrophenyl sulfate	IUPAC Name: 1-nitro-4-sulfooxy-benzene, Sulfuric acid mono(4-nitrophenyl) ester, p-Nitrophenol sulfate, p-Nitrophenyl sulfate	C6H4NO6S	-1	Extracellular
4ppan	D-4'-Phosphopantothenate	(R)-4'-Phosphopantothenate	C9H15NO8P	-3	Cytosol
4ppan	D-4'-Phosphopantothenate	(R)-4'-Phosphopantothenate	C9H15NO8P	-3	Mitochondria
4ppcys	N-((R)-4-Phosphopantothenoyl)-L-cysteine	(R)-4'-Phosphopantothenoyl-L-cysteine	C12H20N2O9PS	-3	Cytosol
4pyrdx	4-Pyridoxate	4-Pyridoxic acid	C8H9NO4	0	Cytosol
4pyrdx	4-Pyridoxate	4-Pyridoxic acid	C8H9NO4	0	Extracellular
4tmeabut	4-Trimethylammoniobutanal		C7H16NO	1	Cytosol
4tmeabut	4-Trimethylammoniobutanal		C7H16NO	1	Mitochondria
4tmeabutn	4-Trimethylammoniobutanoate		C7H15NO2	0	Cytosol
56dihindlcrbxlt	5,6-Dihydroxyindole-2-carboxylate		C9H6NO4	-1	Cytosol
56dthm	5,6-Dihydrothymine	5,6-Dihydro-5-methyluracil, Dihydrothymine	C5H8N2O2	0	Cytosol
56dura	5,6-dihydrouracil	2, 3H)-Pyrimidinedione, 4(1H, 4-dihydroxypyrimidine, 5, 6-Dihydro-2, Dihydrouracile, Hydrouracil, dihydro-, dihydrouracil	C4H6N2O2	0	Cytosol
5a2opntn	5-Amino-2-oxopentanoate	2-Oxo-5-amino-pentanoate, 2-Oxo-5-aminopentanoate, alpha-Keto-delta-aminopentanoate	C5H9NO3	0	Peroxisome
5adtststerone	5alpha-Dihydrotestosterone	17beta-Hydroxy-5alpha-androstan-3-one, 17beta-Hydroxyandrostan-3-one, 5alpha-Dihydrotestosterone, Androstanolone	C19H30O2	0	Cytosol
5adtststerone	5alpha-Dihydrotestosterone	17beta-Hydroxy-5alpha-androstan-3-one, 17beta-Hydroxyandrostan-3-one, 5alpha-Dihydrotestosterone, Androstanolone	C19H30O2	0	Extracellular
5adtststerone	5alpha-Dihydrotestosterone	17beta-Hydroxy-5alpha-androstan-3-one, 17beta-Hydroxyandrostan-3-one, 5alpha-Dihydrotestosterone, Androstanolone	C19H30O2	0	Endoplasmic Reticulum
5adtststeroneglc	5alpha-Dihydrotestosterone glucuronide		C25H38O8	0	Cytosol
5adtststeroneglc	5alpha-Dihydrotestosterone glucuronide		C25H38O8	0	Extracellular
5adtststeroneglc	5alpha-Dihydrotestosterone glucuronide		C25H38O8	0	Endoplasmic Reticulum
5adtststerones	5alpha-Dihydrotestosterone sulfate		C19H29O5S	-1	Cytosol
5adtststerones	5alpha-Dihydrotestosterone sulfate		C19H29O5S	-1	Extracellular
5aizc	5-amino-1-(5-phospho-D-ribosyl)imidazole-4-carboxylate	1-(5'-Phosphoribosyl)-4-carboxy-5-aminoimidazole, 1-(5'-Phosphoribosyl)-5-amino-4-carboxyimidazole, 1-(5'-Phosphoribosyl)-5-amino-4-imidazolecarboxylate, 1-(5-Phospho-D-ribosyl)-5-amino-4-imidazolecarboxylate, 5'-Phosphoribosyl-4-carboxy-5-aminoimidazole, 5'-Phosphoribosyl-5-amino-4-imidazolecarboxylate	C9H11N3O9P	-3	Cytosol
5aop	5-Amino-4-oxopentanoate	5-Amino-4-oxovaleric acid, 5-Aminolevulinate	C5H9NO3	0	Cytosol
5aop	5-Amino-4-oxopentanoate	5-Amino-4-oxovaleric acid, 5-Aminolevulinate	C5H9NO3	0	Mitochondria
5dhf	pentaglutamyl folate (DHF)		C39H43N11O18	-6	Cytosol
5dhf	pentaglutamyl folate (DHF)		C39H43N11O18	-6	Extracellular
5dhf	pentaglutamyl folate (DHF)		C39H43N11O18	-6	Lysosome
5dhf	pentaglutamyl folate (DHF)		C39H43N11O18	-6	Mitochondria
5dpmev	(R)-5-Diphosphomevalonate		C6H10O10P2	-4	Peroxisome
5forthf	5-Formiminotetrahydrofolate		C20H22N8O6	-2	Cytosol
5fthf	5-Formyltetrahydrofolate	Folinic acid, L(-)-5-Formyl-5,6,7,8-tetrahydrofolic acid	C20H21N7O7	-2	Cytosol

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
5fthf	5-Formyltetrahydrofolate	Folinic acid, L(-)-5-Formyl-5,6,7,8-tetrahydrofolic acid	C20H21N7O7	-2	Extracellular
5g2oxpt	5-Guanidino-2-oxopentanoate	2-Oxo-5-guanidino-pentanoate, 2-Oxo-5-guanidinopentanoate, 5-Guanidino-2-oxo-pentanoate	C6H11N3O3	0	Peroxisome
5homeprazole	5 hydroxy omeprazole		C17H19N3O4S	0	Cytosol
5homeprazole	5 hydroxy omeprazole		C17H19N3O4S	0	Extracellular
5hoxindact	5-Hydroxyindoleacetaldehyde		C10H9NO2	0	Cytosol
5hoxindact	5-Hydroxyindoleacetaldehyde		C10H9NO2	0	Mitochondria
5hoxindoa	5-Hydroxyindoleacetate		C10H8NO3	-1	Cytosol
5hoxindoa	5-Hydroxyindoleacetate		C10H8NO3	-1	Mitochondria
5hoxnfkyn	5-Hydroxy-N-formylkynurenine		C11H12N2O5	0	Cytosol
5HPET	5-Hydroperoxy-6-trans-8,11,14-cis-eicosatetraenoate	(6E,8Z,11Z,14Z)-(5S)-5-Hydroperoxyeicosa-6,8,11,14-tetraenoate, 5-HPETE, 5-Hydroperoxy-6-trans-8,11,14-cis-eicosatetraenoate	C20H31O4	-1	Cytosol
5htrp	5-Hydroxy-L-tryptophan	5-HTP	C11H12N2O3	0	Cytosol
5htrp	5-Hydroxy-L-tryptophan	5-HTP	C11H12N2O3	0	Extracellular
5hxkyn	5-Hydroxykynurenine		C10H12N2O4	0	Cytosol
5hxkynam	5-Hydroxykynurenamine		C9H13N2O2	1	Cytosol
5mdr1p	5-Methylthio-5-deoxy-D-ribose 1-phosphate	5-Methylthio-D-ribose 1-phosphate, S5-Methyl-5-thio-D-ribose 1-phosphate	C6H11O7PS	-2	Cytosol
5mdru1p	5-Methylthio-5-deoxy-D-ribulose 1-phosphate		C6H11O7PS	-2	Cytosol
5moxact	5-Methoxyindoleacetate		C11H10NO3	-1	Cytosol
5mta	5-Methylthioadenosine	5'-Deoxy-5'-(methylthio)adenosine, 5'-Methylthioadenosine, 5'-S-Methylthioadenosine, Methylthioadenosine	C11H15N5O3S	0	Cytosol
5mthf	5-Methyltetrahydrofolate	5-methyl-5,6,7,8-tetrahydrofolate, N5-methyl-5,6,7,8-tetrahydrofolate, N5-methyl-tetrahydrofolate	C20H24N7O6	-1	Cytosol
5mthf	5-Methyltetrahydrofolate	5-methyl-5,6,7,8-tetrahydrofolate, N5-methyl-5,6,7,8-tetrahydrofolate, N5-methyl-tetrahydrofolate	C20H24N7O6	-1	Extracellular
5oxpro	5-Oxoproline	5-Oxoproline, 5-Pyrrolidone-2-carboxylic acid, Pyroglutamate, Pyroglutamic acid	C5H6NO3	-1	Cytosol
5pmev	(R)-5-Phosphomevalonate	(R)-5-Phosphomevaloonic acid, (R)-Mevalonic acid 5-phosphate	C6H10O7P	-3	Peroxisome
5thf	pentaglutamyl folate (THF)		C39H45N11O18	-6	Cytosol
5thf	pentaglutamyl folate (THF)		C39H45N11O18	-6	Extracellular
5thf	pentaglutamyl folate (THF)		C39H45N11O18	-6	Lysosome
5thf	pentaglutamyl folate (THF)		C39H45N11O18	-6	Mitochondria
6a2ohxnt	6-Amino-2-oxohexanoate	2-Oxo-6-aminocaproate	C6H11NO3	0	Peroxisome
6dhf	haxglutamyl folate (DHF)		C44H49N12O21	-7	Cytosol
6dhf	haxglutamyl folate (DHF)		C44H49N12O21	-7	Extracellular
6dhf	haxglutamyl folate (DHF)		C44H49N12O21	-7	Lysosome
6dhf	haxglutamyl folate (DHF)		C44H49N12O21	-7	Mitochondria
6hoxmelatn	6-Hydroxymelatonin		C13H16N2O3	0	Cytosol
6htststerone	6 beta hydroxy testosterone		C19H28O3	0	Cytosol
6htststerone	6 beta hydroxy testosterone		C19H28O3	0	Extracellular
6htststerone	6 beta hydroxy testosterone		C19H28O3	0	Endoplasmic Reticulum
6pgc	6-Phospho-D-gluconate	6-phosphogluconic acid, D-gluconate 6-phosphate	C6H10O10P	-3	Cytosol
6pgc	6-Phospho-D-gluconate	6-phosphogluconic acid, D-gluconate 6-phosphate	C6H10O10P	-3	Endoplasmic Reticulum
6pgl	6-phospho-D-glucono-1,5-lactone	D-Glucono-1,5-lactone 6-phosphate	C6H9O9P	-2	Cytosol
6pgl	6-phospho-D-glucono-1,5-lactone	D-Glucono-1,5-lactone 6-phosphate	C6H9O9P	-2	Endoplasmic Reticulum
6pthp	6-Pyruvoyl-5,6,7,8-tetrahydropterin	6-Pyruvoyl-tetrahydropterin, 6-Pyruvoyltetrahydropterin	C9H11N5O3	0	Cytosol
6pthp	6-Pyruvoyl-5,6,7,8-tetrahydropterin	6-Pyruvoyl-tetrahydropterin, 6-Pyruvoyltetrahydropterin	C9H11N5O3	0	Nucleus
6thf	hexaglutamyl folate (THF)		C44H51N12O21	-7	Cytosol
6thf	hexaglutamyl folate (THF)		C44H51N12O21	-7	Extracellular
6thf	hexaglutamyl folate (THF)		C44H51N12O21	-7	Lysosome
6thf	hexaglutamyl folate (THF)		C44H51N12O21	-7	Mitochondria
7dhchsterol	7-Dehydrocholesterol	7-dien-3beta-ol, Cholesta-5, Provitamin D3	C27H44O	0	Cytosol
7dhchsterol	7-Dehydrocholesterol	7-dien-3beta-ol, Cholesta-5, Provitamin D3	C27H44O	0	Endoplasmic Reticulum
7dhf	heptaglutamyl folate (DHF)		C49H55N13O24	-8	Cytosol
7dhf	heptaglutamyl folate (DHF)		C49H55N13O24	-8	Extracellular
7dhf	heptaglutamyl folate (DHF)		C49H55N13O24	-8	Lysosome
7dhf	heptaglutamyl folate (DHF)		C49H55N13O24	-8	Mitochondria
7thf	heptaglutamyl folate (THF)		C49H57N13O24	-8	Cytosol
7thf	heptaglutamyl folate (THF)		C49H57N13O24	-8	Extracellular
7thf	heptaglutamyl folate (THF)		C49H57N13O24	-8	Lysosome
7thf	heptaglutamyl folate (THF)		C49H57N13O24	-8	Mitochondria
9-cis-retfa	fatty acid 9-cis-retinol		C20H29OFULLR2CO	0	Cytosol
9-cis-retfa	fatty acid 9-cis-retinol		C20H29OFULLR2CO	0	Extracellular
aacoa	Acetoacetyl-CoA	3-acetoacetyl-CoA, 3-ketobutanoyl-CoA, 3-ketobutyroyl-CoA, 3-oxobutanoyl-CoA, 3-oxobutyroyl-CoA, Acetoacetyl coenzyme A	C25H36N7O18P3S	-4	Cytosol
aacoa	Acetoacetyl-CoA	3-acetoacetyl-CoA, 3-ketobutanoyl-CoA, 3-ketobutyroyl-CoA, 3-oxobutanoyl-CoA, 3-oxobutyroyl-CoA, Acetoacetyl coenzyme A	C25H36N7O18P3S	-4	Mitochondria

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
aacoa	Acetoacetyl-CoA	3-acetoacetyl-CoA, 3-ketobutanoyl-CoA, 3-ketobutyroyl-CoA, 3-oxobutanoyl-CoA, 3-oxobutyroyl-CoA, Acetoacetyl coenzyme A	C25H36N7O18P3S	-4	Peroxisome
aact	Aminoacetone	1-Amino-2-propanone	C3H8NO	1	Cytosol
aact	Aminoacetone	1-Amino-2-propanone	C3H8NO	1	Mitochondria
abt	L-Arabinitol	L-Arabinol, L-Arabitol, L-Lyxitol	C5H12O5	0	Cytosol
abt	L-Arabinitol	L-Arabinol, L-Arabitol, L-Lyxitol	C5H12O5	0	Extracellular
ac	Acetate	Acetic acid, Ethanoic acid, Ethylic acid, Methanecarboxylic acid, Vinegar acid, vinegar	C2H3O2	-1	Cytosol
ac	Acetate	Acetic acid, Ethanoic acid, Ethylic acid, Methanecarboxylic acid, Vinegar acid, vinegar	C2H3O2	-1	Extracellular
ac	Acetate	Acetic acid, Ethanoic acid, Ethylic acid, Methanecarboxylic acid, Vinegar acid, vinegar	C2H3O2	-1	Golgi Apparatus
ac	Acetate	Acetic acid, Ethanoic acid, Ethylic acid, Methanecarboxylic acid, Vinegar acid, vinegar	C2H3O2	-1	Mitochondria
acac	Acetoacetate	3-Oxobutanoic acid, Acetoacetic acid, beta-Ketobutyric acid	C4H5O3	-1	Cytosol
acac	Acetoacetate	3-Oxobutanoic acid, Acetoacetic acid, beta-Ketobutyric acid	C4H5O3	-1	Extracellular
acac	Acetoacetate	3-Oxobutanoic acid, Acetoacetic acid, beta-Ketobutyric acid	C4H5O3	-1	Mitochondria
acac	Acetoacetate	3-Oxobutanoic acid, Acetoacetic acid, beta-Ketobutyric acid	C4H5O3	-1	Peroxisome
acACP	Acetyl-ACP		C13H23N2O8PRS	-1	Cytosol
acald	Acetaldehyde	Aceteldehyde, Acetic aldehyde, Aldehyde, Aldehyde C(2), Ethanal, Ethyl aldehyde, acetylaldehyde	C2H4O	0	Cytosol
acald	Acetaldehyde	Aceteldehyde, Acetic aldehyde, Aldehyde, Aldehyde C(2), Ethanal, Ethyl aldehyde, acetylaldehyde	C2H4O	0	Extracellular
acald	Acetaldehyde	Aceteldehyde, Acetic aldehyde, Aldehyde, Aldehyde C(2), Ethanal, Ethyl aldehyde, acetylaldehyde	C2H4O	0	Mitochondria
acald	Acetaldehyde	Aceteldehyde, Acetic aldehyde, Aldehyde, Aldehyde C(2), Ethanal, Ethyl aldehyde, acetylaldehyde	C2H4O	0	Endoplasmic Reticulum
acald	Acetaldehyde	Aceteldehyde, Acetic aldehyde, Aldehyde, Aldehyde C(2), Ethanal, Ethyl aldehyde, acetylaldehyde	C2H4O	0	Peroxisome
accoa	Acetyl-CoA	Acetyl coenzyme A	C23H34N7O17P3S	-4	Cytosol
accoa	Acetyl-CoA	Acetyl coenzyme A	C23H34N7O17P3S	-4	Golgi Apparatus
accoa	Acetyl-CoA	Acetyl coenzyme A	C23H34N7O17P3S	-4	Mitochondria
accoa	Acetyl-CoA	Acetyl coenzyme A	C23H34N7O17P3S	-4	Nucleus
accoa	Acetyl-CoA	Acetyl coenzyme A	C23H34N7O17P3S	-4	Endoplasmic Reticulum
accoa	Acetyl-CoA	Acetyl coenzyme A	C23H34N7O17P3S	-4	Peroxisome
acetol	Acetol	1-Hydroxy-2-propanone, 2-Ketopropyl alcohol, Acetone alcohol, Hydroxyacetone, Methylketol, Pyruvic alcohol, Pyruvinalcohol	C3H6O2	0	Cytosol
acetone	Acetone	2-Propanone, Dimethyl ketone	C3H6O	0	Cytosol
acetone	Acetone	2-Propanone, Dimethyl ketone	C3H6O	0	Extracellular
acetone	Acetone	2-Propanone, Dimethyl ketone	C3H6O	0	Mitochondria
acg5p	N-Acetyl-L-glutamyl 5-phosphate	N-Acetyl-L-glutamate 5-phosphate	C7H9NO8P	-3	Mitochondria
acg5sa	N-Acetyl-L-glutamate 5-semialdehyde	2-Acetamido-5-oxopentanoate	C7H10NO4	-1	Mitochondria
acgagbside_hs	alpha GalNAc globoside (homo sapiens)	GalNAc alpha globoside	C52H92N3O27FULLRCO	0	Cytosol
acgagbside_hs	alpha GalNAc globoside (homo sapiens)	GalNAc alpha globoside	C52H92N3O27FULLRCO	0	Golgi Apparatus
acgagbside_hs	alpha GalNAc globoside (homo sapiens)	GalNAc alpha globoside	C52H92N3O27FULLRCO	0	Lysosome
acgal	N-Acetyl-D-galactosamine	2-Acetamido-2-deoxy-D-galactose, GalNAc, N-Acetyl-D-chondrosamine	C8H15NO6	0	Cytosol
acgal	N-Acetyl-D-galactosamine	2-Acetamido-2-deoxy-D-galactose, GalNAc, N-Acetyl-D-chondrosamine	C8H15NO6	0	Golgi Apparatus
acgal	N-Acetyl-D-galactosamine	2-Acetamido-2-deoxy-D-galactose, GalNAc, N-Acetyl-D-chondrosamine	C8H15NO6	0	Lysosome
acgal1p	N-Acetyl-D-galactosamine 1-phosphate		C8H14NO9P	-2	Cytosol
acgalfuc12gal14acglcgalgluside_hs	(Gal)2 (GalNAc)1 (Glc)1 (GlcNAc)1 (LFuc)1 (Cer)1		C58H102N3O31FULLRCO	0	Golgi Apparatus
acgalfucgalacgalfuc12gal14acglcgalgluside_hs	Type IIIA glycolipid	(Gal)3 (GalNAc)2 (Glc)1 (GlcNAc)1 (LFuc)2 (Cer)1	C78H135N4O45FULLRCO	0	Cytosol
acgalfucgalacgalfuc12gal14acglcgalgluside_hs	Type IIIA glycolipid	(Gal)3 (GalNAc)2 (Glc)1 (GlcNAc)1 (LFuc)2 (Cer)1	C78H135N4O45FULLRCO	0	Extracellular
acgalfucgalacgalfuc12gal14acglcgalgluside_hs	Type IIIA glycolipid	(Gal)3 (GalNAc)2 (Glc)1 (GlcNAc)1 (LFuc)2 (Cer)1	C78H135N4O45FULLRCO	0	Golgi Apparatus
acgalfucgalacgalfucgalacglcgal14acglcgalgluside_hs	Type IIIAb	(Gal)4 (GalNAc)2 (Glc)1 (GlcNAc)2 (LFuc)2 (Cer)1	C92H158N5O55FULLRCO	0	Cytosol
acgalfucgalacgalfucgalacglcgal14acglcgalgluside_hs	Type IIIAb	(Gal)4 (GalNAc)2 (Glc)1 (GlcNAc)2 (LFuc)2 (Cer)1	C92H158N5O55FULLRCO	0	Extracellular
acgalfucgalacgalfucgalacglcgal14acglcgalgluside_hs	Type IIIAb	(Gal)4 (GalNAc)2 (Glc)1 (GlcNAc)2 (LFuc)2 (Cer)1	C92H158N5O55FULLRCO	0	Golgi Apparatus
acgalfucgalacglcgal14acglcgalgluside_hs	(Gal)3 (GalNAc)1 (Glc)1 (GlcNAc)2 (LFuc)1 (Cer)1		C72H125N4O41FULLRCO	0	Golgi Apparatus
acgalfucgalacglcgalgluside_hs	Type IA glycolipid	(Gal)2 (GalNAc)1 (Glc)1 (GlcNAc)1 (LFuc)1 (Cer)1	C58H102N3O31FULLRCO	0	Golgi Apparatus
acgam	N-Acetyl-D-glucosamine	2-Acetamido-2-deoxy-D-glucose, GlcNAc, N-Acetylchitosamine	C8H15NO6	0	Cytosol

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
acgam	N-Acetyl-D-glucosamine	2-Acetamido-2-deoxy-D-glucose, GlcNAc, N-Acetylchitosamine	C8H15NO6	0	Extracellular
acgam	N-Acetyl-D-glucosamine	2-Acetamido-2-deoxy-D-glucose, GlcNAc, N-Acetylchitosamine	C8H15NO6	0	Lysosome
acgam1p	N-Acetyl-D-glucosamine 1-phosphate		C8H14NO9P	-2	Cytosol
acgam6p	N-Acetyl-D-glucosamine 6-phosphate		C8H14NO9P	-2	Cytosol
acgbgbside_hs	beta GalNAc globoside (homo sapiens)	IV3GalNAcb-Gb4Cer	C52H92N3O27FULLRCO	0	Cytosol
acgbgbside_hs	beta GalNAc globoside (homo sapiens)	IV3GalNAcb-Gb4Cer	C52H92N3O27FULLRCO	0	Golgi Apparatus
acgbgbside_hs	beta GalNAc globoside (homo sapiens)	IV3GalNAcb-Gb4Cer	C52H92N3O27FULLRCO	0	Lysosome
acglc13galacglcgal14acglcgalgluside_hs	nLc7Cer		C66H115N4O37FULLRCO	0	Golgi Apparatus
acglcgal14acglcgalgluside_hs	nLc5Cer	(Gal)2 (Glc)1 (GlcNAc)2 (Cer)1	C52H92N3O27FULLRCO	0	Golgi Apparatus
acglcgalacglcgal14acglcgalgluside_hs	(Gal)3 (Glc)1 (GlcNAc)3 (Cer)1		C66H115N4O37FULLRCO	0	Golgi Apparatus
acglcgalgbside_hs	GlcNAc-Gal globoside (homo sapiens)	(Gal)3 (GalNAc)1 (Glc)1 (GlcNAc)1 (Cer)1	C58H102N3O32FULLRCO	0	Golgi Apparatus
acglcgalgluside_hs	(Gal)1 (Glc)1 (GlcNAc)1 (Cer)1	Lc3Cer	C38H69N2O17FULLRCO	0	Golgi Apparatus
acglu	N-Acetyl-L-glutamate	N-Acetyl-L-glutamic acid	C7H9NO5	-2	Mitochondria
acgpail_hs	N-Acetyl-D-glucosaminylphosphatidylinositol		C17H29NO14PFULLRCO2FULLR2CO2	-1	Cytosol
ach	Acetylcholine	Acetylcholine, O-Acetylcholine	C7H16NO2	1	Cytosol
ach	Acetylcholine	Acetylcholine, O-Acetylcholine	C7H16NO2	1	Extracellular
ach	Acetylcholine	Acetylcholine, O-Acetylcholine	C7H16NO2	1	Nucleus
acmana	N-Acetyl-D-mannosamine	2-Acetamido-2-deoxy-D-monnose	C8H15NO6	0	Cytosol
acmanap	N-Acetyl-D-mannosamine 6-phosphate	N-Acetyl-D-mannosamine 6-phosphate, N-Acetylmannosamine 6-phosphate	C8H14NO9P	-2	Cytosol
acn13acngalgbside_hs	sialyl (1,3) sialyl (2,6) galactosylgloboside (homo sapiens)	Disialosyl Gb5;, Disialosylgalactosylgloboside, Disialosylglobopentaosylceramide;, V3NeuAcIV6NeuAc-Gb5Cer;	C72H121N4O43FULLRCO	-2	Cytosol
acn13acngalgbside_hs	sialyl (1,3) sialyl (2,6) galactosylgloboside (homo sapiens)	Disialosyl Gb5;, Disialosylgalactosylgloboside, Disialosylglobopentaosylceramide;, V3NeuAcIV6NeuAc-Gb5Cer;	C72H121N4O43FULLRCO	-2	Extracellular
acn13acngalgbside_hs	sialyl (1,3) sialyl (2,6) galactosylgloboside (homo sapiens)	Disialosyl Gb5;, Disialosylgalactosylgloboside, Disialosylglobopentaosylceramide;, V3NeuAcIV6NeuAc-Gb5Cer;	C72H121N4O43FULLRCO	-2	Golgi Apparatus
acn23acngalgbside_hs	sialyl (2,3) sialyl (2,6) galactosylgloboside (homo sapiens)	(Gal)3 (GalNAc)1 (Glc)1 (Neu5Ac)2 (Cer)1	C72H121N4O43FULLRCO	-2	Cytosol
acn23acngalgbside_hs	sialyl (2,3) sialyl (2,6) galactosylgloboside (homo sapiens)	(Gal)3 (GalNAc)1 (Glc)1 (Neu5Ac)2 (Cer)1	C72H121N4O43FULLRCO	-2	Extracellular
acn23acngalgbside_hs	sialyl (2,3) sialyl (2,6) galactosylgloboside (homo sapiens)	(Gal)3 (GalNAc)1 (Glc)1 (Neu5Ac)2 (Cer)1	C72H121N4O43FULLRCO	-2	Golgi Apparatus
acnacngal14acglcgalgluside_hs	3',8'-LD1	(Gal)2 (Glc)1 (GlcNAc)1 (Neu5Ac)2 (Cer)1	C66H111N4O38FULLRCO	-2	Cytosol
acnacngal14acglcgalgluside_hs	3',8'-LD1	(Gal)2 (Glc)1 (GlcNAc)1 (Neu5Ac)2 (Cer)1	C66H111N4O38FULLRCO	-2	Extracellular
acnacngal14acglcgalgluside_hs	3',8'-LD1	(Gal)2 (Glc)1 (GlcNAc)1 (Neu5Ac)2 (Cer)1	C66H111N4O38FULLRCO	-2	Golgi Apparatus
acnacngalgbside_hs	disialyl galactosylgloboside (homo sapiens)	V3(NeuAc)2-Gb5Cer	C72H121N4O43FULLRCO	-2	Cytosol
acnacngalgbside_hs	disialyl galactosylgloboside (homo sapiens)	V3(NeuAc)2-Gb5Cer	C72H121N4O43FULLRCO	-2	Extracellular
acnacngalgbside_hs	disialyl galactosylgloboside (homo sapiens)	V3(NeuAc)2-Gb5Cer	C72H121N4O43FULLRCO	-2	Golgi Apparatus
acnam	N-Acetylneuraminate	5-Acetamido-3,5-dideoxy-D-glycero-D-galacto-2-nonulosonic acid, N-Acetylneuraminic acid, Neu5Ac	C11H18NO9	-1	Cytosol
acnam	N-Acetylneuraminate	5-Acetamido-3,5-dideoxy-D-glycero-D-galacto-2-nonulosonic acid, N-Acetylneuraminic acid, Neu5Ac	C11H18NO9	-1	Lysosome
acnam	N-Acetylneuraminate	5-Acetamido-3,5-dideoxy-D-glycero-D-galacto-2-nonulosonic acid, N-Acetylneuraminic acid, Neu5Ac	C11H18NO9	-1	Nucleus
acnamp	N-Acetylneuraminate 9-phosphate		C11H17NO12P	-3	Cytosol
acngal14acglcgalgluside_hs	Sialyl-3-paragloboside	(Gal)2 (Glc)1 (GlcNAc)1 (Neu5Ac)1 (Cer)1, 3'-LM1;, IV3-a-Neu5Ac-nLc4Cer;, Sialyl-3-paragloboside;, snLc4Cer	C55H95N3O30FULLRCO	-1	Golgi Apparatus
acngalacglcgal14acglcgalgluside_hs	VI3NeuAc-nLc6Cer	(Gal)3 (Glc)1 (GlcNAc)2 (Neu5Ac)1 (Cer)1	C69H118N4O40FULLRCO	-1	Cytosol
acngalacglcgal14acglcgalgluside_hs	VI3NeuAc-nLc6Cer	(Gal)3 (Glc)1 (GlcNAc)2 (Neu5Ac)1 (Cer)1	C69H118N4O40FULLRCO	-1	Extracellular
acngalacglcgal14acglcgalgluside_hs	VI3NeuAc-nLc6Cer	(Gal)3 (Glc)1 (GlcNAc)2 (Neu5Ac)1 (Cer)1	C69H118N4O40FULLRCO	-1	Golgi Apparatus
acngalacglcgalgluside_hs	(Gal)3 (Glc)1 (GlcNAc)1 (Cer)1		C55H95N3O30FULLRCO	-1	Golgi Apparatus
acngalgbside_hs	sialyl galactosylgloboside (homo sapiens)	MSGG, Monosialyl-Gb5, Monosialylgalactosylgloboside, SSEA-4, V3NeuAc-Gb5Cer	C61H105N3O35FULLRCO	-1	Golgi Apparatus
acorn	N2-Acetyl-L-ornithine		C7H14N2O3	0	Cytosol
ACP	acyl carrier protein		C11H21N2O7PRS	-1	Cytosol
ACP	acyl carrier protein		C11H21N2O7PRS	-1	Mitochondria
acrn	O-Acetylcarnitine		C9H17NO4	0	Cytosol
acrn	O-Acetylcarnitine		C9H17NO4	0	Mitochondria
acrn	O-Acetylcarnitine		C9H17NO4	0	Endoplasmic Reticulum
acrn	O-Acetylcarnitine		C9H17NO4	0	Peroxisome
ade	Adenine	1H-Purin-6-amine, 6-Aminopurine, A, Ade, Adeninimine, Vitamin B4	C5H5N5	0	Cytosol
ade	Adenine	1H-Purin-6-amine, 6-Aminopurine, A, Ade, Adeninimine, Vitamin B4	C5H5N5	0	Extracellular
ade	Adenine	1H-Purin-6-amine, 6-Aminopurine, A, Ade, Adeninimine, Vitamin B4	C5H5N5	0	Lysosome
adhap_hs	acyl-dihydroxyacetone phosphate		C3H4O6PFULLRCO	-2	Cytosol

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
adhap_hs	acyl-dihydroxyacetone phosphate		C3H4O6PFULLRCO	-2	Peroxisome
adn	Adenosine	9-B-D-ribofuranosyl-9H-purin-6-amine, 9-beta-D-Ribofuranosyladenine, Adenine riboside, Adenocard, rA	C10H13N5O4	0	Cytosol
adn	Adenosine	9-B-D-ribofuranosyl-9H-purin-6-amine, 9-beta-D-Ribofuranosyladenine, Adenine riboside, Adenocard, rA	C10H13N5O4	0	Extracellular
adn	Adenosine	9-B-D-ribofuranosyl-9H-purin-6-amine, 9-beta-D-Ribofuranosyladenine, Adenine riboside, Adenocard, rA	C10H13N5O4	0	Lysosome
adn	Adenosine	9-B-D-ribofuranosyl-9H-purin-6-amine, 9-beta-D-Ribofuranosyladenine, Adenine riboside, Adenocard, rA	C10H13N5O4	0	Mitochondria
adocbl	Adenosylcobalamin	(5, (5'-Deoxy-5'-adenosyl)cobamide coenzyme, 5, 5 Deoxy-5'-adenosyl vitamin B12, 5'-Deoxy-5'-adenosyl-5, 5'-Deoxy-5'-adenosylcobalamin, 6-Dimethylbenzimidazolyl)cobamide coenzyme, 6-Dimethylbenzimidazolyl-5-deoxyadenosyl-cobamide, 6-Dimethylbenzimidazolyl-Co-5'-deoxy-5'-adenosylcobamide, 6-dimethylbenzimidazolyl)cobamide coenzyme, 6-dimethylbenzimidazolylcobamide, Adenosylcobalamin, Calomide, Cobalamin coenzyme, Cobamamide, Coenzyme B12, DMBC coenzyme, Deoxyadenosylcobalamin, Dibencozide Funacomide, Vitamin B12 coenzyme, a-(5	C72H100CoN18O17P	0	Mitochondria
adp	ADP	Adenosine 5'-diphosphate	C10H12N5O10P2	-3	Cytosol
adp	ADP	Adenosine 5'-diphosphate	C10H12N5O10P2	-3	Extracellular
adp	ADP	Adenosine 5'-diphosphate	C10H12N5O10P2	-3	Mitochondria
adp	ADP	Adenosine 5'-diphosphate	C10H12N5O10P2	-3	Nucleus
adp	ADP	Adenosine 5'-diphosphate	C10H12N5O10P2	-3	Endoplasmic Reticulum
adp	ADP	Adenosine 5'-diphosphate	C10H12N5O10P2	-3	Peroxisome
adpglc	ADPglucose	Adenosine diphosphoglucose	C16H23N5O15P2	-2	Cytosol
adpman	ADPmannose		C16H23N5O15P2	-2	Cytosol
adprbp	ADPribose 2'-phosphate		C15H20N5O17P3	-4	Cytosol
adprbp	ADPribose 2'-phosphate		C15H20N5O17P3	-4	Extracellular
adprib	ADPribose	ADP-D-ribose, ADP-ribose, adenine-diphosphate-ribose, adenosine diphosphate ribose	C15H21N5O14P2	-2	Cytosol
adprib	ADPribose	ADP-D-ribose, ADP-ribose, adenine-diphosphate-ribose, adenosine diphosphate ribose	C15H21N5O14P2	-2	Extracellular
adprib	ADPribose	ADP-D-ribose, ADP-ribose, adenine-diphosphate-ribose, adenosine diphosphate ribose	C15H21N5O14P2	-2	Mitochondria
adrn	adrenic acid	adrenic acid(22:4,n-6), docosa-7,10,13,16-tetraenoic acid	C22H35O2	-1	Cytosol
adrn	adrenic acid	adrenic acid(22:4,n-6), docosa-7,10,13,16-tetraenoic acid	C22H35O2	-1	Extracellular
adrn	adrenic acid	adrenic acid(22:4,n-6), docosa-7,10,13,16-tetraenoic acid	C22H35O2	-1	Peroxisome
adrncoa	adrenyl coenzyme A		C43H66N7O17P3S	-4	Cytosol
adrncoa	adrenyl coenzyme A		C43H66N7O17P3S	-4	Mitochondria
adrncoa	adrenyl coenzyme A		C43H66N7O17P3S	-4	Peroxisome
adrncrn	Adrenyl carnitine	adrenic acid carnitine	C29H49NO4	0	Cytosol
adrncrn	Adrenyl carnitine	adrenic acid carnitine	C29H49NO4	0	Mitochondria
adrnl	Adrenaline	(R)-(-)-Adnephrine, (R)-(-)-Adrenaline, (R)-(-)-Epinephrine, (R)-(-)-Epirenamine, 2-benzenediol, 4-[(1R)-1-Hydroxy-2-(methylamino)ethyl]-1, L-Adrenaline	C9H14NO3	1	Cytosol
adrnl	Adrenaline	(R)-(-)-Adnephrine, (R)-(-)-Adrenaline, (R)-(-)-Epinephrine, (R)-(-)-Epirenamine, 2-benzenediol, 4-[(1R)-1-Hydroxy-2-(methylamino)ethyl]-1, L-Adrenaline	C9H14NO3	1	Extracellular
adsel	Adenylylselenate	Adenosine-5'-phosphoselenate	C10H12N5O10PSe	-2	Cytosol
aflatoxin	aflatoxin B1	2,3-Epoxyaflatoxin B1, Aflatoxin B1 2,3-epoxide, Aflatoxin B1 8,9-epoxide, Aflatoxin B1 8,9-oxide, Aflatoxin B1 epoxide, Aflatoxin B1-2,3-oxide [MeSH: aflatoxin B1-2,3-oxide]	C17H12O6	0	Cytosol
aflatoxin	aflatoxin B1	2,3-Epoxyaflatoxin B1, Aflatoxin B1 2,3-epoxide, Aflatoxin B1 8,9-epoxide, Aflatoxin B1 8,9-oxide, Aflatoxin B1 epoxide, Aflatoxin B1-2,3-oxide [MeSH: aflatoxin B1-2,3-oxide]	C17H12O6	0	Extracellular
agm	Agmatine	(4-Aminobutyl) guanidine	C5H16N4	2	Mitochondria
ahandrostan	3alpha-Hydroxy-5beta-androstan-17-one	3alpha-Hydroxy-5beta-androstan-17-one, 3alpha-Hydroxyetiocholan-17-one, Etiocholan-3alpha-ol-17-one	C19H30O2	0	Endoplasmic Reticulum
ahandrostanglc	Etiocholan-3alpha-ol-17-one 3-glucuronide		C25H38O8	0	Cytosol
ahandrostanglc	Etiocholan-3alpha-ol-17-one 3-glucuronide		C25H38O8	0	Extracellular
ahandrostanglc	Etiocholan-3alpha-ol-17-one 3-glucuronide		C25H38O8	0	Endoplasmic Reticulum
ahcys	S-Adenosyl-L-homocysteine	S-Adenosylhomocysteine	C14H20N6O5S	0	Cytosol
ahcys	S-Adenosyl-L-homocysteine	S-Adenosylhomocysteine	C14H20N6O5S	0	Mitochondria
ahcys	S-Adenosyl-L-homocysteine	S-Adenosylhomocysteine	C14H20N6O5S	0	Nucleus

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
ahcys	S-Adenosyl-L-homocysteine	S-Adenosylhomocysteine	C14H20N6O5S	0	Endoplasmic Reticulum
ahdt	2-Amino-4-hydroxy-6-(erythro-1,2,3-trihydroxypropyl)dihydropteridine triphosphate	2-Amino-4-hydroxy-6-(erythro-1,2,3-trihydroxypropyl)dihydropteridine triphosphate;, 6-(L-erythro-1,2-Dihydroxypropyl 3-triphosphate)-7,dihydropterin;, 6-[(1S,2R)-1,2-Dihydroxy-3-triphosphooxypropyl]-7,8-dihydropterin, H2-neopterin triphosphate, dihydroneopterin triphosphate	C9H12N5O13P3	-4	Cytosol
ahdt	2-Amino-4-hydroxy-6-(erythro-1,2,3-trihydroxypropyl)dihydropteridine triphosphate	2-Amino-4-hydroxy-6-(erythro-1,2,3-trihydroxypropyl)dihydropteridine triphosphate;, 6-(L-erythro-1,2-Dihydroxypropyl 3-triphosphate)-7,dihydropterin;, 6-[(1S,2R)-1,2-Dihydroxy-3-triphosphooxypropyl]-7,8-dihydropterin, H2-neopterin triphosphate, dihydroneopterin triphosphate	C9H12N5O13P3	-4	Nucleus
aicar	5-Amino-1-(5-Phospho-D-ribosyl)imidazole-4-carboxamide	1-(5'-Phosphoribosyl)-5-amino-4-imidazolecarboxamide, 5'-Phospho-ribosyl-5-amino-4-imidazole carboxamide, 5'-Phosphoribosyl-5-amino-4-imidazolecarboxamide, 5-Aminoimidazole-4-carboxamide ribotide, 5-Phosphoribosyl-4-carbamoyl-5-aminoimidazole, AICAR	C9H13N4O8P	-2	Cytosol
air	5-amino-1-(5-phospho-D-ribosyl)imidazole	1-(5'-Phosphoribosyl)-5-aminoimidazole, 1-(5-Phospho-D-ribosyl)-5-aminoimidazole, 5'-Phosphoribosyl-5-aminoimidazole, AIR, Aminoimidazole ribotide	C8H12N3O7P	-2	Cytosol
ak2g_hs	1-alkyl 2-acylglycerol		C5H10O2FULLRFULLR2CO2	0	Cytosol
ak2gchol_hs	1-alkyl 2-acylglycerol 3-phosphocholine		C10H20O5NPFULLRFULLR2CO	0	Cytosol
ak2gp_hs	1-alkyl 2-acylglycerol 3-phosphate		C5H9O6PFULLRFULLR2CO	-2	Cytosol
ak2gpe_hs	1-alkyl 2-acylglycerol 3-phosphoethanolamine		C7H16O5NPFULLRFULLR2CO	0	Cytosol
ak2lgchol_hs	1-alkyl 2-lysoglycerol 3-phosphocholine	1-Organyl-2-lyso-sn-glycero-3-phosphocholine, 1-Radyl-2-lyso-sn-glycero-3-phosphocholine	C10H21O5NPFULLR	0	Cytosol
ak2lgchol_hs	1-alkyl 2-lysoglycerol 3-phosphocholine	1-Organyl-2-lyso-sn-glycero-3-phosphocholine, 1-Radyl-2-lyso-sn-glycero-3-phosphocholine	C10H21O5NPFULLR	0	Extracellular
akdhap_hs	1-alkyldihydroxyacetone phosphate		C3H4O6PFULLRC2H4	-2	Cytosol
akdhap_hs	1-alkyldihydroxyacetone phosphate		C3H4O6PFULLRC2H4	-2	Peroxisome
akg	2-Oxoglutarate	2-Ketoglutaric acid, Oxoglutaric acid, alpha-Ketoglutarate, alpha-Ketoglutaric Acid	C5H4O5	-2	Cytosol
akg	2-Oxoglutarate	2-Ketoglutaric acid, Oxoglutaric acid, alpha-Ketoglutarate, alpha-Ketoglutaric Acid	C5H4O5	-2	Extracellular
akg	2-Oxoglutarate	2-Ketoglutaric acid, Oxoglutaric acid, alpha-Ketoglutarate, alpha-Ketoglutaric Acid	C5H4O5	-2	Mitochondria
akg	2-Oxoglutarate	2-Ketoglutaric acid, Oxoglutaric acid, alpha-Ketoglutarate, alpha-Ketoglutaric Acid	C5H4O5	-2	Endoplasmic Reticulum
akg	2-Oxoglutarate	2-Ketoglutaric acid, Oxoglutaric acid, alpha-Ketoglutarate, alpha-Ketoglutaric Acid	C5H4O5	-2	Peroxisome
akgp_hs	1-alkylglycerol 3-phosphate (homo sapiens)		C4H10O4PFULLRCO2	-2	Cytosol
ala-B	beta-Alanine	3-Aminopropanoate, 3-aminopropionic acid	C3H7NO2	0	Cytosol
ala-B	beta-Alanine	3-Aminopropanoate, 3-aminopropionic acid	C3H7NO2	0	Extracellular
ala-B	beta-Alanine	3-Aminopropanoate, 3-aminopropionic acid	C3H7NO2	0	Mitochondria
ala-D	D-Alanine	D-2-Aminopropionic acid	C3H7NO2	0	Cytosol
ala-D	D-Alanine	D-2-Aminopropionic acid	C3H7NO2	0	Extracellular
ala-D	D-Alanine	D-2-Aminopropionic acid	C3H7NO2	0	Lysosome
ala-D	D-Alanine	D-2-Aminopropionic acid	C3H7NO2	0	Peroxisome
ala-L	L-Alanine	L-2-Aminopropionic acid, L-alpha-Alanine	C3H7NO2	0	Cytosol
ala-L	L-Alanine	L-2-Aminopropionic acid, L-alpha-Alanine	C3H7NO2	0	Extracellular
ala-L	L-Alanine	L-2-Aminopropionic acid, L-alpha-Alanine	C3H7NO2	0	Lysosome
ala-L	L-Alanine	L-2-Aminopropionic acid, L-alpha-Alanine	C3H7NO2	0	Mitochondria
ala-L	L-Alanine	L-2-Aminopropionic acid, L-alpha-Alanine	C3H7NO2	0	Peroxisome
aldstrn	Aldosterone	11beta,21-Dihydroxy-3,20-dioxo-4-pregnen-18-al, Aldosterone	C21H28O5	0	Cytosol
aldstrn	Aldosterone	11beta,21-Dihydroxy-3,20-dioxo-4-pregnen-18-al, Aldosterone	C21H28O5	0	Extracellular
aldstrn	Aldosterone	11beta,21-Dihydroxy-3,20-dioxo-4-pregnen-18-al, Aldosterone	C21H28O5	0	Mitochondria
alkylR1oh	hydroxy alkyl chain		C2H5OFULLR	0	Peroxisome
alpa_hs	lysophosphatidic acid (homo sapiens)		C3H6O5PFULLRCO2	-2	Cytosol
alpa_hs	lysophosphatidic acid (homo sapiens)		C3H6O5PFULLRCO2	-2	Mitochondria
alpam	S-aminomethyldihydrolipoamide		C9H21N2OS2	1	Mitochondria

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
alpro	S-Aminomethyldihydrolipoylprotein		CH6NS2X	1	Mitochondria
am6sa	2-Aminomuconate 6-semialdehyde	2-Aminomuconate semialdehyde	C6H7NO3	0	Cytosol
amet	S-Adenosyl-L-methionine	Acylcarnitine, S-Adenosylmethionine	C15H23N6O5S	1	Cytosol
amet	S-Adenosyl-L-methionine	Acylcarnitine, S-Adenosylmethionine	C15H23N6O5S	1	Mitochondria
amet	S-Adenosyl-L-methionine	Acylcarnitine, S-Adenosylmethionine	C15H23N6O5S	1	Nucleus
amet	S-Adenosyl-L-methionine	Acylcarnitine, S-Adenosylmethionine	C15H23N6O5S	1	Endoplasmic Reticulum
ametam	S-Adenosylmethioninamine	(5-Deoxy-5-adenosyl)(3-aminopropyl)methylsulfonium salt, S-Adenosyl-L-methioninamine	C14H24N6O3S	2	Cytosol
amp	AMP	5'-AMP, 5'-Adenosine monophosphate, 5'-Adenylic acid, Adenosine 5'-monophosphate, Adenosine 5'-phosphate, Adenylate, Adenylic acid	C10H12N5O7P	-2	Cytosol
amp	AMP	5'-AMP, 5'-Adenosine monophosphate, 5'-Adenylic acid, Adenosine 5'-monophosphate, Adenosine 5'-phosphate, Adenylate, Adenylic acid	C10H12N5O7P	-2	Extracellular
amp	AMP	5'-AMP, 5'-Adenosine monophosphate, 5'-Adenylic acid, Adenosine 5'-monophosphate, Adenosine 5'-phosphate, Adenylate, Adenylic acid	C10H12N5O7P	-2	Golgi Apparatus
amp	AMP	5'-AMP, 5'-Adenosine monophosphate, 5'-Adenylic acid, Adenosine 5'-monophosphate, Adenosine 5'-phosphate, Adenylate, Adenylic acid	C10H12N5O7P	-2	Lysosome
amp	AMP	5'-AMP, 5'-Adenosine monophosphate, 5'-Adenylic acid, Adenosine 5'-monophosphate, Adenosine 5'-phosphate, Adenylate, Adenylic acid	C10H12N5O7P	-2	Mitochondria
amp	AMP	5'-AMP, 5'-Adenosine monophosphate, 5'-Adenylic acid, Adenosine 5'-monophosphate, Adenosine 5'-phosphate, Adenylate, Adenylic acid	C10H12N5O7P	-2	Endoplasmic Reticulum
amp	AMP	5'-AMP, 5'-Adenosine monophosphate, 5'-Adenylic acid, Adenosine 5'-monophosphate, Adenosine 5'-phosphate, Adenylate, Adenylic acid	C10H12N5O7P	-2	Peroxisome
amuco	2-Aminomuconate	2-Aminomuconic acid, o-Aminomuconate	C6H6NO4	-1	Cytosol
andrstandn	androstanedione	5beta-Androstane-3,17-dione	C19H28O2	0	Endoplasmic Reticulum
andrstndn	Androstenedione	4-Androstene-3,17-dione, Androst-4-ene-3,17-dione	C19H26O2	0	Endoplasmic Reticulum
andrstrn	Androsterone	3alpha-Hydroxy-5alpha-androstan-17-one	C19H30O2	0	Cytosol
andrstrn	Androsterone	3alpha-Hydroxy-5alpha-androstan-17-one	C19H30O2	0	Extracellular
andrstrn	Androsterone	3alpha-Hydroxy-5alpha-androstan-17-one	C19H30O2	0	Endoplasmic Reticulum
andrstrnglc	androsterone glucuronide		C25H38O8	0	Cytosol
andrstrnglc	androsterone glucuronide		C25H38O8	0	Extracellular
andrstrnglc	androsterone glucuronide		C25H38O8	0	Endoplasmic Reticulum
anth	Anthranilate	2-Aminobenzoate, Anthranilic acid, Vitamin L, Vitamin L1, o-Aminobenzoic acid	C7H6NO2	-1	Cytosol
antipyrene	antipyrene	Analgesine, Anodynine, Antipirin, Antipyrin, Apirelina, Parodyne, Phenazon [MeSH: pyrazon], Phenazone [MeSH: Antipyrine], Phenazonum, antipyrine [MeSH: Antipyrine]	C11H12N2O	0	Cytosol
antipyrene	antipyrene	Analgesine, Anodynine, Antipirin, Antipyrin, Apirelina, Parodyne, Phenazon [MeSH: pyrazon], Phenazone [MeSH: Antipyrine], Phenazonum, antipyrine [MeSH: Antipyrine]	C11H12N2O	0	Extracellular
ap4a	P1,P4-Bis(5'-adenosyl) tetraphosphate	AppppA	C20H24N10O19P4	-4	Cytosol
apnnox	alpha-Pinene-oxide	alpha-Pinene-oxide	C10H16O	0	Cytosol
apnnox	alpha-Pinene-oxide	alpha-Pinene-oxide	C10H16O	0	Extracellular
apoC	Apocarboxlase (no lys residue)		XH	0	Cytosol
apoC	Apocarboxlase (no lys residue)		XH	0	Mitochondria
apoC-Lys	Apocarboxylase (Lys residue)		C6H13N2OX	0	Cytosol
apoC-Lys	Apocarboxylase (Lys residue)		C6H13N2OX	0	Mitochondria
apoC-Lys_btn	Holocarboxylase (biotin covalent bound to Lys residue of apoC)		C16H27N4O3SX	0	Cytosol
apoC-Lys_btn	Holocarboxylase (biotin covalent bound to Lys residue of apoC)		C16H27N4O3SX	0	Mitochondria
appnn	(+)-alpha-Pinene	(+)-alpha-Pinene	C10H16	0	Cytosol
appnn	(+)-alpha-Pinene	(+)-alpha-Pinene	C10H16	0	Extracellular
aprgstrn	20alpha-Hydroxyprogesterone	20(S)-Hydroxyprogesterone, 20alpha-Dihydroprogesterone, 20alpha-Hydroxy-4-pregnen-3-one, 20alpha-Hydroxypregn-4-en-3-one, 20alpha-Hydroxyprogesterone, Progesterol-20alpha	C21H32O2	0	Cytosol
aprgstrn	20alpha-Hydroxyprogesterone	20(S)-Hydroxyprogesterone, 20alpha-Dihydroprogesterone, 20alpha-Hydroxy-4-pregnen-3-one, 20alpha-Hydroxypregn-4-en-3-one, 20alpha-Hydroxyprogesterone, Progesterol-20alpha	C21H32O2	0	Extracellular
aprut	N-Acetylputrescine		C6H15N2O	1	Cytosol
aps	Adenosine 5'-phosphosulfate	APS, Adenylylsulfate	C10H12N5O10PS	-2	Cytosol
aqcobal	Aquacob(III)alamin	Aquacobalamin	C62H93CoN13O15P	0	Cytosol
aqcobal	Aquacob(III)alamin	Aquacobalamin	C62H93CoN13O15P	0	Extracellular

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
arab-L	L-Arabinose		C5H10O5	0	Cytosol
arab-L	L-Arabinose		C5H10O5	0	Extracellular
arach	Arachidic acid	Arachidic acid, Eicosanoic acid, Icosanoic acid	C20H39O2	-1	Cytosol
arach	Arachidic acid	Arachidic acid, Eicosanoic acid, Icosanoic acid	C20H39O2	-1	Extracellular
arachcoa	arachidyl coenzyme A		C41H70N7O17P3S	-4	Cytosol
arachcoa	arachidyl coenzyme A		C41H70N7O17P3S	-4	Mitochondria
arachcoa	arachidyl coenzyme A		C41H70N7O17P3S	-4	Peroxisome
arachcrn	arachidyl carnitine	arachidic acid - carnitine	C27H53NO4	0	Cytosol
arachcrn	arachidyl carnitine	arachidic acid - carnitine	C27H53NO4	0	Mitochondria
arachd	arachidonic acid	(5Z,8Z,11Z,14Z)-Icosatetraenoic acid, Arachidonate, Arachidonic acid, cis-5,8,11,14-Eicosatetraenoic acid, eicosanoate 20:4	C20H31O2	-1	Cytosol
arachd	arachidonic acid	(5Z,8Z,11Z,14Z)-Icosatetraenoic acid, Arachidonate, Arachidonic acid, cis-5,8,11,14-Eicosatetraenoic acid, eicosanoate 20:4	C20H31O2	-1	Extracellular
arachd	arachidonic acid	(5Z,8Z,11Z,14Z)-Icosatetraenoic acid, Arachidonate, Arachidonic acid, cis-5,8,11,14-Eicosatetraenoic acid, eicosanoate 20:4	C20H31O2	-1	Endoplasmic Reticulum
arachdcoa	C20:4-CoA	Arachidonyl-CoA, arachidonate CoA, arachidonic acid Coenzyme A	C41H62N7O17P3S	-4	Cytosol
arachdcoa	C20:4-CoA	Arachidonyl-CoA, arachidonate CoA, arachidonic acid Coenzyme A	C41H62N7O17P3S	-4	Mitochondria
arachdcoa	C20:4-CoA	Arachidonyl-CoA, arachidonate CoA, arachidonic acid Coenzyme A	C41H62N7O17P3S	-4	Peroxisome
arachdcrn	C20:4 carnitine	Arachidonate carnitine	C27H45NO4	0	Cytosol
arachdcrn	C20:4 carnitine	Arachidonate carnitine	C27H45NO4	0	Mitochondria
arg-D	D-Arginine	D-2-Amino-5-guanidinovaleric acid	C6H15N4O2	1	Peroxisome
arg-L	L-Arginine	(S)-2-Amino-5-guanidinovaleric acid, Arg, Arginine	C6H15N4O2	1	Cytosol
arg-L	L-Arginine	(S)-2-Amino-5-guanidinovaleric acid, Arg, Arginine	C6H15N4O2	1	Extracellular
arg-L	L-Arginine	(S)-2-Amino-5-guanidinovaleric acid, Arg, Arginine	C6H15N4O2	1	Mitochondria
argsuc	N(omega)-(L-Arginino)succinate	L-Argininosuccinate, L-Argininosuccinic acid, L-Arginosuccinic acid, N-(L-Arginino)succinate	C10H17N4O6	-1	Cytosol
ascb-L	L-Ascorbate	Ascorbate, Ascorbic acid, L-Ascorbic acid, Vitamin C	C6H8O6	0	Cytosol
ascb-L	L-Ascorbate	Ascorbate, Ascorbic acid, L-Ascorbic acid, Vitamin C	C6H8O6	0	Extracellular
asn-L	L-Asparagine	2-Amino-3-carbamoylpropanoic acid, 2-Aminosuccinamic acid, Arg	C4H8N2O3	0	Cytosol
asn-L	L-Asparagine	2-Amino-3-carbamoylpropanoic acid, 2-Aminosuccinamic acid, Arg	C4H8N2O3	0	Extracellular
asn-L	L-Asparagine	2-Amino-3-carbamoylpropanoic acid, 2-Aminosuccinamic acid, Arg	C4H8N2O3	0	Mitochondria
Asn-X-Ser/Thr	protein-linked asparagine residue (N-glycosylation site)		XH	0	Lysosome
Asn-X-Ser/Thr	protein-linked asparagine residue (N-glycosylation site)		XH	0	Endoplasmic Reticulum
asp-D	D-Aspartate	D-2-Aminobutanedioic acid, D-Aspartic acid	C4H6NO4	-1	Cytosol
asp-D	D-Aspartate	D-2-Aminobutanedioic acid, D-Aspartic acid	C4H6NO4	-1	Extracellular
asp-D	D-Aspartate	D-2-Aminobutanedioic acid, D-Aspartic acid	C4H6NO4	-1	Peroxisome
asp-L	L-Aspartate	2-aminosuccinic acid, Asp, L-Aspartic acid	C4H6NO4	-1	Cytosol
asp-L	L-Aspartate	2-aminosuccinic acid, Asp, L-Aspartic acid	C4H6NO4	-1	Extracellular
asp-L	L-Aspartate	2-aminosuccinic acid, Asp, L-Aspartic acid	C4H6NO4	-1	Mitochondria
atp	ATP	5'-adenylate triphosphate, Adenosine 5'-triphosphate	C10H12N5O13P3	-4	Cytosol
atp	ATP	5'-adenylate triphosphate, Adenosine 5'-triphosphate	C10H12N5O13P3	-4	Extracellular
atp	ATP	5'-adenylate triphosphate, Adenosine 5'-triphosphate	C10H12N5O13P3	-4	Mitochondria
atp	ATP	5'-adenylate triphosphate, Adenosine 5'-triphosphate	C10H12N5O13P3	-4	Nucleus
atp	ATP	5'-adenylate triphosphate, Adenosine 5'-triphosphate	C10H12N5O13P3	-4	Endoplasmic Reticulum
atp	ATP	5'-adenylate triphosphate, Adenosine 5'-triphosphate	C10H12N5O13P3	-4	Peroxisome
avite1	alpha-Tocopherol	Aquasol E, Ephanyl, Eprolin, Esorb, Pheryl-E, Phytogermine, Vita plus E, Vita plus Ealpha-Tocopherol, Viteolin, Waynecomycin	C29H50O2	0	Cytosol
avite1	alpha-Tocopherol	Aquasol E, Ephanyl, Eprolin, Esorb, Pheryl-E, Phytogermine, Vita plus E, Vita plus Ealpha-Tocopherol, Viteolin, Waynecomycin	C29H50O2	0	Extracellular
avite2	alpha-Tocotrienol	1721-51-3, 2H-1-Benzopyran-6-ol, 3,4-dihydro-2,5,7,8-tetramethyl-2-(4,8,12-trimethyl-3,7,11-tridecatrienyl)-, CHEMID001721513, Tocotrienol, alpha, zeta1-Tocopherol	C29H44O2	0	Cytosol

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
avite2	alpha-Tocotrienol	1721-51-3, 2H-1-Benzopyran-6-ol, 3,4-dihydro-2,5,7,8-tetramethyl-2-(4,8,12-trimethyl-3,7,11-tridecatrienyl)-, CHEMID001721513, Tocotrienol, alpha, zeta1-Tocopherol	C29H44O2	0	Extracellular
b2coa	Crotonoyl-CoA	2-Butenoyl-CoA, But-2-enoyl-CoA, Crotonyl-CoA, trans-But-2-enoyl-CoA	C25H36N7O17P3S	-4	Mitochondria
b2coa	Crotonoyl-CoA	2-Butenoyl-CoA, But-2-enoyl-CoA, Crotonyl-CoA, trans-But-2-enoyl-CoA	C25H36N7O17P3S	-4	Peroxisome
bamppald	beta-Aminopropion aldehyde		C3H8NO	1	Cytosol
bamppald	beta-Aminopropion aldehyde		C3H8NO	1	Mitochondria
bdg2hc	cis-beta-D-Glucosyl-2-hydroxycinnamate	beta-D-Glucosyl-2-coumarinate	C15H18O8	0	Cytosol
betald	Betaine aldehyde		C5H12NO	1	Cytosol
betald	Betaine aldehyde		C5H12NO	1	Mitochondria
bhb	(R)-3-Hydroxybutanoate	(R)-3-Hydroxybutanoic acid, (R)-3-Hydroxybutyric acid, 3-hydroxybutyrate	C4H7O3	-1	Cytosol
bhb	(R)-3-Hydroxybutanoate	(R)-3-Hydroxybutanoic acid, (R)-3-Hydroxybutyric acid, 3-hydroxybutyrate	C4H7O3	-1	Extracellular
bhb	(R)-3-Hydroxybutanoate	(R)-3-Hydroxybutanoic acid, (R)-3-Hydroxybutyric acid, 3-hydroxybutyrate	C4H7O3	-1	Mitochondria
bildglcur	Bilirubin beta-diglucuronide	Bilirubin bis-glucuronoside	C45H50N4O18	-2	Cytosol
bildglcur	Bilirubin beta-diglucuronide	Bilirubin bis-glucuronoside	C45H50N4O18	-2	Extracellular
bildglcur	Bilirubin beta-diglucuronide	Bilirubin bis-glucuronoside	C45H50N4O18	-2	Endoplasmic Reticulum
bilglcur	Bilirubin monoglucuronide	Bilirubin-glucuronoside	C39H44N4O12	0	Cytosol
bilglcur	Bilirubin monoglucuronide	Bilirubin-glucuronoside	C39H44N4O12	0	Extracellular
bilglcur	Bilirubin monoglucuronide	Bilirubin-glucuronoside	C39H44N4O12	0	Endoplasmic Reticulum
bilirub	Bilirubin		C33H34N4O6	-2	Cytosol
bilirub	Bilirubin		C33H34N4O6	-2	Extracellular
bilirub	Bilirubin		C33H34N4O6	-2	Endoplasmic Reticulum
biliverd	Biliverdin		C33H32N4O6	-2	Cytosol
biocyt	Biocytin	N6-D-Biotinyl-L-lysine, epsilon-N-Biotinyl-L-lysine	C16H28N4O4S	0	Cytosol
biocyt	Biocytin	N6-D-Biotinyl-L-lysine, epsilon-N-Biotinyl-L-lysine	C16H28N4O4S	0	Extracellular
biocyt	Biocytin	N6-D-Biotinyl-L-lysine, epsilon-N-Biotinyl-L-lysine	C16H28N4O4S	0	Mitochondria
biocyt	Biocytin	N6-D-Biotinyl-L-lysine, epsilon-N-Biotinyl-L-lysine	C16H28N4O4S	0	Nucleus
btamp	Biotinyl-5'-AMP		C20H27N7O9PS	-1	Cytosol
btamp	Biotinyl-5'-AMP		C20H27N7O9PS	-1	Mitochondria
btcoa	Butanoyl-CoA	Butyryl-CoA	C25H38N7O17P3S	-4	Mitochondria
btn	Biotin	Coenzyme R, D-Biotin, Vitamin B7, Vitamin H	C10H15N2O3S	-1	Cytosol
btn	Biotin	Coenzyme R, D-Biotin, Vitamin B7, Vitamin H	C10H15N2O3S	-1	Extracellular
btn	Biotin	Coenzyme R, D-Biotin, Vitamin B7, Vitamin H	C10H15N2O3S	-1	Mitochondria
btn	Biotin	Coenzyme R, D-Biotin, Vitamin B7, Vitamin H	C10H15N2O3S	-1	Nucleus
but	Butyrate (n-C4:0)	Butanoate, Butanoic acid, Butyric acid	C4H7O2	-1	Cytosol
but	Butyrate (n-C4:0)	Butanoate, Butanoic acid, Butyric acid	C4H7O2	-1	Extracellular
but	Butyrate (n-C4:0)	Butanoate, Butanoic acid, Butyric acid	C4H7O2	-1	Mitochondria
bvite	beta-tocopherol	148-03-8, 2H-1-Benzopyran-6-ol, 3,4-dihydro-2,5,8-trimethyl-2-((4R,8R)-4,8,12-trimethyltridecyl)-, (2R)-rel-, 2H-1-Benzopyran-6-ol, 3,4-dihydro-2,5,8-trimethyl-2-(4,8,12-trimethyltridecyl)-, 3,4-Dihydro-2,5,8-trimethyl-2-(4,8,12-trimethyltridecyl)-2H-benzopyran-6-ol, CHEMID000148038, EINECS 205-708-5	C28H48O2	0	Cytosol
bvite	beta-tocopherol	148-03-8, 2H-1-Benzopyran-6-ol, 3,4-dihydro-2,5,8-trimethyl-2-((4R,8R)-4,8,12-trimethyltridecyl)-, (2R)-rel-, 2H-1-Benzopyran-6-ol, 3,4-dihydro-2,5,8-trimethyl-2-(4,8,12-trimethyltridecyl)-, 3,4-Dihydro-2,5,8-trimethyl-2-(4,8,12-trimethyltridecyl)-2H-benzopyran-6-ol, CHEMID000148038, EINECS 205-708-5	C28H48O2	0	Extracellular
bz	Benzoate	Benzenecarboxylic acid, Benzoic acid, Dracylic acid, Phenylformic acid	C7H5O2	-1	Cytosol
bz	Benzoate	Benzenecarboxylic acid, Benzoic acid, Dracylic acid, Phenylformic acid	C7H5O2	-1	Extracellular
bz	Benzoate	Benzenecarboxylic acid, Benzoic acid, Dracylic acid, Phenylformic acid	C7H5O2	-1	Endoplasmic Reticulum
c226coa	cervonyl coenzyme A	C226-CoA, Docosahexaenoic acid coenzyme a, cervonic acid coenzyme a, docosa-4,7,10,13,16,19-hexaenoic acid coenzyme a	C43H62N7O17P3S	-4	Cytosol
c226coa	cervonyl coenzyme A	C226-CoA, Docosahexaenoic acid coenzyme a, cervonic acid coenzyme a, docosa-4,7,10,13,16,19-hexaenoic acid coenzyme a	C43H62N7O17P3S	-4	Mitochondria
c226coa	cervonyl coenzyme A	C226-CoA, Docosahexaenoic acid coenzyme a, cervonic acid coenzyme a, docosa-4,7,10,13,16,19-hexaenoic acid coenzyme a	C43H62N7O17P3S	-4	Peroxisome
c226crn	cervonyl carnitine	cervonic acid carnitine	C29H45NO4	0	Cytosol
c226crn	cervonyl carnitine	cervonic acid carnitine	C29H45NO4	0	Mitochondria
c2m26dcoa	cis-2-Methyl-5-isopropylhexa-2,5-dienoyl-CoA		C31H46N7O17P3S	-4	Mitochondria
c2m26dcoa	cis-2-Methyl-5-isopropylhexa-2,5-dienoyl-CoA		C31H46N7O17P3S	-4	Peroxisome

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
ca2	Calcium	Ca2+	Ca	2	Cytosol
ca2	Calcium	Ca2+	Ca	2	Extracellular
cala	N-Carbamoyl-beta-alanine	3-Ureidopropanoate, 3-Ureidopropionate, beta-Ureidopropionic acid	C4H7N2O3	-1	Cytosol
camp	cAMP	3',5'-Cyclic AMP, Adenosine 3[-,5[-cyclic monophosphate, Cyclic adenylic acid	C10H11N5O6P	-1	Cytosol
camp	cAMP	3',5'-Cyclic AMP, Adenosine 3[-,5[-cyclic monophosphate, Cyclic adenylic acid	C10H11N5O6P	-1	Extracellular
camp	cAMP	3',5'-Cyclic AMP, Adenosine 3[-,5[-cyclic monophosphate, Cyclic adenylic acid	C10H11N5O6P	-1	Golgi Apparatus
carn	L-Carnosine	L-Carnosine, Nalpha-(beta-alanyl)-L-histidine	C9H14N4O3	0	Cytosol
caro	beta-Carotene		C40H56	0	Cytosol
caro	beta-Carotene		C40H56	0	Extracellular
carveol	(E)-carveol	(-)-trans-Carveol, (E)-carveol	C10H16O	0	Cytosol
carveol	(E)-carveol	(-)-trans-Carveol, (E)-carveol	C10H16O	0	Extracellular
cbasp	N-Carbamoyl-L-aspartate		C5H6N2O5	-2	Cytosol
cbl1	Cob(I)alamin	Cbl, Vitamin B12s	C62H88CoN13O14P	-1	Mitochondria
cbl2	Cob(II)alamin	Vitamin B12r	C62H92CoN13O14P	0	Cytosol
cbl2	Cob(II)alamin	Vitamin B12r	C62H92CoN13O14P	0	Mitochondria
cbp	Carbamoyl phosphate		CH2NO5P	-2	Cytosol
cbp	Carbamoyl phosphate		CH2NO5P	-2	Mitochondria
cbp	Carbamoyl phosphate		CH2NO5P	-2	Endoplasmic Reticulum
cca_d3	Calcitroic acid (D3)	1alpha(OH)-23-carboxy-24,25,26,27-tetranor-D3	C22H33O4	-1	Cytosol
cca_d3	Calcitroic acid (D3)	1alpha(OH)-23-carboxy-24,25,26,27-tetranor-D3	C22H33O4	-1	Extracellular
cca_d3	Calcitroic acid (D3)	1alpha(OH)-23-carboxy-24,25,26,27-tetranor-D3	C22H33O4	-1	Mitochondria
cdp	CDP	Cytidine 5'-diphosphate, Cytidine diphosphate	C9H12N3O11P2	-3	Cytosol
cdp	CDP	Cytidine 5'-diphosphate, Cytidine diphosphate	C9H12N3O11P2	-3	Mitochondria
cdp	CDP	Cytidine 5'-diphosphate, Cytidine diphosphate	C9H12N3O11P2	-3	Nucleus
cdpchol	CDPcholine	Cydine 5'-diphosphocholine	C14H25N4O11P2	-1	Cytosol
cdpdag_hs	CDP diacylglycerol (homo sapiens)	CDP-diacylglycerol	C12H17N3O11P2FULLRCO2FULLR2CO2	-2	Cytosol
cdpdag_hs	CDP diacylglycerol (homo sapiens)	CDP-diacylglycerol	C12H17N3O11P2FULLRCO2FULLR2CO2	-2	Mitochondria
cdpea	CDPethanolamine		C11H19N4O11P2	-1	Cytosol
cgly	Cys-Gly	L-Cysteinylglycine	C5H10N2O3S	0	Cytosol
cgly	Cys-Gly	L-Cysteinylglycine	C5H10N2O3S	0	Extracellular
chito2pdol_L	N,N'-Diacetylchitobiosyldiphosphodolichol, human liver homolog	Chitobiosyldiphosphodolichol	C1240H2028N20O170P20	-20	Cytosol
chito2pdol_U	N,N'-Diacetylchitobiosyldiphosphodolichol, human uterine homolog	Chitobiosyldiphosphodolichol	C1185H1940N20O170P20	-20	Cytosol
chlstol	Cholesta-7,24-dien-3beta-ol	Cholesta-7,24-dien-3beta-ol	C27H44O	0	Endoplasmic Reticulum
chol	Choline	Bilineurine	C5H14NO	1	Cytosol
chol	Choline	Bilineurine	C5H14NO	1	Extracellular
chol	Choline	Bilineurine	C5H14NO	1	Golgi Apparatus
chol	Choline	Bilineurine	C5H14NO	1	Mitochondria
chol	Choline	Bilineurine	C5H14NO	1	Nucleus
chol	Choline	Bilineurine	C5H14NO	1	Endoplasmic Reticulum
cholate	Cholate	12alpha-Trihydroxy-5beta-cholanate, 12alpha-Trihydroxy-5beta-cholanic acid, 3alpha, 7alpha, Cholic acid, bile acid	C24H39O5	-1	Cytosol
cholate	Cholate	12alpha-Trihydroxy-5beta-cholanate, 12alpha-Trihydroxy-5beta-cholanic acid, 3alpha, 7alpha, Cholic acid, bile acid	C24H39O5	-1	Extracellular
cholcoa	Choloyl-CoA	3-alpha-7-alpha-12-alpha-trihydroxy-5-beta-cholan-24-one-CoA, Choloyl-CoA	C45H70N7O20P3S	-4	Peroxisome
cholcoads	3alpha,7alpha,12alpha-Trihydroxy-5beta-cholest-24-enoyl-CoA	25(S)-3-alpha-7-alpha-12-alpha-trihydroxy-5-beta-cholest-24-enoyl-CoA, 3alpha,7alpha,12alpha-Trihydroxy-5beta-cholest-24-enoyl-CoA	C48H74N7O20P3S	-4	Peroxisome
cholcoaone	3alpha,7alpha,12alpha-Trihydroxy-5beta-24-oxocholestanoyl-CoA	3-alpha-7-alpha-12-alpha-trihydroxy-5-beta-cholest-24-one-CoA, 3alpha,7alpha,12alpha-Trihydroxy-5beta-24-oxocholestanoyl-CoA	C48H74N7O21P3S	-4	Peroxisome
cholcoar	3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestanoyl-CoA	25(R) 3-alpha-7-alpha-12-alpha-trihydroxy-5-beta-cholestanoyl-CoA, 3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestanoyl-CoA	C48H76N7O20P3S	-4	Endoplasmic Reticulum
cholcoar	3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestanoyl-CoA	25(R) 3-alpha-7-alpha-12-alpha-trihydroxy-5-beta-cholestanoyl-CoA, 3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestanoyl-CoA	C48H76N7O20P3S	-4	Peroxisome
cholcoas	3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestanoyl-CoA(S)	25(S)-3-alpha-7-alpha-12-alpha-trihydroxy-5-beta-cholestanoyl-coa	C48H76N7O20P3S	-4	Endoplasmic Reticulum
cholcoas	3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestanoyl-CoA(S)	25(S)-3-alpha-7-alpha-12-alpha-trihydroxy-5-beta-cholestanoyl-coa	C48H76N7O20P3S	-4	Peroxisome
cholp	Choline phosphate	O-Phosphocholine, Phosphocholine, Phosphorylcholine	C5H13NO4P	-1	Cytosol
cholp	Choline phosphate	O-Phosphocholine, Phosphocholine, Phosphorylcholine	C5H13NO4P	-1	Golgi Apparatus
cholp	Choline phosphate	O-Phosphocholine, Phosphocholine, Phosphorylcholine	C5H13NO4P	-1	Lysosome

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
chsterol	Cholesterol	Cholest-5-en-3beta-ol	C27H46O	0	Cytosol
chsterol	Cholesterol	Cholest-5-en-3beta-ol	C27H46O	0	Extracellular
chsterol	Cholesterol	Cholest-5-en-3beta-ol	C27H46O	0	Golgi Apparatus
chsterol	Cholesterol	Cholest-5-en-3beta-ol	C27H46O	0	Lysosome
chsterol	Cholesterol	Cholest-5-en-3beta-ol	C27H46O	0	Mitochondria
chsterol	Cholesterol	Cholest-5-en-3beta-ol	C27H46O	0	Endoplasmic Reticulum
chsterols	cholesterol sulfate		C27H45O4S	-1	Cytosol
chsterols	cholesterol sulfate		C27H45O4S	-1	Endoplasmic Reticulum
chtn	chitin	beta-1,4-poly-N-acetyl-D-glucosamine	C24H41N3O16	0	Cytosol
chtn	chitin	beta-1,4-poly-N-acetyl-D-glucosamine	C24H41N3O16	0	Extracellular
cit	Citrate	2, 2-Hydroxy-1, 2-Hydroxytricarballylic acid, 3-propanetricarboxylic acid, Citric acid	C6H5O7	-3	Cytosol
cit	Citrate	2, 2-Hydroxy-1, 2-Hydroxytricarballylic acid, 3-propanetricarboxylic acid, Citric acid	C6H5O7	-3	Extracellular
cit	Citrate	2, 2-Hydroxy-1, 2-Hydroxytricarballylic acid, 3-propanetricarboxylic acid, Citric acid	C6H5O7	-3	Mitochondria
citmcoa-L	L-Citramalyl-CoA	(3S)-Citramalyl-CoA	C26H37N7O20P3S	-5	Mitochondria
citr-L	L-Citrulline	2-Amino-5-ureidovaleric acid, Citrulline, N5-(aminocarbonyl)-L-Ornithine	C6H13N3O3	0	Cytosol
citr-L	L-Citrulline	2-Amino-5-ureidovaleric acid, Citrulline, N5-(aminocarbonyl)-L-Ornithine	C6H13N3O3	0	Mitochondria
cl	Chloride	Cl-	Cl	-1	Cytosol
cl	Chloride	Cl-	Cl	-1	Extracellular
clpn_hs	cardiolipin (homo sapiens)		C9H16O9P2FULLRCO2FULLR2CO2FULLRCO2FULLR2CO2	-2	Cytosol
clpnd	clupanodonic acid	docosa-7,10,13,16,19-pentaenoic acid, docosapentaenoic acid (n-3)	C22H33O2	-1	Cytosol
clpnd	clupanodonic acid	docosa-7,10,13,16,19-pentaenoic acid, docosapentaenoic acid (n-3)	C22H33O2	-1	Extracellular
clpndcoa	clupanodonyl CoA	clupanodonyl Coenzyme A, docosa-7,10,13,16,19-pentaenoyl coenzyme A	C43H64N7O17P3S	-4	Cytosol
clpndcoa	clupanodonyl CoA	clupanodonyl Coenzyme A, docosa-7,10,13,16,19-pentaenoyl coenzyme A	C43H64N7O17P3S	-4	Mitochondria
clpndcoa	clupanodonyl CoA	clupanodonyl Coenzyme A, docosa-7,10,13,16,19-pentaenoyl coenzyme A	C43H64N7O17P3S	-4	Peroxisome
clpndcrn	clupanodonyl carnitine		C29H47NO4	0	Cytosol
clpndcrn	clupanodonyl carnitine		C29H47NO4	0	Mitochondria
cmp	CMP	3'-Cytidylic Acid, Cytidine-2'(3')-monophosphoric acid, Cytidine-2[(3[)-monophosphoric acid, Cytidine-5'-monophosphate, Cytidylic acid	C9H12N3O8P	-2	Cytosol
cmp	CMP	3'-Cytidylic Acid, Cytidine-2'(3')-monophosphoric acid, Cytidine-2[(3[)-monophosphoric acid, Cytidine-5'-monophosphate, Cytidylic acid	C9H12N3O8P	-2	Extracellular
cmp	CMP	3'-Cytidylic Acid, Cytidine-2'(3')-monophosphoric acid, Cytidine-2[(3[)-monophosphoric acid, Cytidine-5'-monophosphate, Cytidylic acid	C9H12N3O8P	-2	Golgi Apparatus
cmp	CMP	3'-Cytidylic Acid, Cytidine-2'(3')-monophosphoric acid, Cytidine-2[(3[)-monophosphoric acid, Cytidine-5'-monophosphate, Cytidylic acid	C9H12N3O8P	-2	Lysosome
cmp	CMP	3'-Cytidylic Acid, Cytidine-2'(3')-monophosphoric acid, Cytidine-2[(3[)-monophosphoric acid, Cytidine-5'-monophosphate, Cytidylic acid	C9H12N3O8P	-2	Mitochondria
cmp	CMP	3'-Cytidylic Acid, Cytidine-2'(3')-monophosphoric acid, Cytidine-2[(3[)-monophosphoric acid, Cytidine-5'-monophosphate, Cytidylic acid	C9H12N3O8P	-2	Nucleus
cmp2amep	CMP-2-aminoethylphosphonate	CMPciliatine	C11H19N4O10P2	-1	Cytosol
cmpacna	CMP-N-acetylneuraminate	CMP-Neu5Ac	C20H29N4O16P	-2	Cytosol
cmpacna	CMP-N-acetylneuraminate	CMP-Neu5Ac	C20H29N4O16P	-2	Golgi Apparatus
cmpacna	CMP-N-acetylneuraminate	CMP-Neu5Ac	C20H29N4O16P	-2	Nucleus
cmpntm2amep	CMP-N-trimethyl-2-aminoethylphosphonate	CMP-2-trimethylaminoethylphosphonate	C14H25N4O10P2	-1	Cytosol
cmusa	2-Amino-3-carboxymuconate semialdehyde		C7H6NO5	-1	Cytosol
co	Carbon monoxide		CO	0	Cytosol
co	Carbon monoxide		CO	0	Extracellular
co2	CO2	Carbon dioxide, Carbonic anhydride	CO2	0	Cytosol
co2	CO2	Carbon dioxide, Carbonic anhydride	CO2	0	Extracellular
co2	CO2	Carbon dioxide, Carbonic anhydride	CO2	0	Golgi Apparatus
co2	CO2	Carbon dioxide, Carbonic anhydride	CO2	0	Mitochondria
co2	CO2	Carbon dioxide, Carbonic anhydride	CO2	0	Nucleus
co2	CO2	Carbon dioxide, Carbonic anhydride	CO2	0	Endoplasmic Reticulum
co2	CO2	Carbon dioxide, Carbonic anhydride	CO2	0	Peroxisome
coa	Coenzyme A	CoA, CoA-SH, CoASH	C21H32N7O16P3S	-4	Cytosol
coa	Coenzyme A	CoA, CoA-SH, CoASH	C21H32N7O16P3S	-4	Golgi Apparatus
coa	Coenzyme A	CoA, CoA-SH, CoASH	C21H32N7O16P3S	-4	Lysosome
coa	Coenzyme A	CoA, CoA-SH, CoASH	C21H32N7O16P3S	-4	Mitochondria
coa	Coenzyme A	CoA, CoA-SH, CoASH	C21H32N7O16P3S	-4	Nucleus
coa	Coenzyme A	CoA, CoA-SH, CoASH	C21H32N7O16P3S	-4	Endoplasmic Reticulum
coa	Coenzyme A	CoA, CoA-SH, CoASH	C21H32N7O16P3S	-4	Peroxisome
coke	cocaine	beta-Cocain, l-Cocain	C17H21NO4	0	Endoplasmic Reticulum

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
core2	Core 2	beta-D-Galactosyl-1,3-(N-acetyl-beta-D-glucosaminyl-1,6)-N-acetyl-D-galactosaminyl-R	C22H37N2O15X	0	Golgi Apparatus
core3	Core 3	N-Acetyl-beta-D-glucosaminyl-1,3-N-acetyl-D-galactosaminyl-R	C16H27N2O10X	0	Golgi Apparatus
core4	Core 4	N-Acetyl-beta-D-glucosaminyl-1,6-(N-acetyl-beta-glucosaminyl-1,3)-N-acetyl-D-galactosaminyl-R	C24H40N3O15X	0	Golgi Apparatus
core5	Core 5		C16H27N2O10X	0	Golgi Apparatus
core6	Core 6		C16H27N2O10X	0	Golgi Apparatus
core6	Core 6		C16H27N2O10X	0	Lysosome
core7	Core 7		C16H27N2O10X	0	Golgi Apparatus
core8	Core 8		C14H24NO10X	0	Golgi Apparatus
cortsn	Cortisone	11, 17alpha, 20-trione, 21-Dihydroxy-4-pregnene-3, Kendall's compound E, Reichstein's substance Fa	C21H28O5	0	Endoplasmic Reticulum
coucoa	p-coumaroyl-CoA	4-Coumaroyl-CoA;, 4-Hydroxycinnamoyl-CoA	C30H38N7O18P3S1	-4	Mitochondria
coumarin	coumarin	1,2-Benzopyrone, 2-Propenoic acid, 3-(2-hydroxyphenyl)-, d-lactone, 2H-1-Benzopyran-2-one, 5,6-Benzo-2-pyrone, Benzo-a-pyrone, Coumarine, Coumarinic anhydride, Cumarin, Rattex, Tonka bean camphor, cis-o-Coumarinic acid lactone, o-Hydroxycinnamic acid lactone	C9H6O2	0	Cytosol
coumarin	coumarin	1,2-Benzopyrone, 2-Propenoic acid, 3-(2-hydroxyphenyl)-, d-lactone, 2H-1-Benzopyran-2-one, 5,6-Benzo-2-pyrone, Benzo-a-pyrone, Coumarine, Coumarinic anhydride, Cumarin, Rattex, Tonka bean camphor, cis-o-Coumarinic acid lactone, o-Hydroxycinnamic acid lactone	C9H6O2	0	Extracellular
cpppg3	Coproporphyrinogen III		C36H40N4O8	-4	Cytosol
creat	Creatine	Methylglycocyamine, alpha-Methylguanidino aceti acid	C4H9N3O2	0	Cytosol
creat	Creatine	Methylglycocyamine, alpha-Methylguanidino aceti acid	C4H9N3O2	0	Extracellular
creat	Creatine	Methylglycocyamine, alpha-Methylguanidino aceti acid	C4H9N3O2	0	Mitochondria
crm_hs	ceramide (homo sapiens)	Ceramide, N-Acylsphingosine	C18H36NO2FULLRCO	0	Cytosol
crm_hs	ceramide (homo sapiens)	Ceramide, N-Acylsphingosine	C18H36NO2FULLRCO	0	Golgi Apparatus
crm_hs	ceramide (homo sapiens)	Ceramide, N-Acylsphingosine	C18H36NO2FULLRCO	0	Lysosome
crm_hs	ceramide (homo sapiens)	Ceramide, N-Acylsphingosine	C18H36NO2FULLRCO	0	Endoplasmic Reticulum
crmp_hs	Ceramide 1-phosphate	Ceramide 1-phosphate, Ceramide phosphate	C18H35NO5PFULLRCO	-2	Cytosol
crmp_hs	Ceramide 1-phosphate	Ceramide 1-phosphate, Ceramide phosphate	C18H35NO5PFULLRCO	-2	Extracellular
crn	L-Carnitine	(S)-Carnitine, 3-Carboxy-2-hydroxy-N, L-gamma-Trimethyl-beta-hydroxybutyrobetaine, N-trimethyl-1-propanaminium, Vitamin BT	C7H15NO3	0	Cytosol
crn	L-Carnitine	(S)-Carnitine, 3-Carboxy-2-hydroxy-N, L-gamma-Trimethyl-beta-hydroxybutyrobetaine, N-trimethyl-1-propanaminium, Vitamin BT	C7H15NO3	0	Extracellular
crn	L-Carnitine	(S)-Carnitine, 3-Carboxy-2-hydroxy-N, L-gamma-Trimethyl-beta-hydroxybutyrobetaine, N-trimethyl-1-propanaminium, Vitamin BT	C7H15NO3	0	Mitochondria
crn	L-Carnitine	(S)-Carnitine, 3-Carboxy-2-hydroxy-N, L-gamma-Trimethyl-beta-hydroxybutyrobetaine, N-trimethyl-1-propanaminium, Vitamin BT	C7H15NO3	0	Endoplasmic Reticulum
crn	L-Carnitine	(S)-Carnitine, 3-Carboxy-2-hydroxy-N, L-gamma-Trimethyl-beta-hydroxybutyrobetaine, N-trimethyl-1-propanaminium, Vitamin BT	C7H15NO3	0	Peroxisome
crtn	Creatinine	1-Methylglycocyamidine	C4H7N3O	0	Cytosol
crtsl	Cortisol	11beta, 17alpha, 20-dione, 21-Trihydroxy-4-pregnene-3, Hydrocortisone, Kendall's compound F Reichstein's substance M	C21H30O5	0	Cytosol
crtsl	Cortisol	11beta, 17alpha, 20-dione, 21-Trihydroxy-4-pregnene-3, Hydrocortisone, Kendall's compound F Reichstein's substance M	C21H30O5	0	Mitochondria
crtsl	Cortisol	11beta, 17alpha, 20-dione, 21-Trihydroxy-4-pregnene-3, Hydrocortisone, Kendall's compound F Reichstein's substance M	C21H30O5	0	Endoplasmic Reticulum
crtstrn	Corticosterone	11beta,21-Dihydroxy-4-pregnene-3,20-dione, Kendall's compound B, Reichstein's substance H	C21H30O4	0	Cytosol
crtstrn	Corticosterone	11beta,21-Dihydroxy-4-pregnene-3,20-dione, Kendall's compound B, Reichstein's substance H	C21H30O4	0	Mitochondria
crtstrn	Corticosterone	11beta,21-Dihydroxy-4-pregnene-3,20-dione, Kendall's compound B, Reichstein's substance H	C21H30O4	0	Endoplasmic Reticulum
crvnc	cervonic acid, C22:6 n-3	DHE, Docosahexaenoic acid, docosa-4,7,10,13,16,19-hexaenoic acid	C22H31O2	-1	Cytosol
crvnc	cervonic acid, C22:6 n-3	DHE, Docosahexaenoic acid, docosa-4,7,10,13,16,19-hexaenoic acid	C22H31O2	-1	Extracellular

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
cs,hs_linkage	chondroitin sulfate/heparan sulfate linkage region (GlcA-(Gal)2-Xyl-L-Ser (protein))		C23H36O20X	-1	Golgi Apparatus
cs_a	chondroitin sulfate A (GalNAc4S-GlcA), free chain	(GalNAc4S-GlcA)2-Gal4S-Gal-Xyl	C45H67N2O46S3	-5	Lysosome
cs_a,b,e_pre1	chondroitin sulfate A (GalNAc4S-GlcA), B (IdoA2S-GalNAc4S), and E (GalNAc4,6diS-GlcA), precursor 1	GalNAc4S-GlcA-Gal4S-Gal-Xyl-L-Ser (protein)	C31H47NO31S2X	-3	Golgi Apparatus
cs_a,b_pre2	chondroitin sulfate A (GalNAc4S-GlcA) and B (IdoA2S-GalNAc4S), precursor 2	GlcA-GalNAc4S-GlcA-Gal4S-Gal-Xyl-L-Ser	C37H54NO37S2X	-4	Golgi Apparatus
cs_a,b_pre3	chondroitin sulfate A (GalNAc4S-GlcA) and B (IdoA2S-GalNAc4S), precursor 3	GalNAc-GlcA-GalNAc4S-GlcA-Gal4S-Gal-Xyl-L-Ser	C45H67N2O42S2X	-4	Golgi Apparatus
cs_a_deg1	chondroitin sulfate A (GalNAc4S-GlcA), degradation product 1	GalNAc-GlcA-GalNAc4S-GlcA-Gal4S-Gal-Xyl	C45H68N2O43S2	-4	Lysosome
cs_a_deg2	chondroitin sulfate A (GalNAc4S-GlcA), degradation product 2	GlcA-GalNAc4S-GlcA-Gal4S-Gal-Xyl	C37H55NO38S2	-4	Lysosome
cs_a_deg3	chondroitin sulfate A (GalNAc4S-GlcA), degradation product 3	GalNAc4S-GlcA-Gal4S-Gal-Xyl	C31H48NO32S2	-3	Lysosome
cs_a_deg4	chondroitin sulfate A (GalNAc4S-GlcA), degradation product 4	GalNAc-GlcA-Gal4S-Gal-Xyl	C31H49NO29S	-2	Lysosome
cs_a_deg5	chondroitin sulfate A (GalNAc4S-GlcA), degradation product 5	GlcA-Gal4S-Gal-Xyl	C23H36O24S	-2	Lysosome
cs_b	chondroitin sulfate B / dermatan sulfate (IdoA2S-GalNAc4S), free chain	GalNAc4S-IdoA2S-GalNAc4S-GlcA-Gal4S-Gal-Xyl	C45H66N2O49S4	-6	Lysosome
cs_b_deg1	chondroitin sulfate B / dermatan sulfate (IdoA2S-GalNAc4S), degradation product 1	GalNAc-IdoA2S-GalNAc4S-GlcA-Gal4S-Gal-Xyl	C45H67N2O46S3	-5	Lysosome
cs_b_deg2	chondroitin sulfate B / dermatan sulfate (IdoA2S-GalNAc4S), degradation product 2	IdoA2S-GalNAc4S-GlcA-Gal4S-Gal-Xyl	C37H54NO41S3	-5	Lysosome
cs_b_deg3	chondroitin sulfate B / dermatan sulfate (IdoA2S-GalNAc4S), degradation product 3	IdoA-GalNAc4S-GlcA-Gal4S-Gal-Xyl	C37H55NO38S2	-4	Lysosome
cs_b_pre4	chondroitin sulfate B (IdoA2S-GalNAc4S), precursor 4	GalNAc-IdoA-GalNAc4S-GlcA-Gal4S-Gal-Xyl-L-Ser	C45H67N2O42S2X	-4	Golgi Apparatus
cs_b_pre5	chondroitin sulfate B (IdoA2S-GalNAc4s), precursor 5		C45H66N2O45S3X	-5	Golgi Apparatus
cs_c	chondroitin sulfate C (GalNAc6S-GlcA), free chain	(GalNAc6S-GlcA)2-Gal6S-Gal-Xyl	C45H67N2O46S3	-5	Lysosome
cs_c,d,e_pre1	chondroitin sulfate C (GalNAc6S-GlcA) and D (GlcNAc6S-GlcA2S), precursor 1	GalNAc6S-GlcA-Gal6S-Gal-Xyl-L-Ser (protein)	C31H47NO31S2X	-3	Golgi Apparatus
cs_c_deg1	chondroitin sulfate C (GalNAc6S-GlcA), degradation product 1	GalNAc-GlcA-GalNAc6S-GlcA-Gal6S-Gal-Xyl	C45H68N2O43S2	-4	Lysosome
cs_c_deg2	chondroitin sulfate C (GalNAc6S-GlcA), degradation product 2	GlcA-GalNAc6S-GlcA-Gal6S-Gal-Xyl	C37H55NO38S2	-4	Lysosome
cs_c_deg3	chondroitin sulfate C (GalNAc6S-GlcA), degradation product 3	GalNAc6S-GlcA-Gal6S-Gal-Xyl	C31H48NO32S2	-3	Lysosome
cs_c_deg4	chondroitin sulfate C (GalNAc6S-GlcA), degradation product 4	GalNAc-GlcA-Gal6S-Gal-Xyl	C31H49NO29S	-2	Lysosome
cs_c_deg5	chondroitin sulfate C (GalNAc6S-GlcA), degradation product 5	GlcA-Gal6S-Gal-Xyl	C23H36O24S	-2	Lysosome
cs_c_pre2	chondroitin sulfate C (GalNAc6S-GlcA), precursor 2	GlcA-GalNAc6S-GlcA-Gal6S-Gal-Xyl-L-Ser (protein)	C37H54NO37S2X	-4	Golgi Apparatus
cs_c_pre3	chondroitin sulfate C (GalNAc6S-GlcA), precursor 3	GalNAc-GlcA-GalNAc6S-GlcA-Gal6S-Gal-Xyl-L-Ser (protein)	C45H67N2O42S2X	-4	Golgi Apparatus
cs_d	chondroitin sulfate D (GlcNAc6S-GlcA2S), free chain	(GalNAc6S-GlcA2S)2-Gal6S-Gal-Xyl	C45H65N2O52S5	-7	Lysosome
cs_d_deg1	chondroitin sulfate D (GlcNAc6S-GlcA2S), degradation product 1	GalNAc-GlcA2S-GalNAc6S-GlcA2S-Gal6S-Gal-Xyl	C45H66N2O49S4	-6	Lysosome
cs_d_deg2	chondroitin sulfate D (GlcNAc6S-GlcA2S), degradation product 2	GlcA2S-GalNAc6S-GlcA2S-Gal6S-Gal-Xyl	C37H53NO44S4	-6	Lysosome
cs_d_deg3	chondroitin sulfate D (GlcNAc6S-GlcA2S), degradation product 3	GlcA-GalNAc6S-GlcA2S-Gal6S-Gal-Xyl	C37H54NO41S3	-5	Lysosome
cs_d_deg4	chondroitin sulfate D (GlcNAc6S-GlcA2S), degradation product 4	GalNAc6S-GlcA2S-Gal6S-Gal-Xyl	C31H47NO35S3	-4	Lysosome
cs_d_deg5	chondroitin sulfate D (GlcNAc6S-GlcA2S), degradation product 5	GalNAc-GlcA2S-Gal6S-Gal-Xyl	C31H48NO32S2	-3	Lysosome
cs_d_deg6	chondroitin sulfate D (GlcNAc6S-GlcA2S), degradation product 6	GlcA2S-Gal6S-Gal-Xyl	C23H35O27S2	-3	Lysosome
cs_d_pre2	chondroitin sulfate D (GlcNAc6S-GlcA2S) precursor 2	GalNAc6S-GlcA2S-Gal6S-Gal-Xyl-L-Ser (protein)	C31H46NO34S3X	-4	Golgi Apparatus
cs_d_pre3	chondroitin sulfate D (GlcNAc6S-GlcA2S), precursor 3	GlcA-GalNAc6S-GlcA2S-Gal6S-Gal-Xyl-L-Ser (protein)	C37H53NO40S3X	-5	Golgi Apparatus
cs_d_pre4	chondroitin sulfate D (GlcNAc6S-GlcA2S), precursor 4	GalNAc-GlcA-GalNAc6S-GlcA2S-Gal6S-Gal-Xyl-L-Ser (protein)	C45H66N2O45S3X	-5	Golgi Apparatus
cs_d_pre5	chondroitin sulfate D (GlcNAc6S-GlcA2S), precursor 5	GalNAc6S-GlcA-GalNAc6S-GlcA2S-Gal6S-Gal-Xyl-L-Ser (protein)	C45H65N2O48S4X	-6	Golgi Apparatus
cs_e	chondroitin sulfate E (GalNAc4,6diS-GlcA), free chain	(GalNAc4,6diS-GlcA)2-Gal4,6diS-Gal-Xyl	C45H64N2O55S6	-8	Lysosome
cs_e_deg1	chondroitin sulfate E (GalNAc4,6diS-GlcA), degradation product 1	GalNAc6S-GlcA-GalNAc4,6diS-GlcA-Gal4,6diS-Gal-Xyl	C45H65N2O52S5	-7	Lysosome
cs_e_deg2	chondroitin sulfate E (GalNAc4,6diS-GlcA), degradation product 2	GalNAc-GlcA-GalNAc4,6diS-GlcA-Gal4,6diS-Gal-Xyl	C45H66N2O49S4	-6	Lysosome
cs_e_deg3	chondroitin sulfate E (GalNAc4,6diS-GlcA), degradation product 3	GlcA-GalNAc4,6diS-GlcA-Gal4,6diS-Gal-Xyl	C37H53NO44S4	-6	Lysosome
cs_e_deg4	chondroitin sulfate E (GalNAc4,6diS-GlcA), degradation product 4	GalNAc4,6diS-GlcA-Gal4,6diS-Gal-Xyl	C31H46NO38S4	-5	Lysosome
cs_e_deg5	chondroitin sulfate E (GalNAc4,6diS-GlcA), degradation product 5	GalNAc6S-GlcA-Gal4,6diS-Gal-Xyl	C31H47NO35S3	-4	Lysosome
cs_e_deg6	chondroitin sulfate E (GalNAc4,6diS-GlcA), degradation product 6	GalNAc-GlcA-Gal4,6diS-Gal-Xyl	C31H48NO32S2	-3	Lysosome
cs_e_deg7	chondroitin sulfate E (GalNAc4,6diS-GlcA), degradation product 7	GlcA-Gal4,6diS-Gal-Xyl	C23H35O27S2	-3	Lysosome
cs_e_pre2	chondroitin sulfate E (GalNAc4,6diS-GlcA), precursor 2	GalNAc4,6diS-GlcA-Gal4,6diS-Gal-Xyl-L-Ser (protein)	C31H45NO37S4X	-5	Golgi Apparatus
cs_e_pre3	chondroitin sulfate E (GalNAc4,6diS-GlcA), precursor 3	GlcA-GalNAc4,6diS-GlcA-Gal4,6diS-Gal-Xyl-L-Ser (protein)	C37H52NO43S4X	-6	Golgi Apparatus
cs_e_pre4	chondroitin sulfate E (GalNAc4,6diS-GlcA), precursor 4	GalNAc-GlcA-GalNAc4,6diS-GlcA-Gal4,6diS-Gal-Xyl-L-Ser (protein)	C45H65N2O48S4X	-6	Golgi Apparatus

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
cs_e_pre5a	chondroitin sulfate E (GalNAc4,6diS-GlcA), precursor 5a	GalNAc4S-GlcA-GalNAc4,6diS-GlcA-Gal4,6diS-Gal-Xyl-L-Ser (protein)	C45H64N2O51S5X	-7	Golgi Apparatus
cs_e_pre5b	chondroitin sulfate E (GalNAc4,6diS-GlcA), precursor 5b	GalNAc6S-GlcA-GalNAc4,6diS-GlcA-Gal4,6diS-Gal-Xyl-L-Ser (protein)	C45H64N2O51S5X	-7	Golgi Apparatus
cs_pre	chondroitin sulfate precursor (GalNAc-GlcA-(Gal)2-Xyl-L-Ser (protein))	GalNAc-GlcA-(Gal)2-Xyl-L-Ser (protein)	C31H49NO25X	-1	Golgi Apparatus
csn	Cytosine		C4H5N3O	0	Cytosol
csn	Cytosine		C4H5N3O	0	Extracellular
cspg_a	chondroitin sulfate A (GalNAc4S-GlcA) proteoglycan	(GalNAc4S-GlcA)2-Gal4S-Gal-Xyl-L-Ser (protein)	C45H66N2O45S3X	-5	Extracellular
cspg_a	chondroitin sulfate A (GalNAc4S-GlcA) proteoglycan	(GalNAc4S-GlcA)2-Gal4S-Gal-Xyl-L-Ser (protein)	C45H66N2O45S3X	-5	Golgi Apparatus
cspg_a	chondroitin sulfate A (GalNAc4S-GlcA) proteoglycan	(GalNAc4S-GlcA)2-Gal4S-Gal-Xyl-L-Ser (protein)	C45H66N2O45S3X	-5	Lysosome
cspg_b	chondroitin sulfate B / dermatan sulfate (IdoA2S-GalNAc4S proteoglycan	GalNAc4S-IdoA2S-GalNAc4S-GlcA-Gal4S-Gal-Xyl-L-Ser	C45H65N2O48S4X	-6	Extracellular
cspg_b	chondroitin sulfate B / dermatan sulfate (IdoA2S-GalNAc4S proteoglycan	GalNAc4S-IdoA2S-GalNAc4S-GlcA-Gal4S-Gal-Xyl-L-Ser	C45H65N2O48S4X	-6	Golgi Apparatus
cspg_b	chondroitin sulfate B / dermatan sulfate (IdoA2S-GalNAc4S proteoglycan	GalNAc4S-IdoA2S-GalNAc4S-GlcA-Gal4S-Gal-Xyl-L-Ser	C45H65N2O48S4X	-6	Lysosome
cspg_c	chondroitin sulfate C (GalNAc6S-GlcA) proteoglycan	(GalNAc6S-GlcA)2-Gal6S-Gal-Xyl-L-Ser (protein)	C45H66N2O45S3X	-5	Extracellular
cspg_c	chondroitin sulfate C (GalNAc6S-GlcA) proteoglycan	(GalNAc6S-GlcA)2-Gal6S-Gal-Xyl-L-Ser (protein)	C45H66N2O45S3X	-5	Golgi Apparatus
cspg_c	chondroitin sulfate C (GalNAc6S-GlcA) proteoglycan	(GalNAc6S-GlcA)2-Gal6S-Gal-Xyl-L-Ser (protein)	C45H66N2O45S3X	-5	Lysosome
cspg_d	chondroitin sulfate D (GlcNAc6S-GlcA2S) proteoglycan	(GalNAc6S-GlcA2S)2-Gal6S-Gal-Xyl-L-Ser (protein)	C45H64N2O51S5X	-7	Extracellular
cspg_d	chondroitin sulfate D (GlcNAc6S-GlcA2S) proteoglycan	(GalNAc6S-GlcA2S)2-Gal6S-Gal-Xyl-L-Ser (protein)	C45H64N2O51S5X	-7	Golgi Apparatus
cspg_d	chondroitin sulfate D (GlcNAc6S-GlcA2S) proteoglycan	(GalNAc6S-GlcA2S)2-Gal6S-Gal-Xyl-L-Ser (protein)	C45H64N2O51S5X	-7	Lysosome
cspg_e	chondroitin sulfate E (GalNAc4,6diS-GlcA) proteoglycan	(GalNAc4,6diS-GlcA)2-Gal4,6diS-Gal-Xyl-L-Ser (protein)	C45H63N2O54S6X	-8	Extracellular
cspg_e	chondroitin sulfate E (GalNAc4,6diS-GlcA) proteoglycan	(GalNAc4,6diS-GlcA)2-Gal4,6diS-Gal-Xyl-L-Ser (protein)	C45H63N2O54S6X	-8	Golgi Apparatus
cspg_e	chondroitin sulfate E (GalNAc4,6diS-GlcA) proteoglycan	(GalNAc4,6diS-GlcA)2-Gal4,6diS-Gal-Xyl-L-Ser (protein)	C45H63N2O54S6X	-8	Lysosome
ctp	CTP	Cytidine 5'-triphosphate, Cytidine triphosphate	C9H12N3O14P3	-4	Cytosol
ctp	CTP	Cytidine 5'-triphosphate, Cytidine triphosphate	C9H12N3O14P3	-4	Mitochondria
ctp	CTP	Cytidine 5'-triphosphate, Cytidine triphosphate	C9H12N3O14P3	-4	Nucleus
cyan	Hydrogen cyanide	CN-, Cyano	CHN	0	Cytosol
cyan	Hydrogen cyanide	CN-, Cyano	CHN	0	Extracellular
cyan	Hydrogen cyanide	CN-, Cyano	CHN	0	Mitochondria
cysam	Cysteamine		C2H8NS	1	Cytosol
cys-L	L-Cysteine	Cys, L-2-Amino-3-mercaptopropionic acid	C3H7NO2S	0	Cytosol
cys-L	L-Cysteine	Cys, L-2-Amino-3-mercaptopropionic acid	C3H7NO2S	0	Extracellular
cys-L	L-Cysteine	Cys, L-2-Amino-3-mercaptopropionic acid	C3H7NO2S	0	Mitochondria
cyst-L	L-Cystathionine		C7H14N2O4S	0	Cytosol
cytd	Cytidine	1-beta-ribofuranosylosine, 4-amino-1-beta-D-ribofuranosyl-2(1H)-pyrimidinone, cytosine riboside	C9H13N3O5	0	Cytosol
cytd	Cytidine	1-beta-ribofuranosylosine, 4-amino-1-beta-D-ribofuranosyl-2(1H)-pyrimidinone, cytosine riboside	C9H13N3O5	0	Extracellular
cytd	Cytidine	1-beta-ribofuranosylosine, 4-amino-1-beta-D-ribofuranosyl-2(1H)-pyrimidinone, cytosine riboside	C9H13N3O5	0	Lysosome
cytd	Cytidine	1-beta-ribofuranosylosine, 4-amino-1-beta-D-ribofuranosyl-2(1H)-pyrimidinone, cytosine riboside	C9H13N3O5	0	Mitochondria
cytd	Cytidine	1-beta-ribofuranosylosine, 4-amino-1-beta-D-ribofuranosyl-2(1H)-pyrimidinone, cytosine riboside	C9H13N3O5	0	Nucleus
dad-2	Deoxyadenosine	2'-Deoxyadenosine, dA	C10H13N5O3	0	Cytosol
dad-2	Deoxyadenosine	2'-Deoxyadenosine, dA	C10H13N5O3	0	Extracellular
dad-2	Deoxyadenosine	2'-Deoxyadenosine, dA	C10H13N5O3	0	Lysosome
dad-5	5'-Deoxyadenosine		C10H13N5O3	0	Extracellular
dadp	dADP	2'-Deoxyadenosine 5'-diphosphate	C10H12N5O9P2	-3	Cytosol
dadp	dADP	2'-Deoxyadenosine 5'-diphosphate	C10H12N5O9P2	-3	Mitochondria
dadp	dADP	2'-Deoxyadenosine 5'-diphosphate	C10H12N5O9P2	-3	Nucleus
dag_hs	diacylglycerol (homo sapiens)		C3H6OFULLRCO2FULLR2CO2	0	Cytosol
dag_hs	diacylglycerol (homo sapiens)		C3H6OFULLRCO2FULLR2CO2	0	Extracellular
dag_hs	diacylglycerol (homo sapiens)		C3H6OFULLRCO2FULLR2CO2	0	Nucleus
dag_hs	diacylglycerol (homo sapiens)		C3H6OFULLRCO2FULLR2CO2	0	Endoplasmic Reticulum
dak2gpe_hs	1-alkenyl 2-acylglycerol 3-phosphoethanolamine plasmalogen (homo sapiens)	plasmalogen	C7H14O5NPFULLRFULLR2CO	0	Cytosol
damp	dAMP	2'-Deoxyadenosine 5'-monophosphate, 2'-Deoxyadenosine 5'-phosphate, Deoxyadenosine monophosphate, Deoxyadenylic acid	C10H12N5O6P	-2	Cytosol

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
damp	dAMP	2'-Deoxyadenosine 5'-monophosphate, 2'-Deoxyadenosine 5'-phosphate, Deoxyadenosine monophosphate, Deoxyadenylic acid	C10H12N5O6P	-2	Lysosome
datp	dATP	2'-Deoxyadenosine 5'-triphosphate, Deoxyadenosine 5'-triphosphate, Deoxyadenosine triphosphate	C10H12N5O12P3	-4	Cytosol
datp	dATP	2'-Deoxyadenosine 5'-triphosphate, Deoxyadenosine 5'-triphosphate, Deoxyadenosine triphosphate	C10H12N5O12P3	-4	Mitochondria
datp	dATP	2'-Deoxyadenosine 5'-triphosphate, Deoxyadenosine 5'-triphosphate, Deoxyadenosine triphosphate	C10H12N5O12P3	-4	Nucleus
dcacoa	Decanoyl-CoA (n-C10:0CoA)		C31H50N7O17P3S	-4	Cytosol
dcacoa	Decanoyl-CoA (n-C10:0CoA)		C31H50N7O17P3S	-4	Peroxisome
dcamp	N6-(1,2-Dicarboxyethyl)-AMP	Adenylosuccinate, Adenylosuccinic acid	C14H14N5O11P	-4	Cytosol
dcdp	dCDP	2'-Deoxycytidine 5'-diphosphate, 2'-Deoxycytidine diphosphate	C9H12N3O10P2	-3	Cytosol
dcdp	dCDP	2'-Deoxycytidine 5'-diphosphate, 2'-Deoxycytidine diphosphate	C9H12N3O10P2	-3	Mitochondria
dcdp	dCDP	2'-Deoxycytidine 5'-diphosphate, 2'-Deoxycytidine diphosphate	C9H12N3O10P2	-3	Nucleus
dcholcoa	chenodeoxycholoyl coenzyme a	Chenodeoxycholoyl-CoA, bile acid	C45H70N7O19P3S	-4	Peroxisome
dcmp	dCMP	2'-Deoxycytidine 5'-monophosphate, Deoxycytidine monophosphate, Deoxycytidylate, Deoxycytidylic acid	C9H12N3O7P	-2	Cytosol
dcmp	dCMP	2'-Deoxycytidine 5'-monophosphate, Deoxycytidine monophosphate, Deoxycytidylate, Deoxycytidylic acid	C9H12N3O7P	-2	Lysosome
dcmp	dCMP	2'-Deoxycytidine 5'-monophosphate, Deoxycytidine monophosphate, Deoxycytidylate, Deoxycytidylic acid	C9H12N3O7P	-2	Mitochondria
dcmp	dCMP	2'-Deoxycytidine 5'-monophosphate, Deoxycytidine monophosphate, Deoxycytidylate, Deoxycytidylic acid	C9H12N3O7P	-2	Nucleus
dcsptn1	docosa-4,7,10,13,16-pentaenoic acid (n-6)	(All-Z)-4,7,10,13,16-docosapentaenoic acid, 4,7,10,13,16-Docasapentaenoic acid, (all-Z), 4,7,10,13,16-Docosapentaenoic acid, (all-Z)-, docosa-4,7,10,13,16-pentaenoic acid	C22H33O2	-1	Cytosol
dcsptn1	docosa-4,7,10,13,16-pentaenoic acid (n-6)	(All-Z)-4,7,10,13,16-docosapentaenoic acid, 4,7,10,13,16-Docasapentaenoic acid, (all-Z), 4,7,10,13,16-Docosapentaenoic acid, (all-Z)-, docosa-4,7,10,13,16-pentaenoic acid	C22H33O2	-1	Extracellular
dcsptn1coa	docosa-4,7,10,13,16-pentaenoyl coenzyme A		C43H64N7O17P3S	-4	Cytosol
dcsptn1coa	docosa-4,7,10,13,16-pentaenoyl coenzyme A		C43H64N7O17P3S	-4	Mitochondria
dcsptn1coa	docosa-4,7,10,13,16-pentaenoyl coenzyme A		C43H64N7O17P3S	-4	Peroxisome
dcsptn1crn	docosa-4,7,10,13,16-pentaenoyl carnitine		C29H47NO4	0	Cytosol
dcsptn1crn	docosa-4,7,10,13,16-pentaenoyl carnitine		C29H47NO4	0	Mitochondria
dctp	dCTP	2'-Deoxycytidine 5'-triphosphate, Deoxycytidine 5'-triphosphate, Deoxycytidine triphosphate	C9H12N3O13P3	-4	Cytosol
dctp	dCTP	2'-Deoxycytidine 5'-triphosphate, Deoxycytidine 5'-triphosphate, Deoxycytidine triphosphate	C9H12N3O13P3	-4	Mitochondria
dctp	dCTP	2'-Deoxycytidine 5'-triphosphate, Deoxycytidine 5'-triphosphate, Deoxycytidine triphosphate	C9H12N3O13P3	-4	Nucleus
dcyt	Deoxycytidine	2'-Deoxycytidine, dC	C9H13N3O4	0	Cytosol
dcyt	Deoxycytidine	2'-Deoxycytidine, dC	C9H13N3O4	0	Extracellular
dcyt	Deoxycytidine	2'-Deoxycytidine, dC	C9H13N3O4	0	Lysosome
dcyt	Deoxycytidine	2'-Deoxycytidine, dC	C9H13N3O4	0	Mitochondria
dcyt	Deoxycytidine	2'-Deoxycytidine, dC	C9H13N3O4	0	Nucleus
dd2coa	trans-Dodec-2-enoyl-CoA	2-trans-Dodecenoyl-CoA	C33H52N7O17P3S	-4	Mitochondria
dd3coa	3-dodecenoyl CoA	3-cis-Dodecenoyl-CoA	C33H52N7O17P3S	-4	Mitochondria
ddca	Dodecanoate (n-C12:0)	Dodecanoic acid, Dodecylcarboxylate, Lauric acid	C12H23O2	-1	Cytosol
ddcaACP	Dodecanoyl-ACP (n-C12:0ACP)	Dodecanoyl-[acp], Dodecanoyl-[acyl-carrier protein], Fatty Acid C12 ACP, Lauroyl ACP	C23H43N2O8PRS	-1	Cytosol
ddcacoa	Dodecanoyl-CoA (n-C12:0CoA)	Lauroyl coenzyme A, Lauroyl-CoA	C33H54N7O17P3S	-4	Cytosol
ddcacoa	Dodecanoyl-CoA (n-C12:0CoA)	Lauroyl coenzyme A, Lauroyl-CoA	C33H54N7O17P3S	-4	Peroxisome
ddsmsterol	7-Dehydrodesmosterol	7-Dehydrodesmosterol	C27H42O	0	Endoplasmic Reticulum
debrisoquine	debrisoquine	2(1H)-Isoquinolinecarboximidamide, 3,4-dihydro-, 3,4-Dihydro-2(1H)-isoquinolinecarboxamidine, 3,4-Dihydro-2(1H)-isoquinolinecarboximidamide, Debrisoquin [MeSH: Debrisoquin], Debrisoquine [MeSH: Debrisoquin], Isocaramidine	C10H14N3	1	Cytosol
debrisoquine	debrisoquine	2(1H)-Isoquinolinecarboximidamide, 3,4-dihydro-, 3,4-Dihydro-2(1H)-isoquinolinecarboxamidine, 3,4-Dihydro-2(1H)-isoquinolinecarboximidamide, Debrisoquin [MeSH: Debrisoquin], Debrisoquine [MeSH: Debrisoquin], Isocaramidine	C10H14N3	1	Extracellular
decdp	all trans Decaprenyl diphosphate		C50H81O7P2	-3	Cytosol
decdp	all trans Decaprenyl diphosphate		C50H81O7P2	-3	Mitochondria
dedol_L	Dehydrodolichol, human liver homolog		C1080H1748O10	0	Cytosol
dedol_U	Dehydrodolichol, human uterine homolog		C1025H1660O10	0	Cytosol

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
dedoldp_L	Dehydrodolichol diphosphate, human liver homolog	Dehydrodolichyl diphosphate	C1080H1738O70P20	-30	Cytosol
dedoldp_U	Dehydrodolichol diphosphate, human uterine homolog		C1025H1650O70P20	-30	Cytosol
dedolp_L	Dehydrodolichol phosphate, human liver homolog		C1080H1738O40P10	-20	Cytosol
dedolp_U	Dehydrodolichol phosphate, human uterine homolog		C1025H1650O40P10	-20	Cytosol
dem2emgacpail_prot_hs	deacylated-(phosphoethanolaminyl-dimannosyl),(phosphoethanolaminyl)-mannosyl-glucosaminyl-acylphosphatidylinositol	{[Prot-PE-(Man)2],[PE]}-Man-GlcN-PI	C37H70N3O34P3FULLRCO2FULLR2CO2X	0	Endoplasmic Reticulum
dgchol	Chenodeoxyglycocholate	Chenodeoxyglycocholate	C26H43NO5	0	Cytosol
dgchol	Chenodeoxyglycocholate	Chenodeoxyglycocholate	C26H43NO5	0	Extracellular
dgchol	Chenodeoxyglycocholate	Chenodeoxyglycocholate	C26H43NO5	0	Peroxisome
dgcholcoa	Chenodeoxyglycocholoyl-CoA	Chenodeoxyglycocholoyl-CoA	C45H70N7O19P3S	-4	Peroxisome
dgdp	dGDP	2'-Deoxyguanosine 5'-diphosphate	C10H12N5O10P2	-3	Cytosol
dgdp	dGDP	2'-Deoxyguanosine 5'-diphosphate	C10H12N5O10P2	-3	Mitochondria
dgdp	dGDP	2'-Deoxyguanosine 5'-diphosphate	C10H12N5O10P2	-3	Nucleus
dgmp	dGMP	2'-Deoxyguanosine 5'-monophosphate, 2'-Deoxyguanosine 5'-phosphate, Deoxyguanosine monophosphate, Deoxyguanylic acid	C10H12N5O7P	-2	Cytosol
dgmp	dGMP	2'-Deoxyguanosine 5'-monophosphate, 2'-Deoxyguanosine 5'-phosphate, Deoxyguanosine monophosphate, Deoxyguanylic acid	C10H12N5O7P	-2	Lysosome
dgmp	dGMP	2'-Deoxyguanosine 5'-monophosphate, 2'-Deoxyguanosine 5'-phosphate, Deoxyguanosine monophosphate, Deoxyguanylic acid	C10H12N5O7P	-2	Mitochondria
dgpi_prot_hs	deacylated-glycophosphatidylinositol (GPI)-anchored protein	{[(Prot-PE-Man),(PE)-Man],[PE]}-Man-GlcN-PI	C39H76N4O37P4FULLRCO2FULLR2CO2X	0	Endoplasmic Reticulum
dgsn	Deoxyguanosine	2'-Deoxyguanosine, 2'-deoxyguanosine hemihydrat	C10H13N5O4	0	Cytosol
dgsn	Deoxyguanosine	2'-Deoxyguanosine, 2'-deoxyguanosine hemihydrat	C10H13N5O4	0	Extracellular
dgsn	Deoxyguanosine	2'-Deoxyguanosine, 2'-deoxyguanosine hemihydrat	C10H13N5O4	0	Lysosome
dgsn	Deoxyguanosine	2'-Deoxyguanosine, 2'-deoxyguanosine hemihydrat	C10H13N5O4	0	Mitochondria
dgtp	dGTP	2'-Deoxyguanosine 5'-triphosphate, Deoxyguanosine 5'-triphosphate, Deoxyguanosine triphosphate	C10H12N5O13P3	-4	Cytosol
dgtp	dGTP	2'-Deoxyguanosine 5'-triphosphate, Deoxyguanosine 5'-triphosphate, Deoxyguanosine triphosphate	C10H12N5O13P3	-4	Mitochondria
dgtp	dGTP	2'-Deoxyguanosine 5'-triphosphate, Deoxyguanosine 5'-triphosphate, Deoxyguanosine triphosphate	C10H12N5O13P3	-4	Nucleus
dha	Dihydroxyacetone	1, 3-Dihydroxy-2-propanone, 3-Dihydroxyacetone, 3-Dihydroxypropan-2-one, Glycerone	C3H6O3	0	Cytosol
dhap	Dihydroxyacetone phosphate	Glycerone phosphate	C3H5O6P	-2	Cytosol
dhap	Dihydroxyacetone phosphate	Glycerone phosphate	C3H5O6P	-2	Peroxisome
dhbpt	6,7-Dihydrobiopterin	Dihydrobiopterin, Quinoid-dihydrobiopterin	C9H13N5O3	0	Cytosol
dhcholestanate	3alpha,7alpha-Dihydroxy-5beta-cholestanate	3alpha,7alpha-Dihydroxy-5beta-cholestanate, 3alpha,7alpha-Dihydroxy-5beta-cholestanoate	C27H45O4	-1	Mitochondria
dhcholestanate	3alpha,7alpha-Dihydroxy-5beta-cholestanate	3alpha,7alpha-Dihydroxy-5beta-cholestanate, 3alpha,7alpha-Dihydroxy-5beta-cholestanoate	C27H45O4	-1	Endoplasmic Reticulum
dhcholestanate	3alpha,7alpha-Dihydroxy-5beta-cholestanate	3alpha,7alpha-Dihydroxy-5beta-cholestanate, 3alpha,7alpha-Dihydroxy-5beta-cholestanoate	C27H45O4	-1	Peroxisome
dhcholestancoa	3alpha,7alpha-Dihydroxy-5beta-cholestanoyl-CoA	3alpha,7alpha-Dihydroxy-5beta-cholestanoyl-CoA	C48H76N7O19P3S	-4	Endoplasmic Reticulum
dhcholestancoa	3alpha,7alpha-Dihydroxy-5beta-cholestanoyl-CoA	3alpha,7alpha-Dihydroxy-5beta-cholestanoyl-CoA	C48H76N7O19P3S	-4	Peroxisome
dhcholoylcoa	3alpha,7alpha-Dihydroxy-5beta-cholest-24-enoyl-CoA	3alpha,7alpha-Dihydroxy-5beta-cholest-24-enoyl-CoA	C48H74N7O19P3S	-4	Endoplasmic Reticulum
dhcholoylcoa	3alpha,7alpha-Dihydroxy-5beta-cholest-24-enoyl-CoA	3alpha,7alpha-Dihydroxy-5beta-cholest-24-enoyl-CoA	C48H74N7O19P3S	-4	Peroxisome
dhcrm_hs	dihydroceramide (homo sapiens)	N-Acylsphinganine	C18H38NO2FULLRCO	0	Cytosol
dhdascb	Dehydroascorbate	DHA, Dehydroascorbic acid	C6H6O6	0	Cytosol
dhdascb	Dehydroascorbate	DHA, Dehydroascorbic acid	C6H6O6	0	Extracellular
dhea	Dehydroepiandrosterone	3beta-Hydroxyandrost-5-en-17-one, DHA, DHEA, Dehydroisoandrosterone	C19H28O2	0	Cytosol
dhea	Dehydroepiandrosterone	3beta-Hydroxyandrost-5-en-17-one, DHA, DHEA, Dehydroisoandrosterone	C19H28O2	0	Endoplasmic Reticulum
dheas	Dehydroepiandrosterone sulfate	3beta-Hydroxyandrost-5-en-17-one 3-sulfate, Dehydroepiandrosterone sulfate	C19H27O5S	-1	Cytosol
dheas	Dehydroepiandrosterone sulfate	3beta-Hydroxyandrost-5-en-17-one 3-sulfate, Dehydroepiandrosterone sulfate	C19H27O5S	-1	Extracellular
dheas	Dehydroepiandrosterone sulfate	3beta-Hydroxyandrost-5-en-17-one 3-sulfate, Dehydroepiandrosterone sulfate	C19H27O5S	-1	Endoplasmic Reticulum
dhf	7,8-Dihydrofolate	7,8-Dihydrofolic acid, Dihydrofolate, Dihydrofolic acid	C19H19N7O6	-2	Cytosol
dhf	7,8-Dihydrofolate	7,8-Dihydrofolic acid, Dihydrofolate, Dihydrofolic acid	C19H19N7O6	-2	Extracellular
dhf	7,8-Dihydrofolate	7,8-Dihydrofolic acid, Dihydrofolate, Dihydrofolic acid	C19H19N7O6	-2	Lysosome
dhf	7,8-Dihydrofolate	7,8-Dihydrofolic acid, Dihydrofolate, Dihydrofolic acid	C19H19N7O6	-2	Mitochondria

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
dhlam	Dihydrolipoamide	Dihydrothioctamide	C8H17NOS2	0	Mitochondria
dhlpro	Dihydrolipolprotein		H2S2X	0	Mitochondria
dhocholoylcoa	3alpha,7alpha,12alpha,26-Tetrahydroxy-5beta-cholestane	3alpha,7alpha,12alpha,26-Tetrahydroxy-5beta-cholestane, 3alpha,7alpha-Dihydroxy-5beta-24-oxocholestanoyl-CoA, 5beta-Cholestane-3alpha,7alpha,12alpha,26-tetraol	C48H74N7O20P3S	-4	Peroxisome
dhor-S	(S)-Dihydroorotate	(S)-4, 5-Dihydroorotate, Dihydro-L-orotic acid, L-Dihydroorotate, L-Dihydroorotic acid	C5H5N2O4	-1	Cytosol
didp	dIDP	2'-Deoxyinosine 5'-diphosphate, 2'-Deoxyinosine-5-diphosphate	C10H11N4O10P2	-3	Cytosol
didp	dIDP	2'-Deoxyinosine 5'-diphosphate, 2'-Deoxyinosine-5-diphosphate	C10H11N4O10P2	-3	Mitochondria
didp	dIDP	2'-Deoxyinosine 5'-diphosphate, 2'-Deoxyinosine-5-diphosphate	C10H11N4O10P2	-3	Nucleus
digalsgalside_hs	Digalactosylceramidesulfate	Digalactosylceramidesulfate	C30H55NO15SFULLRCO	-1	Cytosol
digalsgalside_hs	Digalactosylceramidesulfate	Digalactosylceramidesulfate	C30H55NO15SFULLRCO	-1	Extracellular
digalsgalside_hs	Digalactosylceramidesulfate	Digalactosylceramidesulfate	C30H55NO15SFULLRCO	-1	Golgi Apparatus
digalside_hs	Digalactosylceramide	Gal-Gal-Cer, Gal-alpha1->4Gal-beta1->1'Cer	C30H56NO12FULLRCO	0	Cytosol
digalside_hs	Digalactosylceramide	Gal-Gal-Cer, Gal-alpha1->4Gal-beta1->1'Cer	C30H56NO12FULLRCO	0	Golgi Apparatus
digalside_hs	Digalactosylceramide	Gal-Gal-Cer, Gal-alpha1->4Gal-beta1->1'Cer	C30H56NO12FULLRCO	0	Lysosome
dimp	dIMP	2'-Deoxyinosine 5'-phosphate	C10H11N4O7P	-2	Cytosol
din	Deoxyinosine	2'-deoxy-inosine	C10H12N4O4	0	Cytosol
din	Deoxyinosine	2'-deoxy-inosine	C10H12N4O4	0	Extracellular
ditp	dITP	2'-Deoxyinosine 5'-triphosphate, 2'-Deoxyinosine-5-triphosphate	C10H11N4O13P3	-4	Cytosol
ditp	dITP	2'-Deoxyinosine 5'-triphosphate, 2'-Deoxyinosine-5-triphosphate	C10H11N4O13P3	-4	Mitochondria
ditp	dITP	2'-Deoxyinosine 5'-triphosphate, 2'-Deoxyinosine-5-triphosphate	C10H11N4O13P3	-4	Nucleus
dkmpp	2,3-diketo-5-methylthio-1-phosphopentane	1-phospho-2,3-diketo-5-methylthiopentane	C6H9O6PS	-2	Cytosol
dlnlcg	dihomo-gamma-linolenic acid (n-6)	(Z,Z,Z)-8,11,14-Eicosatrienoate, (Z,Z,Z)-8,11,14-Icosatrienoate, 8,11,14-Eicosatrienoate, 8,11,14-Icosatrienoate, Dihomo-gamma-linolenic acid, icos-6,9,12-trienoic acid	C20H33O2	-1	Cytosol
dlnlcg	dihomo-gamma-linolenic acid (n-6)	(Z,Z,Z)-8,11,14-Eicosatrienoate, (Z,Z,Z)-8,11,14-Icosatrienoate, 8,11,14-Eicosatrienoate, 8,11,14-Icosatrienoate, Dihomo-gamma-linolenic acid, icos-6,9,12-trienoic acid	C20H33O2	-1	Extracellular
dlnlcgcoa	dihomo-gamma-linolenyl coenzyme A		C41H64N7O17P3S	-4	Cytosol
dlnlcgcoa	dihomo-gamma-linolenyl coenzyme A		C41H64N7O17P3S	-4	Mitochondria
dlnlcgcrn	dihomo-gamma-linolenyl carnitine		C27H47NO4	0	Cytosol
dlnlcgcrn	dihomo-gamma-linolenyl carnitine		C27H47NO4	0	Mitochondria
dmantipyrine	demethylated antipyrine		C10H10N2O	0	Cytosol
dmantipyrine	demethylated antipyrine		C10H10N2O	0	Extracellular
dmgly	N,N-Dimethylglycine	Dimethylglycine	C4H9NO2	0	Cytosol
dmgly	N,N-Dimethylglycine	Dimethylglycine	C4H9NO2	0	Mitochondria
dmhptcoa	2,6 dimethylheptanoyl-CoA	dimethyl heptanoyl coenzyme A	C30H52N7O17P3S	-4	Cytosol
dmhptcoa	2,6 dimethylheptanoyl-CoA	dimethyl heptanoyl coenzyme A	C30H52N7O17P3S	-4	Mitochondria
dmhptcrn	2,6 dimethylheptanoyl carnitine	dimethyl heptanoyl carnitine	C16H35NO4	0	Cytosol
dmhptcrn	2,6 dimethylheptanoyl carnitine	dimethyl heptanoyl carnitine	C16H35NO4	0	Extracellular
dmhptcrn	2,6 dimethylheptanoyl carnitine	dimethyl heptanoyl carnitine	C16H35NO4	0	Mitochondria
dmnoncoa	4,8 dimethylnonanoyl-CoA	4,8 dimethylnonanoyl coenzyme a	C32H54N7O17P3S	-4	Cytosol
dmnoncoa	4,8 dimethylnonanoyl-CoA	4,8 dimethylnonanoyl coenzyme a	C32H54N7O17P3S	-4	Mitochondria
dmnoncoa	4,8 dimethylnonanoyl-CoA	4,8 dimethylnonanoyl coenzyme a	C32H54N7O17P3S	-4	Peroxisome
dmnoncrn	4,8 dimethylnonanoyl carnitine		C18H37NO4	0	Mitochondria
dmnoncrn	4,8 dimethylnonanoyl carnitine		C18H37NO4	0	Peroxisome
dmpp	Dimethylallyl diphosphate	2-Isopentenyl diphosphate, Prenyl diphosphate, delta2-Isopentenyl diphosphate, dimethylallyl pyrophosphate	C5H9O7P2	-3	Cytosol
dmpp	Dimethylallyl diphosphate	2-Isopentenyl diphosphate, Prenyl diphosphate, delta2-Isopentenyl diphosphate, dimethylallyl pyrophosphate	C5H9O7P2	-3	Peroxisome
dna	DNA		C10H17O8PR2	0	Nucleus
dna5mtc	DNA 5-methylcytosine		C11H19O8PR2	0	Nucleus
dnad	Deamino-NAD+	Deamido-NAD+	C21H24N6O15P2	-2	Cytosol
dnad	Deamino-NAD+	Deamido-NAD+	C21H24N6O15P2	-2	Mitochondria
dnad	Deamino-NAD+	Deamido-NAD+	C21H24N6O15P2	-2	Nucleus
doldp_L	Dolichol diphosphate, human liver homolog		C1080H1758O70P20	-30	Endoplasmic Reticulum
doldp_U	Dolichol diphosphate, human uterine homolog		C1025H1670O70P20	-30	Endoplasmic Reticulum
dolglcp_L	Dolichyl beta-D-glucosyl phosphate, human liver homolog		C1140H1868O90P10	-10	Cytosol
dolglcp_L	Dolichyl beta-D-glucosyl phosphate, human liver homolog		C1140H1868O90P10	-10	Endoplasmic Reticulum
dolglcp_U	Dolichyl beta-D-glucosyl phosphate, human uterine homolog		C1085H1780O90P10	-10	Cytosol
dolglcp_U	Dolichyl beta-D-glucosyl phosphate, human uterine homolog		C1085H1780O90P10	-10	Endoplasmic Reticulum
dolichol_L	Dolichol, human liver homolog		C1080H1768O10	0	Cytosol
dolichol_L	Dolichol, human liver homolog		C1080H1768O10	0	Endoplasmic Reticulum
dolichol_U	Dolichol, human uterine homolog		C1025H1680O10	0	Cytosol
dolichol_U	Dolichol, human uterine homolog		C1025H1680O10	0	Endoplasmic Reticulum

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
dolmanp_L	Dolichyl phosphate D-mannose, human liver homolog	Dolichyl D-mannosyl phosphate	C1140H1868O90P10	-10	Cytosol
dolmanp_L	Dolichyl phosphate D-mannose, human liver homolog	Dolichyl D-mannosyl phosphate	C1140H1868O90P10	-10	Endoplasmic Reticulum
dolmanp_U	Dolichyl phosphate D-mannose, human uterine homolog	Dolichyl D-mannosyl phosphate	C1085H1780O90P10	-10	Cytosol
dolmanp_U	Dolichyl phosphate D-mannose, human uterine homolog	Dolichyl D-mannosyl phosphate	C1085H1780O90P10	-10	Endoplasmic Reticulum
dolp_L	Dolichol phosphate, human liver homolog	Dolichyl phosphate	C1080H1758O40P10	-20	Cytosol
dolp_L	Dolichol phosphate, human liver homolog	Dolichyl phosphate	C1080H1758O40P10	-20	Endoplasmic Reticulum
dolp_U	Dolichol phosphate, human uterine homolog		C1025H1670O40P10	-20	Cytosol
dolp_U	Dolichol phosphate, human uterine homolog		C1025H1670O40P10	-20	Endoplasmic Reticulum
dopa	Dopamine	2-(3,4-Dihydroxyphenyl)ethylamine, 3,4-Dihydroxyphenethylamine, 4-(2-Aminoethyl)-1,2-benzenediol, 4-(2-Aminoethyl)benzene-1,2-diol	C8H12NO2	1	Cytosol
dopa	Dopamine	2-(3,4-Dihydroxyphenyl)ethylamine, 3,4-Dihydroxyphenethylamine, 4-(2-Aminoethyl)-1,2-benzenediol, 4-(2-Aminoethyl)benzene-1,2-diol	C8H12NO2	1	Extracellular
dopaqn	Dopaquinone		C9H9NO4	0	Cytosol
dopasf	Dopamine 3-O-sulfate		C8H11NO5S	0	Cytosol
dopasf	Dopamine 3-O-sulfate		C8H11NO5S	0	Extracellular
dpcoa	Dephospho-CoA		C21H33N7O13P2S	-2	Cytosol
dpcoa	Dephospho-CoA		C21H33N7O13P2S	-2	Lysosome
drib	Deoxyribose	2-Deoxy-D-ribose, 2-Deoxy-beta-D-erythro-pentose, Thyminose	C5H10O4	0	Cytosol
drib	Deoxyribose	2-Deoxy-D-ribose, 2-Deoxy-beta-D-erythro-pentose, Thyminose	C5H10O4	0	Extracellular
dsmsterol	Desmosterol	24-Dehydrocholesterol, Cholesta-5,24-dien-3beta-ol, Desmosterol	C27H44O	0	Endoplasmic Reticulum
dsT_antigen	disialyl-T antigen		C36H56N3O26X	-2	Golgi Apparatus
dtdp	dTDP	Thymidine 5'-diphosphate	C10H13N2O11P2	-3	Cytosol
dtdp	dTDP	Thymidine 5'-diphosphate	C10H13N2O11P2	-3	Mitochondria
dtdp	dTDP	Thymidine 5'-diphosphate	C10H13N2O11P2	-3	Nucleus
dtdp4d6dg	dTDP-4-dehydro-6-deoxy-D-glucose	dTDP-4-oxo-6-deoxy-D-glucose	C16H22N2O15P2	-2	Cytosol
dtdp4d6dm	dTDP-4-dehydro-6-deoxy-L-mannose	dTDP-4-oxo-6-deoxy-L-mannose, dTDP-4-oxo-L-rhamnose	C16H22N2O15P2	-2	Cytosol
dtdpglu	dTDPglucose	dTDP-D-glucose	C16H24N2O16P2	-2	Cytosol
dtdprmn	dTDP-L-rhamnose	dTDP-6-deoxy-L-mannose, dTDP-L-rhamnose	C16H24N2O15P2	-2	Cytosol
dtmp	dTMP	5'-Thymidylic acid, Deoxythymidine 5'-phosphate, Deoxythymidylic acid, Thymidine 5'-phosphate, Thymidine monophosphate, Thymidylate, Thymidylic acid	C10H13N2O8P	-2	Cytosol
dtmp	dTMP	5'-Thymidylic acid, Deoxythymidine 5'-phosphate, Deoxythymidylic acid, Thymidine 5'-phosphate, Thymidine monophosphate, Thymidylate, Thymidylic acid	C10H13N2O8P	-2	Lysosome
dtmp	dTMP	5'-Thymidylic acid, Deoxythymidine 5'-phosphate, Deoxythymidylic acid, Thymidine 5'-phosphate, Thymidine monophosphate, Thymidylate, Thymidylic acid	C10H13N2O8P	-2	Mitochondria
dtt	Dithiothreitol	1, 3-butanediol, 4-Dimercapto-2, 4-Dithiothreitol, DTT, threo-1	C4H10O2S2	0	Cytosol
dttOX	Oxidized dithiothreitol		C4H8O2S2	0	Cytosol
dttp	dTTP	TTP, Thymidine 5'-triphosphate, Thymidine triphosphate	C10H13N2O14P3	-4	Cytosol
dttp	dTTP	TTP, Thymidine 5'-triphosphate, Thymidine triphosphate	C10H13N2O14P3	-4	Mitochondria
dttp	dTTP	TTP, Thymidine 5'-triphosphate, Thymidine triphosphate	C10H13N2O14P3	-4	Nucleus
dudp	dUDP	2'-Deoxyuridine 5'-diphosphate	C9H11N2O11P2	-3	Cytosol
dudp	dUDP	2'-Deoxyuridine 5'-diphosphate	C9H11N2O11P2	-3	Mitochondria
dudp	dUDP	2'-Deoxyuridine 5'-diphosphate	C9H11N2O11P2	-3	Nucleus
dump	dUMP	2'-Deoxyuridine 5'-phosphate, Deoxyuridine 5'-phosphate, Deoxyuridine monophosphate, Deoxyuridylic acid	C9H11N2O8P	-2	Cytosol
dump	dUMP	2'-Deoxyuridine 5'-phosphate, Deoxyuridine 5'-phosphate, Deoxyuridine monophosphate, Deoxyuridylic acid	C9H11N2O8P	-2	Mitochondria
dump	dUMP	2'-Deoxyuridine 5'-phosphate, Deoxyuridine 5'-phosphate, Deoxyuridine monophosphate, Deoxyuridylic acid	C9H11N2O8P	-2	Nucleus
duri	Deoxyuridine	2'-Deoxyuridine, 2-Deoxyuridine	C9H12N2O5	0	Cytosol
duri	Deoxyuridine	2'-Deoxyuridine, 2-Deoxyuridine	C9H12N2O5	0	Extracellular
duri	Deoxyuridine	2'-Deoxyuridine, 2-Deoxyuridine	C9H12N2O5	0	Mitochondria
duri	Deoxyuridine	2'-Deoxyuridine, 2-Deoxyuridine	C9H12N2O5	0	Nucleus
dutp	dUTP	2'-Deoxyuridine 5'-triphosphate	C9H11N2O14P3	-4	Cytosol
dutp	dUTP	2'-Deoxyuridine 5'-triphosphate	C9H11N2O14P3	-4	Mitochondria
dutp	dUTP	2'-Deoxyuridine 5'-triphosphate	C9H11N2O14P3	-4	Nucleus
dxtrn	phosphorylase-limit dextrin (glycogenin-1,6{4[1,4-Glc], 4[1,4-Glc]})		C48H81O41X	0	Cytosol
e4hglu	L-erythro-4-Hydroxyglutamate		C5H8NO5	-1	Cytosol
e4hglu	L-erythro-4-Hydroxyglutamate		C5H8NO5	-1	Mitochondria
e4p	D-Erythrose 4-phosphate	4-phospho D-erythrose	C4H7O7P	-2	Cytosol
eaflatoxin	8,9 epxoy aflatoxin B1		C17H12O7	0	Cytosol
eaflatoxin	8,9 epxoy aflatoxin B1		C17H12O7	0	Extracellular

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
eandrstrn	epiandrosterone	16alpha-Hydroxydehydroepiandrosterone, 5-Androstene-3beta,16alpha-diol-17-one	C19H28O3	0	Endoplasmic Reticulum
ebastine	ebastine	4-Diphenylmethoxy-1-(3-(4-tert-butylbenzoyl)propyl)piperidine, Ebastel, Ebastina, Ebastine, Ebastinum, Kestine, ebastine	C32H39NO2	0	Cytosol
ebastine	ebastine	4-Diphenylmethoxy-1-(3-(4-tert-butylbenzoyl)propyl)piperidine, Ebastel, Ebastina, Ebastine, Ebastinum, Kestine, ebastine	C32H39NO2	0	Extracellular
ebastine	ebastine	4-Diphenylmethoxy-1-(3-(4-tert-butylbenzoyl)propyl)piperidine, Ebastel, Ebastina, Ebastine, Ebastinum, Kestine, ebastine	C32H39NO2	0	Endoplasmic Reticulum
ebastineoh	hydroxylated ebastine		C32H39NO3	0	Cytosol
ebastineoh	hydroxylated ebastine		C32H39NO3	0	Extracellular
ebastineoh	hydroxylated ebastine		C32H39NO3	0	Endoplasmic Reticulum
ecgon	ecgonine		C9H14NO3	-1	Endoplasmic Reticulum
egme	ecgonine methyl ester		C10H17NO3	0	Endoplasmic Reticulum
eicostet	eicosatetranoic acid	8,11,14,17-Eicosatetraenoic acid	C20H31O2	-1	Cytosol
eicostet	eicosatetranoic acid	8,11,14,17-Eicosatetraenoic acid	C20H31O2	-1	Extracellular
eicostetcoa	eicosatetranoyl coenzyme A	8,11,14,17-Eicosatetraenoic acid coenzyme a	C41H62N7O17P3S	-4	Cytosol
eicostetcoa	eicosatetranoyl coenzyme A	8,11,14,17-Eicosatetraenoic acid coenzyme a	C41H62N7O17P3S	-4	Mitochondria
eicostetcrn	Eicosatetranoyl carnitine		C27H45NO4	0	Cytosol
eicostetcrn	Eicosatetranoyl carnitine		C27H45NO4	0	Mitochondria
elaid	elaidic acid	(E)-9-Octadecenoic acid, (E)-Oleic acid, 9-Octadecenoic acid, (E)-, 9-trans-Octadecenoic acid, D9-trans-Octadecenoic acid, Elaidinsaure, acide elaidique, elaidic acid, trans-9-Octadecenoic acid, trans-D9-Octadecenoic acid, trans-Elaidic acid, trans-Oleic acid	C18H33O2	-1	Cytosol
elaid	elaidic acid	(E)-9-Octadecenoic acid, (E)-Oleic acid, 9-Octadecenoic acid, (E)-, 9-trans-Octadecenoic acid, D9-trans-Octadecenoic acid, Elaidinsaure, acide elaidique, elaidic acid, trans-9-Octadecenoic acid, trans-D9-Octadecenoic acid, trans-Elaidic acid, trans-Oleic acid	C18H33O2	-1	Extracellular
elaidcrn	Elaidic carnitine	elaidic acid carnitine	C25H47NO4	0	Cytosol
elaidcrn	Elaidic carnitine	elaidic acid carnitine	C25H47NO4	0	Mitochondria
em2emgacpail_hs	(phosphoethanolaminyl-dimannosyl),(phosphoethanolaminyl)-mannosyl-glucosaminyl-acylphosphatidylinositol (H7)	[PE-(Man)2-],[PE-]Man-GlcN-acylPI	C53H100N3O35P3FULLRCO2FULLR2CO2	0	Endoplasmic Reticulum
em2emgacpail_prot_hs	(phosphoethanolaminyl-dimannosyl),(phosphoethanolaminyl)-mannosyl-glucosaminyl-acylphosphatidylinositol	{[PE-(Man)2],[PE]}-Man-GlcN-acylPI-prot	C53H100N3O35P3FULLRCO2FULLR2CO2X	0	Endoplasmic Reticulum
em3gacpail_hs	phosphoethanolaminyl-trimannosyl-glucosaminyl-acylphosphatidylinositol (H6')	PE-(Man)3-GlcN-acylPI	C51H94N2O32P2FULLRCO2FULLR2CO2	0	Endoplasmic Reticulum
emem2gacpail_hs	(phosphoethanolaminyl-mannosyl),(phosphoethanolaminyl)-dimannosyl-glucosaminyl-acylphosphatidylinositol (H7')	[PE-Man-],[PE-](Man)2-GlcN-acylPI	C53H100N3O35P3FULLRCO2FULLR2CO2	0	Endoplasmic Reticulum
emgacpail_hs	phosphoethanolaminyl-mannosyl-glucosylaminyl-acylphosphatidylinositol (H5)	PE-Man-GlcN-acylPI	C39H74N2O22P2FULLRCO2FULLR2CO2	0	Endoplasmic Reticulum
eryth	L-Erythrulose	L-glycero-Tetrulose	C4H8O4	0	Cytosol
estradiol	Estradiol	Estradiol-17beta, beta-Estradiol	C18H24O2	0	Cytosol
estradiol	Estradiol	Estradiol-17beta, beta-Estradiol	C18H24O2	0	Endoplasmic Reticulum
estradiolglc	estradiol glucuronide	Estradiol-17beta 3-glucuronide	C24H32O8	0	Cytosol
estradiolglc	estradiol glucuronide	Estradiol-17beta 3-glucuronide	C24H32O8	0	Extracellular
estradiolglc	estradiol glucuronide	Estradiol-17beta 3-glucuronide	C24H32O8	0	Endoplasmic Reticulum
estriol	estriol	1,3,5(10)-Estratriene-3,16-alpha,17beta-triol, Estriol	C18H24O3	0	Cytosol
estriol	estriol	1,3,5(10)-Estratriene-3,16-alpha,17beta-triol, Estriol	C18H24O3	0	Endoplasmic Reticulum
estriolglc	16-Glucuronide-estriol	16-Glucuronide, 16-Glucuronide-estriol, 16alpha,17beta-Estriol 16-(beta-D-glucuronide)	C24H32O9	0	Cytosol
estriolglc	16-Glucuronide-estriol	16-Glucuronide, 16-Glucuronide-estriol, 16alpha,17beta-Estriol 16-(beta-D-glucuronide)	C24H32O9	0	Extracellular
estriolglc	16-Glucuronide-estriol	16-Glucuronide, 16-Glucuronide-estriol, 16alpha,17beta-Estriol 16-(beta-D-glucuronide)	C24H32O9	0	Endoplasmic Reticulum
estrone	Estrone	3, 3-Hydroxy-1, 5(10)-estratrien-17-one	C18H22O2	0	Cytosol
estrone	Estrone	3, 3-Hydroxy-1, 5(10)-estratrien-17-one	C18H22O2	0	Endoplasmic Reticulum
estroneglc	estrone glucuronide		C24H30O8	0	Cytosol
estroneglc	estrone glucuronide		C24H30O8	0	Extracellular
estroneglc	estrone glucuronide		C24H30O8	0	Endoplasmic Reticulum
estrones	Estrone 3-sulfate	Estrone 3-sulfate	C18H21O5S	-1	Cytosol
estrones	Estrone 3-sulfate	Estrone 3-sulfate	C18H21O5S	-1	Extracellular
estrones	Estrone 3-sulfate	Estrone 3-sulfate	C18H21O5S	-1	Endoplasmic Reticulum
etfox	Electron transfer flavoprotein oxidized		R	0	Mitochondria
etfrd	Electron transfer flavoprotein reduced		RH2	0	Mitochondria
etha	Ethanolamine	Aminoethanol, Hydroxyethylamine	C2H8NO	1	Cytosol
ethamp	Ethanolamine phosphate	O-Phosphoethanolamine, O-Phosphorylethanolamine, Phosphoethanolamine	C2H7NO4P	-1	Cytosol

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
ethamp	Ethanolamine phosphate	O-Phosphoethanolamine, O-Phosphorylethanolamine, Phosphoethanolamine	C2H7NO4P	-1	Endoplasmic Reticulum
etoh	Ethanol	Ethyl alcohol, Methylcarbinol	C2H6O	0	Cytosol
etoh	Ethanol	Ethyl alcohol, Methylcarbinol	C2H6O	0	Extracellular
etoh	Ethanol	Ethyl alcohol, Methylcarbinol	C2H6O	0	Peroxisome
f1a	F1alpha		C22H37N2O15X	0	Golgi Apparatus
f1a	F1alpha		C22H37N2O15X	0	Lysosome
f1p	D-Fructose 1-phosphate	Fructofuranose 1-phosphate, Fructose 1-phosphate	C6H11O9P	-2	Cytosol
f26bp	D-Fructose 2,6-bisphosphate		C6H10O12P2	-4	Cytosol
f5hoxkyn	Formyl-5-hydroxykynurenamine		C10H13N2O3	1	Cytosol
f6p	D-Fructose 6-phosphate	D-Fructose 6-phosphoric acid, Neuberg ester, beta-D-Fructose 6-phosphate	C6H11O9P	-2	Cytosol
fad	Flavin adenine dinucleotide oxidized	FAD, Flavin adenine dinucleotide, Riboflavine 5'-adenosine diphosphate	C27H31N9O15P2	-2	Cytosol
fad	Flavin adenine dinucleotide oxidized	FAD, Flavin adenine dinucleotide, Riboflavine 5'-adenosine diphosphate	C27H31N9O15P2	-2	Mitochondria
fad	Flavin adenine dinucleotide oxidized	FAD, Flavin adenine dinucleotide, Riboflavine 5'-adenosine diphosphate	C27H31N9O15P2	-2	Endoplasmic Reticulum
fad	Flavin adenine dinucleotide oxidized	FAD, Flavin adenine dinucleotide, Riboflavine 5'-adenosine diphosphate	C27H31N9O15P2	-2	Peroxisome
fadh2	Flavin adenine dinucleotide reduced	flavin adenine dinucleotide (reduced form)	C27H33N9O15P2	-2	Cytosol
fadh2	Flavin adenine dinucleotide reduced	flavin adenine dinucleotide (reduced form)	C27H33N9O15P2	-2	Mitochondria
fadh2	Flavin adenine dinucleotide reduced	flavin adenine dinucleotide (reduced form)	C27H33N9O15P2	-2	Endoplasmic Reticulum
fadh2	Flavin adenine dinucleotide reduced	flavin adenine dinucleotide (reduced form)	C27H33N9O15P2	-2	Peroxisome
fald	Formaldehyde	Formalin, Methanal, Methylene oxide, Oxomethane, Oxomethylene	CH2O	0	Cytosol
fald	Formaldehyde	Formalin, Methanal, Methylene oxide, Oxomethane, Oxomethylene	CH2O	0	Lysosome
fald	Formaldehyde	Formalin, Methanal, Methylene oxide, Oxomethane, Oxomethylene	CH2O	0	Mitochondria
fald	Formaldehyde	Formalin, Methanal, Methylene oxide, Oxomethane, Oxomethylene	CH2O	0	Peroxisome
fdp	D-Fructose 1,6-bisphosphate	beta-D-fructofuranose-1,6-diphosphate, fbp, fructose diphosphate, fructose-1,6-bisphosphate	C6H10O12P2	-4	Cytosol
fe2	Fe2+	Fe(II), Iron, Iron dication, Reduced Iron	Fe	2	Cytosol
fe2	Fe2+	Fe(II), Iron, Iron dication, Reduced Iron	Fe	2	Extracellular
fe2	Fe2+	Fe(II), Iron, Iron dication, Reduced Iron	Fe	2	Mitochondria
fe3	Fe3+	Fe(III), Iron trication	Fe	3	Extracellular
fgam	N2-Formyl-N1-(5-phospho-D-ribosyl)glycinamide	5'-Phosphoribosyl-N-formylglycinamide, N-Formyl-GAR, N-Formylglycinamide ribonucleotide	C8H13N2O9P	-2	Cytosol
ficytC	Ferricytochrome c		C42H54FeN8O6S2	3	Mitochondria
fmn	FMN	Flavin mononucleotide, Riboflavin-5-phosphate	C17H19N4O9P	-2	Cytosol
fn2m2masn	N4-{N-Acetyl-beta-D-glucosaminyl-(1,2)-alpha-D-mannosyl-(1,3)-[N-acetyl-beta-D-glucosaminyl-(1,2)-alpha-D-mannosyl-(1,6)]-beta-D-mannosyl-(1,4)-N-acetyl-beta-D-glucosaminyl-(1,4)-[alpha-L-fucosyl-(1,6)]-N-acetyl-beta-D-glucosaminyl}asparagine		C56H93N4O39X	0	Golgi Apparatus
fna5moxam	Formyl-N-acetyl-5-methoxykynurenamine		C13H16N2O4	0	Cytosol
focytC	Ferrocytochrome C		C42H54FeN8O6S2	2	Mitochondria
fol	Folate	Folic acid, Pteroylglutamic acid	C19H18N7O6	-1	Cytosol
fol	Folate	Folic acid, Pteroylglutamic acid	C19H18N7O6	-1	Extracellular
for	Formate	Formic acid, Hydrogencarboxylic acid, Methanoic acid, aminic acid	CH1O2	-1	Cytosol
for	Formate	Formic acid, Hydrogencarboxylic acid, Methanoic acid, aminic acid	CH1O2	-1	Extracellular
for	Formate	Formic acid, Hydrogencarboxylic acid, Methanoic acid, aminic acid	CH1O2	-1	Mitochondria
for	Formate	Formic acid, Hydrogencarboxylic acid, Methanoic acid, aminic acid	CH1O2	-1	Nucleus
for	Formate	Formic acid, Hydrogencarboxylic acid, Methanoic acid, aminic acid	CH1O2	-1	Endoplasmic Reticulum
forglu	N-Formimidoyl-L-glutamate	N-Formimino-L-glutamate	C6H8N2O4	-2	Cytosol
formcoa	Formyl-CoA		C22H36N7O17P3S	0	Cytosol
formcoa	Formyl-CoA		C22H36N7O17P3S	0	Peroxisome
fpram	2-(Formamido)-N1-(5-phospho-D-ribosyl)acetamidine	1-(5'-Phosphoribosyl)-N-formylglycinamidine, 2-(Formamido)-N1-(5'-phosphoribosyl)acetamidine, 5'-Phosphoribosyl-N-formylglycinamidine, 5'-PhosphoribosylformylglycinamidineC8H15N3O8P	C8H15N3O8P	-1	Cytosol
fprica	5-Formamido-1-(5-phospho-D-ribosyl)imidazole-4-carboxamide	1-(5'-Phosphoribosyl)-5-formamido-4-imidazolecarboxamide, 5'-Phosphoribosyl-5-formamido-4-imidazolecarboxamide, 5-Formamido-1-(5-phosphoribosyl)imidazole-4-carboxamide	C10H13N4O9P	-2	Cytosol
frdp	Farnesyl diphosphate	2-trans,6-trans-Farnesyl diphosphate, FPP, Farnesyl pyrophosphate, trans,trans-Farnesyl diphosphate	C15H25O7P2	-3	Cytosol
frdp	Farnesyl diphosphate	2-trans,6-trans-Farnesyl diphosphate, FPP, Farnesyl pyrophosphate, trans,trans-Farnesyl diphosphate	C15H25O7P2	-3	Endoplasmic Reticulum
frdp	Farnesyl diphosphate	2-trans,6-trans-Farnesyl diphosphate, FPP, Farnesyl pyrophosphate, trans,trans-Farnesyl diphosphate	C15H25O7P2	-3	Peroxisome

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
fru	D-Fructose	D-Arabino-hexulose, Fruit sugar, Levulose	C6H12O6	0	Cytosol
fru	D-Fructose	D-Arabino-hexulose, Fruit sugar, Levulose	C6H12O6	0	Extracellular
fuc12gal14acglcgalgluside_hs	Type IIH glycolipid	(Gal)2 (Glc)1 (GlcNAc)1 (LFuc)1 (Cer)1, IV2-a-Fuc-nLc4Cer;, IV2Fuc-nLc4Cer;	C50H89N2O26FULLRCO	0	Golgi Apparatus
fuc132galacglcgal14acglcgalgluside_hs	V3Fuc-nLc6Cer	(Gal)3 (Glc)1 (GlcNAc)2 (LFuc)1 (Cer)1, Lex	C64H112N3O36FULLRCO	0	Golgi Apparatus
fuc13galacglcgal14acglcgalguside_hs	III3Fuc-nLc6Cer	(Gal)3 (Glc)1 (GlcNAc)2 (LFuc)1 (Cer)1	C64H112N3O36FULLRCO	0	Cytosol
fuc13galacglcgal14acglcgalguside_hs	III3Fuc-nLc6Cer	(Gal)3 (Glc)1 (GlcNAc)2 (LFuc)1 (Cer)1	C64H112N3O36FULLRCO	0	Extracellular
fuc13galacglcgal14acglcgalguside_hs	III3Fuc-nLc6Cer	(Gal)3 (Glc)1 (GlcNAc)2 (LFuc)1 (Cer)1	C64H112N3O36FULLRCO	0	Golgi Apparatus
fuc14galacglcgalgluside_hs	Lea glycolipid	(Gal)2 (Glc)1 (GlcNAc)1 (LFuc)1 (Cer)1, Fuc-Lc4Cer, III4-a-Fuc-Lc4Cer	C50H89N2O26FULLRCO	0	Cytosol
fuc14galacglcgalgluside_hs	Lea glycolipid	(Gal)2 (Glc)1 (GlcNAc)1 (LFuc)1 (Cer)1, Fuc-Lc4Cer, III4-a-Fuc-Lc4Cer	C50H89N2O26FULLRCO	0	Extracellular
fuc14galacglcgalgluside_hs	Lea glycolipid	(Gal)2 (Glc)1 (GlcNAc)1 (LFuc)1 (Cer)1, Fuc-Lc4Cer, III4-a-Fuc-Lc4Cer	C50H89N2O26FULLRCO	0	Golgi Apparatus
fuc1p-L	L-Fucose 1-phosphate	6-Deoxy-L-galactose 1-phosphate, L-Fucose 1-phosphate	C6H11O8P	-2	Cytosol
fucacgalfucgalacglcgalgluside_hs	(Gal)2 (GalNAc)1 (Glc)1 (GlcNAc)1 (LFuc)2 (Cer)1	ALeb	C64H112N3O35FULLRCO	0	Cytosol
fucacgalfucgalacglcgalgluside_hs	(Gal)2 (GalNAc)1 (Glc)1 (GlcNAc)1 (LFuc)2 (Cer)1	ALeb	C64H112N3O35FULLRCO	0	Extracellular
fucacgalfucgalacglcgalgluside_hs	(Gal)2 (GalNAc)1 (Glc)1 (GlcNAc)1 (LFuc)2 (Cer)1	ALeb	C64H112N3O35FULLRCO	0	Golgi Apparatus
fucacngal14acglcgalgluside_hs	IV3-a-NeuAc,III3-a-Fuc-nLc4Cer	(Gal)2 (Glc)1 (GlcNAc)1 (LFuc)1 (Neu5Ac)1 (Cer)1, IV3-a-NeuAc,III3-a-Fuc-nLc4Cer, IV3NeuAc,III3Fuc-nLc4Cer;	C61H105N3O34FULLRCO	-1	Cytosol
fucacngal14acglcgalgluside_hs	IV3-a-NeuAc,III3-a-Fuc-nLc4Cer	(Gal)2 (Glc)1 (GlcNAc)1 (LFuc)1 (Neu5Ac)1 (Cer)1, IV3-a-NeuAc,III3-a-Fuc-nLc4Cer, IV3NeuAc,III3Fuc-nLc4Cer;	C61H105N3O34FULLRCO	-1	Extracellular
fucacngal14acglcgalgluside_hs	IV3-a-NeuAc,III3-a-Fuc-nLc4Cer	(Gal)2 (Glc)1 (GlcNAc)1 (LFuc)1 (Neu5Ac)1 (Cer)1, IV3-a-NeuAc,III3-a-Fuc-nLc4Cer, IV3NeuAc,III3Fuc-nLc4Cer;	C61H105N3O34FULLRCO	-1	Golgi Apparatus
fucacngalacglcgalgluside_hs	IV3-a-Neu5Ac,III4-a-Fuc-Lc4Cer	(Gal)2 (Glc)1 (GlcNAc)1 (LFuc)1 (Neu5Ac)1 (Cer)1, Fuc-3'-isoLM1	C61H105N3O34FULLRCO	-1	Cytosol
fucacngalacglcgalgluside_hs	IV3-a-Neu5Ac,III4-a-Fuc-Lc4Cer	(Gal)2 (Glc)1 (GlcNAc)1 (LFuc)1 (Neu5Ac)1 (Cer)1, Fuc-3'-isoLM1	C61H105N3O34FULLRCO	-1	Extracellular
fucacngalacglcgalgluside_hs	IV3-a-Neu5Ac,III4-a-Fuc-Lc4Cer	(Gal)2 (Glc)1 (GlcNAc)1 (LFuc)1 (Neu5Ac)1 (Cer)1, Fuc-3'-isoLM1	C61H105N3O34FULLRCO	-1	Golgi Apparatus
fucfuc12gal14acglcgalgluside_hs	Ley glycolipid	(Gal)2 (Glc)1 (GlcNAc)1 (LFuc)2 (Cer)1, III3,IV2Fuc-nLc4Cer;, IV2-a-Fuc,III3-a-Fuc-nLc4Cer;	C56H99N2O30FULLRCO	0	Cytosol
fucfuc12gal14acglcgalgluside_hs	Ley glycolipid	(Gal)2 (Glc)1 (GlcNAc)1 (LFuc)2 (Cer)1, III3,IV2Fuc-nLc4Cer;, IV2-a-Fuc,III3-a-Fuc-nLc4Cer;	C56H99N2O30FULLRCO	0	Extracellular
fucfuc12gal14acglcgalgluside_hs	Ley glycolipid	(Gal)2 (Glc)1 (GlcNAc)1 (LFuc)2 (Cer)1, III3,IV2Fuc-nLc4Cer;, IV2-a-Fuc,III3-a-Fuc-nLc4Cer;	C56H99N2O30FULLRCO	0	Golgi Apparatus
fucfuc132galacglcgal14acglcgalgluside_hs	V3Fuc,III3Fuc-nLc6Cer	(Gal)3 (Glc)1 (GlcNAc)2 (LFuc)2 (Cer)1, dimeric Lex	C70H122N3O40FULLRCO	0	Cytosol
fucfuc132galacglcgal14acglcgalgluside_hs	V3Fuc,III3Fuc-nLc6Cer	(Gal)3 (Glc)1 (GlcNAc)2 (LFuc)2 (Cer)1, dimeric Lex	C70H122N3O40FULLRCO	0	Extracellular
fucfuc132galacglcgal14acglcgalgluside_hs	V3Fuc,III3Fuc-nLc6Cer	(Gal)3 (Glc)1 (GlcNAc)2 (LFuc)2 (Cer)1, dimeric Lex	C70H122N3O40FULLRCO	0	Golgi Apparatus
fucfucfucgalacglc13galacglcgal14acglcgalgluside_hs	(Gal)4 (Glc)1 (GlcNAc)3 (LFuc)3 (Cer)1	trimeric Lex	C90H155N4O54FULLRCO	0	Cytosol
fucfucfucgalacglc13galacglcgal14acglcgalgluside_hs	(Gal)4 (Glc)1 (GlcNAc)3 (LFuc)3 (Cer)1	trimeric Lex	C90H155N4O54FULLRCO	0	Extracellular
fucfucfucgalacglc13galacglcgal14acglcgalgluside_hs	(Gal)4 (Glc)1 (GlcNAc)3 (LFuc)3 (Cer)1	trimeric Lex	C90H155N4O54FULLRCO	0	Golgi Apparatus
fucfucfucgalacglcgal14acglcgalgluside_hs	(Gal)3 (Glc)1 (GlcNAc)2 (LFuc)3 (Cer)1		C76H132N3O44FULLRCO	0	Cytosol
fucfucfucgalacglcgal14acglcgalgluside_hs	(Gal)3 (Glc)1 (GlcNAc)2 (LFuc)3 (Cer)1		C76H132N3O44FULLRCO	0	Extracellular
fucfucfucgalacglcgal14acglcgalgluside_hs	(Gal)3 (Glc)1 (GlcNAc)2 (LFuc)3 (Cer)1		C76H132N3O44FULLRCO	0	Golgi Apparatus
fucfucgalacglc13galacglcgal14acglcgalgluside_hs	(Gal)4 (Glc)1 (GlcNAc)3 (LFuc)2 (Cer)1	dimeric Lex	C84H145N4O50FULLRCO	0	Golgi Apparatus
fucfucgalacglcgal14acglcgalgluside_hs	(Gal)3 (Glc)1 (GlcNAc)2 (LFuc)2 (Cer)1		C70H122N3O40FULLRCO	0	Golgi Apparatus
fucfucgalacglcgalacglcgal14acglcgalgluside_hs	(Gal)4 (Glc)1 (GlcNAc)3 (LFuc)2 (Cer)1		C84H145N4O50FULLRCO	0	Golgi Apparatus
fucfucgalacglcgalgluside_hs	Leb glycolipid	(Gal)2 (Glc)1 (GlcNAc)1 (LFuc)2 (Cer)1, IV2-a-Fuc,III4-a-Fuc-Lc4Cer, IV2Fuc,III4Fuc-Lc4Cer	C56H99N2O30FULLRCO	0	Cytosol
fucfucgalacglcgalgluside_hs	Leb glycolipid	(Gal)2 (Glc)1 (GlcNAc)1 (LFuc)2 (Cer)1, IV2-a-Fuc,III4-a-Fuc-Lc4Cer, IV2Fuc,III4Fuc-Lc4Cer	C56H99N2O30FULLRCO	0	Extracellular
fucfucgalacglcgalgluside_hs	Leb glycolipid	(Gal)2 (Glc)1 (GlcNAc)1 (LFuc)2 (Cer)1, IV2-a-Fuc,III4-a-Fuc-Lc4Cer, IV2Fuc,III4Fuc-Lc4Cer	C56H99N2O30FULLRCO	0	Golgi Apparatus
fucgal14acglcgalgluside_hs	Lacto-N-fucopentaosyl III ceramide	(Gal)2 (Glc)1 (GlcNAc)1 (LFuc)1 (Cer)1, III3-a-Fuc-nLc4Cer;, III3Fuc-nLc4Cer;, LNF III cer;, Lacto-N-fucopentaosyl III ceramide;, SSEA-1	C50H89N2O26FULLRCO	0	Cytosol

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
fucgal14acglcgalgluside_hs	Lacto-N-fucopentaosyl III ceramide	(Gal)2 (Glc)1 (GlcNAc)1 (LFuc)1 (Cer)1, III3-a-Fuc-nLc4Cer;, III3Fuc-nLc4Cer;, LNF III cer;, Lacto-N-fucopentaosyl III ceramide;, SSEA-1	C50H89N2O26FULLRCO	0	Extracellular
fucgal14acglcgalgluside_hs	Lacto-N-fucopentaosyl III ceramide	(Gal)2 (Glc)1 (GlcNAc)1 (LFuc)1 (Cer)1, III3-a-Fuc-nLc4Cer;, III3Fuc-nLc4Cer;, LNF III cer;, Lacto-N-fucopentaosyl III ceramide;, SSEA-1	C50H89N2O26FULLRCO	0	Golgi Apparatus
fucgalacgalfuc12gal14acglcgalgluside_hs	Type IIIH glycolipid	(Gal)3 (GalNAc)1 (Glc)1 (GlcNAc)1 (LFuc)2 (Cer)1	C70H122N3O40FULLRCO	0	Golgi Apparatus
fucgalacgalfucgalacglcgal14acglcgalgluside_hs	(Gal)4 (GalNAc)1 (Glc)1 (GlcNAc)2 (LFuc)2 (Cer)1		C84H145N4O50FULLRCO	0	Golgi Apparatus
fucgalacglc13galacglcgal14acglcgalgluside_hs	(Gal)4 (Glc)1 (GlcNAc)3 (LFuc)1 (Cer)1	Lex	C78H135N4O46FULLRCO	0	Golgi Apparatus
fucgalacglcgal14acglcgalgluside_hs	VI2Fuc-nLc6	(Gal)3 (Glc)1 (GlcNAc)2 (LFuc)1 (Cer)1	C64H112N3O36FULLRCO	0	Golgi Apparatus
fucgalacglcgalgluside_hs	Type IH glycolipid	(Gal)2 (Glc)1 (GlcNAc)1 (LFuc)1 (Cer)1, IV2-a-Fuc-Lc4Cer, IV2Fuc-Lc4Cer	C50H89N2O26FULLRCO	0	Golgi Apparatus
fucgalfucgalacglcgalgluside_hs	(Gal)3 (Glc)1 (GlcNAc)1 (LFuc)2 (Cer)1		C62H109N2O35FULLRCO	0	Cytosol
fucgalfucgalacglcgalgluside_hs	(Gal)3 (Glc)1 (GlcNAc)1 (LFuc)2 (Cer)1		C62H109N2O35FULLRCO	0	Extracellular
fucgalfucgalacglcgalgluside_hs	(Gal)3 (Glc)1 (GlcNAc)1 (LFuc)2 (Cer)1		C62H109N2O35FULLRCO	0	Golgi Apparatus
fucgalgbside_hs	fucosyl galactosylgloboside (homo sapiens)	(Gal)3 (GalNAc)1 (Glc)1 (LFuc)1 (Cer)1, Fuc-Gal-globoside, Globo-H	C56H99N2O31FULLRCO	0	Cytosol
fucgalgbside_hs	fucosyl galactosylgloboside (homo sapiens)	(Gal)3 (GalNAc)1 (Glc)1 (LFuc)1 (Cer)1, Fuc-Gal-globoside, Globo-H	C56H99N2O31FULLRCO	0	Extracellular
fucgalgbside_hs	fucosyl galactosylgloboside (homo sapiens)	(Gal)3 (GalNAc)1 (Glc)1 (LFuc)1 (Cer)1, Fuc-Gal-globoside, Globo-H	C56H99N2O31FULLRCO	0	Golgi Apparatus
fuc-L	L-Fucose	6-Deoxy-L-galactose	C6H12O5	0	Cytosol
fuc-L	L-Fucose	6-Deoxy-L-galactose	C6H12O5	0	Extracellular
fuc-L	L-Fucose	6-Deoxy-L-galactose	C6H12O5	0	Lysosome
fum	Fumarate	Fumaric acid, Trans-butenedioic acid, allomaleic acid, boletic acid	C4H2O4	-2	Cytosol
fum	Fumarate	Fumaric acid, Trans-butenedioic acid, allomaleic acid, boletic acid	C4H2O4	-2	Mitochondria
g1m6masnB1	glucosyl-(alpha-D-mannosyl)6-beta-D-mannosyl-diacetylchitobiosyl-L-asparagine (protein)		C64H107N2O50X	0	Golgi Apparatus
g1m6masnB1	glucosyl-(alpha-D-mannosyl)6-beta-D-mannosyl-diacetylchitobiosyl-L-asparagine (protein)		C64H107N2O50X	0	Endoplasmic Reticulum
g1m7masnB	glucosyl-(alpha-D-mannosyl)7-beta-D-mannosyl-diacetylchitobiosyl-L-asparagine, isoform B (protein)		C70H117N2O55X	0	Golgi Apparatus
g1m7masnB	glucosyl-(alpha-D-mannosyl)7-beta-D-mannosyl-diacetylchitobiosyl-L-asparagine, isoform B (protein)		C70H117N2O55X	0	Endoplasmic Reticulum
g1m7masnC	glucosyl-(alpha-D-mannosyl)7-beta-D-mannosyl-diacetylchitobiosyl-L-asparagine, isoform C (protein)		C70H117N2O55X	0	Golgi Apparatus
g1m7masnC	glucosyl-(alpha-D-mannosyl)7-beta-D-mannosyl-diacetylchitobiosyl-L-asparagine, isoform C (protein)		C70H117N2O55X	0	Endoplasmic Reticulum
g1m8masn	(alpha-D-Glucosyl)-(alpha-D-mannosyl)8-beta-D-mannosyl-diacetylchitobiosyl-L-asparagine (protein)		C76H127N2O60X	0	Golgi Apparatus
g1m8masn	(alpha-D-Glucosyl)-(alpha-D-mannosyl)8-beta-D-mannosyl-diacetylchitobiosyl-L-asparagine (protein)		C76H127N2O60X	0	Endoplasmic Reticulum
g1m8mpdol_L	alpha-D-Glucosyl-(alpha-D-mannosyl)8-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human liver homolog		C1840H3028N20O670P20	-20	Endoplasmic Reticulum
g1m8mpdol_U	alpha-D-Glucosyl-(alpha-D-mannosyl)8-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human uterine homolog		C1785H2940N20O670P20	-20	Endoplasmic Reticulum
g1p	D-Glucose 1-phosphate	Cori ester, Glucose 1-phosphate, alpha-D-Glucose phosphate	C6H11O9P	-2	Cytosol
g2m8masn	(alpha-D-Glucosyl)2-(alpha-D-mannosyl)8-beta-D-mannosy diacetylchitobiosyl-L-asparagine (protein)		C82H137N2O65X	0	Golgi Apparatus
g2m8masn	(alpha-D-Glucosyl)2-(alpha-D-mannosyl)8-beta-D-mannosy diacetylchitobiosyl-L-asparagine (protein)		C82H137N2O65X	0	Endoplasmic Reticulum
g2m8mpdol_L	(alpha-D-Glucosyl)2-(alpha-D-mannosyl)8-beta-D-mannosy diacetylchitobiosyldiphosphodolichol, human liver homolog		C1900H3128N20O720P20	-20	Endoplasmic Reticulum
g2m8mpdol_U	(alpha-D-Glucosyl)2-(alpha-D-mannosyl)8-beta-D-mannosy diacetylchitobiosyldiphosphodolichol, human uterine homolog		C1845H3040N20O720P20	-20	Endoplasmic Reticulum
g3m8masn	(alpha-D-Glucosyl)3-(alpha-D-mannosyl)8-beta-D-mannosy diacetylchitobiosyl-L-asparagine (protein)		C88H147N2O70X	0	Golgi Apparatus
g3m8masn	(alpha-D-Glucosyl)3-(alpha-D-mannosyl)8-beta-D-mannosy diacetylchitobiosyl-L-asparagine (protein)		C88H147N2O70X	0	Endoplasmic Reticulum
g3m8mpdol_L	(alpha-D-Glucosyl)3-(alpha-D-mannosyl)8-beta-D-mannosy diacetylchitobiosyldiphosphodolichol, human liver homolog		C1960H3228N20O770P20	-20	Endoplasmic Reticulum
g3m8mpdol_U	(alpha-D-Glucosyl)3-(alpha-D-mannosyl)8-beta-D-mannosy diacetylchitobiosyldiphosphodolichol, human uterine homolog		C1905H3140N20O770P20	-20	Endoplasmic Reticulum

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
g3p	Glyceraldehyde 3-phosphate	(2R)-2-Hydroxy-3-(phosphonooxy)-propanal, D-glyceraldehyde 3-phosphate	C3H5O6P	-2	Cytosol
g3pc	sn-Glycero-3-phosphocholine	Glycerophosphocholine	C8H20NO6P	0	Cytosol
g6p	D-Glucose 6-phosphate	Glucose 6-phosphate, Robinson ester, alpha-D-Glucose 6-phosphate	C6H11O9P	-2	Cytosol
g6p	D-Glucose 6-phosphate	Glucose 6-phosphate, Robinson ester, alpha-D-Glucose 6-phosphate	C6H11O9P	-2	Endoplasmic Reticulum
ga1_hs	GA1 (homo sapiens)	(Gal)2 (GalNAc)1 (Glc)1 (Cer)1	C44H79N2O22FULLRCO	0	Golgi Apparatus
ga2_hs	GA2 (homo sapiens)	(Gal)1 (GalNAc)1 (Glc)1 (Cer)1	C38H69N2O17FULLRCO	0	Golgi Apparatus
gacpail_hs	glucosaminyl-acylphosphatidylinositol	GlcN-acylPI	C31H58NO14PFULLRCO2FULLR2CO2	0	Cytosol
gacpail_hs	glucosaminyl-acylphosphatidylinositol	GlcN-acylPI	C31H58NO14PFULLRCO2FULLR2CO2	0	Endoplasmic Reticulum
gal	D-Galactose	Galactose, alpha-Galactose(D)	C6H12O6	0	Cytosol
gal	D-Galactose	Galactose, alpha-Galactose(D)	C6H12O6	0	Extracellular
gal	D-Galactose	Galactose, alpha-Galactose(D)	C6H12O6	0	Lysosome
gal14acglcgalgluside_hs	Lactoneotetraosylceramide	(Gal)2 (Glc)1 (GlcNAc)1 (Cer)1, LA1;, Lacto-N-neotetraosylceramide;, Lactoneotetraosylceramide;, Neolactotetraosylceramide;, Paragloboside;, nLcCer	C44H79N2O22FULLRCO	0	Golgi Apparatus
gal1p	alpha-D-Galactose 1-phosphate	D-Galactose 1-phosphate, alpha-D-Galactose 1-phosphate	C6H11O9P	-2	Cytosol
galacgalfuc12gal14acglcgalgluside_hs	(Gal)3 (GalNAc)1 (Glc)1 (GlcNAc)1 (LFuc)1 (Cer)1		C64H112N3O36FULLRCO	0	Golgi Apparatus
galacgalfucgalacglcgal14acglcgalgluside_hs	(Gal)4 (GalNAc)1 (Glc)1 (GlcNAc)2 (LFuc)1 (Cer)1		C78H135N4O46FULLRCO	0	Golgi Apparatus
galacglc13galacglcgal14acglcgalgluside_hs	nLc8Cer	(Gal)4 (Glc)1 (GlcNAc)3 (Cer)1	C72H125N4O42FULLRCO	0	Golgi Apparatus
galacglcgal14acglcgalgluside_hs	i-antigen	(Gal)3 (Glc)1 (GlcNAc)2 (Cer)1, nLc6Cer;	C58H102N3O32FULLRCO	0	Golgi Apparatus
galacglcgalacglcgal14acglcgalgluside_hs	I-antigen	(Gal)4 (Glc)1 (GlcNAc)3 (Cer)1, LacNAc-Lc6Cer; Lactoisooctaosylceramide, iso-nLc8Cer;	C72H125N4O42FULLRCO	0	Golgi Apparatus
galacglcgalgbside_hs	Gal-GlcNAc-Gal globoside (homo sapiens)	(Gal)4 (GalNAc)1 (Glc)1 (GlcNAc)1 (Cer)1	C64H112N3O37FULLRCO	0	Cytosol
galacglcgalgbside_hs	Gal-GlcNAc-Gal globoside (homo sapiens)	(Gal)4 (GalNAc)1 (Glc)1 (GlcNAc)1 (Cer)1	C64H112N3O37FULLRCO	0	Extracellular
galacglcgalgbside_hs	Gal-GlcNAc-Gal globoside (homo sapiens)	(Gal)4 (GalNAc)1 (Glc)1 (GlcNAc)1 (Cer)1	C64H112N3O37FULLRCO	0	Golgi Apparatus
galacglcgalgluside_hs	Lc4Cer	(Gal)2 (Glc)1 (GlcNAc)1 (Cer)1	C44H79N2O22FULLRCO	0	Golgi Apparatus
galfuc12gal14acglcgalgluside_hs	(Gal)3 (Glc)1 (GlcNAc)1 (LFuc)1 (Cer)1		C56H99N2O31FULLRCO	0	Cytosol
galfuc12gal14acglcgalgluside_hs	(Gal)3 (Glc)1 (GlcNAc)1 (LFuc)1 (Cer)1		C56H99N2O31FULLRCO	0	Extracellular
galfuc12gal14acglcgalgluside_hs	(Gal)3 (Glc)1 (GlcNAc)1 (LFuc)1 (Cer)1		C56H99N2O31FULLRCO	0	Golgi Apparatus
galfucgalacglcgal14acglcgalgluside_hs	(Gal)4 (Glc)1 (GlcNAc)2 (LFuc)1 (Cer)1		C70H122N3O41FULLRCO	0	Cytosol
galfucgalacglcgal14acglcgalgluside_hs	(Gal)4 (Glc)1 (GlcNAc)2 (LFuc)1 (Cer)1		C70H122N3O41FULLRCO	0	Extracellular
galfucgalacglcgal14acglcgalgluside_hs	(Gal)4 (Glc)1 (GlcNAc)2 (LFuc)1 (Cer)1		C70H122N3O41FULLRCO	0	Golgi Apparatus
galfucgalacglcgalgluside_hs	Type IB glycolipid	(Gal)3 (Glc)1 (GlcNAc)1 (LFuc)1 (Cer)1	C56H99N2O31FULLRCO	0	Golgi Apparatus
galgalfucfucgalacglcgalacglcgal14acglcgalgluside_hs	(Gal)6 (Glc)1 (GlcNAc)3 (LFuc)2 (Cer)1		C96H165N4O60FULLRCO	0	Cytosol
galgalfucfucgalacglcgalacglcgal14acglcgalgluside_hs	(Gal)6 (Glc)1 (GlcNAc)3 (LFuc)2 (Cer)1		C96H165N4O60FULLRCO	0	Extracellular
galgalfucfucgalacglcgalacglcgal14acglcgalgluside_hs	(Gal)6 (Glc)1 (GlcNAc)3 (LFuc)2 (Cer)1		C96H165N4O60FULLRCO	0	Golgi Apparatus
galgalgalthcrm_hs	Gal-Gal-Gal-Gal-Gal-Glc-Cer (homo sapiens)	Gal(alpha 1->3)-Gal(alpha 1->3)-Gal(alpha 1->3)-Gal(alpha 1->3)-Gal(alpha 1->4)-Gal(beta 1->4)-Glc(beta 1->4)-Cer, Gal-Gal-Gal-Gal-Gal-Glu-Cer	C54H96NO32FULLRCO	0	Cytosol
galgalgalthcrm_hs	Gal-Gal-Gal-Gal-Gal-Glc-Cer (homo sapiens)	Gal(alpha 1->3)-Gal(alpha 1->3)-Gal(alpha 1->3)-Gal(alpha 1->3)-Gal(alpha 1->4)-Gal(beta 1->4)-Glc(beta 1->4)-Cer, Gal-Gal-Gal-Gal-Gal-Glu-Cer	C54H96NO32FULLRCO	0	Extracellular
galgalgalthcrm_hs	Gal-Gal-Gal-Gal-Gal-Glc-Cer (homo sapiens)	Gal(alpha 1->3)-Gal(alpha 1->3)-Gal(alpha 1->3)-Gal(alpha 1->3)-Gal(alpha 1->4)-Gal(beta 1->4)-Glc(beta 1->4)-Cer, Gal-Gal-Gal-Gal-Gal-Glu-Cer	C54H96NO32FULLRCO	0	Golgi Apparatus
galgalthcrm_hs	Gal-Gal-Gal-Gal-Glc-Cer (homo sapiens)	Gal(alpha 1->3)-Gal(alpha 1->3)-Gal(alpha 1->4)-Gal(beta 1->4)-Glc(beta 1->4)-Cer, Gal-Gal-Gal-Glu-Cer	C48H86NO27FULLRCO	0	Golgi Apparatus
galgbside_hs	galactosylgloboside (homo sapiens)	Gal-GalNac-Gal-Gal-Glc-Cer, Gb5Cer, SSEA-3, galactose globoside	C50H89N2O27FULLRCO	0	Golgi Apparatus
galgluside_hs	galactosyl glucosyl ceramide	(Gal)1 (Glc)1 (Cer)1, Cer-Glc-Gal, Gal-Glc-Cer	C30H56NO12FULLRCO	0	Cytosol
galgluside_hs	galactosyl glucosyl ceramide	(Gal)1 (Glc)1 (Cer)1, Cer-Glc-Gal, Gal-Glc-Cer	C30H56NO12FULLRCO	0	Golgi Apparatus
galgluside_hs	galactosyl glucosyl ceramide	(Gal)1 (Glc)1 (Cer)1, Cer-Glc-Gal, Gal-Glc-Cer	C30H56NO12FULLRCO	0	Lysosome
galside_hs	galactocerebroside (homo sapiens)	1-beta-D-galactoceramide, Cer-Gal	C24H46NO7FULLRCO	0	Cytosol
galside_hs	galactocerebroside (homo sapiens)	1-beta-D-galactoceramide, Cer-Gal	C24H46NO7FULLRCO	0	Golgi Apparatus
galside_hs	galactocerebroside (homo sapiens)	1-beta-D-galactoceramide, Cer-Gal	C24H46NO7FULLRCO	0	Lysosome
galt	Galactitol	Dulcitol, Dulcose	C6H14O6	0	Cytosol
galthcrm_hs	Gal-Gal-Gal-Glc-Cer (homo sapiens)	Gal(alpha 1->3)-Gal(alpha 1->4)-Gal(beta 1->4)-Glc(beta 1->4)-Cer, Gal-Gal-Gal-Glu-Cer	C42H76NO22FULLRCO	0	Golgi Apparatus

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
gam	D-Glucosamine	2-Amino-2-deoxy-D-glucose, Chitosamine, GlcN	C6H14NO5	1	Cytosol
gam	D-Glucosamine	2-Amino-2-deoxy-D-glucose, Chitosamine, GlcN	C6H14NO5	1	Extracellular
gam6p	D-Glucosamine 6-phosphate	D-Glucosamine phosphate	C6H13NO8P	-1	Cytosol
gar	N1-(5-Phospho-D-ribosyl)glycinamide	5'-Phosphoribosylglycinamide, GAR, Glycinamide ribonucleotide	C7H14N2O8P	-1	Cytosol
gbside_hs	globoside (homo sapiens)	GalNac-Gal-Gal-Glc-Cer, Gb4Cer, P-antigen	C44H79N2O22FULLRCO	0	Cytosol
gbside_hs	globoside (homo sapiens)	GalNac-Gal-Gal-Glc-Cer, Gb4Cer, P-antigen	C44H79N2O22FULLRCO	0	Extracellular
gbside_hs	globoside (homo sapiens)	GalNac-Gal-Gal-Glc-Cer, Gb4Cer, P-antigen	C44H79N2O22FULLRCO	0	Golgi Apparatus
gbside_hs	globoside (homo sapiens)	GalNac-Gal-Gal-Glc-Cer, Gb4Cer, P-antigen	C44H79N2O22FULLRCO	0	Lysosome
gcald	Glycolaldehyde	Hydroxyacetaldehyde	C2H4O2	0	Cytosol
gcald	Glycolaldehyde	Hydroxyacetaldehyde	C2H4O2	0	Mitochondria
gchola	glycocholate	5-beta-cholanic acid-3-alpha-7-alpha-12-alpha-triol N-(carboxymethyl)-amide, Glycocholate, Glycocholic acid, bile acid	C26H43NO6	0	Cytosol
gchola	glycocholate	5-beta-cholanic acid-3-alpha-7-alpha-12-alpha-triol N-(carboxymethyl)-amide, Glycocholate, Glycocholic acid, bile acid	C26H43NO6	0	Extracellular
gchola	glycocholate	5-beta-cholanic acid-3-alpha-7-alpha-12-alpha-triol N-(carboxymethyl)-amide, Glycocholate, Glycocholic acid, bile acid	C26H43NO6	0	Peroxisome
gd1a_hs	GD1a (homo sapiens)	(Gal)2 (GalNAc)1 (Glc)1 (Neu5Ac)2 (Cer)1	C66H111N4O38FULLRCO	-2	Golgi Apparatus
gd1alpha_hs	GD1a (homo sapiens)	(Gal)2 (GalNAc)1 (Glc)1 (Neu5Ac)2 (Cer)1	C66H111N4O38FULLRCO	-2	Golgi Apparatus
gd1b_hs	GD1b (homo sapiens)	(Gal)2 (GalNAc)1 (Glc)1 (Neu5Ac)2 (Cer)1	C66H111N4O38FULLRCO	-2	Golgi Apparatus
gd1b2_hs	GD1beta (homo sapiens)	(Gal)2 (GalNAc)1 (Glc)1 (Neu5Ac)2 (Cer)1	C66H111N4O38FULLRCO	-2	Cytosol
gd1b2_hs	GD1beta (homo sapiens)	(Gal)2 (GalNAc)1 (Glc)1 (Neu5Ac)2 (Cer)1	C66H111N4O38FULLRCO	-2	Extracellular
gd1b2_hs	GD1beta (homo sapiens)	(Gal)2 (GalNAc)1 (Glc)1 (Neu5Ac)2 (Cer)1	C66H111N4O38FULLRCO	-2	Golgi Apparatus
gd1c_hs	GD1c (homo sapiens)	(Gal)2 (GalNAc)1 (Glc)1 (Neu5Ac)2 (Cer)1	C66H111N4O38FULLRCO	-2	Cytosol
gd1c_hs	GD1c (homo sapiens)	(Gal)2 (GalNAc)1 (Glc)1 (Neu5Ac)2 (Cer)1	C66H111N4O38FULLRCO	-2	Extracellular
gd1c_hs	GD1c (homo sapiens)	(Gal)2 (GalNAc)1 (Glc)1 (Neu5Ac)2 (Cer)1	C66H111N4O38FULLRCO	-2	Golgi Apparatus
gd2_hs	GD2 (homo sapiens)	(Gal)1 (GalNAc)1 (Glc)1 (Neu5Ac)2 (Cer)1	C60H101N4O33FULLRCO	-2	Golgi Apparatus
gd3_hs	GD3 (homo sapiens)	(Gal)1 (Glc)1 (Neu5Ac)2 (Cer)1, CD60a	C52H88N3O28FULLRCO	-2	Cytosol
gd3_hs	GD3 (homo sapiens)	(Gal)1 (Glc)1 (Neu5Ac)2 (Cer)1, CD60a	C52H88N3O28FULLRCO	-2	Golgi Apparatus
gdchola	glycochenodeoxycholate	Glycochenodeoxycholate, bile acid, bile salt	C26H43NO5	0	Cytosol
gdchola	glycochenodeoxycholate	Glycochenodeoxycholate, bile acid, bile salt	C26H43NO5	0	Extracellular
gdchola	glycochenodeoxycholate	Glycochenodeoxycholate, bile acid, bile salt	C26H43NO5	0	Peroxisome
gdp	GDP	Guanosine 5'-diphosphate, Guanosine diphosphate	C10H12N5O11P2	-3	Cytosol
gdp	GDP	Guanosine 5'-diphosphate, Guanosine diphosphate	C10H12N5O11P2	-3	Extracellular
gdp	GDP	Guanosine 5'-diphosphate, Guanosine diphosphate	C10H12N5O11P2	-3	Golgi Apparatus
gdp	GDP	Guanosine 5'-diphosphate, Guanosine diphosphate	C10H12N5O11P2	-3	Mitochondria
gdp	GDP	Guanosine 5'-diphosphate, Guanosine diphosphate	C10H12N5O11P2	-3	Nucleus
gdpddman	GDP-4-dehydro-6-deoxy-D-mannose	GDP-4-dehydro-6-deoxy-D-mannose, GDP-4-dehydro-6-deoxy-D-talose, GDP-4-dehydro-D-rhamnose, GDP-4-oxo-6-deoxy-D-mannose	C16H21N5O15P2	-2	Cytosol
gdpfuc	GDP-L-fucose		C16H23N5O15P2	-2	Cytosol
gdpfuc	GDP-L-fucose		C16H23N5O15P2	-2	Golgi Apparatus
gdpmann	GDP-D-mannose		C16H23N5O16P2	-2	Cytosol
ggdp	Geranylgeranyl diphosphate	GGPP, Geranylgeranyl pyrophosphate, all-trans-Geranylgeranyl diphosphate, all-trans-Geranylgeranyl pyrophosphate	C20H33O7P2	-3	Cytosol
ggn	primed glycogenin (glycogenin-8[1,4-Glc])		C48H81O41X	0	Cytosol
glac	D-glucurono-6,3-lactone		C6H8O6	0	Cytosol
glac	D-glucurono-6,3-lactone		C6H8O6	0	Mitochondria
glac	D-glucurono-6,3-lactone		C6H8O6	0	Endoplasmic Reticulum
glc1man	glucose-1,3-mannose oligosaccharide		C12H22O11	0	Golgi Apparatus
glc2man	(2)[glucose-1,3]-mannose oligosaccharide		C18H32O16	0	Golgi Apparatus
glc3man	glucose-1,2-(2)[glucose-1,3]-mannose oligosaccharide		C24H42O21	0	Golgi Apparatus
glc-D	D-Glucose	Dextrose, Glucose, Grape sugar, alpha-D-Glucose, beta-D-Glucose	C6H12O6	0	Cytosol
glc-D	D-Glucose	Dextrose, Glucose, Grape sugar, alpha-D-Glucose, beta-D-Glucose	C6H12O6	0	Extracellular
glc-D	D-Glucose	Dextrose, Glucose, Grape sugar, alpha-D-Glucose, beta-D-Glucose	C6H12O6	0	Golgi Apparatus
glc-D	D-Glucose	Dextrose, Glucose, Grape sugar, alpha-D-Glucose, beta-D-Glucose	C6H12O6	0	Lysosome
glc-D	D-Glucose	Dextrose, Glucose, Grape sugar, alpha-D-Glucose, beta-D-Glucose	C6H12O6	0	Endoplasmic Reticulum
glcr	D-Glucarate	D-Glucaric acid, D-Glucosaccharic acid, D-Saccharic acid, L-Gularic acid	C6H8O8	-2	Cytosol

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
glcr	D-Glucarate	D-Glucaric acid, D-Glucosaccharic acid, D-Saccharic acid, L-Gularic acid	C6H8O8	-2	Mitochondria
glcur	D-Glucuronate	GlcA, Glucuronate, Glucuronic acid	C6H9O7	-1	Cytosol
glcur	D-Glucuronate	GlcA, Glucuronate, Glucuronic acid	C6H9O7	-1	Lysosome
glcur	D-Glucuronate	GlcA, Glucuronate, Glucuronic acid	C6H9O7	-1	Endoplasmic Reticulum
glcur1p	D-Glucuronate 1-phosphate	GlcA-1P	C6H8O10P	-3	Cytosol
gln-L	L-Glutamine	Gln, L-2-Aminoglutaramic acid	C5H10N2O3	0	Cytosol
gln-L	L-Glutamine	Gln, L-2-Aminoglutaramic acid	C5H10N2O3	0	Extracellular
gln-L	L-Glutamine	Gln, L-2-Aminoglutaramic acid	C5H10N2O3	0	Mitochondria
glu5p	L-Glutamate 5-phosphate	L-Glutamyl 5-phosphate	C5H8NO7P	-2	Mitochondria
glu5sa	L-Glutamate 5-semialdehyde	L-Glutamate gamma-semialdehyde	C5H9NO3	0	Cytosol
glu5sa	L-Glutamate 5-semialdehyde	L-Glutamate gamma-semialdehyde	C5H9NO3	0	Mitochondria
gluala	5-L-Glutamyl-L-alanine		C8H13N2O5	-1	Extracellular
glucys	gamma-L-Glutamyl-L-cysteine	5-L-Glutamyl-L-cysteine, L-gamma-Glutamylcysteine	C8H13N2O5S	-1	Cytosol
glu-L	L-Glutamate	Glu, L-Glutamic acid, L-Glutaminic acid	C5H8NO4	-1	Cytosol
glu-L	L-Glutamate	Glu, L-Glutamic acid, L-Glutaminic acid	C5H8NO4	-1	Extracellular
glu-L	L-Glutamate	Glu, L-Glutamic acid, L-Glutaminic acid	C5H8NO4	-1	Lysosome
glu-L	L-Glutamate	Glu, L-Glutamic acid, L-Glutaminic acid	C5H8NO4	-1	Mitochondria
glu-L	L-Glutamate	Glu, L-Glutamic acid, L-Glutaminic acid	C5H8NO4	-1	Endoplasmic Reticulum
gluside_hs	glucocerebroside (homo sapiens)	1-beta-D-glucoceramide, Cer-Glu, glucosyl ceramide	C24H46NO7FULLRCO	0	Cytosol
gluside_hs	glucocerebroside (homo sapiens)	1-beta-D-glucoceramide, Cer-Glu, glucosyl ceramide	C24H46NO7FULLRCO	0	Golgi Apparatus
gluside_hs	glucocerebroside (homo sapiens)	1-beta-D-glucoceramide, Cer-Glu, glucosyl ceramide	C24H46NO7FULLRCO	0	Lysosome
gluside_hs	glucocerebroside (homo sapiens)	1-beta-D-glucoceramide, Cer-Glu, glucosyl ceramide	C24H46NO7FULLRCO	0	Endoplasmic Reticulum
glutcoa	Glutaryl-CoA		C26H37N7O19P3S	-5	Mitochondria
glx	Glyoxylate	Acetic acid, Glyoxalate, Glyoxylic acid	C2H1O3	-1	Cytosol
glx	Glyoxylate	Acetic acid, Glyoxalate, Glyoxylic acid	C2H1O3	-1	Mitochondria
glx	Glyoxylate	Acetic acid, Glyoxalate, Glyoxylic acid	C2H1O3	-1	Peroxisome
gly	Glycine	Aminoacetic acid, Gly	C2H5NO2	0	Cytosol
gly	Glycine	Aminoacetic acid, Gly	C2H5NO2	0	Extracellular
gly	Glycine	Aminoacetic acid, Gly	C2H5NO2	0	Lysosome
gly	Glycine	Aminoacetic acid, Gly	C2H5NO2	0	Mitochondria
gly	Glycine	Aminoacetic acid, Gly	C2H5NO2	0	Peroxisome
glyald	D-Glyceraldehyde	(R)-glyceraldehyde	C3H6O3	0	Cytosol
glyb	Glycine betaine	Betaine, Trimethylaminoacetate	C5H11NO2	0	Cytosol
glyb	Glycine betaine	Betaine, Trimethylaminoacetate	C5H11NO2	0	Extracellular
glyb	Glycine betaine	Betaine, Trimethylaminoacetate	C5H11NO2	0	Mitochondria
glyc	Glycerol	1,2,3-trihydroxypropane, 3-propanetriol, Glycerin	C3H8O3	0	Cytosol
glyc	Glycerol	1,2,3-trihydroxypropane, 3-propanetriol, Glycerin	C3H8O3	0	Extracellular
glyc	Glycerol	1,2,3-trihydroxypropane, 3-propanetriol, Glycerin	C3H8O3	0	Mitochondria
glyc3p	Glycerol 3-phosphate	Glycerophosphoric acid, Phosphatidyl glycerol, sn-Glycerol 3-phosphate, sn-Gro-1-P	C3H7O6P	-2	Cytosol
glyc3p	Glycerol 3-phosphate	Glycerophosphoric acid, Phosphatidyl glycerol, sn-Glycerol 3-phosphate, sn-Gro-1-P	C3H7O6P	-2	Mitochondria
glyclt	Glycolate	Glycolic acid, Hydroxyacetic acid	C2H3O3	-1	Cytosol
glyclt	Glycolate	Glycolic acid, Hydroxyacetic acid	C2H3O3	-1	Mitochondria
glyclt	Glycolate	Glycolic acid, Hydroxyacetic acid	C2H3O3	-1	Peroxisome
glyc-R	(R)-Glycerate	D-Glycerate, Glycerate, Glyceric acid	C3H5O4	-1	Cytosol
glyc-S	(S)-Glycerate	L-glycerate	C3H5O4	-1	Cytosol
glyc-S	(S)-Glycerate	L-glycerate	C3H5O4	-1	Extracellular
glygn1	glycogen, structure 1 (glycogenin-11[1,4-Glc])		C66H111O56X	0	Cytosol
glygn2	glycogen, structure 2 (glycogenin-1,6-{7[1,4-Glc], 4[1,4-Glc]})		C66H111O56X	0	Cytosol
glygn2	glycogen, structure 2 (glycogenin-1,6-{7[1,4-Glc], 4[1,4-Glc]})		C66H111O56X	0	Extracellular
glygn3	glycogen, structure 3 (glycogenin-7[1,4-Glc])		C42H71O36X	0	Cytosol
glygn4	glycogen, structure 4 (glycogenin-1,6-{2[1,4-Glc], [1,4-Glc]})		C18H31O16X	0	Extracellular
glygn5	glycogen, structure 5 (glycogenin-2[1,4-Glc])		C12H21O11X	0	Extracellular
gm1_hs	ganglioside GM1 (homo sapiens)	Cer-Glc-Gal-NeuAc-GlaNAc-Gal	C55H95N3O30FULLRCO	-1	Golgi Apparatus
gm1a_hs	GM1alpha (homo sapiens)	III6NeuAc-Gg4Cer	C55H95N3O30FULLRCO	-1	Golgi Apparatus
gm1b_hs	GM1b (homo sapiens)	(Gal)2 (GalNAc)1 (Glc)1 (Neu5Ac)1 (Cer)1	C55H95N3O30FULLRCO	-1	Golgi Apparatus
gm2_hs	ganglioside GM2 (homo sapiens)	Cer-Glc-Gal-NeuAc-GalNAc	C49H85N3O25FULLRCO	-1	Golgi Apparatus
gm2a_hs	GM2alpha (homo sapiens)	(Gal)1 (GalNAc)1 (Glc)1 (Neu5Ac)1 (Cer)1	C49H85N3O25FULLRCO	-1	Golgi Apparatus
gm3_hs	ganglioside GM3 (homo sapiens)	Cer-Glc-Gal-NeuAc	C41H72N2O20FULLRCO	-1	Golgi Apparatus
gmp	GMP	Guanosine 5'-monophosphate, Guanosine 5'-phosphate, Guanosine monophosphate, Guanylic acid	C10H12N5O8P	-2	Cytosol
gmp	GMP	Guanosine 5'-monophosphate, Guanosine 5'-phosphate, Guanosine monophosphate, Guanylic acid	C10H12N5O8P	-2	Extracellular
gmp	GMP	Guanosine 5'-monophosphate, Guanosine 5'-phosphate, Guanosine monophosphate, Guanylic acid	C10H12N5O8P	-2	Golgi Apparatus
gmp	GMP	Guanosine 5'-monophosphate, Guanosine 5'-phosphate, Guanosine monophosphate, Guanylic acid	C10H12N5O8P	-2	Lysosome

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
gmp	GMP	Guanosine 5'-monophosphate, Guanosine 5'-phosphate, Guanosine monophosphate, Guanylic acid	C10H12N5O8P	-2	Mitochondria
gmp	GMP	Guanosine 5'-monophosphate, Guanosine 5'-phosphate, Guanosine monophosphate, Guanylic acid	C10H12N5O8P	-2	Nucleus
gncore1	GlcNAc-alpha-1,4-Core 1		C22H37N2O15X	0	Golgi Apparatus
gncore2	GlcNAc-alpha-1,4-Core 2		C30H50N3O20X	0	Golgi Apparatus
gp1c_hs	GP1c (homo sapiens)	(Gal)2 (GalNAc)1 (Glc)1 (Neu5Ac)5 (Cer)1	C99H159N7O62FULLRCO	-5	Cytosol
gp1c_hs	GP1c (homo sapiens)	(Gal)2 (GalNAc)1 (Glc)1 (Neu5Ac)5 (Cer)1	C99H159N7O62FULLRCO	-5	Extracellular
gp1c_hs	GP1c (homo sapiens)	(Gal)2 (GalNAc)1 (Glc)1 (Neu5Ac)5 (Cer)1	C99H159N7O62FULLRCO	-5	Golgi Apparatus
gp1calpha_hs	GP1c alpha (homo sapiens)	(Gal)2 (GalNAc)1 (Glc)1 (Neu5Ac)5 (Cer)1	C99H159N7O62FULLRCO	-5	Cytosol
gp1calpha_hs	GP1c alpha (homo sapiens)	(Gal)2 (GalNAc)1 (Glc)1 (Neu5Ac)5 (Cer)1	C99H159N7O62FULLRCO	-5	Extracellular
gp1calpha_hs	GP1c alpha (homo sapiens)	(Gal)2 (GalNAc)1 (Glc)1 (Neu5Ac)5 (Cer)1	C99H159N7O62FULLRCO	-5	Golgi Apparatus
gpail_hs	D-glucosaminylphosphatidylinositol		C15H28NO13PFULLRCO2FULLR2CO2	0	Cytosol
gpi_hs	glycophosphatidylinositol (GPI) anchor precursor (3-(phosphoethanolaminyl-mannosyl)-glucosaminyl-acylphosphatidylinositol) (H8)	{[PE-Man-],[PE-]Man},{PE-}Man-GlcN-acylPI	C55H106N4O38P4FULLRCO2FULLR2CO2	0	Endoplasmic Reticulum
gpi_prot_hs	glycophosphatidylinositol (GPI)-anchored protein	{[(Prot-PE-Man),(PE)-Man],[PE]}-Man-GlcN-acylPI	C55H106N4O38P4FULLRCO2FULLR2CO2X	0	Endoplasmic Reticulum
gpi_sig	glycophosphatidylinositol (GPI) signal sequence (C-terminal peptide)		Y	0	Endoplasmic Reticulum
gq1b_hs	GQ1b (homo sapiens)	(Gal)2 (GalNAc)1 (Glc)1 (Neu5Ac)4 (Cer)1	C88H143N6O54FULLRCO	-4	Cytosol
gq1b_hs	GQ1b (homo sapiens)	(Gal)2 (GalNAc)1 (Glc)1 (Neu5Ac)4 (Cer)1	C88H143N6O54FULLRCO	-4	Extracellular
gq1b_hs	GQ1b (homo sapiens)	(Gal)2 (GalNAc)1 (Glc)1 (Neu5Ac)4 (Cer)1	C88H143N6O54FULLRCO	-4	Golgi Apparatus
gq1balpha_hs	GQ1balpha (homo sapiens)	(Gal)2 (GalNAc)1 (Glc)1 (Neu5Ac)4 (Cer)1	C88H143N6O54FULLRCO	-4	Cytosol
gq1balpha_hs	GQ1balpha (homo sapiens)	(Gal)2 (GalNAc)1 (Glc)1 (Neu5Ac)4 (Cer)1	C88H143N6O54FULLRCO	-4	Extracellular
gq1balpha_hs	GQ1balpha (homo sapiens)	(Gal)2 (GalNAc)1 (Glc)1 (Neu5Ac)4 (Cer)1	C88H143N6O54FULLRCO	-4	Golgi Apparatus
gq1c_hs	GQ1c (homo sapiens)	(Gal)2 (GalNAc)1 (Glc)1 (Neu5Ac)4 (Cer)1	C88H143N6O54FULLRCO	-4	Golgi Apparatus
grdp	Geranyl diphosphate	GPP	C10H17O7P2	-3	Cytosol
grdp	Geranyl diphosphate	GPP	C10H17O7P2	-3	Peroxisome
gsn	Guanosine	Guanine riboside, rG	C10H13N5O5	0	Cytosol
gsn	Guanosine	Guanine riboside, rG	C10H13N5O5	0	Extracellular
gsn	Guanosine	Guanine riboside, rG	C10H13N5O5	0	Lysosome
gsn	Guanosine	Guanine riboside, rG	C10H13N5O5	0	Mitochondria
gt1a_hs	GT1a (homo sapiens)	(Gal)2 (GalNAc)1 (Glc)1 (Neu5Ac)3 (Cer)1	C77H127N5O46FULLRCO	-3	Cytosol
gt1a_hs	GT1a (homo sapiens)	(Gal)2 (GalNAc)1 (Glc)1 (Neu5Ac)3 (Cer)1	C77H127N5O46FULLRCO	-3	Extracellular
gt1a_hs	GT1a (homo sapiens)	(Gal)2 (GalNAc)1 (Glc)1 (Neu5Ac)3 (Cer)1	C77H127N5O46FULLRCO	-3	Golgi Apparatus
gt1alpha_hs	GT1aalpha (homo sapiens)	(Gal)2 (GalNAc)1 (Glc)1 (Neu5Ac)3 (Cer)1	C77H127N5O46FULLRCO	-3	Golgi Apparatus
gt1b_hs	GT1b (homo sapiens)	(Gal)2 (GalNAc)1 (Glc)1 (Neu5Ac)3 (Cer)1	C77H127N5O46FULLRCO	-3	Golgi Apparatus
gt1c_hs	GT1c (homo sapiens)	(Gal)2 (GalNAc)1 (Glc)1 (Neu5Ac)3 (Cer)1	C77H127N5O46FULLRCO	-3	Golgi Apparatus
gt2_hs	GT2 (homo sapiens)	(Gal)1 (GalNAc)1 (Glc)1 (Neu5Ac)3 (Cer)1	C71H117N5O41FULLRCO	-3	Golgi Apparatus
gt3_hs	GT3 (homo sapiens)	(Gal)1 (Glc)1 (Neu5Ac)3 (Cer)1	C63H104N4O36FULLRCO	-3	Cytosol
gt3_hs	GT3 (homo sapiens)	(Gal)1 (Glc)1 (Neu5Ac)3 (Cer)1	C63H104N4O36FULLRCO	-3	Golgi Apparatus
gthox	Oxidized glutathione	Glutathione disulfide, L-Glutathione oxidized	C20H30N6O12S2	-2	Cytosol
gthox	Oxidized glutathione	Glutathione disulfide, L-Glutathione oxidized	C20H30N6O12S2	-2	Extracellular
gthox	Oxidized glutathione	Glutathione disulfide, L-Glutathione oxidized	C20H30N6O12S2	-2	Mitochondria
gthrd	Reduced glutathione	5-L-Glutamyl-L-cysteinylglycine, Glutathione, N-(gamma-L-Glutamyl-L-cysteinyl)glycine, gamma-L-Glutamyl-L-cysteinyl-glycine	C10H16N3O6S	-1	Cytosol
gthrd	Reduced glutathione	5-L-Glutamyl-L-cysteinylglycine, Glutathione, N-(gamma-L-Glutamyl-L-cysteinyl)glycine, gamma-L-Glutamyl-L-cysteinyl-glycine	C10H16N3O6S	-1	Extracellular
gthrd	Reduced glutathione	5-L-Glutamyl-L-cysteinylglycine, Glutathione, N-(gamma-L-Glutamyl-L-cysteinyl)glycine, gamma-L-Glutamyl-L-cysteinyl-glycine	C10H16N3O6S	-1	Mitochondria
gthrd	Reduced glutathione	5-L-Glutamyl-L-cysteinylglycine, Glutathione, N-(gamma-L-Glutamyl-L-cysteinyl)glycine, gamma-L-Glutamyl-L-cysteinyl-glycine	C10H16N3O6S	-1	Endoplasmic Reticulum
gtp	GTP	Guanosine 5'-triphosphate	C10H12N5O14P3	-4	Cytosol
gtp	GTP	Guanosine 5'-triphosphate	C10H12N5O14P3	-4	Extracellular
gtp	GTP	Guanosine 5'-triphosphate	C10H12N5O14P3	-4	Mitochondria
gtp	GTP	Guanosine 5'-triphosphate	C10H12N5O14P3	-4	Nucleus
gua	Guanine	2-Amino-6-hydroxypurine, 2-Aminohypoxanthine, G	C5H5N5O	0	Cytosol

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
gua	Guanine	2-Amino-6-hydroxypurine, 2-Aminohypoxanthine, G	C5H5N5O	0	Extracellular
gudac	Guanidinoacetate	Glycocyamine, Guanidinoacetic acid, Guanidoacetic acid, N-Amidinoglycine	C3H7N3O2	0	Cytosol
gullac	L-Gulono-1,4-lactone	L-Gulonic acid gamma-lactone, L-Gulono-gamma-lactone, L-Gulonolactone, gamma-Gulonolactone	C6H10O6	0	Cytosol
gullac	L-Gulono-1,4-lactone	L-Gulonic acid gamma-lactone, L-Gulono-gamma-lactone, L-Gulonolactone, gamma-Gulonolactone	C6H10O6	0	Endoplasmic Reticulum
guln	L-Gulonate	Gulonate, Gulonic acid, L-Gulonic acid	C6H11O7	-1	Cytosol
guln	L-Gulonate	Gulonate, Gulonic acid, L-Gulonic acid	C6H11O7	-1	Endoplasmic Reticulum
h	H+	Hydrogen Ion, Proton	H	1	Cytosol
h	H+	Hydrogen Ion, Proton	H	1	Extracellular
h	H+	Hydrogen Ion, Proton	H	1	Golgi Apparatus
h	H+	Hydrogen Ion, Proton	H	1	Lysosome
h	H+	Hydrogen Ion, Proton	H	1	Mitochondria
h	H+	Hydrogen Ion, Proton	H	1	Nucleus
h	H+	Hydrogen Ion, Proton	H	1	Endoplasmic Reticulum
h	H+	Hydrogen Ion, Proton	H	1	Peroxisome
h2co3	carbonic acid		H2CO3	0	Cytosol
h2co3	carbonic acid		H2CO3	0	Mitochondria
h2o	H2O	Dihydrogen oxide, Water	H2O	0	Cytosol
h2o	H2O	Dihydrogen oxide, Water	H2O	0	Extracellular
h2o	H2O	Dihydrogen oxide, Water	H2O	0	Golgi Apparatus
h2o	H2O	Dihydrogen oxide, Water	H2O	0	Lysosome
h2o	H2O	Dihydrogen oxide, Water	H2O	0	Mitochondria
h2o	H2O	Dihydrogen oxide, Water	H2O	0	Nucleus
h2o	H2O	Dihydrogen oxide, Water	H2O	0	Endoplasmic Reticulum
h2o	H2O	Dihydrogen oxide, Water	H2O	0	Peroxisome
h2o2	Hydrogen peroxide	H2O2, hydrogen dioxide, peroxide	H2O2	0	Cytosol
h2o2	Hydrogen peroxide	H2O2, hydrogen dioxide, peroxide	H2O2	0	Extracellular
h2o2	Hydrogen peroxide	H2O2, hydrogen dioxide, peroxide	H2O2	0	Lysosome
h2o2	Hydrogen peroxide	H2O2, hydrogen dioxide, peroxide	H2O2	0	Mitochondria
h2o2	Hydrogen peroxide	H2O2, hydrogen dioxide, peroxide	H2O2	0	Nucleus
h2o2	Hydrogen peroxide	H2O2, hydrogen dioxide, peroxide	H2O2	0	Peroxisome
ha	hyaluronan	Hyaluronate, Hyaluronic acid	C28H40N2O22	-2	Extracellular
ha	hyaluronan	Hyaluronate, Hyaluronic acid	C28H40N2O22	-2	Lysosome
ha_deg1	hyaluronan degradation product 1		C22H33N2O16	-1	Lysosome
ha_pre1	hyaluronan biosynthesis, precursor 1		C14H20NO11	-1	Extracellular
ha_pre1	hyaluronan biosynthesis, precursor 1		C14H20NO11	-1	Lysosome
hco3	Bicarbonate	Acid carbonate, HCO3-, Hydrogencarbonate	CHO3	-1	Cytosol
hco3	Bicarbonate	Acid carbonate, HCO3-, Hydrogencarbonate	CHO3	-1	Extracellular
hco3	Bicarbonate	Acid carbonate, HCO3-, Hydrogencarbonate	CHO3	-1	Mitochondria
hcoumarin	hydroxy coumarin	7 hydroxy coumarin	C9H6O3	0	Cytosol
hcoumarin	hydroxy coumarin	7 hydroxy coumarin	C9H6O3	0	Extracellular
hcys-L	L-Homocysteine	L-2-Amino-4-mercaptobutyric acid, L-Homocysteine	C4H9NO2S	0	Cytosol
hdca	Hexadecanoate (n-C16:0)	Cetylic acid, Hexadecanoic acid, Hexadecylic acid, Palmitic acid, palmitate	C16H31O2	-1	Cytosol
hdca	Hexadecanoate (n-C16:0)	Cetylic acid, Hexadecanoic acid, Hexadecylic acid, Palmitic acid, palmitate	C16H31O2	-1	Extracellular
hdca	Hexadecanoate (n-C16:0)	Cetylic acid, Hexadecanoic acid, Hexadecylic acid, Palmitic acid, palmitate	C16H31O2	-1	Endoplasmic Reticulum
hdca	Hexadecanoate (n-C16:0)	Cetylic acid, Hexadecanoic acid, Hexadecylic acid, Palmitic acid, palmitate	C16H31O2	-1	Peroxisome
hdcea	Hexadecenoate (n-C16:1)	(9Z)-Hexadecenoic acid, Palmitoleic acid, cis-9-Hexadecenoic acid, hexadecenoic acid	C16H29O2	-1	Cytosol
hdcea	Hexadecenoate (n-C16:1)	(9Z)-Hexadecenoic acid, Palmitoleic acid, cis-9-Hexadecenoic acid, hexadecenoic acid	C16H29O2	-1	Extracellular
hdcecrn	Hexadecenoyl carnitine		C23H43NO4	0	Cytosol
hdcecrn	Hexadecenoyl carnitine		C23H43NO4	0	Mitochondria
hdcoa	Hexadecenoyl-CoA (n-C16:1CoA)	(2E)-Hexadecenoyl-CoA, palmitoleic coenzyme A, trans-2-Hexadecenoyl-CoA, trans-Hexadec-2-enoyl-CoA	C37H60N7O17P3S	-4	Cytosol
hdcoa	Hexadecenoyl-CoA (n-C16:1CoA)	(2E)-Hexadecenoyl-CoA, palmitoleic coenzyme A, trans-2-Hexadecenoyl-CoA, trans-Hexadec-2-enoyl-CoA	C37H60N7O17P3S	-4	Mitochondria
hdd2coa	trans-Hexadec-2-enoyl-CoA		C37H60N7O17P3S	-4	Cytosol
hdd2coa	trans-Hexadec-2-enoyl-CoA		C37H60N7O17P3S	-4	Mitochondria
hdd2coa	trans-Hexadec-2-enoyl-CoA		C37H60N7O17P3S	-4	Peroxisome
hdd2crn	trans-Hexadec-2-enoyl carnitine		C23H43NO4	0	Cytosol
hdd2crn	trans-Hexadec-2-enoyl carnitine		C23H43NO4	0	Mitochondria
hdeACP	cis-hexadec-9-enoyl-[acyl-carrier protein] (n-C16:1)	Hexadecenoyl-ACP (n-C16:1ACP), cis-palmitol-9-eoyl-[acyl-carrier protein] (n-C16:1)	C27H49N2O8PRS	-1	Cytosol
hestratriol	4,17 dihydroxy estradiol	4 hydroxy 17 beta estradiol	C18H24O3	0	Cytosol
hestratriol	4,17 dihydroxy estradiol	4 hydroxy 17 beta estradiol	C18H24O3	0	Extracellular
hestratriol	4,17 dihydroxy estradiol	4 hydroxy 17 beta estradiol	C18H24O3	0	Endoplasmic Reticulum
hexc	hexacosanoate (n-C26:0)	cerotic acid, hexacosanoic acid	C26H51O2	-1	Cytosol
hexc	hexacosanoate (n-C26:0)	cerotic acid, hexacosanoic acid	C26H51O2	-1	Extracellular
hexccoa	Hexacosanoyl-CoA (n-C26:0CoA)	cerotic acid coenzyme a, cerotoyl-CoA	C47H82N7O17P3S	-4	Cytosol
hexccoa	Hexacosanoyl-CoA (n-C26:0CoA)	cerotic acid coenzyme a, cerotoyl-CoA	C47H82N7O17P3S	-4	Mitochondria
hexccoa	Hexacosanoyl-CoA (n-C26:0CoA)	cerotic acid coenzyme a, cerotoyl-CoA	C47H82N7O17P3S	-4	Peroxisome

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
hexccrn	hexacosanoyl carnitine		C33H65NO4	0	Cytosol
hexccrn	hexacosanoyl carnitine		C33H65NO4	0	Mitochondria
hgentis	Homogentisate	2,5-Dihydroxyphenylacetate, 2,5-Dihydroxyphenylacetic acid, Homogentisic acid	C8H7O4	-1	Cytosol
his-L	L-Histidine	(S)-alpha-Amino-1H-imidazole-4-propionic acid, Glyoxaline-5-alanine, His	C6H9N3O2	0	Cytosol
his-L	L-Histidine	(S)-alpha-Amino-1H-imidazole-4-propionic acid, Glyoxaline-5-alanine, His	C6H9N3O2	0	Extracellular
hista	Histamine		C5H10N3	1	Cytosol
hista	Histamine		C5H10N3	1	Extracellular
hLkynr	3-Hydroxy-L-kynurenine		C10H12N2O4	0	Cytosol
hmbil	Hydroxymethylbilane		C40H38N4O17	-8	Cytosol
hmgcoa	Hydroxymethylglutaryl-CoA	(S)-3-Hydroxy-3-methylglutaryl-CoA, 3-Hydroxy-3-methylglutaryl-CoA, HMG-CoA, Hydroxymethylglutaroyl coenzyme A	C27H39N7O20P3S	-5	Cytosol
hmgcoa	Hydroxymethylglutaryl-CoA	(S)-3-Hydroxy-3-methylglutaryl-CoA, 3-Hydroxy-3-methylglutaryl-CoA, HMG-CoA, Hydroxymethylglutaroyl coenzyme A	C27H39N7O20P3S	-5	Mitochondria
hmgcoa	Hydroxymethylglutaryl-CoA	(S)-3-Hydroxy-3-methylglutaryl-CoA, 3-Hydroxy-3-methylglutaryl-CoA, HMG-CoA, Hydroxymethylglutaroyl coenzyme A	C27H39N7O20P3S	-5	Endoplasmic Reticulum
hmgcoa	Hydroxymethylglutaryl-CoA	(S)-3-Hydroxy-3-methylglutaryl-CoA, 3-Hydroxy-3-methylglutaryl-CoA, HMG-CoA, Hydroxymethylglutaroyl coenzyme A	C27H39N7O20P3S	-5	Peroxisome
hnifedipine	hydroxy nifedipine		C17H18N2O7	0	Cytosol
hom-L	L-Homoserine	2-Amino-4-hydroxybutyric acid	C4H9NO3	0	Cytosol
hom-L	L-Homoserine	2-Amino-4-hydroxybutyric acid	C4H9NO3	0	Extracellular
homoval	Homovanillate	Homovanillic acid	C9H9O4	-1	Cytosol
hpdca	heptadecanoate	Heptadecanoic acid;, Margaric acid, n-Heptadecanoic Acid;	C17H33O2	-1	Cytosol
hpdca	heptadecanoate	Heptadecanoic acid;, Margaric acid, n-Heptadecanoic Acid;	C17H33O2	-1	Extracellular
hpdcacoa	heptadecanoyl coa	Heptadecanoic acid coa, Margaric acid coa, n-Heptadecanoic Acid coenzyme a	C38H64N7O17P3S	-4	Cytosol
hpdcacoa	heptadecanoyl coa	Heptadecanoic acid coa, Margaric acid coa, n-Heptadecanoic Acid coenzyme a	C38H64N7O17P3S	-4	Mitochondria
hpdcacrn	heptadecanoyl carnitine	heptadecanoate carnitine, heptadecanoyl acid carnitine	C24H47NO4	0	Cytosol
hpdcacrn	heptadecanoyl carnitine	heptadecanoate carnitine, heptadecanoyl acid carnitine	C24H47NO4	0	Mitochondria
hpyr	Hydroxypyruvate	3-Hydroxypyruvate, 3-Hydroxypyruvic acid, Hydroxypyruvic acid	C3H3O4	-1	Cytosol
hpyr	Hydroxypyruvate	3-Hydroxypyruvate, 3-Hydroxypyruvic acid, Hydroxypyruvic acid	C3H3O4	-1	Mitochondria
hpyr	Hydroxypyruvate	3-Hydroxypyruvate, 3-Hydroxypyruvic acid, Hydroxypyruvic acid	C3H3O4	-1	Peroxisome
hretn	4 hydroxy retinoic acid		C20H27O3	-1	Cytosol
hretn	4 hydroxy retinoic acid		C20H27O3	-1	Nucleus
hs	heparan sulfate, free chain		C79H114N5O102S12	-13	Lysosome
hs_deg1	heparan sulfate, degradation product 1		C79H115N5O99S11	-12	Lysosome
hs_deg10	heparan sulfate, degradation product 10		C55H80N3O70S8	-9	Lysosome
hs_deg11	heparan sulfate, degradation product 11		C55H81N3O67S7	-8	Lysosome
hs_deg12	heparan sulfate, degradation product 12		C55H82N3O64S6	-7	Lysosome
hs_deg13	heparan sulfate, degradation product 13		C55H83N3O61S5	-6	Lysosome
hs_deg14	heparan sulfate, degradation product 14		C57H84N3O62S5	-7	Lysosome
hs_deg15	heparan sulfate, degradation product 15		C49H71N2O57S5	-7	Lysosome
hs_deg16	heparan sulfate, degradation product 16		C49H72N2O54S4	-6	Lysosome
hs_deg17	heparan sulfate, degradation product 17		C43H65N2O48S4	-5	Lysosome
hs_deg18	heparan sulfate, degradation product 18		C43H66N2O45S3	-4	Lysosome
hs_deg19	heparan sulfate, degradation product 19		C43H67N2O42S2	-3	Lysosome
hs_deg2	heparan sulfate, degradation product 2		C79H116N5O96S10	-11	Lysosome
hs_deg20	heparan sulfate, degradation product 20		C45H68N2O43S2	-4	Lysosome
hs_deg21	heparan sulfate, degradation product 21		C37H55NO38S2	-4	Lysosome
hs_deg22	heparan sulfate, degradation product 22		C37H56NO35S	-3	Lysosome
hs_deg23	heparan sulfate, degradation product 23		C31H49NO29S	-2	Lysosome
hs_deg24	heparan sulfate, degradation product 24	GlcNAc-GlcA-(Gal)2-Xyl	C31H50NO26	-1	Lysosome
hs_deg25	heparan sulfate, degradation product 25		C23H37O21	-1	Lysosome
hs_deg3	heparan sulfate, degradation product 3		C81H117N5O97S10	-12	Lysosome
hs_deg4	heparan sulfate, degradation product 4		C73H104N4O92S10	-12	Lysosome
hs_deg5	heparan sulfate, degradation product 5		C67H97N4O86S10	-11	Lysosome
hs_deg6	heparan sulfate, degradation product 6		C67H98N4O83S9	-10	Lysosome
hs_deg7	heparan sulfate, degradation product 7		C67H99N4O80S8	-9	Lysosome
hs_deg8	heparan sulfate, degradation product 8		C69H100N4O81S8	-10	Lysosome
hs_deg9	heparan sulfate, degradation product 9		C61H87N3O76S8	-10	Lysosome
hs_pre1	heparan sulfate, precursor 1	GlcNAc-GlcA-Gal-Gal-Xyl-L-Ser (protein)	C31H49NO25X	-1	Golgi Apparatus
hs_pre10	heparan sulfate, precursor 10	(GlcN2S-GlcA)4-GlcNAc-GlcA-Gal-Gal-Xyl-L-Ser (protein)	C79H121N5O77S4X	-5	Golgi Apparatus
hs_pre11	heparan sulfate, precursor 11	(GlcN2S-IdoA-GlcN2S-GlcA)2-GlcNAc-GlcA-Gal-Gal-Xyl-L-Ser (protein)	C79H121N5O77S4X	-5	Golgi Apparatus
hs_pre12	heparan sulfate, precursor 12	GlcN2S-IdoA-GlcN2S-GlcA2S-GlcN2S-IdoA2S-GlcN2S-GlcA-GlcNAc-GlcA-Gal-Gal-Xyl-L-Ser (protein)	C79H119N5O83S6X	-7	Golgi Apparatus

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
hs_pre13	heparan sulfate, precursor 13	GlcN2S-IdoA-GlcN2,6diS-GlcA2S-GlcN2,6diS-IdoA2S-GlcN2,6diS-GlcA-GlcNAc-GlcA-Gal-Gal-Xyl-L-Ser (protein)	C79H116N5O92S9X	-10	Golgi Apparatus
hs_pre14	heparan sulfate, precursor 14		C79H115N5O95S10X	-11	Golgi Apparatus
hs_pre15	heparan sulfate, precursor 15		C79H114N5O98S11X	-12	Golgi Apparatus
hs_pre2	heparan sulfate, precursor 2	GlcA-GlcNAc-GlcA-Gal-Gal-Xyl-L-Ser (protein)	C37H56NO31X	-2	Golgi Apparatus
hs_pre3	heparan sulfate, precursor 3	GlcNAc-GlcA-GlcNAc-GlcA-Gal-Gal-Xyl-L-Ser (protein)	C45H69N2O36X	-2	Golgi Apparatus
hs_pre4	heparan sulfate, precursor 4	GlcA-GlcNAc-GlcA-GlcNAc-GlcA-Gal-Gal-Xyl-L-Ser (protein)	C51H76N2O42X	-3	Golgi Apparatus
hs_pre5	heparan sulfate, precursor 5	(GlcNAc-GlcA)2-GlcNAc-GlcA-Gal-Gal-Xyl-L-Ser (protein)	C59H89N3O47X	-3	Golgi Apparatus
hs_pre6	heparan sulfate, precursor 6	GlcA-(GlcNAc-GlcA)2-GlcNAc-GlcA-Gal-Gal-Xyl-L-Ser (protein)	C65H96N3O53X	-4	Golgi Apparatus
hs_pre7	heparan sulfate, precursor 7	(GlcNAc-GlcA)3-GlcNAc-GlcA-Gal-Gal-Xyl-L-Ser (protein)	C73H109N4O58X	-4	Golgi Apparatus
hs_pre8	heparan sulfate, precursor 8	GlcA-(GlcNAc-GlcA)3-GlcNAc-GlcA-Gal-Gal-Xyl-L-Ser (protein)	C79H116N4O64X	-5	Golgi Apparatus
hs_pre9	heparan sulfate, precursor 9	(GlcNAc-GlcA)4-GlcNAc-GlcA-Gal-Gal-Xyl-L-Ser (protein)	C87H129N5O69X	-5	Golgi Apparatus
hspg	heparan sulfate proteoglycan	GlcN2S-IdoA-GlcN2,6diS-GlcA2S-GlcN2,3,6triS-IdoA2S-GlcN2,6diS-GlcA-GlcNAc-GlcA-Gal-Gal-Xyl-L-Ser (protein), Heparan sulfate;, Heparin monosulfate, Heparin sulfate;, Heparitin sulfate;	C79H113N5O101S12X	-13	Extracellular
hspg	heparan sulfate proteoglycan	GlcN2S-IdoA-GlcN2,6diS-GlcA2S-GlcN2,3,6triS-IdoA2S-GlcN2,6diS-GlcA-GlcNAc-GlcA-Gal-Gal-Xyl-L-Ser (protein), Heparan sulfate;, Heparin monosulfate, Heparin sulfate;, Heparitin sulfate;	C79H113N5O101S12X	-13	Golgi Apparatus
hspg	heparan sulfate proteoglycan	GlcN2S-IdoA-GlcN2,6diS-GlcA2S-GlcN2,3,6triS-IdoA2S-GlcN2,6diS-GlcA-GlcNAc-GlcA-Gal-Gal-Xyl-L-Ser (protein), Heparan sulfate;, Heparin monosulfate, Heparin sulfate;, Heparitin sulfate;	C79H113N5O101S12X	-13	Lysosome
htaxol	hydroxylated taxol	6 alpha hydroxy paclitaxel, 6 alpha hydroxy taxol	C47H31NO15	0	Cytosol
htaxol	hydroxylated taxol	6 alpha hydroxy paclitaxel, 6 alpha hydroxy taxol	C47H31NO15	0	Extracellular
hxan	Hypoxanthine	1,7-Dihydro-6H-purin-6-one, 6-Hydroxypurine, Purine-6-ol	C5H4N4O	0	Cytosol
hxan	Hypoxanthine	1,7-Dihydro-6H-purin-6-one, 6-Hydroxypurine, Purine-6-ol	C5H4N4O	0	Extracellular
hxan	Hypoxanthine	1,7-Dihydro-6H-purin-6-one, 6-Hydroxypurine, Purine-6-ol	C5H4N4O	0	Lysosome
hxan	Hypoxanthine	1,7-Dihydro-6H-purin-6-one, 6-Hydroxypurine, Purine-6-ol	C5H4N4O	0	Peroxisome
hxdcal	Hexadecanal	16-Hexadecanal, Palmitaldehyde	C16H32O	0	Endoplasmic Reticulum
hyptaur	Hypotaurine	2-Aminoethanesulfinic acid	C2H6NO2S	-1	Cytosol
i	Iodide	I-	I	-1	Cytosol
i	Iodide	I-	I	-1	Extracellular
ibcoa	Isobutyryl-CoA	2-Methylpropanoyl-CoA, 2-Methylpropionyl-CoA	C25H38N7O17P3S	-4	Mitochondria
icit	Isocitrate	1-Hydroxypropane-1, 1-Hydroxytricarballylic acid, 2, 3-tricarboxylic acid, Isocitric acid	C6H5O7	-3	Cytosol
icit	Isocitrate	1-Hydroxypropane-1, 1-Hydroxytricarballylic acid, 2, 3-tricarboxylic acid, Isocitric acid	C6H5O7	-3	Mitochondria
icit	Isocitrate	1-Hydroxypropane-1, 1-Hydroxytricarballylic acid, 2, 3-tricarboxylic acid, Isocitric acid	C6H5O7	-3	Peroxisome
id3acald	Indole-3-acetaldehyde	2-(Indol-3-yl)acetaldehyde, Indoleacetaldehyde	C10H9NO	0	Cytosol
id3acald	Indole-3-acetaldehyde	2-(Indol-3-yl)acetaldehyde, Indoleacetaldehyde	C10H9NO	0	Mitochondria
idour	L-Iduronate	D-Ido-hexuronic acid, IdoA, L-Iduronic acid	C6H9O7	-1	Cytosol
idour	L-Iduronate	D-Ido-hexuronic acid, IdoA, L-Iduronic acid	C6H9O7	-1	Lysosome
idp	IDP	5'-inosinate diphosphate, Inosine 5'-diphosphate, Inosine diphosphate	C10H11N4O11P2	-3	Cytosol
idp	IDP	5'-inosinate diphosphate, Inosine 5'-diphosphate, Inosine diphosphate	C10H11N4O11P2	-3	Extracellular
idp	IDP	5'-inosinate diphosphate, Inosine 5'-diphosphate, Inosine diphosphate	C10H11N4O11P2	-3	Mitochondria
idp	IDP	5'-inosinate diphosphate, Inosine 5'-diphosphate, Inosine diphosphate	C10H11N4O11P2	-3	Nucleus
ile-L	L-Isoleucine	2-Amino-3-methylvaleric acid, Ile	C6H13NO2	0	Cytosol
ile-L	L-Isoleucine	2-Amino-3-methylvaleric acid, Ile	C6H13NO2	0	Extracellular
ile-L	L-Isoleucine	2-Amino-3-methylvaleric acid, Ile	C6H13NO2	0	Mitochondria
im4ac	Imidazole-4-acetate	4-Imidazoleacetate, Imidazoleacetic acid	C5H5N2O2	-1	Cytosol
im4ac	Imidazole-4-acetate	4-Imidazoleacetate, Imidazoleacetic acid	C5H5N2O2	-1	Mitochondria
im4act	Imidazole-4-acetaldehyde	Imidazole acetaldehyde	C5H6N2O	0	Cytosol
im4act	Imidazole-4-acetaldehyde	Imidazole acetaldehyde	C5H6N2O	0	Mitochondria
imp	IMP	5'-Inosinate, 5'-Inosine monophosphate, 5'-Inosinic acid, Inosine 5'-monophosphate, Inosine 5'-phosphate, Inosine monophosphate, Inosinic acid	C10H11N4O8P	-2	Cytosol

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
imp	IMP	5'-Inosinate, 5'-Inosine monophosphate, 5'-Inosinic acid, Inosine 5'-monophosphate, Inosine 5'-phosphate, Inosine monophosphate, Inosinic acid	C10H11N4O8P	-2	Extracellular
imp	IMP	5'-Inosinate, 5'-Inosine monophosphate, 5'-Inosinic acid, Inosine 5'-monophosphate, Inosine 5'-phosphate, Inosine monophosphate, Inosinic acid	C10H11N4O8P	-2	Mitochondria
ind3ac	Indole-3-acetate	3-indoleacetate, Indole-3-acetic acid, Indoleacetate, Indoleacetic acid	C10H8NO2	-1	Cytosol
ind3ac	Indole-3-acetate	3-indoleacetate, Indole-3-acetic acid, Indoleacetate, Indoleacetic acid	C10H8NO2	-1	Mitochondria
inost	myo-Inositol	1D-myo-Inositol, 1L-myo-Inositol, Bios I, Cyclohexitol, D-myo-Inositol, Dambose, Inositol, L-myo-Inositol, Meat sugar, meso-Inositol	C6H12O6	0	Cytosol
inost	myo-Inositol	1D-myo-Inositol, 1L-myo-Inositol, Bios I, Cyclohexitol, D-myo-Inositol, Dambose, Inositol, L-myo-Inositol, Meat sugar, meso-Inositol	C6H12O6	0	Extracellular
ins	Inosine	Hypoxanthine ribonucleoside	C10H12N4O5	0	Cytosol
ins	Inosine	Hypoxanthine ribonucleoside	C10H12N4O5	0	Extracellular
ins	Inosine	Hypoxanthine ribonucleoside	C10H12N4O5	0	Lysosome
ins	Inosine	Hypoxanthine ribonucleoside	C10H12N4O5	0	Mitochondria
iodine	Iodine	I2	I2	0	Cytosol
ipdp	Isopentenyl diphosphate	Isopentenyl pyrophosphate, Isoprenyl pyrophosphate, delta3-Isopentenyl diphosphate, delta3-methyl-3-butenyl diphosphate	C5H9O7P2	-3	Cytosol
ipdp	Isopentenyl diphosphate	Isopentenyl pyrophosphate, Isoprenyl pyrophosphate, delta3-Isopentenyl diphosphate, delta3-methyl-3-butenyl diphosphate	C5H9O7P2	-3	Peroxisome
itaccoa	Itaconyl-CoA		C26H35N7O19P3S	-5	Mitochondria
itacon	Itaconate	Itaconic acid, Methylenesuccinic acid	C5H4O4	-2	Mitochondria
itp	ITP	Inosine 5'-triphosphate, Inosine triphosphate, Inosine tripolyphosphate	C10H11N4O14P3	-4	Cytosol
itp	ITP	Inosine 5'-triphosphate, Inosine triphosphate, Inosine tripolyphosphate	C10H11N4O14P3	-4	Mitochondria
itp	ITP	Inosine 5'-triphosphate, Inosine triphosphate, Inosine tripolyphosphate	C10H11N4O14P3	-4	Nucleus
ivcoa	Isovaleryl-CoA	3-Methylbutanoyl-CoA	C26H40N7O17P3S	-4	Mitochondria
k	potassium	K+, Potassium	K	1	Cytosol
k	potassium	K+, Potassium	K	1	Extracellular
k	potassium	K+, Potassium	K	1	Golgi Apparatus
kdn	2-keto-3-deoxy-D-glycero-D-galactononic acid	3-deoxy-D-glycero-D-galacto-nonulsonic acid, a-D-KDN, deaminoneuraminic acid	C9H15O9	-1	Cytosol
kdnp	2-keto-3-deoxy-D-glycero-D-galactononic acid 9-phosphate		C9H14O12P	-3	Cytosol
ksi	keratan sulfate I		C247H393N17O213S12X	-13	Extracellular
ksi	keratan sulfate I		C247H393N17O213S12X	-13	Golgi Apparatus
ksi	keratan sulfate I		C247H393N17O213S12X	-13	Lysosome
ksi_deg1	keratan sulfate I, degradation product 1		C241H383N17O209S12X	-13	Extracellular
ksi_deg1	keratan sulfate I, degradation product 1		C241H383N17O209S12X	-13	Lysosome
ksi_deg10	keratan sulfate I, degradation product 10		C188H302N13O163S9	-9	Lysosome
ksi_deg11	keratan sulfate I, degradation product 11		C180H289N12O158S9	-9	Lysosome
ksi_deg12	keratan sulfate I, degradation product 12		C174H279N12O153S9	-9	Lysosome
ksi_deg13	keratan sulfate I, degradation product 13		C174H280N12O150S8	-8	Lysosome
ksi_deg14	keratan sulfate I, degradation product 14		C166H267N11O145S8	-8	Lysosome
ksi_deg15	keratan sulfate I, degradation product 15		C160H257N11O140S8	-8	Lysosome
ksi_deg16	keratan sulfate I, degradation product 16		C160H258N11O137S7	-7	Lysosome
ksi_deg17	keratan sulfate I, degradation product 17		C152H245N10O132S7	-7	Lysosome
ksi_deg18	keratan sulfate I, degradation product 18		C146H235N10O127S7	-7	Lysosome
ksi_deg19	keratan sulfate I, degradation product 19		C146H236N10O124S6	-6	Lysosome
ksi_deg2	keratan sulfate I, degradation product 2		C241H384N17O210S12	-13	Lysosome
ksi_deg20	keratan sulfate I, degradation product 20		C138H223N9O119S6	-6	Lysosome
ksi_deg21	keratan sulfate I, degradation product 21		C132H213N9O114S6	-6	Lysosome
ksi_deg22	keratan sulfate I, degradation product 22		C132H214N9O111S5	-5	Lysosome
ksi_deg23	keratan sulfate I, degradation product 23		C124H201N8O106S5	-5	Lysosome
ksi_deg24	keratan sulfate I, degradation product 24		C118H191N8O101S5	-5	Lysosome
ksi_deg25	keratan sulfate I, degradation product 25		C118H192N8O98S4	-4	Lysosome
ksi_deg26	keratan sulfate I, degradation product 26		C110H179N7O93S4	-4	Lysosome
ksi_deg27	keratan sulfate I, degradation product 27		C104H169N7O88S4	-4	Lysosome
ksi_deg28	keratan sulfate I, degradation product 28		C104H170N7O85S3	-3	Lysosome
ksi_deg29	keratan sulfate I, degradation product 29		C96H157N6O80S3	-3	Lysosome
ksi_deg3	keratan sulfate I, degradation product 3		C233H371N16O205S12	-13	Lysosome
ksi_deg30	keratan sulfate I, degradation product 30		C90H147N6O75S3	-3	Lysosome
ksi_deg31	keratan sulfate I, degradation product 31		C90H148N6O72S2	-2	Lysosome
ksi_deg32	keratan sulfate I, degradation product 32		C82H135N5O67S2	-2	Lysosome
ksi_deg33	keratan sulfate I, degradation product 33		C76H125N5O62S2	-2	Lysosome
ksi_deg34	keratan sulfate I, degradation product 34		C76H126N5O59S1	-1	Lysosome
ksi_deg35	keratan sulfate I, degradation product 35		C68H113N4O54S1	-1	Lysosome
ksi_deg36	keratan sulfate I, degradation product 36		C62H103N4O49S1	-1	Lysosome
ksi_deg37	keratan sulfate I, degradation product 37		C62H104N4O46	0	Lysosome
ksi_deg38	keratan sulfate I, degradation product 38		C54H91N3O41	0	Lysosome
ksi_deg39	keratan sulfate I, degradation product 39		C48H81N3O36	0	Lysosome
ksi_deg4	keratan sulfate I, degradation product 4		C222H355N15O197S12	-12	Lysosome
ksi_deg40	keratan sulfate I, degradation product 40		C40H68N2O31	0	Lysosome
ksi_deg41	keratan sulfate I, degradation product 41		C34H58N2O26	0	Lysosome

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
ksi_deg5	keratan sulfate I, degradation product 5		C222H356N15O194S11	-11	Lysosome
ksi_deg6	keratan sulfate I, degradation product 6		C210H336N15O184S11	-11	Lysosome
ksi_deg7	keratan sulfate I, degradation product 7		C210H337N15O181S10	-10	Lysosome
ksi_deg8	keratan sulfate I, degradation product 8		C194H311N13O171S10	-10	Lysosome
ksi_deg9	keratan sulfate I, degradation product 9		C188H301N13O166S10	-10	Lysosome
ksi_pre1	keratan sulfate I biosynthesis, precursor 1		C79H129N5O57X	-1	Golgi Apparatus
ksi_pre10	keratan sulfate I biosynthesis, precursor 10		C129H209N9O98S2X	-3	Golgi Apparatus
ksi_pre11	keratan sulfate I biosynthesis, precursor 11		C129H208N9O101S3X	-4	Golgi Apparatus
ksi_pre12	keratan sulfate I biosynthesis, precursor 12		C135H218N9O106S3X	-4	Golgi Apparatus
ksi_pre13	keratan sulfate I biosynthesis, precursor 13		C143H231N10O111S3X	-4	Golgi Apparatus
ksi_pre14	keratan sulfate I biosynthesis, precursor 14		C143H230N10O114S4X	-5	Golgi Apparatus
ksi_pre15	keratan sulfate I biosynthesis, precursor 15		C149H240N10O119S4X	-5	Golgi Apparatus
ksi_pre16	keratan sulfate I biosynthesis, precursor 16		C157H253N11O124S4X	-5	Golgi Apparatus
ksi_pre17	keratan sulfate I biosynthesis, precursor 17		C157H252N11O127S5X	-6	Golgi Apparatus
ksi_pre18	keratan sulfate I biosynthesis, precursor 18		C163H262N11O132S5X	-6	Golgi Apparatus
ksi_pre19	keratan sulfate I biosynthesis, precursor 19		C171H275N12O137S5X	-6	Golgi Apparatus
ksi_pre2	keratan sulfate I biosynthesis, precursor 2		C87H142N6O62X	-1	Golgi Apparatus
ksi_pre20	keratan sulfate I biosynthesis, precursor 20		C171H274N12O140S6X	-7	Golgi Apparatus
ksi_pre21	keratan sulfate I biosynthesis, precursor 21		C177H284N12O145S6X	-7	Golgi Apparatus
ksi_pre22	keratan sulfate I biosynthesis, precursor 22		C185H297N13O150S6X	-7	Golgi Apparatus
ksi_pre23	keratan sulfate I biosynthesis, precursor 23		C185H296N13O153S7X	-8	Golgi Apparatus
ksi_pre24	keratan sulfate I biosynthesis, precursor 24		C191H306N13O158S7X	-8	Golgi Apparatus
ksi_pre25	keratan sulfate I biosynthesis, precursor 25		C199H319N14O163S7X	-8	Golgi Apparatus
ksi_pre26	keratan sulfate I biosynthesis, precursor 26		C199H318N14O166S8X	-9	Golgi Apparatus
ksi_pre27	keratan sulfate I biosynthesis, precursor 27		C205H328N14O171S8X	-9	Golgi Apparatus
ksi_pre28	keratan sulfate I biosynthesis, precursor 28		C213H341N15O176S8X	-9	Golgi Apparatus
ksi_pre29	keratan sulfate I biosynthesis, precursor 29		C213H340N15O179S9X	-10	Golgi Apparatus
ksi_pre3	keratan sulfate I biosynthesis, precursor 3		C93H152N6O67X	-1	Golgi Apparatus
ksi_pre30	keratan sulfate I biosynthesis, precursor 30		C219H350N15O184S9X	-10	Golgi Apparatus
ksi_pre31	keratan sulfate I biosynthesis, precursor 31		C227H363N16O189S9X	-10	Golgi Apparatus
ksi_pre32	keratan sulfate I biosynthesis, precursor 32		C227H362N16O192S10X	-11	Golgi Apparatus
ksi_pre33	keratan sulfate I biosynthesis, precursor 33		C233H372N16O197S10X	-11	Golgi Apparatus
ksi_pre34	keratan sulfate I biosynthesis, precursor 34		C241H385N17O202S10X	-11	Golgi Apparatus
ksi_pre35	keratan sulfate I biosynthesis, precursor 35		C241H384N17O205S11X	-12	Golgi Apparatus
ksi_pre36	keratan sulfate I biosynthesis, precursor 36		C247H394N17O210S11X	-12	Golgi Apparatus
ksi_pre4	keratan sulfate I biosynthesis, precursor 4		C101H165N7O72X	-1	Golgi Apparatus
ksi_pre5	keratan sulfate I biosynthesis, precursor 5		C101H164N7O75SX	-2	Golgi Apparatus
ksi_pre6	keratan sulfate I biosynthesis, precursor 6		C107H174N7O80SX	-2	Golgi Apparatus
ksi_pre7	keratan sulfate I biosynthesis, precursor 7		C115H187N8O85SX	-2	Golgi Apparatus
ksi_pre8	keratan sulfate I biosynthesis, precursor 8		C115H186N8O88S2X	-3	Golgi Apparatus
ksi_pre9	keratan sulfate I biosynthesis, precursor 9		C121H196N8O93S2X	-3	Golgi Apparatus
ksii_core2	keratan sulfate II (core 2-linked)		C81H129N6O67S3X	-4	Extracellular
ksii_core2	keratan sulfate II (core 2-linked)		C81H129N6O67S3X	-4	Golgi Apparatus
ksii_core2	keratan sulfate II (core 2-linked)		C81H129N6O67S3X	-4	Lysosome
ksii_core2_deg1	keratan sulfate II (core 2-linked), degradation product 1		C70H113N5O59S3X	-3	Lysosome
ksii_core2_deg2	keratan sulfate II (core 2-linked), degradation product 2		C70H114N5O56S2X	-2	Lysosome
ksii_core2_deg3	keratan sulfate II (core 2-linked), degradation product 3		C58H94N5O46S2X	-2	Lysosome
ksii_core2_deg4	keratan sulfate II (core 2-linked), degradation product 4		C58H95N5O43SX	-1	Lysosome
ksii_core2_deg5	keratan sulfate II (core 2-linked), degradation product 5		C50H82N4O38SX	-1	Lysosome
ksii_core2_deg6	keratan sulfate II (core 2-linked), degradation product 6		C44H72N4O33SX	-1	Lysosome
ksii_core2_deg7	keratan sulfate II (core 2-linked), degradation product 7		C44H73N4O30X	0	Lysosome
ksii_core2_deg8	keratan sulfate II (core 2-linked), degradation product 8		C36H60N3O25X	0	Lysosome
ksii_core2_deg9	keratan sulfate II (core 2-linked), degradation product 9		C30H50N3O20X	0	Lysosome
ksii_core2_pre1	keratan sulfate II biosynthesis, precursor 1		C33H53N3O23X	-1	Golgi Apparatus
ksii_core2_pre10	keratan sulfate II biosynthesis, precursor 10		C81H130N6O64S2X	-3	Golgi Apparatus
ksii_core2_pre2	keratan sulfate II biosynthesis, precursor 2		C39H63N3O28X	-1	Golgi Apparatus
ksii_core2_pre3	keratan sulfate II biosynthesis, precursor 3		C47H76N4O33X	-1	Golgi Apparatus
ksii_core2_pre4	keratan sulfate II biosynthesis, precursor 4		C53H86N4O38X	-1	Golgi Apparatus
ksii_core2_pre5	keratan sulfate II biosynthesis, precursor 5		C61H99N5O43X	-1	Golgi Apparatus
ksii_core2_pre6	keratan sulfate II biosynthesis, precursor 6		C61H98N5O46SX	-2	Golgi Apparatus
ksii_core2_pre7	keratan sulfate II biosynthesis, precursor 7		C67H108N5O51SX	-2	Golgi Apparatus
ksii_core2_pre8	keratan sulfate II biosynthesis, precursor 8		C75H121N6O56SX	-2	Golgi Apparatus
ksii_core2_pre9	keratan sulfate II biosynthesis, precursor 9		C75H120N6O59S2X	-3	Golgi Apparatus
ksii_core4	keratan sulfate II (core 4-linked)		C89H142N7O72S3X	-4	Extracellular
ksii_core4	keratan sulfate II (core 4-linked)		C89H142N7O72S3X	-4	Golgi Apparatus
ksii_core4	keratan sulfate II (core 4-linked)		C89H142N7O72S3X	-4	Lysosome
ksii_core4_deg1	keratan sulfate II (core 4-linked), degradation product 1		C78H126N6O64S3X	-3	Lysosome
ksii_core4_deg2	keratan sulfate II (core 4-linked), degradation product 2		C78H127N6O61S2X	-2	Lysosome
ksii_core4_deg3	keratan sulfate II (core 4-linked), degradation product 3		C66H107N6O51S2X	-2	Lysosome
ksii_core4_deg4	keratan sulfate II (core 4-linked), degradation product 4		C66H108N6O48SX	-1	Lysosome
ksii_core4_pre1	keratan sulfate II biosynthesis, precursor 1		C36H60N3O25X	0	Golgi Apparatus
ksii_core4_pre10	keratan sulfate II biosynthesis, precursor 10		C89H143N7O69S2X	-3	Golgi Apparatus
ksii_core4_pre2	keratan sulfate II boisynthesis, precursor 2		C47H76N4O33X	-1	Golgi Apparatus
ksii_core4_pre3	keratan sulfate II biosynthesis, precursor 3		C55H89N5O38X	-1	Golgi Apparatus
ksii_core4_pre4	keratan sulfate II biosynthesis, precursor 4		C61H99N5O43X	-1	Golgi Apparatus

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
ksii_core4_pre5	keratan sulfate II biosynthesis, precursor 5		C69H112N6O48X	-1	Golgi Apparatus
ksii_core4_pre6	keratan sulfate II biosynthesis, precursor 6		C69H111N6O51SX	-2	Golgi Apparatus
ksii_core4_pre7	keratan sulfate II biosynthesis, precursor 7		C75H121N6O56SX	-2	Golgi Apparatus
ksii_core4_pre8	keratan sulfate II biosynthesis, precursor 8		C83H134N7O61SX	-2	Golgi Apparatus
ksii_core4_pre9	keratan sulfate II biosynthesis, precursor 9		C83H133N7O64S2X	-3	Golgi Apparatus
kynate	4-Hydroxy-2-quinolinecarboxylic acid	4-Hydroxy-2-quinolinecarboxylic acid, Kynurenate, Kynurenic acid	C10H6NO3	-1	Cytosol
L2aadp	L-2-Aminoadipate	L-2-Aminoadipic acid, L-alpha-Aminoadipate, L-alpha-Aminoadipic acid	C6H10NO4	-1	Cytosol
L2aadp	L-2-Aminoadipate	L-2-Aminoadipic acid, L-alpha-Aminoadipate, L-alpha-Aminoadipic acid	C6H10NO4	-1	Mitochondria
L2aadp6sa	L-2-Aminoadipate 6-semialdehyde		C6H11NO3	0	Cytosol
L2aadp6sa	L-2-Aminoadipate 6-semialdehyde		C6H11NO3	0	Mitochondria
l2fn2m2masn	{[galactosyl-(1,4)-N-Acetyl-glucosaminyl-(1,2)-mannosyl-(1,3)-],[N-acetyl-glucosaminyl-(1,2)-mannosyl-(1,6)-]mannosyl-(1,4)-N-acetyl-glucosaminyl-(1,4)-[fucosyl-(1,6)]-N-acetyl-glucosaminyl}asparagine		C68H113N4O49X	0	Golgi Apparatus
l2n2m2mn	de-Fuc, reducing GlcNAc removed, de-Sia form of PA6 (w/ peptide linkage)		C54H91N3O41	0	Cytosol
l2n2m2mn	de-Fuc, reducing GlcNAc removed, de-Sia form of PA6 (w/ peptide linkage)		C54H91N3O41	0	Lysosome
l2xser	(Gal)2-Xyl-L-Ser (protein)		C17H29O14X	0	Golgi Apparatus
lac-D	D-Lactate	(R)-Lactate, D-2-Hydroxypropanoic acid, D-2-Hydroxypropionic acid, D-Lactic acid	C3H5O3	-1	Cytosol
lac-D	D-Lactate	(R)-Lactate, D-2-Hydroxypropanoic acid, D-2-Hydroxypropionic acid, D-Lactic acid	C3H5O3	-1	Extracellular
lac-D	D-Lactate	(R)-Lactate, D-2-Hydroxypropanoic acid, D-2-Hydroxypropionic acid, D-Lactic acid	C3H5O3	-1	Mitochondria
lac-L	L-Lactate	(S)-Lactate, Hydroxypropionic acid, L-Lactic acid	C3H5O3	-1	Cytosol
lac-L	L-Lactate	(S)-Lactate, Hydroxypropionic acid, L-Lactic acid	C3H5O3	-1	Extracellular
lac-L	L-Lactate	(S)-Lactate, Hydroxypropionic acid, L-Lactic acid	C3H5O3	-1	Mitochondria
lald-D	D-Lactaldehyde	(R)-Lactaldehyde, D-2-Hydroxypropionaldehyde	C3H6O2	0	Cytosol
lald-D	D-Lactaldehyde	(R)-Lactaldehyde, D-2-Hydroxypropionaldehyde	C3H6O2	0	Mitochondria
lald-L	L-Lactaldehyde	(S)-Lactaldehyde, L-2-Hydroxypropionaldehyde	C3H6O2	0	Cytosol
lald-L	L-Lactaldehyde	(S)-Lactaldehyde, L-2-Hydroxypropionaldehyde	C3H6O2	0	Mitochondria
lanost	Lanosterol		C30H50O	0	Cytosol
lanost	Lanosterol		C30H50O	0	Endoplasmic Reticulum
lcts	Lactose	1-beta-D-Galactopyranosyl-4-alpha-D-glucopyranose, Milk sugar, lactobiose	C12H22O11	0	Cytosol
lcts	Lactose	1-beta-D-Galactopyranosyl-4-alpha-D-glucopyranose, Milk sugar, lactobiose	C12H22O11	0	Extracellular
lcts	Lactose	1-beta-D-Galactopyranosyl-4-alpha-D-glucopyranose, Milk sugar, lactobiose	C12H22O11	0	Golgi Apparatus
lcts	Lactose	1-beta-D-Galactopyranosyl-4-alpha-D-glucopyranose, Milk sugar, lactobiose	C12H22O11	0	Lysosome
Lcyst	L-Cysteate	2-Amino-3-sulfopropionic acid, 3-Sulfoalanine, L-Cysteic acid	C3H6NO5S	-1	Cytosol
Lcyst	L-Cysteate	2-Amino-3-sulfopropionic acid, 3-Sulfoalanine, L-Cysteic acid	C3H6NO5S	-1	Mitochondria
Lcystin	L-Cystine	L-Dicysteine, L-alpha-Diamino-beta-dithiolactic acid	C6H12N2O4S2	0	Cytosol
Lcystin	L-Cystine	L-Dicysteine, L-alpha-Diamino-beta-dithiolactic acid	C6H12N2O4S2	0	Extracellular
L-dpchrm	L-Dopachrome	2-L-Carboxy-2,3-dihydroindole-5,6-quinone	C9H6NO4	-1	Cytosol
leuktrA4	Leukotriene A4	(7E,9E,11Z,14Z)-(5S,6S)-5,6-Epoxyeicosa-7,9,11,14-tetraenoate, (7E,9E,11Z,14Z)-(5S,6S)-5,6-Epoxyicosa-7,9,11,14-tetr, LTA4, Leukotriene A4	C20H29O3	-1	Cytosol
leuktrA4	Leukotriene A4	(7E,9E,11Z,14Z)-(5S,6S)-5,6-Epoxyeicosa-7,9,11,14-tetraenoate, (7E,9E,11Z,14Z)-(5S,6S)-5,6-Epoxyicosa-7,9,11,14-tetr, LTA4, Leukotriene A4	C20H29O3	-1	Endoplasmic Reticulum
leuktrB4	Leukotriene B4	(6Z,8E,10E,14Z)-(5S,12R)-5,12-Dihydroxyeicosa-6,8,10,14-tetraenoate, (6Z,8E,10E,14Z)-(5S,12R)-5,12-Dihydroxyicosa-6,8,10,14-tetraenoate, Leukotriene B4	C20H31O4	-1	Cytosol
leuktrB4	Leukotriene B4	(6Z,8E,10E,14Z)-(5S,12R)-5,12-Dihydroxyeicosa-6,8,10,14-tetraenoate, (6Z,8E,10E,14Z)-(5S,12R)-5,12-Dihydroxyicosa-6,8,10,14-tetraenoate, Leukotriene B4	C20H31O4	-1	Endoplasmic Reticulum
leuktrB4wcooh	w-carboxy leukotriene B4	20 carboxy leukotriene B4, omega carboxy leukotriene B4, omega carboxylated leukotriene B4	C20H28O6	-2	Endoplasmic Reticulum
leuktrB4woh	w-hydroxyl leukotriene B4	20 hydroxy leukotriene B4, omega hydroxy leukotriene B4, omega-hydroxylated leukotriene B4	C20H31O5	-1	Endoplasmic Reticulum
leuktrC4	Leukotriene C4		C30H45N3O9S	-2	Cytosol
leuktrC4	Leukotriene C4		C30H45N3O9S	-2	Extracellular

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
leuktrC4	Leukotriene C4		C30H45N3O9S	-2	Endoplasmic Reticulum
leuktrD4	Leukotriene D4	LTD4, Leukotriene D4	C25H39N2O6S	-1	Cytosol
leuktrD4	Leukotriene D4	LTD4, Leukotriene D4	C25H39N2O6S	-1	Endoplasmic Reticulum
leuktrE4	leukotriene E4	5S-hydroxy,6R-(S-cysteinyl),7E,9E,11Z,14Z-eicosatetraenoic acid, C05952, LMFA03020002, LTE4, leukotriene E4	C23H36NO5S	-1	Cytosol
leuktrF4	leukotriene F4	C06462, LTF4, Leukotriene F4	C28H42N2O8S	-2	Cytosol
leu-L	L-Leucine	2-amino-4-methylvaleric acid, Leu	C6H13NO2	0	Cytosol
leu-L	L-Leucine	2-amino-4-methylvaleric acid, Leu	C6H13NO2	0	Extracellular
leu-L	L-Leucine	2-amino-4-methylvaleric acid, Leu	C6H13NO2	0	Mitochondria
Lfmkynr	L-Formylkynurenine	N-Formyl-L-kynurenine	C11H12N2O4	0	Cytosol
lgnc	lignoceric acid	Lignoceric acid, Tetracosanoic acid	C24H47O2	-1	Cytosol
lgnc	lignoceric acid	Lignoceric acid, Tetracosanoic acid	C24H47O2	-1	Extracellular
lgnccoa	lignocericyl coenzyme A		C45H78N7O17P3S	-4	Cytosol
lgnccoa	lignocericyl coenzyme A		C45H78N7O17P3S	-4	Mitochondria
lgnccoa	lignocericyl coenzyme A		C45H78N7O17P3S	-4	Peroxisome
lgnccrn	lignoceryl carnitine		C31H61NO4	0	Cytosol
lgnccrn	lignoceryl carnitine		C31H61NO4	0	Mitochondria
lgt-S	(R)-S-Lactoylglutathione		C13H20N3O8S	-1	Cytosol
lgt-S	(R)-S-Lactoylglutathione		C13H20N3O8S	-1	Mitochondria
limnen	Limonene	Limonene	C10H16	0	Cytosol
limnen	Limonene	Limonene	C10H16	0	Extracellular
lipoate	Lipoate	Lipoic acid, Thioctic acid, alpha-Lipoic acid	C8H14O2S2	0	Cytosol
lipoate	Lipoate	Lipoic acid, Thioctic acid, alpha-Lipoic acid	C8H14O2S2	0	Extracellular
Lkynr	L-Kynurenine	3-Anthraniloyl-L-alanine	C10H12N2O3	0	Cytosol
lneldc	linoelaidic acid (all trans C18:2)	9-cis,11-trans-Octadecadienoate, C18:2, Linoelaidic acid	C18H31O2	-1	Cytosol
lneldc	linoelaidic acid (all trans C18:2)	9-cis,11-trans-Octadecadienoate, C18:2, Linoelaidic acid	C18H31O2	-1	Extracellular
lneldcACP	linoelaidic acid ACP (all trans)		C29H51N2O8PRS	-1	Cytosol
lneldccoa	linoelaidyl coenzyme A		C39H62N7O17P3S	-4	Cytosol
lneldccoa	linoelaidyl coenzyme A		C39H62N7O17P3S	-4	Mitochondria
lneldccrn	Linoelaidyl carnitine		C25H45NO4	0	Cytosol
lneldccrn	Linoelaidyl carnitine		C25H45NO4	0	Mitochondria
lnlc	linoleic acid (all cis C18:2) n-6	9,12-Octadecadienoic acid, 9-cis,12-cis-Octadecadienoate, 9-cis,12-cis-Octadecadienoic acid, Linoleate, Linoleic acid	C18H31O2	-1	Cytosol
lnlc	linoleic acid (all cis C18:2) n-6	9,12-Octadecadienoic acid, 9-cis,12-cis-Octadecadienoate, 9-cis,12-cis-Octadecadienoic acid, Linoleate, Linoleic acid	C18H31O2	-1	Extracellular
lnlcACP	linoleic acid ACP (all cis)		C29H51N2O8PRS	-1	Cytosol
lnlccoa	linoleic coenzyme A	linoleic acid coenzyme A, linoleic coenzyme A	C39H62N7O17P3S	-4	Cytosol
lnlccoa	linoleic coenzyme A	linoleic acid coenzyme A, linoleic coenzyme A	C39H62N7O17P3S	-4	Mitochondria
lnlccrn	Linoleyl carnitine	linoleic acid carnitine	C25H45NO4	0	Cytosol
lnlccrn	Linoleyl carnitine	linoleic acid carnitine	C25H45NO4	0	Mitochondria
lnlnca	alpha-Linolenic acid, C18:3, n-3	(9Z,12Z,15Z)-Octadecatrienoic acid, 9,12,15-Octadecatrienoic acid, Linolenate, alpha-Linolenic acid	C18H29O2	-1	Cytosol
lnlnca	alpha-Linolenic acid, C18:3, n-3	(9Z,12Z,15Z)-Octadecatrienoic acid, 9,12,15-Octadecatrienoic acid, Linolenate, alpha-Linolenic acid	C18H29O2	-1	Extracellular
lnlncacoa	alpha-Linolenoyl-CoA	alpha-Linolenoyl-CoA	C39H60N7O17P3S	-4	Cytosol
lnlncacoa	alpha-Linolenoyl-CoA	alpha-Linolenoyl-CoA	C39H60N7O17P3S	-4	Mitochondria
lnlncacrn	alpha-linolenyl carnitine		C25H43NO4	0	Cytosol
lnlncacrn	alpha-linolenyl carnitine		C25H43NO4	0	Mitochondria
lnlncg	gamma-linolenic acid	6,9,12-Octadecatrienoic acid, gamma-Linolenic acid	C18H29O2	-1	Cytosol
lnlncg	gamma-linolenic acid	6,9,12-Octadecatrienoic acid, gamma-Linolenic acid	C18H29O2	-1	Extracellular
lnlncgcoa	gamma-linolenoyl-CoA	gamma-Linolenoyl-CoA	C39H60N7O17P3S	-4	Cytosol
lnlncgcoa	gamma-linolenoyl-CoA	gamma-Linolenoyl-CoA	C39H60N7O17P3S	-4	Mitochondria
lnlncgcoa	gamma-linolenoyl-CoA	gamma-Linolenoyl-CoA	C39H60N7O17P3S	-4	Peroxisome
lnlncgcrn	gamma-linolenyl carnitine		C25H43NO4	0	Cytosol
lnlncgcrn	gamma-linolenyl carnitine		C25H43NO4	0	Mitochondria
lpam	Lipoamide	Thioctic Acid Amide	C8H15NOS2	0	Mitochondria
lpchol_hs	lysophosphatidylcholine (homo sapiens)	1-Acyl-sn-glycero-3-phosphocholine;, 1-Acyl-sn-glycerol-3-phosphocholine;, 2-Lysolecithin;, 2-Lysophosphatidylcholine, alpha-Acylglycerophosphocholine;, lysolecithin	C8H19NO5PFULLRCO2	0	Cytosol
lpchol_hs	lysophosphatidylcholine (homo sapiens)	1-Acyl-sn-glycero-3-phosphocholine;, 1-Acyl-sn-glycerol-3-phosphocholine;, 2-Lysolecithin;, 2-Lysophosphatidylcholine, alpha-Acylglycerophosphocholine;, lysolecithin	C8H19NO5PFULLRCO2	0	Extracellular
Lpipecol	L-Pipecolate	2-Piperidinecarboxylic acid, Pipecolic acid, Pipecolinic acid	C6H11NO2	0	Peroxisome
lpro	Lipoylprotein		S2X	0	Mitochondria
lthstrl	5alpha-Cholest-7-en-3beta-ol	5alpha-Cholest-7-en-3beta-ol, Lathosterol	C27H46O	0	Endoplasmic Reticulum
lum3	Lumisterol 3		C27H44O	0	Cytosol
lxser	Gal-Xyl-L-Ser (protein)		C11H19O9X	0	Golgi Apparatus

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
lys-L	L-Lysine	2,6-diaminohexanoic acid, Lys, Lysine acid	C6H15N2O2	1	Cytosol
lys-L	L-Lysine	2,6-diaminohexanoic acid, Lys, Lysine acid	C6H15N2O2	1	Extracellular
lys-L	L-Lysine	2,6-diaminohexanoic acid, Lys, Lysine acid	C6H15N2O2	1	Mitochondria
lys-L	L-Lysine	2,6-diaminohexanoic acid, Lys, Lysine acid	C6H15N2O2	1	Nucleus
lys-L	L-Lysine	2,6-diaminohexanoic acid, Lys, Lysine acid	C6H15N2O2	1	Peroxisome
lyxnt	L-lyxonate	L-Lyxonic acid	C5H9O6	-1	Cytosol
m(em)3gacpail_hs	mannosyl-3-(phosphoethanolaminyl-mannosyl)-glucosaminyl-acylphosphatidylinositol (M4A)	[({[Man],[PE-]Man-},{PE-}Man-],[PE-]Man-GlcN-acylPI	C61H116N4O43P4FULLRCO2FULLR2CO2	0	Endoplasmic Reticulum
m(em)3gacpail_prot_hs	mannosyl-3-(phosphoethanolaminyl-mannosyl)-glucosaminyl-acylphosphatidylinositol-Protein (M4A)		C61H116N4O43P4FULLRCO2FULLR2CO2X	0	Endoplasmic Reticulum
m1mpdol_L	alpha-D-mannosyl-beta-D-mannosyl-diacylchitobiosyldiphosphodolichol, human liver homolog		C1360H2228N20O270P20	-20	Cytosol
m1mpdol_U	alpha-D-mannosyl-beta-D-mannosyl-diacylchitobiosyldiphosphodolichol, human uterine homolog		C1305H2140N20O270P20	-20	Cytosol
m2emgacpail_hs	(dimannosyl),(phosphoethanolaminyl)-mannosyl-glucosylaminyl-acylphosphatidylinositol (H6)	[(Man)2-],[PE-]Man-GlcN-acylPI	C51H94N2O32P2FULLRCO2FULLR2CO2	0	Endoplasmic Reticulum
m2gacpail_hs	dimannosyl-glucosaminyl-acylphosphatidylinositol (H3)	(Man)2-GlcN-acylPI	C43H78NO24PFULLRCO2FULLR2CO2	0	Endoplasmic Reticulum
m2mn	(alpha-D-mannosyl)2-beta-D-mannosyl-N-acetylglucosamine		C26H45NO21	0	Cytosol
m2mn	(alpha-D-mannosyl)2-beta-D-mannosyl-N-acetylglucosamine		C26H45NO21	0	Lysosome
m2mpdol_L	(alpha-D-mannosyl)2-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human liver homolog		C1420H2328N20O320P20	-20	Cytosol
m2mpdol_U	(alpha-D-mannosyl)2-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human uterine homolog		C1365H2240N20O320P20	-20	Cytosol
m3emgacpail_hs	(trimannosyl),(phosphoethanolaminyl)-mannosyl-glucosaminyl-acylphosphatidylinositol (M4C)	[(Man)3-],[PE-]Man-GlcN-acylPI	C57H104N2O37P2FULLRCO2FULLR2CO2	0	Endoplasmic Reticulum
m3gacpail_hs	trimannosyl-glucosaminyl-acylphosphatidylinositol (H4)	(Man)3-GlcN-acylPI	C49H88NO29PFULLRCO2FULLR2CO2	0	Endoplasmic Reticulum
m3mpdol_L	(alpha-D-mannosyl)3-beta-D-mannosyl-diacetylchitodiphosphodolichol, human liver homolog		C1480H2428N20O370P20	-20	Cytosol
m3mpdol_U	(alpha-D-mannosyl)3-beta-D-mannosyl-diacetylchitodiphosphodolichol, human uterine homolog		C1425H2340N20O370P20	-20	Cytosol
m4masn	(alpha-D-mannosyl)4-beta-D-mannosyl-diacetylchitobiosyl-asparagine (protein)		C46H77N2O35X	0	Golgi Apparatus
m4mpdol_L	(alpha-D-Mannosyl)4-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human liver homolog		C1540H2528N20O420P20	-20	Cytosol
m4mpdol_L	(alpha-D-Mannosyl)4-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human liver homolog		C1540H2528N20O420P20	-20	Endoplasmic Reticulum
m4mpdol_U	(alpha-D-Mannosyl)4-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human uterine homolog		C1485H2440N20O420P20	-20	Cytosol
m4mpdol_U	(alpha-D-Mannosyl)4-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human uterine homolog		C1485H2440N20O420P20	-20	Endoplasmic Reticulum
m5masnB1	(alpha-D-mannosyl)5-beta-D-mannosyl-diacetylchitobiosyl-asparagine (protein)		C52H87N2O40X	0	Golgi Apparatus
m5masnB2	(alpha-D-mannosyl)5-beta-D-mannosyl-diacetylchitobiosyl-asparagine (protein)		C52H87N2O40X	0	Golgi Apparatus
m5masnC	(alpha-D-mannosyl)5-beta-D-mannosyl-diacetylchitobiosyl-asparagine (protein)		C52H87N2O40X	0	Golgi Apparatus
m5mpdol_L	(alpha-D-Mannosyl)5-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human liver homolog		C1600H2628N20O470P20	-20	Endoplasmic Reticulum
m5mpdol_U	(alpha-D-Mannosyl)5-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human uterine homolog		C1545H2540N20O470P20	-20	Endoplasmic Reticulum
m6masnA	(alpha-D-mannosyl)6-beta-D-mannosyl-diacetylchitobiosyl-asparagine (protein)		C58H97N2O45X	0	Golgi Apparatus
m6masnB1	(alpha-D-mannosyl)6-beta-D-mannosyl-diacetylchitobiosyl-asparagine (protein)		C58H97N2O45X	0	Golgi Apparatus
m6masnB2	(alpha-D-mannosyl)6-beta-D-mannosyl-diacetylchitobiosyl-asparagine (protein)		C58H97N2O45X	0	Golgi Apparatus
m6masnC	(alpha-D-mannosyl)6-beta-D-mannosyl-diacetylchitobiosyl-asparagine (protein)		C58H97N2O45X	0	Golgi Apparatus
m6mpdol_L	(alpha-D-Mannosyl)6-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human liver homolog		C1660H2728N20O520P20	-20	Endoplasmic Reticulum
m6mpdol_U	(alpha-D-Mannosyl)6-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human uterine homolog		C1605H2640N20O520P20	-20	Endoplasmic Reticulum
m7masnA	(alpha-D-mannosyl)7-beta-D-mannosyl-diacetylchitobiosyl-asparagine, isoform A (protein)		C64H107N2O50X	0	Golgi Apparatus
m7masnB	(alpha-D-mannosyl)7-beta-D-mannosyl-diacetylchitobiosyl-asparagine, isoform B (protein)		C64H107N2O50X	0	Golgi Apparatus

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
m7masnB	(alpha-D-mannosyl)7-beta-D-mannosyl-diacetylchitobiosyl-asparagine, isoform B (protein)		C64H107N2O50X	0	Endoplasmic Reticulum
m7masnC	(alpha-D-mannosyl)7-beta-D-mannosyl-diacetylchitobiosyl-asparagine, isoform C (protein)		C64H107N2O50X	0	Golgi Apparatus
m7mpdol_L	(alpha-D-Mannosyl)7-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human liver homolog		C1720H2828N20O570P20	-20	Endoplasmic Reticulum
m7mpdol_U	(alpha-D-Mannosyl)7-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human uterine homolog		C1665H2740N20O570P20	-20	Endoplasmic Reticulum
m8masn	(alpha-D-mannosyl)8-beta-D-mannosyl-diacetylchitobiosyl-asparagine (protein)		C70H117N2O55X	0	Golgi Apparatus
m8masn	(alpha-D-mannosyl)8-beta-D-mannosyl-diacetylchitobiosyl-asparagine (protein)		C70H117N2O55X	0	Endoplasmic Reticulum
m8mpdol_L	(alpha-D-Mannosyl)8-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human liver homolog		C1780H2928N20O620P20	-20	Endoplasmic Reticulum
m8mpdol_U	(alpha-D-Mannosyl)8-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol, human uterine homolog		C1725H2840N20O620P20	-20	Endoplasmic Reticulum
mag_hs	monoacylglycerol 2 (homo sapiens)		C3H7O2FULLR2CO2	0	Cytosol
mag_hs	monoacylglycerol 2 (homo sapiens)		C3H7O2FULLR2CO2	0	Extracellular
malACP	Malonyl-[acyl-carrier protein]		C14H22N2O10PRS	-2	Cytosol
malACP	Malonyl-[acyl-carrier protein]		C14H22N2O10PRS	-2	Mitochondria
malcoa	Malonyl-CoA	Malonyl coenzyme A	C24H33N7O19P3S	-5	Cytosol
malcoa	Malonyl-CoA	Malonyl coenzyme A	C24H33N7O19P3S	-5	Mitochondria
malcoa	Malonyl-CoA	Malonyl coenzyme A	C24H33N7O19P3S	-5	Peroxisome
mal-L	L-Malate	(S)-Malate, L-2-Hydroxybutanedioic acid, L-Apple acid, L-Malic acid, Malate	C4H4O5	-2	Cytosol
mal-L	L-Malate	(S)-Malate, L-2-Hydroxybutanedioic acid, L-Apple acid, L-Malic acid, Malate	C4H4O5	-2	Mitochondria
malt	Maltose	1-alpha-D-Glucopyranosyl-4-alpha-D-glucopyranose, Malt sugar	C12H22O11	0	Cytosol
malt	Maltose	1-alpha-D-Glucopyranosyl-4-alpha-D-glucopyranose, Malt sugar	C12H22O11	0	Extracellular
malt	Maltose	1-alpha-D-Glucopyranosyl-4-alpha-D-glucopyranose, Malt sugar	C12H22O11	0	Lysosome
malttr	Maltotriose	Amylotriose, Maltotriose	C18H32O16	0	Cytosol
malttr	Maltotriose	Amylotriose, Maltotriose	C18H32O16	0	Extracellular
malttr	Maltotriose	Amylotriose, Maltotriose	C18H32O16	0	Lysosome
man	D-Mannose	Carubinose, Mannose, Seminose	C6H12O6	0	Cytosol
man	D-Mannose	Carubinose, Mannose, Seminose	C6H12O6	0	Extracellular
man	D-Mannose	Carubinose, Mannose, Seminose	C6H12O6	0	Golgi Apparatus
man	D-Mannose	Carubinose, Mannose, Seminose	C6H12O6	0	Lysosome
man	D-Mannose	Carubinose, Mannose, Seminose	C6H12O6	0	Endoplasmic Reticulum
man1p	D-Mannose 1-phosphate	alpha-D-Mannose 1-phosphate	C6H11O9P	-2	Cytosol
man6p	D-Mannose 6-phosphate		C6H11O9P	-2	Cytosol
melanin	Melanin		C9H6NO4	-1	Cytosol
melatn	Melatonin	Melatonin, N-Acetyl-5-methoxytryptamine	C13H16N2O2	0	Cytosol
mem2emgacpail_hs	({[(mannosyl),(phosphoethanolaminyl)]-dimannosyl},{phosphoethanolaminyl})-mannosyl-glucosaminyl-acylphosphatidylinositol (M4B)	{[Man-],[PE-](Man)2-},{PE-}Man-GlcN-acylPI	C59H110N3O40P3FULLRCO2FULLR2CO2	0	Endoplasmic Reticulum
mem2emgacpail_prot_hs	({[(mannosyl),(phosphoethanolaminyl)]-dimannosyl},{phosphoethanolaminyl})-mannosyl-glucosaminyl-acylphosphatidylinositol-Protein (M4B)		C59H110N3O40P3FULLRCO2FULLR2CO2X	0	Endoplasmic Reticulum
memgacpail_hs	(mannosyl),(phosphoethanolaminyl)-mannosyl-glucosylaminyl-acylphosphatidylinositol (B)	[Man-],[PE-]Man-GlcN-acylPI	C45H84N2O27P2FULLRCO2FULLR2CO2	0	Endoplasmic Reticulum
meoh	Methanol	Methyl alcohol	CH4O1	0	Cytosol
meoh	Methanol	Methyl alcohol	CH4O1	0	Extracellular
meoh	Methanol	Methyl alcohol	CH4O1	0	Lysosome
meoh	Methanol	Methyl alcohol	CH4O1	0	Endoplasmic Reticulum
mepi	Metanephrine	L-Metanephrine	C10H16NO3	1	Cytosol
mepi	Metanephrine	L-Metanephrine	C10H16NO3	1	Extracellular
mercplac	3-Mercaptolactate		C3H5O3S	-1	Cytosol
mercplaccys	3-mercaptolactate-cysteine disulfide		C6H10O5S2N	-1	Cytosol
mercplaccys	3-mercaptolactate-cysteine disulfide		C6H10O5S2N	-1	Extracellular
mercppyr	Mercaptopyruvate	3-Mercaptopyruvate	C3H3O3S	-1	Cytosol
mercppyr	Mercaptopyruvate	3-Mercaptopyruvate	C3H3O3S	-1	Mitochondria
mescoa	Mesaconyl-CoA		C26H35N7O19P3S	-5	Mitochondria
mescon	Mesaconate	2-Methylfumarate, Mesaconic acid, Methylfumaric acid	C5H4O4	-2	Mitochondria
methf	5,10-Methenyltetrahydrofolate	(6R)-5,10-methenyltetrahydrofolate, 5,10-methenyltetrahydrofolate, N5,N10-methenyl-5,6,7,8-tetrahydrofolate, N5,N10-methenyl-tetrahydrofolate	C20H20N7O6	-1	Cytosol
methf	5,10-Methenyltetrahydrofolate	(6R)-5,10-methenyltetrahydrofolate, 5,10-methenyltetrahydrofolate, N5,N10-methenyl-5,6,7,8-tetrahydrofolate, N5,N10-methenyl-tetrahydrofolate	C20H20N7O6	-1	Mitochondria
met-L	L-Methionine	L-2-Amino-4methylthiobutyric acid, Met	C5H11NO2S	0	Cytosol
met-L	L-Methionine	L-2-Amino-4methylthiobutyric acid, Met	C5H11NO2S	0	Extracellular
mev-R	(R)-Mevalonate	3,5-Dihydroxy-3-methylvaleric acid, Mevalonic acid	C6H11O4	-1	Endoplasmic Reticulum
mev-R	(R)-Mevalonate	3,5-Dihydroxy-3-methylvaleric acid, Mevalonic acid	C6H11O4	-1	Peroxisome
mgacpail_hs	mannosyl-glucosaminyl-acylphosphatidylinositiol (H2)	Man-GlcN-acylPI	C37H68NO19PFULLRCO2FULLR2CO2	0	Endoplasmic Reticulum

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
mhista	N-Methylhistamine	1-Methyl-4-(2-aminoethyl)imidazole, Methylhistamine	C6H12N3	1	Cytosol
mi13456p	1D-myo-Inositol 1,3,4,5,6-pentakisphosphate	D-myo-Inositol 1,3,4,5,6-pentakisphosphate, Inositol 1,3,4,5,6-pentakisphosphate	C6H7O21P5	-10	Cytosol
mi13456p	1D-myo-Inositol 1,3,4,5,6-pentakisphosphate	D-myo-Inositol 1,3,4,5,6-pentakisphosphate, Inositol 1,3,4,5,6-pentakisphosphate	C6H7O21P5	-10	Nucleus
mi1345p	1D-myo-Inositol 1,3,4,5-tetrakisphosphate	D-myo-Inositol 1,3,4,5-tetrakisphosphate, Inositol 1,3,4,5-tetrakisphosphate	C6H8O18P4	-8	Cytosol
mi1345p	1D-myo-Inositol 1,3,4,5-tetrakisphosphate	D-myo-Inositol 1,3,4,5-tetrakisphosphate, Inositol 1,3,4,5-tetrakisphosphate	C6H8O18P4	-8	Nucleus
mi1346p	1D-myo-Inositol 1,3,4,6-tetrakisphosphate	D-myo-Inositol 1,3,4,6-tetrakisphosphate, Inositol 1,3,4,6-tetrakisphosphate	C6H8O18P4	-8	Cytosol
mi1346p	1D-myo-Inositol 1,3,4,6-tetrakisphosphate	D-myo-Inositol 1,3,4,6-tetrakisphosphate, Inositol 1,3,4,6-tetrakisphosphate	C6H8O18P4	-8	Nucleus
mi134p	1D-myo-Inositol 1,3,4-trisphosphate	Inositol 1,3,4-trisphosphate	C6H9O15P3	-6	Cytosol
mi13p	1D-myo-Inositol 1,3-bisphosphate	D-myo-Inositol 1,3-bisphosphate, Inositol 1,3-bisphosphate, myo-Inositol 1,3-bisphosphate	C6H10O12P2	-4	Cytosol
mi1456p	1D-myo-Inositol 1,4,5,6-tetrakisphosphate		C6H8O18P4	-8	Nucleus
mi145p	1D-myo-Inositol 1,4,5-trisphosphate	IP3, Inositol 1,4,5-trisphosphate	C6H9O15P3	-6	Cytosol
mi145p	1D-myo-Inositol 1,4,5-trisphosphate	IP3, Inositol 1,4,5-trisphosphate	C6H9O15P3	-6	Nucleus
mi14p	1D-myo-Inositol 1,4-bisphosphate	1D-myo-Inositol 1, 4-bisphosphate, Inositol 1, myo-Inositol 1	C6H10O12P2	-4	Cytosol
mi14p	1D-myo-Inositol 1,4-bisphosphate	1D-myo-Inositol 1, 4-bisphosphate, Inositol 1, myo-Inositol 1	C6H10O12P2	-4	Nucleus
mi1p-D	1D-myo-Inositol 1-phosphate	1D-myo-Inositol 1-monophosphate, 1L-myo-Inositol 1-phosphate, D-myo-Inositol 1-phosphate, Inositol 1-phosphate, L-myo-Inositol 1-phosphate, myo-Inositol 1-phosphate	C6H11O9P	-2	Cytosol
mi1p-D	1D-myo-Inositol 1-phosphate	1D-myo-Inositol 1-monophosphate, 1L-myo-Inositol 1-phosphate, D-myo-Inositol 1-phosphate, Inositol 1-phosphate, L-myo-Inositol 1-phosphate, myo-Inositol 1-phosphate	C6H11O9P	-2	Nucleus
mi3456p	1D-myo-Inositol 3,4,5,6-tetrakisphosphate	D-myo-Inositol 3,4,5,6-tetrakisphosphate, Inositol 3,4,5,6-tetrakisphosphate	C6H8O18P4	-8	Cytosol
mi34p	1D-myo-Inositol 3,4-bisphosphate	D-myo-Inositol 3,4-bisphosphate, Inositol 3,4-bisphosphate	C6H10O12P2	-4	Cytosol
mi3p-D	1D-myo-Inositol 3-phosphate	1D-myo-Inositol 3-monophosphate, D-myo-Inositol 3-monophosphate, D-myo-Inositol 3-phosphate, Inositol 3-monophosphate, Inositol 3-phosphate, myo-Inositol 3-monophosphate, myo-Inositol 3-phosphate	C6H11O9P	-2	Cytosol
mi4p-D	1D-myo-Inositol 4-phosphate	1D-myo-Inositol 4-monophosphate, D-myo-Inositol 4-phosphate, Inositol 4-phosphate	C6H11O9P	-2	Cytosol
micit	methylisocitrate	(2S,3R)-3-Hydroxybutane-1,2,3-tricarboxylate, Methylisocitrate, Methylisocitric acid	C7H7O7	-3	Cytosol
minohp	myo-Inositol hexakisphosphate	1D-myo-Inositol 1, 2, 3, 4, 5, 6-hexakisphosphate, D-myo-Inositol 1, Inositol 1, Phytate, Phytic acid, myo-Inositol 1, myo-Inositol hexakisphosphate	C6H6O24P6	-12	Cytosol
minohp	myo-Inositol hexakisphosphate	1D-myo-Inositol 1, 2, 3, 4, 5, 6-hexakisphosphate, D-myo-Inositol 1, Inositol 1, Phytate, Phytic acid, myo-Inositol 1, myo-Inositol hexakisphosphate	C6H6O24P6	-12	Nucleus
mlthf	5,10-Methylenetetrahydrofolate	5,10-methylene-5,6,7,8-tetrahydrofolate, N5,N10-methylene-5,6,7,8-tetrahydrofolate, N5,N10-methylene-tetrahydrofolate	C20H21N7O6	-2	Cytosol
mlthf	5,10-Methylenetetrahydrofolate	5,10-methylene-5,6,7,8-tetrahydrofolate, N5,N10-methylene-5,6,7,8-tetrahydrofolate, N5,N10-methylene-tetrahydrofolate	C20H21N7O6	-2	Mitochondria
mma	monomethylamine	Methanamine, Methylamine	C1H6N	1	Cytosol
mmcoa-R	(R)-Methylmalonyl-CoA	(R)-2-Methyl-3-oxopropanoyl-CoA, (R)-2-Methyl-oxopropionyl-CoA, (R)-3-Oxo-2-methylpropanoyl-CoA	C25H35N7O19P3S	-5	Mitochondria
mmcoa-S	(S)-Methylmalonyl-CoA	(S)-2-Methyl-3-oxopropanoyl-CoA, (S)-2-Methyl-3-oxopropionyl-CoA, (S)-3-oxo-2-methylpropanoyl-CoA, (S)-Methylmalonyl-coenzyme A	C25H35N7O19P3S	-5	Cytosol
mmcoa-S	(S)-Methylmalonyl-CoA	(S)-2-Methyl-3-oxopropanoyl-CoA, (S)-2-Methyl-3-oxopropionyl-CoA, (S)-3-oxo-2-methylpropanoyl-CoA, (S)-Methylmalonyl-coenzyme A	C25H35N7O19P3S	-5	Mitochondria
mmcoa-S	(S)-Methylmalonyl-CoA	(S)-2-Methyl-3-oxopropanoyl-CoA, (S)-2-Methyl-3-oxopropionyl-CoA, (S)-3-oxo-2-methylpropanoyl-CoA, (S)-Methylmalonyl-coenzyme A	C25H35N7O19P3S	-5	Peroxisome
mn	beta-1,4-mannose-N-acetylglucosamine		C14H25NO11	0	Cytosol
mn	beta-1,4-mannose-N-acetylglucosamine		C14H25NO11	0	Lysosome

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
mpdol_L	beta-D-Mannosyldiacetylchitobiosyldiphosphodolichol, human liver homolog	Man-beta1->4GlcNAc-PP-Dol, beta-1,4-D-Mannosylchitobiosyldiphosphodolichol	C1300H2128N20O220P20	-20	Cytosol
mpdol_U	beta-D-Mannosyldiacetylchitobiosyldiphosphodolichol, human uterine homolog	Man-beta1->4GlcNAc-PP-Dol, beta-1,4-D-Mannosylchitobiosyldiphosphodolichol	C1245H2040N20O220P20	-20	Cytosol
msa	Malonate semialdehyde	3-Oxopropanoate	C3H3O3	-1	Cytosol
msa	Malonate semialdehyde	3-Oxopropanoate	C3H3O3	-1	Mitochondria
mthgxl	Methylglyoxal	2-Ketopropionaldehyde, 2-Oxopropanal, Pyruvaldehyde, Pyruvic aldehyde	C3H4O2	0	Cytosol
mthgxl	Methylglyoxal	2-Ketopropionaldehyde, 2-Oxopropanal, Pyruvaldehyde, Pyruvic aldehyde	C3H4O2	0	Extracellular
myrsACP	Myristoyl-ACP (n-C14:0ACP)	Fatty acid C14:0 ACP, Tetradecanoyl-[acp], Tetradecanoyl-[acyl-carrier protein]	C25H47N2O8PRS	-1	Cytosol
n2m2masn	((N-acetyl-D-glucosaminyl)2-(alpha-D-mannosyl)2-beta-D-mannosyl-diacetylchitobiosyl)-L-asparagine (protein)		C50H83N4O35X	0	Golgi Apparatus
n2m2mn	de-Fuc, reducing GlcNAc removed, de-Sia, de-Gal form of PA6 (w/o peptide linkage)		C42H71N3O31	0	Lysosome
n2m2nm	n2m2nmasn (w/o peptide linkage)		C58H97N5O41	0	Cytosol
n2m2nm	n2m2nmasn (w/o peptide linkage)		C58H97N5O41	0	Lysosome
n2m2nmasn	N-Acetyl-beta-D-glucosaminyl-1,2-alpha-D-mannosyl-1,3-(N-acetyl-beta-D-glucosaminyl-1,2-alpha-D-mannosyl-1,6)-(N-acetyl-beta-D-glucosaminyl-1,4)-beta-D-mannosyl-1,4-N-acetyl-beta-D-glucosaminyl-R		C58H96N5O40X	0	Extracellular
n2m2nmasn	N-Acetyl-beta-D-glucosaminyl-1,2-alpha-D-mannosyl-1,3-(N-acetyl-beta-D-glucosaminyl-1,2-alpha-D-mannosyl-1,6)-(N-acetyl-beta-D-glucosaminyl-1,4)-beta-D-mannosyl-1,4-N-acetyl-beta-D-glucosaminyl-R		C58H96N5O40X	0	Golgi Apparatus
n2m2nmasn	N-Acetyl-beta-D-glucosaminyl-1,2-alpha-D-mannosyl-1,3-(N-acetyl-beta-D-glucosaminyl-1,2-alpha-D-mannosyl-1,6)-(N-acetyl-beta-D-glucosaminyl-1,4)-beta-D-mannosyl-1,4-N-acetyl-beta-D-glucosaminyl-R		C58H96N5O40X	0	Lysosome
n2m2nmn	reducing GlcNAc removed form of n2m2nmasn (w/o peptide)		C50H84N4O36	0	Cytosol
n2m2nmn	reducing GlcNAc removed form of n2m2nmasn (w/o peptide)		C50H84N4O36	0	Lysosome
n3m2masn	((N-acetyl-D-glucosaminyl)3-(alpha-D-mannosyl)2-beta-D-mannosyl-diacetylchitobiosyl)-L-asparagine (protein)		C58H96N5O40X	0	Golgi Apparatus
n4abutn	N4-Acetylaminobutanal		C6H11NO2	0	Cytosol
n4abutn	N4-Acetylaminobutanal		C6H11NO2	0	Mitochondria
n4m2masn	((N-acetyl-D-glucosaminyl)4-(alpha-D-mannosyl)2-beta-D-mannosyl-diacetylchitobiosyl)-L-asparagine (protein)		C66H109N6O45X	0	Golgi Apparatus
n5m2masn	((N-acetyl-D-glucosaminyl)5-(alpha-D-mannosyl)2-beta-D-mannosyl-diacetylchitobiosyl)-L-asparagine (protein)		C74H122N7O50X	0	Golgi Apparatus
na1	Sodium	Na, Natrium	Na	1	Cytosol
na1	Sodium	Na, Natrium	Na	1	Extracellular
na1	Sodium	Na, Natrium	Na	1	Golgi Apparatus
na1	Sodium	Na, Natrium	Na	1	Peroxisome
nac	Nicotinate	3-Pyridinecarboxylic acid, Niacin, Nicotinic acid	C6H4NO2	-1	Cytosol
nac	Nicotinate	3-Pyridinecarboxylic acid, Niacin, Nicotinic acid	C6H4NO2	-1	Extracellular
Nacasp	N-Acetyl-L-aspartate		C6H7NO5	-2	Cytosol
Nacasp	N-Acetyl-L-aspartate		C6H7NO5	-2	Mitochondria
Nacsertn	N-Acetylserotonin	N-Acetyl-5-hydroxytryptamine	C12H14N2O2	0	Cytosol
nad	Nicotinamide adenine dinucleotide	NAD, NAD+, beta-Diphosphopyridine Nucleotide, beta-NAD, beta-Nicotinamide adenine dinucleotide	C21H26N7O14P2	-1	Cytosol
nad	Nicotinamide adenine dinucleotide	NAD, NAD+, beta-Diphosphopyridine Nucleotide, beta-NAD, beta-Nicotinamide adenine dinucleotide	C21H26N7O14P2	-1	Extracellular
nad	Nicotinamide adenine dinucleotide	NAD, NAD+, beta-Diphosphopyridine Nucleotide, beta-NAD, beta-Nicotinamide adenine dinucleotide	C21H26N7O14P2	-1	Mitochondria
nad	Nicotinamide adenine dinucleotide	NAD, NAD+, beta-Diphosphopyridine Nucleotide, beta-NAD, beta-Nicotinamide adenine dinucleotide	C21H26N7O14P2	-1	Nucleus
nad	Nicotinamide adenine dinucleotide	NAD, NAD+, beta-Diphosphopyridine Nucleotide, beta-NAD, beta-Nicotinamide adenine dinucleotide	C21H26N7O14P2	-1	Endoplasmic Reticulum
nad	Nicotinamide adenine dinucleotide	NAD, NAD+, beta-Diphosphopyridine Nucleotide, beta-NAD, beta-Nicotinamide adenine dinucleotide	C21H26N7O14P2	-1	Peroxisome
nadh	Nicotinamide adenine dinucleotide - reduced	DPNH, NADH	C21H27N7O14P2	-2	Cytosol
nadh	Nicotinamide adenine dinucleotide - reduced	DPNH, NADH	C21H27N7O14P2	-2	Mitochondria
nadh	Nicotinamide adenine dinucleotide - reduced	DPNH, NADH	C21H27N7O14P2	-2	Endoplasmic Reticulum
nadh	Nicotinamide adenine dinucleotide - reduced	DPNH, NADH	C21H27N7O14P2	-2	Peroxisome
nadp	Nicotinamide adenine dinucleotide phosphate	NADP, NADP+, beta-Nicotinamide adenine dinucleotide phosphate	C21H25N7O17P3	-3	Cytosol
nadp	Nicotinamide adenine dinucleotide phosphate	NADP, NADP+, beta-Nicotinamide adenine dinucleotide phosphate	C21H25N7O17P3	-3	Extracellular
nadp	Nicotinamide adenine dinucleotide phosphate	NADP, NADP+, beta-Nicotinamide adenine dinucleotide phosphate	C21H25N7O17P3	-3	Mitochondria
nadp	Nicotinamide adenine dinucleotide phosphate	NADP, NADP+, beta-Nicotinamide adenine dinucleotide phosphate	C21H25N7O17P3	-3	Nucleus

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
nadp	Nicotinamide adenine dinucleotide phosphate	NADP, NADP+, beta-Nicotinamide adenine dinucleotide phosphate	C21H25N7O17P3	-3	Endoplasmic Reticulum
nadp	Nicotinamide adenine dinucleotide phosphate	NADP, NADP+, beta-Nicotinamide adenine dinucleotide phosphate	C21H25N7O17P3	-3	Peroxisome
nadph	Nicotinamide adenine dinucleotide phosphate - reduced	NADPH, TPNH, beta-triphosphopyridine nucleotide	C21H26N7O17P3	-4	Cytosol
nadph	Nicotinamide adenine dinucleotide phosphate - reduced	NADPH, TPNH, beta-triphosphopyridine nucleotide	C21H26N7O17P3	-4	Mitochondria
nadph	Nicotinamide adenine dinucleotide phosphate - reduced	NADPH, TPNH, beta-triphosphopyridine nucleotide	C21H26N7O17P3	-4	Nucleus
nadph	Nicotinamide adenine dinucleotide phosphate - reduced	NADPH, TPNH, beta-triphosphopyridine nucleotide	C21H26N7O17P3	-4	Endoplasmic Reticulum
nadph	Nicotinamide adenine dinucleotide phosphate - reduced	NADPH, TPNH, beta-triphosphopyridine nucleotide	C21H26N7O17P3	-4	Peroxisome
naglc2p_L	N-Acetyl-D-glucosaminyldiphosphodolichol, human liver homolog	N-Acetyl-D-glucosaminyl-diphosphodolichol	C1160H1898N10O120P20	-20	Cytosol
naglc2p_U	N-Acetyl-D-glucosaminyldiphosphodolichol, human uterine homolog		C1105H1810N10O120P20	-20	Cytosol
ncam	Nicotinamide	Niacinamide, Nicotinic acid amide, Vitamin PP	C6H6N2O	0	Cytosol
ncam	Nicotinamide	Niacinamide, Nicotinic acid amide, Vitamin PP	C6H6N2O	0	Extracellular
Ndmelys	Protein N6,N6-dimethyl-L-lysine	Protein N6,N6-dimethyl-L-lysine	C2H7X	2	Nucleus
nformanth	N-Formylanthranilate	2-(Formylamino)-benzoic acid, Formylanthranilate	C8H6NO3	-1	Cytosol
nh4	Ammonium	NH3	H4N	1	Cytosol
nh4	Ammonium	NH3	H4N	1	Extracellular
nh4	Ammonium	NH3	H4N	1	Mitochondria
nh4	Ammonium	NH3	H4N	1	Nucleus
nh4	Ammonium	NH3	H4N	1	Endoplasmic Reticulum
nh4	Ammonium	NH3	H4N	1	Peroxisome
nicrns	Nicotinate D-ribonucleoside		C11H13NO6	0	Cytosol
nicrnt	Nicotinate D-ribonucleotide	Nicotinate ribonucleotide, Nicotinic acid ribonucleotide, beta-Nicotinate D-ribonucleotide	C11H12NO9P	-2	Cytosol
nicrnt	Nicotinate D-ribonucleotide	Nicotinate ribonucleotide, Nicotinic acid ribonucleotide, beta-Nicotinate D-ribonucleotide	C11H12NO9P	-2	Mitochondria
nicrnt	Nicotinate D-ribonucleotide	Nicotinate ribonucleotide, Nicotinic acid ribonucleotide, beta-Nicotinate D-ribonucleotide	C11H12NO9P	-2	Nucleus
nifedipine	nifedipine	Adalat [MeSH: Nifedipine], Hexadilat, Introcar, Kordafen, Nifedicor, Oxcord, Procardia, Procardia [MeSH: Nifedipine], Tibricol, nifedipine [MeSH: Nifedipine]	C17H18N2O6	0	Cytosol
nifedipine	nifedipine	Adalat [MeSH: Nifedipine], Hexadilat, Introcar, Kordafen, Nifedicor, Oxcord, Procardia, Procardia [MeSH: Nifedipine], Tibricol, nifedipine [MeSH: Nifedipine]	C17H18N2O6	0	Extracellular
nm2masn	(N-acetyl-D-glucosaminyl-(alpha-D-mannosyl)2-beta-D-mannosyl-diacetylchitobiosyl)-L-asparagine (protein)		C42H70N3O30X	0	Golgi Apparatus
nm4masn	(N-acetyl-D-glucosaminyl-(alpha-D-mannosyl)4-beta-D-mannosyl-diacetylchitobiosyl)-L-asparagine (protein)		C54H90N3O40X	0	Golgi Apparatus
Nmelys	Histone N6-methyl-L-lysine		CXH4	1	Nucleus
nmn	NMN	Nicotinamide D-ribonucleotide, Nicotinamide mononucleotide, Nicotinamide ribonucleotide	C11H14N2O8P	-1	Cytosol
nmn	NMN	Nicotinamide D-ribonucleotide, Nicotinamide mononucleotide, Nicotinamide ribonucleotide	C11H14N2O8P	-1	Mitochondria
nmn	NMN	Nicotinamide D-ribonucleotide, Nicotinamide mononucleotide, Nicotinamide ribonucleotide	C11H14N2O8P	-1	Nucleus
nmptrc	N-Methylputrescine		C5H16N2	2	Cytosol
nmthsrtn	N-Methylserotonin		C11H15N2O	1	Cytosol
no	Nitric oxide	NO, Nitrogen monoxide	NO	0	Cytosol
no	Nitric oxide	NO, Nitrogen monoxide	NO	0	Extracellular
normete-L	L-Normetanephrine		C9H14NO3	1	Cytosol
npthl	Naphthalene		C10H8	0	Cytosol
npthl	Naphthalene		C10H8	0	Extracellular
nrpphr	Norepinephrine	2-benzenediol, 4-[(1R)-2-Amino-1-hydroxyethyl]-1 Arterenol, L-Noradrenaline, Noradrenaline	C8H12NO3	1	Cytosol
nrpphr	Norepinephrine	2-benzenediol, 4-[(1R)-2-Amino-1-hydroxyethyl]-1 Arterenol, L-Noradrenaline, Noradrenaline	C8H12NO3	1	Extracellular
nrpphrsf	Sulfate derivative of norepinephrine		C8H11NO6S	0	Cytosol
nrpphrsf	Sulfate derivative of norepinephrine		C8H11NO6S	0	Extracellular
nrvnc	nervonic acid	(Z)-15-Tetracosenoic acid, Nervonic acid, tetracos-15-enoic acid	C24H45O2	-1	Cytosol
nrvnc	nervonic acid	(Z)-15-Tetracosenoic acid, Nervonic acid, tetracos-15-enoic acid	C24H45O2	-1	Extracellular
nrvnccoa	nervonyl coenzyme A		C45H76N7O17P3S	-4	Cytosol
nrvnccoa	nervonyl coenzyme A		C45H76N7O17P3S	-4	Mitochondria
nrvnccoa	nervonyl coenzyme A		C45H76N7O17P3S	-4	Peroxisome
nrvnccrn	Nervonyl carnitine	nervonic acid - carnitine	C31H59NO4	0	Cytosol
nrvnccrn	Nervonyl carnitine	nervonic acid - carnitine	C31H59NO4	0	Mitochondria
ntm2amep	N-Trimethyl-2-aminoethylphosphonate	2-Trimethylaminoethylphosphonate	C5H13NO3P	-1	Cytosol
Ntmelys	Protein N6,N6,N6-trimethyl-L-lysine	Protein N6,N6,N6-trimethyl-L-lysine	C3H10X	3	Nucleus
Ntmelys	Protein N6,N6,N6-trimethyl-L-lysine	Protein N6,N6,N6-trimethyl-L-lysine	C3H10X	3	Endoplasmic Reticulum

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
nwharg	N-(omega)-Hydroxyarginine		C6H15N4O3	1	Cytosol
o2	O2	Oxygen, dioxygen	O2	0	Cytosol
o2	O2	Oxygen, dioxygen	O2	0	Extracellular
o2	O2	Oxygen, dioxygen	O2	0	Mitochondria
o2	O2	Oxygen, dioxygen	O2	0	Nucleus
o2	O2	Oxygen, dioxygen	O2	0	Endoplasmic Reticulum
o2	O2	Oxygen, dioxygen	O2	0	Peroxisome
o2s	Superoxide anion	O2 free radical, O2.-	O2	-1	Cytosol
o2s	Superoxide anion	O2 free radical, O2.-	O2	-1	Extracellular
o2s	Superoxide anion	O2 free radical, O2.-	O2	-1	Mitochondria
o2s	Superoxide anion	O2 free radical, O2.-	O2	-1	Nucleus
o2s	Superoxide anion	O2 free radical, O2.-	O2	-1	Peroxisome
oaa	Oxaloacetate	2-oxobutanedioic acid, Oxalacetic acid, Oxaloacetic acid, Oxosuccinic acid	C4H2O5	-2	Cytosol
oaa	Oxaloacetate	2-oxobutanedioic acid, Oxalacetic acid, Oxaloacetic acid, Oxosuccinic acid	C4H2O5	-2	Mitochondria
oaa	Oxaloacetate	2-oxobutanedioic acid, Oxalacetic acid, Oxaloacetic acid, Oxosuccinic acid	C4H2O5	-2	Peroxisome
oagd3_hs	9-O-Acetylated GD3 (homo sapiens)	(Gal)1 (Glc)1 (Neu5Ac)1 (Neu5Ac9Ac)1 (Cer)1, 9-O-Ac-GD3, 9-O-Acetyl-GD3, 9-O-Acetylated GD3 CD60b	C54H90N3O29FULLRCO	-2	Cytosol
oagd3_hs	9-O-Acetylated GD3 (homo sapiens)	(Gal)1 (Glc)1 (Neu5Ac)1 (Neu5Ac9Ac)1 (Cer)1, 9-O-Ac-GD3, 9-O-Acetyl-GD3, 9-O-Acetylated GD3 CD60b	C54H90N3O29FULLRCO	-2	Extracellular
oagd3_hs	9-O-Acetylated GD3 (homo sapiens)	(Gal)1 (Glc)1 (Neu5Ac)1 (Neu5Ac9Ac)1 (Cer)1, 9-O-Ac-GD3, 9-O-Acetyl-GD3, 9-O-Acetylated GD3 CD60b	C54H90N3O29FULLRCO	-2	Golgi Apparatus
oagt3_hs	9-O-Acetylated GT3 (homo sapiens)	(Gal)1 (Glc)1 (Neu5Ac)2 (Neu5Ac9Ac)1 (Cer)1, 9-O-Ac-GT3, 9-O-Acetylated GT3	C65H106N4O37FULLRCO	-3	Cytosol
oagt3_hs	9-O-Acetylated GT3 (homo sapiens)	(Gal)1 (Glc)1 (Neu5Ac)2 (Neu5Ac9Ac)1 (Cer)1, 9-O-Ac-GT3, 9-O-Acetylated GT3	C65H106N4O37FULLRCO	-3	Extracellular
oagt3_hs	9-O-Acetylated GT3 (homo sapiens)	(Gal)1 (Glc)1 (Neu5Ac)2 (Neu5Ac9Ac)1 (Cer)1, 9-O-Ac-GT3, 9-O-Acetylated GT3	C65H106N4O37FULLRCO	-3	Golgi Apparatus
occoa	Octanoyl-CoA (n-C8:0CoA)		C29H46N7O17P3S	-4	Cytosol
occoa	Octanoyl-CoA (n-C8:0CoA)		C29H46N7O17P3S	-4	Mitochondria
occoa	Octanoyl-CoA (n-C8:0CoA)		C29H46N7O17P3S	-4	Peroxisome
ocdca	octadecanoate (n-C18:0)	Octadecanoic acid, Stearate, Stearic acid	C18H35O2	-1	Cytosol
ocdca	octadecanoate (n-C18:0)	Octadecanoic acid, Stearate, Stearic acid	C18H35O2	-1	Extracellular
ocdcaACP	Octadecanoyl-ACP (n-C18:0ACP)	stearoyl-ACP	C29H55N2O8PRS	-1	Cytosol
ocdcea	octadecenoate (n-C18:1)	(9Z)-Octadecenoic acid, (Z)-Octadec-9-enoic acid, Oleic acid, octadecenoic acid, oleate	C18H33O2	-1	Cytosol
ocdcea	octadecenoate (n-C18:1)	(9Z)-Octadecenoic acid, (Z)-Octadec-9-enoic acid, Oleic acid, octadecenoic acid, oleate	C18H33O2	-1	Extracellular
ocdcya	octadecadienoate (n-C18:2)	9,12-Octadecadienoic acid, octadecadienoic acid	C18H31O2	-1	Cytosol
ocdcyaACP	Octadecynoyl-ACP (n-C18:2ACP)		C29H51N2O8PRS	-1	Cytosol
octa	octanoate (n-C8:0)	Caprylic acid, Octanoic acid, Octylic acid	C8H15O2	-1	Cytosol
octa	octanoate (n-C8:0)	Caprylic acid, Octanoic acid, Octylic acid	C8H15O2	-1	Extracellular
octeACP	cis-octadec-11-enoyl-[acyl-carrier protein] (n-C18:1)	Octadecenoyl-ACP (n-C18:1ACP), cis-vacc-11-enoyl-[acyl-carrier protein] (n-C18:1)	C29H53N2O8PRS	-1	Cytosol
od2coa	trans-Octadec-2-enoyl-CoA	elaidic acid coenzyme A	C39H64N7O17P3S	-4	Cytosol
od2coa	trans-Octadec-2-enoyl-CoA	elaidic acid coenzyme A	C39H64N7O17P3S	-4	Mitochondria
odecoa	Octadecenoyl-CoA (n-C18:1CoA)	Oleoyl-CoA	C39H64N7O17P3S	-4	Cytosol
odecoa	Octadecenoyl-CoA (n-C18:1CoA)	Oleoyl-CoA	C39H64N7O17P3S	-4	Mitochondria
odecoa	Octadecenoyl-CoA (n-C18:1CoA)	Oleoyl-CoA	C39H64N7O17P3S	-4	Peroxisome
odecrn	octadecenoyl carnitine		C25H47NO4	0	Cytosol
odecrn	octadecenoyl carnitine		C25H47NO4	0	Mitochondria
oh1	hydroxide ion	HO-, OH-	HO	-1	Cytosol
oh1	hydroxide ion	HO-, OH-	HO	-1	Extracellular
oh1	hydroxide ion	HO-, OH-	HO	-1	Mitochondria
omeprazole	omeprazole	Demeprazol, Dudencer, Emeproton, Epirazole, Gastrimut, Gastroloc, Gibancer, Indurgan, Inhibitron, omeprazole [MeSH: Omeprazole]	C17H19N3O3S	0	Cytosol
omeprazole	omeprazole	Demeprazol, Dudencer, Emeproton, Epirazole, Gastrimut, Gastroloc, Gibancer, Indurgan, Inhibitron, omeprazole [MeSH: Omeprazole]	C17H19N3O3S	0	Extracellular
onpthl	naphthalene epoxide		C10H8O	0	Cytosol
onpthl	naphthalene epoxide		C10H8O	0	Extracellular
oretn	4-oxo-retonoic acid		C20H27O3	-1	Cytosol
oretn	4-oxo-retonoic acid		C20H27O3	-1	Nucleus
orn	Ornithine	2,5-Diaminopentanoate, 2,5-Diaminopentanoic acid, 2,5-Diaminovaleric acid, L-Ornithine	C5H13N2O2	1	Cytosol
orn	Ornithine	2,5-Diaminopentanoate, 2,5-Diaminopentanoic acid, 2,5-Diaminovaleric acid, L-Ornithine	C5H13N2O2	1	Extracellular
orn	Ornithine	2,5-Diaminopentanoate, 2,5-Diaminopentanoic acid, 2,5-Diaminovaleric acid, L-Ornithine	C5H13N2O2	1	Mitochondria
orn-D	D-Ornithine		C5H13N2O2	1	Peroxisome
orot	Orotate	Orotic acid, Uracil-6-carboxylic acid	C5H3N2O4	-1	Cytosol
orot5p	Orotidine 5'-phosphate	Orotidylic acid	C10H10N2O11P	-3	Cytosol
oxa	Oxalate	Ethanedioic acid, Oxalic acid	C2O4	-2	Cytosol

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
oxa	Oxalate	Ethanedioic acid, Oxalic acid	C2O4	-2	Extracellular
oxa	Oxalate	Ethanedioic acid, Oxalic acid	C2O4	-2	Peroxisome
pa_hs	phosphatidic acid (homo sapiens)	phosphatidate	C3H5O4PFULLRCO2FULLR2CO2	-2	Cytosol
pa_hs	phosphatidic acid (homo sapiens)	phosphatidate	C3H5O4PFULLRCO2FULLR2CO2	-2	Golgi Apparatus
pa_hs	phosphatidic acid (homo sapiens)	phosphatidate	C3H5O4PFULLRCO2FULLR2CO2	-2	Mitochondria
pa_hs	phosphatidic acid (homo sapiens)	phosphatidate	C3H5O4PFULLRCO2FULLR2CO2	-2	Nucleus
pa_hs	phosphatidic acid (homo sapiens)	phosphatidate	C3H5O4PFULLRCO2FULLR2CO2	-2	Endoplasmic Reticulum
pac	Phenylacetic acid	Benzeneacetiic acid, Benzylformic acid, Phenylacetate	C8H7O2	-1	Cytosol
pacald	Phenylacetaldehyde	alpha-Tolualdehyde	C8H8O	0	Cytosol
paf_hs	1-alkyl 2-acteylglycerol 3-phosphocholine (homo sapiens)	1-Alkyl-2-acetyl-sn-glycero-3-phosphocholine, PA platelet activating factor	C11H23O4NPFULLRCO2	0	Cytosol
paf_hs	1-alkyl 2-acteylglycerol 3-phosphocholine (homo sapiens)	1-Alkyl-2-acetyl-sn-glycero-3-phosphocholine, PA platelet activating factor	C11H23O4NPFULLRCO2	0	Extracellular
pail_hs	phosphatidylinositol (homo sapiens)	PtdIns	C9H16O9PFULLRCO2FULLR2CO2	-1	Cytosol
pail_hs	phosphatidylinositol (homo sapiens)	PtdIns	C9H16O9PFULLRCO2FULLR2CO2	-1	Nucleus
pail_hs	phosphatidylinositol (homo sapiens)	PtdIns	C9H16O9PFULLRCO2FULLR2CO2	-1	Endoplasmic Reticulum
pail345p_hs	phosphatidylinositol-3,4,5-trisphosphate (Homo sapiens)	PIP3, PtdIns(3,4,5)P3	C9H13O18P4FULLRCO2FULLR2CO2	-7	Cytosol
pail345p_hs	phosphatidylinositol-3,4,5-trisphosphate (Homo sapiens)	PIP3, PtdIns(3,4,5)P3	C9H13O18P4FULLRCO2FULLR2CO2	-7	Nucleus
pail34p_hs	phosphatidylinositol-3,4-bisphosphate (Homo sapiens)		C9H14O15P3FULLRCO2FULLR2CO2	-5	Cytosol
pail34p_hs	phosphatidylinositol-3,4-bisphosphate (Homo sapiens)		C9H14O15P3FULLRCO2FULLR2CO2	-5	Nucleus
pail34p_hs	phosphatidylinositol-3,4-bisphosphate (Homo sapiens)		C9H14O15P3FULLRCO2FULLR2CO2	-5	Endoplasmic Reticulum
pail35p_hs	phosphatidylinositol-3,5-bisphosphate (Homo sapiens)		C9H14O15P3FULLRCO2FULLR2CO2	-5	Cytosol
pail35p_hs	phosphatidylinositol-3,5-bisphosphate (Homo sapiens)		C9H14O15P3FULLRCO2FULLR2CO2	-5	Endoplasmic Reticulum
pail3p_hs	1-Phosphatidyl-1D-myo-inositol 3-phosphate (Homo sapiens)		C9H15O12P2FULLRCO2FULLR2CO2	-3	Cytosol
pail3p_hs	1-Phosphatidyl-1D-myo-inositol 3-phosphate (Homo sapiens)		C9H15O12P2FULLRCO2FULLR2CO2	-3	Nucleus
pail3p_hs	1-Phosphatidyl-1D-myo-inositol 3-phosphate (Homo sapiens)		C9H15O12P2FULLRCO2FULLR2CO2	-3	Endoplasmic Reticulum
pail45p_hs	phosphatidylinositol 4,5-bisphosphate (Homo sapiens)	PIP2, PtdIns(4,5)P2, phosphatidylinositol disphosphate	C9H14O15P3FULLRCO2FULLR2CO2	-5	Cytosol
pail45p_hs	phosphatidylinositol 4,5-bisphosphate (Homo sapiens)	PIP2, PtdIns(4,5)P2, phosphatidylinositol disphosphate	C9H14O15P3FULLRCO2FULLR2CO2	-5	Nucleus
pail4p_hs	1-Phosphatidyl-1D-myo-inositol 4-phosphate (Homo sapiens)	PIP, PtdIns4P	C9H15O12P2FULLRCO2FULLR2CO2	-3	Cytosol
pail4p_hs	1-Phosphatidyl-1D-myo-inositol 4-phosphate (Homo sapiens)	PIP, PtdIns4P	C9H15O12P2FULLRCO2FULLR2CO2	-3	Nucleus
pail4p_hs	1-Phosphatidyl-1D-myo-inositol 4-phosphate (Homo sapiens)	PIP, PtdIns4P	C9H15O12P2FULLRCO2FULLR2CO2	-3	Endoplasmic Reticulum
pail5p_hs	1-Phosphatidyl-1D-myo-inositol 5-phosphate (Homo sapiens)		C9H15O12P2FULLRCO2FULLR2CO2	-3	Cytosol
pail5p_hs	1-Phosphatidyl-1D-myo-inositol 5-phosphate (Homo sapiens)		C9H15O12P2FULLRCO2FULLR2CO2	-3	Nucleus
pail5p_hs	1-Phosphatidyl-1D-myo-inositol 5-phosphate (Homo sapiens)		C9H15O12P2FULLRCO2FULLR2CO2	-3	Endoplasmic Reticulum
palmACP	Palmitoyl-ACP (n-C16:0ACP)	Hexadecanoyl-[acp], Hexadecanoyl-[acyl-carrier protein], fa8-ACP, hexadecanoyl-ACP	C27H51N2O8PRS	-1	Cytosol
pan4p	Pantetheine 4'-phosphate	4'-Phosphopantetheine, Phosphopantetheine	C11H21N2O7PS	-2	Cytosol
pap	Adenosine 3',5'-bisphosphate	3'-Phosphoadenylate, PAP, Phosphoadenosine phosphate	C10H11N5O10P2	-4	Cytosol
pap	Adenosine 3',5'-bisphosphate	3'-Phosphoadenylate, PAP, Phosphoadenosine phosphate	C10H11N5O10P2	-4	Golgi Apparatus
paps	3'-Phosphoadenylyl sulfate	3'-Phospho-5'-adenylyl sulfate, 3'-Phosphoadenosine 5'-phosphosulfate, PAPS	C10H11N5O13P2S	-4	Cytosol
paps	3'-Phosphoadenylyl sulfate	3'-Phospho-5'-adenylyl sulfate, 3'-Phosphoadenosine 5'-phosphosulfate, PAPS	C10H11N5O13P2S	-4	Golgi Apparatus
pchol_hs	Phosphatidylcholine (homo sapiens)		C8H18NO4PFULLRCO2FULLR2CO2	0	Cytosol
pchol_hs	Phosphatidylcholine (homo sapiens)		C8H18NO4PFULLRCO2FULLR2CO2	0	Extracellular
pchol_hs	Phosphatidylcholine (homo sapiens)		C8H18NO4PFULLRCO2FULLR2CO2	0	Golgi Apparatus
pchol_hs	Phosphatidylcholine (homo sapiens)		C8H18NO4PFULLRCO2FULLR2CO2	0	Mitochondria
pchol_hs	Phosphatidylcholine (homo sapiens)		C8H18NO4PFULLRCO2FULLR2CO2	0	Endoplasmic Reticulum
pcollg5hlys	Procollagen 5-hydroxy-L-lysine		C6H14N2O3	0	Cytosol
pcollglys	Procollagen L-lysine		C7H14N3O2R2	1	Cytosol
pcreat	Phosphocreatine		C4H9N3O5P	-1	Cytosol
pcreat	Phosphocreatine		C4H9N3O5P	-1	Mitochondria
pcrn	propionyl-carnitine		C10H19NO4	0	Cytosol
pcrn	propionyl-carnitine		C10H19NO4	0	Mitochondria
pcrn	propionyl-carnitine		C10H19NO4	0	Peroxisome

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
pd3	Previtamin D3		C27H44O	0	Cytosol
pdx5p	Pyridoxine 5'-phosphate	Pyridoxine 5-phosphate, Pyridoxine phosphate	C8H10NO6P	-2	Cytosol
pe_hs	phosphatidylethanolamine (homo sapiens)		C5H12NO4PFULLRCO2FULLR2CO2	0	Cytosol
pe_hs	phosphatidylethanolamine (homo sapiens)		C5H12NO4PFULLRCO2FULLR2CO2	0	Extracellular
pe_hs	phosphatidylethanolamine (homo sapiens)		C5H12NO4PFULLRCO2FULLR2CO2	0	Golgi Apparatus
pe_hs	phosphatidylethanolamine (homo sapiens)		C5H12NO4PFULLRCO2FULLR2CO2	0	Mitochondria
pe_hs	phosphatidylethanolamine (homo sapiens)		C5H12NO4PFULLRCO2FULLR2CO2	0	Endoplasmic Reticulum
peamn	Phenethylamine	2-Phenylethylamine, Phenethylamine, Phenylethylamine, beta-Phenylethylamine	C8H12N	1	Cytosol
pecgon	pseudoecgonine		C9H14NO3	-1	Endoplasmic Reticulum
pecgoncoa	Pseudoecgonyl-CoA		C30H46N8O18P3S	-3	Endoplasmic Reticulum
pep	Phosphoenolpyruvate	PEP, Phosphoenolpyruvic acid	C3H2O6P	-3	Cytosol
pep	Phosphoenolpyruvate	PEP, Phosphoenolpyruvic acid	C3H2O6P	-3	Mitochondria
peplys	Peptidyl-L-lysine	L-Lysine-protein, Protein lysine	XH	0	Extracellular
peplys	Peptidyl-L-lysine	L-Lysine-protein, Protein lysine	XH	0	Nucleus
pepslys	peptide sans lysine	peptide without lysine (cleaved)	X	0	Endoplasmic Reticulum
peracd	Perillic acid		C10H13O2	-1	Cytosol
peracd	Perillic acid		C10H13O2	-1	Mitochondria
perillyl	Perillyl alcohol	(-)-Perillyl alcohol, Perillyl alcohol	C10H16O	0	Cytosol
perillyl	Perillyl alcohol	(-)-Perillyl alcohol, Perillyl alcohol	C10H16O	0	Extracellular
pglyc_hs	phosphatidylglycerol (homo sapiens)		C6H12O6PFULLRCO2FULLR2CO2	-1	Cytosol
pglyc_hs	phosphatidylglycerol (homo sapiens)		C6H12O6PFULLRCO2FULLR2CO2	-1	Extracellular
pgp_hs	phosphatidyl glycerol phosphate (homo sapiens)		C6H11O9P2FULLRCO2FULLR2CO2	-3	Cytosol
phaccoa	Phenylacetyl-CoA		C29H38N7O17P3S	-4	Cytosol
pheacgln	alpha-N-Phenylacetyl-L-glutamine		C13H16N2O4	0	Cytosol
pheacgln	alpha-N-Phenylacetyl-L-glutamine		C13H16N2O4	0	Extracellular
phe-L	L-Phenylalanine	(S)-Phenylalanine, (S)-alpha-amino-beta-phenylpropionic acid, 3-phenylalanine	C9H11NO2	0	Cytosol
phe-L	L-Phenylalanine	(S)-Phenylalanine, (S)-alpha-amino-beta-phenylpropionic acid, 3-phenylalanine	C9H11NO2	0	Extracellular
phe-L	L-Phenylalanine	(S)-Phenylalanine, (S)-alpha-amino-beta-phenylpropionic acid, 3-phenylalanine	C9H11NO2	0	Mitochondria
pheme	Protoheme	Haem, Heme, Heme B, hemeB	C34H30FeN4O4	-2	Cytosol
pheme	Protoheme	Haem, Heme, Heme B, hemeB	C34H30FeN4O4	-2	Extracellular
pheme	Protoheme	Haem, Heme, Heme B, hemeB	C34H30FeN4O4	-2	Mitochondria
phom	O-Phospho-L-homoserine		C4H8NO6P	-2	Cytosol
phpyr	Phenylpyruvate	3-Phenyl-2-oxopropanoate, Phenylpyruvic acid, alpha-Ketohydrocinnamic acid, keto-Phenylpyruvate	C9H7O3	-1	Cytosol
phpyr	Phenylpyruvate	3-Phenyl-2-oxopropanoate, Phenylpyruvic acid, alpha-Ketohydrocinnamic acid, keto-Phenylpyruvate	C9H7O3	-1	Mitochondria
phyQ	Phylloquinone	2-Methyl-3-phytyl-1,4-naphthoquinone, Phylloquinone, Phytonadione, Vitamin K1	C31H46O2	0	Cytosol
phyQ	Phylloquinone	2-Methyl-3-phytyl-1,4-naphthoquinone, Phylloquinone, Phytonadione, Vitamin K1	C31H46O2	0	Extracellular
phyt	phytanic acid	Phytanate, Phytanic acid	C20H39O2	-1	Cytosol
phyt	phytanic acid	Phytanate, Phytanic acid	C20H39O2	-1	Extracellular
phyt	phytanic acid	Phytanate, Phytanic acid	C20H39O2	-1	Peroxisome
phyt2ohcoa	2-Hydroxyphytanoyl-CoA		C41H70N7O18P3S	-4	Peroxisome
phytcoa	phytanyl coa	Phytanoyl-CoA, phytanic acid coenzyme a, phytanyl coa, phytanyl coenzyme a	C41H70N7O17P3S	-4	Cytosol
phytcoa	phytanyl coa	Phytanoyl-CoA, phytanic acid coenzyme a, phytanyl coa, phytanyl coenzyme a	C41H70N7O17P3S	-4	Peroxisome
pi	Phosphate	Orthophosphate, Phosphoric acid, Pi	HO4P	-2	Cytosol
pi	Phosphate	Orthophosphate, Phosphoric acid, Pi	HO4P	-2	Extracellular
pi	Phosphate	Orthophosphate, Phosphoric acid, Pi	HO4P	-2	Golgi Apparatus
pi	Phosphate	Orthophosphate, Phosphoric acid, Pi	HO4P	-2	Lysosome
pi	Phosphate	Orthophosphate, Phosphoric acid, Pi	HO4P	-2	Mitochondria
pi	Phosphate	Orthophosphate, Phosphoric acid, Pi	HO4P	-2	Nucleus
pi	Phosphate	Orthophosphate, Phosphoric acid, Pi	HO4P	-2	Endoplasmic Reticulum
pi	Phosphate	Orthophosphate, Phosphoric acid, Pi	HO4P	-2	Peroxisome
pmtcoa	Palmitoyl-CoA (n-C16:0CoA)	Hexadecanoyl-CoA	C37H62N7O17P3S	-4	Cytosol
pmtcoa	Palmitoyl-CoA (n-C16:0CoA)	Hexadecanoyl-CoA	C37H62N7O17P3S	-4	Mitochondria
pmtcoa	Palmitoyl-CoA (n-C16:0CoA)	Hexadecanoyl-CoA	C37H62N7O17P3S	-4	Peroxisome
pmtcrn	L-Palmitoylcarnitine		C23H45NO4	0	Cytosol
pmtcrn	L-Palmitoylcarnitine		C23H45NO4	0	Mitochondria
pnto-R	(R)-Pantothenate	D-Pantothenate, Pantothenate, Pantothenic acid	C9H16NO5	-1	Cytosol
pnto-R	(R)-Pantothenate	D-Pantothenate, Pantothenate, Pantothenic acid	C9H16NO5	-1	Extracellular
pnto-R	(R)-Pantothenate	D-Pantothenate, Pantothenate, Pantothenic acid	C9H16NO5	-1	Mitochondria
ppa	Propionate (n-C3:0)	Propanoate, Propanoic acid, Propionic acid	C3H5O2	-1	Cytosol
ppa	Propionate (n-C3:0)	Propanoate, Propanoic acid, Propionic acid	C3H5O2	-1	Extracellular

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
ppa	Propionate (n-C3:0)	Propanoate, Propanoic acid, Propionic acid	C3H5O2	-1	Mitochondria
ppbng	Porphobilinogen		C10H13N2O4	-1	Cytosol
ppcoa	Propanoyl-CoA	Propionyl coenzyme A, Propionyl-CoA	C24H36N7O17P3S	-4	Cytosol
ppcoa	Propanoyl-CoA	Propionyl coenzyme A, Propionyl-CoA	C24H36N7O17P3S	-4	Mitochondria
ppcoa	Propanoyl-CoA	Propionyl coenzyme A, Propionyl-CoA	C24H36N7O17P3S	-4	Peroxisome
ppi	Diphosphate	PPi, Pyrophosphate, Pyrophosphoric acid	HO7P2	-3	Cytosol
ppi	Diphosphate	PPi, Pyrophosphate, Pyrophosphoric acid	HO7P2	-3	Mitochondria
ppi	Diphosphate	PPi, Pyrophosphate, Pyrophosphoric acid	HO7P2	-3	Nucleus
ppi	Diphosphate	PPi, Pyrophosphate, Pyrophosphoric acid	HO7P2	-3	Endoplasmic Reticulum
ppi	Diphosphate	PPi, Pyrophosphate, Pyrophosphoric acid	HO7P2	-3	Peroxisome
ppmi12346p	5-Diphosphoinositol pentakisphosphate	5-PP-InsP5	C6H6O27P7	-13	Cytosol
ppmi12346p	5-Diphosphoinositol pentakisphosphate	5-PP-InsP5	C6H6O27P7	-13	Nucleus
ppmi1346p	Diphosphoinositol tetrakisphosphate		C6H7O24P6	-11	Cytosol
ppmi1346p	Diphosphoinositol tetrakisphosphate		C6H7O24P6	-11	Nucleus
ppp9	Protoporphyrin	Porphyrinogen IX, Protoporphyrin IX	C34H32N4O4	-2	Mitochondria
pppg9	Protoporphyrinogen IX		C34H38N4O4	-2	Cytosol
pppg9	Protoporphyrinogen IX		C34H38N4O4	-2	Mitochondria
pppi	Inorganic triphosphate		HO10P3	-4	Cytosol
pppi	Inorganic triphosphate		HO10P3	-4	Mitochondria
pppi	Inorganic triphosphate		HO10P3	-4	Nucleus
pram	5-Phospho-beta-D-ribosylamine	5-Phospho-D-ribosylamine, 5-Phosphoribosyl-1-amine, 5-Phosphoribosylamine	C5H11NO7P	-1	Cytosol
pre_prot	glycophosphatidylinositol (GPI)-anchored protein precursor		XY	0	Endoplasmic Reticulum
prgnlone	Pregnenolone	3beta-Hydroxypregn-5-en-20-one, 5-Pregnen-3beta-ol-20-one	C21H32O2	0	Cytosol
prgnlone	Pregnenolone	3beta-Hydroxypregn-5-en-20-one, 5-Pregnen-3beta-ol-20-one	C21H32O2	0	Mitochondria
prgnlone	Pregnenolone	3beta-Hydroxypregn-5-en-20-one, 5-Pregnen-3beta-ol-20-one	C21H32O2	0	Endoplasmic Reticulum
prgnlones	pregnenolone sulfate	3beta-Hydroxypregn-5-en-20-one sulfate, 5-Pregnen-3beta-ol-20-one sulfate	C21H31O5S	-1	Cytosol
prgnlones	pregnenolone sulfate	3beta-Hydroxypregn-5-en-20-one sulfate, 5-Pregnen-3beta-ol-20-one sulfate	C21H31O5S	-1	Endoplasmic Reticulum
prgstrn	Progesterone	4-Pregnene-3,20-dione	C21H30O2	0	Cytosol
prgstrn	Progesterone	4-Pregnene-3,20-dione	C21H30O2	0	Endoplasmic Reticulum
prist	pristanic acid	pristanic acid	C19H37O2	-1	Cytosol
prist	pristanic acid	pristanic acid	C19H37O2	-1	Peroxisome
pristanal	pristanal		C19H38O	0	Cytosol
pristanal	pristanal		C19H38O	0	Peroxisome
pristcoa	pristanoyl coa	pristanic acid coenzyme a, pristanoyl coa, pristanoyl coenzyme a	C40H68N7O17P3S	-4	Cytosol
pristcoa	pristanoyl coa	pristanic acid coenzyme a, pristanoyl coa, pristanoyl coenzyme a	C40H68N7O17P3S	-4	Peroxisome
pro-D	D-Proline	D-Pyrrolidine-2-carboxylic acid	C5H9NO2	0	Cytosol
pro-D	D-Proline	D-Pyrrolidine-2-carboxylic acid	C5H9NO2	0	Extracellular
pro-D	D-Proline	D-Pyrrolidine-2-carboxylic acid	C5H9NO2	0	Lysosome
pro-D	D-Proline	D-Pyrrolidine-2-carboxylic acid	C5H9NO2	0	Peroxisome
pro-L	L-Proline	2-Pyrrolidinecarboxylic acid, Pro	C5H9NO2	0	Cytosol
pro-L	L-Proline	2-Pyrrolidinecarboxylic acid, Pro	C5H9NO2	0	Extracellular
pro-L	L-Proline	2-Pyrrolidinecarboxylic acid, Pro	C5H9NO2	0	Lysosome
pro-L	L-Proline	2-Pyrrolidinecarboxylic acid, Pro	C5H9NO2	0	Mitochondria
pro-L	L-Proline	2-Pyrrolidinecarboxylic acid, Pro	C5H9NO2	0	Endoplasmic Reticulum
prostg1	(13E)-11alpha-Hydroxy-9,15-dioxoprost-13-enoate	(13E)-11alpha-Hydroxy-9,15-dioxoprost-13-enoate	C20H31O5	-1	Cytosol
prostgd2	Prostaglandin D2	(5Z, 13-dienoate, 13E)-(15S)-9alpha, 15-Dihydroxy-11-oxoprosta-5	C20H31O5	-1	Cytosol
prostgd2	Prostaglandin D2	(5Z, 13-dienoate, 13E)-(15S)-9alpha, 15-Dihydroxy-11-oxoprosta-5	C20H31O5	-1	Extracellular
prostgd2	Prostaglandin D2	(5Z, 13-dienoate, 13E)-(15S)-9alpha, 15-Dihydroxy-11-oxoprosta-5	C20H31O5	-1	Endoplasmic Reticulum
prostge1	Prostaglandin E1	(13E)-(15S)-11alpha,15-Dihydroxy-9-oxoprost-13-enoate, Alprostadil, Befar, Prink, Prostaglandin E1	C20H33O5	-1	Cytosol
prostge1	Prostaglandin E1	(13E)-(15S)-11alpha,15-Dihydroxy-9-oxoprost-13-enoate, Alprostadil, Befar, Prink, Prostaglandin E1	C20H33O5	-1	Extracellular
prostge2	Prostaglandin E2	(5Z, 13-dienoate, 13E)-(15S)-11alpha, 15-Dihydroxy-9-oxoprost-13-enoate, 15-Dihydroxy-9-oxoprosta-5	C20H31O5	-1	Cytosol
prostge2	Prostaglandin E2	(5Z, 13-dienoate, 13E)-(15S)-11alpha, 15-Dihydroxy-9-oxoprost-13-enoate, 15-Dihydroxy-9-oxoprosta-5	C20H31O5	-1	Extracellular
prostge2	Prostaglandin E2	(5Z, 13-dienoate, 13E)-(15S)-11alpha, 15-Dihydroxy-9-oxoprost-13-enoate, 15-Dihydroxy-9-oxoprosta-5	C20H31O5	-1	Endoplasmic Reticulum
prostgf2	Prostaglandin F2alpha	(+)-Prostaglandin F2a, Amoglandin, Cyclosin, Dinoprost, Enzaprost, Enzaprost F, PGF2a, Panacelan, Prostaglandin F2, Prostaglandin F2a, Prostarmon F, Prostin F 2 alpha, Protamodin, U 14583	C20H33O5	-1	Cytosol

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
prostgf2	Prostaglandin F2alpha	(+)-Prostaglandin F2a, Amoglandin, Cyclosin, Dinoprost, Enzaprost, Enzaprost F, PGF2a, Panacelan, Prostaglandin F2, Prostaglandin F2a, Prostarmon F, Prostin F 2 alpha, Protamodin, U 14583	C20H33O5	-1	Extracellular
prostgh2	Prostaglandin H2	(5Z, 11alpha-Epidioxy-15-hydroxyprosta-5, 13-dienoate, 13E)-(15S)-9alpha	C20H31O5	-1	Cytosol
prostgh2	Prostaglandin H2	(5Z, 11alpha-Epidioxy-15-hydroxyprosta-5, 13-dienoate, 13E)-(15S)-9alpha	C20H31O5	-1	Endoplasmic Reticulum
prostgi2	Prostaglandin I2	$dienoate, (5Z, 13-, 13E)-(15S)-6, 15-dihydroxyprosta-5, 9alpha-Epoxy-11alpha, PGI2, Prostacyclin	C20H31O5	-1	Endoplasmic Reticulum
prpncoa	Propenoyl-CoA	Acryloyl-CoA, Acrylyl-CoA	C24H34N7O17P3S	-4	Mitochondria
prpncoa	Propenoyl-CoA	Acryloyl-CoA, Acrylyl-CoA	C24H34N7O17P3S	-4	Peroxisome
prpp	5-Phospho-alpha-D-ribose 1-diphosphate	5-Phosphoribosyl 1-pyrophosphate, 5-Phosphoribosyl diphosphate, PRPP	C5H8O14P3	-5	Cytosol
ps_hs	phosphatidylserine (homo sapiens)	1,2-Diacyl-sn-glycerol 3-phospho-L-serine, 3-O-sn-Phosphatidyl-L-serine, O3-Phosphatidyl-L-serine, Phosphatidyl-L-serine	C6H11NO6PFULLRCO2FULLR2CO2	-1	Cytosol
ps_hs	phosphatidylserine (homo sapiens)	1,2-Diacyl-sn-glycerol 3-phospho-L-serine, 3-O-sn-Phosphatidyl-L-serine, O3-Phosphatidyl-L-serine, Phosphatidyl-L-serine	C6H11NO6PFULLRCO2FULLR2CO2	-1	Extracellular
ps_hs	phosphatidylserine (homo sapiens)	1,2-Diacyl-sn-glycerol 3-phospho-L-serine, 3-O-sn-Phosphatidyl-L-serine, O3-Phosphatidyl-L-serine, Phosphatidyl-L-serine	C6H11NO6PFULLRCO2FULLR2CO2	-1	Golgi Apparatus
ps_hs	phosphatidylserine (homo sapiens)	1,2-Diacyl-sn-glycerol 3-phospho-L-serine, 3-O-sn-Phosphatidyl-L-serine, O3-Phosphatidyl-L-serine, Phosphatidyl-L-serine	C6H11NO6PFULLRCO2FULLR2CO2	-1	Mitochondria
ps_hs	phosphatidylserine (homo sapiens)	1,2-Diacyl-sn-glycerol 3-phospho-L-serine, 3-O-sn-Phosphatidyl-L-serine, O3-Phosphatidyl-L-serine, Phosphatidyl-L-serine	C6H11NO6PFULLRCO2FULLR2CO2	-1	Endoplasmic Reticulum
pser-L	O-Phospho-L-serine	3-Phosphoserine	C3H6NO6P	-2	Cytosol
ptdca	pentadecanoate	Pentadecanoic acid;, n-Pentadecanoic Acid	C15H29O2	-1	Cytosol
ptdca	pentadecanoate	Pentadecanoic acid;, n-Pentadecanoic Acid	C15H29O2	-1	Extracellular
ptdcacoa	pentadecanoyl Coenzyme A	Pentadecanoic acid coenzyme a, n-Pentadecanoic Acid coa	C36H60N7O17P3S	-4	Cytosol
ptdcacoa	pentadecanoyl Coenzyme A	Pentadecanoic acid coenzyme a, n-Pentadecanoic Acid coa	C36H60N7O17P3S	-4	Mitochondria
ptdcacrn	pendtadenoyl carnitine	Pentadecanoic acid - carnitine, pentadecanoate carnitine	C22H43NO4	0	Cytosol
ptdcacrn	pendtadenoyl carnitine	Pentadecanoic acid - carnitine, pentadecanoate carnitine	C22H43NO4	0	Mitochondria
ptrc	Putrescine	1,4-Butanediamine, 1,4-Diaminobutane, Tetramethylenediamine	C4H14N2	2	Cytosol
ptrc	Putrescine	1,4-Butanediamine, 1,4-Diaminobutane, Tetramethylenediamine	C4H14N2	2	Mitochondria
ptth	Pantetheine		C11H22N2O4S	0	Cytosol
pyam5p	Pyridoxamine 5'-phosphate	Pyridoxamine 5-phosphate, Pyridoxamine phosphate	C8H12N2O5P	-1	Cytosol
pyam5p	Pyridoxamine 5'-phosphate	Pyridoxamine 5-phosphate, Pyridoxamine phosphate	C8H12N2O5P	-1	Mitochondria
pydam	Pyridoxamine	PM	C8H13N2O2	1	Cytosol
pydam	Pyridoxamine	PM	C8H13N2O2	1	Extracellular
pydx	Pyridoxal		C8H9NO3	0	Cytosol
pydx	Pyridoxal		C8H9NO3	0	Extracellular
pydx5p	Pyridoxal 5'-phosphate	Pyridoxal 5-phosphate, Pyridoxal phosphate	C8H8NO6P	-2	Cytosol
pydx5p	Pyridoxal 5'-phosphate	Pyridoxal 5-phosphate, Pyridoxal phosphate	C8H8NO6P	-2	Mitochondria
pydxn	Pyridoxine	Pyridoxol, vitamin b6	C8H11NO3	0	Cytosol
pydxn	Pyridoxine	Pyridoxol, vitamin b6	C8H11NO3	0	Extracellular
pylald	Perillyl aldehyde	Perillaldehyde	C10H14O	0	Cytosol
pylald	Perillyl aldehyde	Perillaldehyde	C10H14O	0	Mitochondria
pyr	Pyruvate	2-Ketopropionic Acid, 2-Oxopropanoate, 2-Oxopropanoic acid, Pyroracemic acid, Pyruvic acid, alpha-Ketopropionic acid	C3H3O3	-1	Cytosol
pyr	Pyruvate	2-Ketopropionic Acid, 2-Oxopropanoate, 2-Oxopropanoic acid, Pyroracemic acid, Pyruvic acid, alpha-Ketopropionic acid	C3H3O3	-1	Extracellular
pyr	Pyruvate	2-Ketopropionic Acid, 2-Oxopropanoate, 2-Oxopropanoic acid, Pyroracemic acid, Pyruvic acid, alpha-Ketopropionic acid	C3H3O3	-1	Mitochondria
pyr	Pyruvate	2-Ketopropionic Acid, 2-Oxopropanoate, 2-Oxopropanoic acid, Pyroracemic acid, Pyruvic acid, alpha-Ketopropionic acid	C3H3O3	-1	Peroxisome
q10	Ubiquinone-10	ubidecarenone	C59H90O4	0	Cytosol
q10	Ubiquinone-10	ubidecarenone	C59H90O4	0	Mitochondria
q10h2	Ubiquinol-10		C59H92O4	0	Cytosol
q10h2	Ubiquinol-10		C59H92O4	0	Mitochondria

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
quln	Quinolinate	2,3-Pyridinedicarboxylic acid, Pyridine-2,3-dicarboxylate, Quinolinic acid	C7H3NO4	-2	Cytosol
R1coa_hs	R group 1 Coenzyme A homo sapiens		XCO2C21H31N7O15P3S	-4	Cytosol
R1coa_hs	R group 1 Coenzyme A homo sapiens		XCO2C21H31N7O15P3S	-4	Endoplasmic Reticulum
r1p	alpha-D-Ribose 1-phosphate	D-Ribose 1-phosphate, Ribose 1-phosphate	C5H9O8P	-2	Cytosol
R2coa_hs	R group 2 Coenzyme A homo sapiens		XCO2C21H31N7O15P3S	-4	Cytosol
R2coa_hs	R group 2 Coenzyme A homo sapiens		XCO2C21H31N7O15P3S	-4	Endoplasmic Reticulum
R3coa_hs	R group 3 Coenzyme A homo sapiens		XCO2C21H31N7O15P3S	-4	Cytosol
R4coa_hs	R group 4 Coenzyme A homo sapiens		XCO2C21H31N7O15P3S	-4	Cytosol
R5coa_hs	R group 5 Coenzyme A homo sapiens		XCO2C21H31N7O15P3S	-4	Cytosol
r5p	alpha-D-Ribose 5-phosphate	D-Ribose 5-phosphate, D-Ribose-5-phosphate, Ribose 5-phosphate	C5H9O8P	-2	Cytosol
r5p	alpha-D-Ribose 5-phosphate	D-Ribose 5-phosphate, D-Ribose-5-phosphate, Ribose 5-phosphate	C5H9O8P	-2	Mitochondria
R6coa_hs	R group 6 Coenzyme A homo sapiens		XCO2C21H31N7O15P3S	-4	Cytosol
rbl-D	D-Ribulose	D-Arabinoketose, D-Arabinulose, D-Erythro-2-pentulose, D-Riboketose	C5H10O5	0	Cytosol
rbt	Ribitol	Adonitol	C5H12O5	0	Cytosol
rbt	Ribitol	Adonitol	C5H12O5	0	Extracellular
retfa	fatty acid retinol		C20H29OFULLR2CO	0	Cytosol
retfa	fatty acid retinol		C20H29OFULLR2CO	0	Extracellular
retinal	Retinal	Retinene, Vitamin A aldehyde, all-trans-Retinal, all-trans-Retinene, all-trans-Vitamin A aldehyde	C20H28O	0	Cytosol
retinal-11-cis	cis-11-retinal	11-cis-Retinal;, 11-cis-Retinene, 11-cis-Vitamin A aldehyde;	C20H28O	0	Cytosol
retinal-cis-13	cis-13-retinal		C20H28O	0	Cytosol
retinal-cis-9	cis-9-retinal		C20H28O	0	Cytosol
retinol	Retinol	Vitamin A, Vitamin A1, all-trans-Retinol	C20H30O	0	Cytosol
retinol	Retinol	Vitamin A, Vitamin A1, all-trans-Retinol	C20H30O	0	Extracellular
retinol-9-cis	9-cis-retinol		C20H30O	0	Cytosol
retinol-9-cis	9-cis-retinol		C20H30O	0	Extracellular
retinol-cis-11	cis-11-retinol		C20H30O	0	Cytosol
retinol-cis-11	cis-11-retinol		C20H30O	0	Extracellular
retinol-cis-13	cis-13-retinol		C20H30O	0	Cytosol
retn	Retinoate	(all-E)-, (all-E)-3, 2, 3, 4, 6, 6-trimethyl-1-cyclohexen-1-yl)-, 6-trimethyl-1-cyclohexen-1-yl)-6-trimethyl-1-cyclohexene-1-yl)-2, 7-Dimethyl-9-(2 7-dimethyl-9-(2, 8-Nonatetraenoic acid, 8-nonatetraenoic acid, 8-nonatetraenoic acid (ECL), AGN 100335, Acide retinoique (French) (DSL), German) (EINECS), Retin A, Retinoic acid, Ro 1-5488, Tretin M, Vitamin A acid, Vitamin A1 acid, all-(E)-Retinoic acid, all-trans-, all-trans-Retinoate, all-trans-Retinoic acid, all-trans-Tretinoin, all-trans-Vitamin A acid, all-trans-b-Retinoic acid, b-Retinoi acid, trans-Retinoic acid, tretinoin (English, tretinoine (French) (EINECS)	C20H27O2	-1	Cytosol
retn	Retinoate	(all-E)-, (all-E)-3, 2, 3, 4, 6, 6-trimethyl-1-cyclohexen-1-yl)-, 6-trimethyl-1-cyclohexen-1-yl)-6-trimethyl-1-cyclohexene-1-yl)-2, 7-Dimethyl-9-(2 7-dimethyl-9-(2, 8-Nonatetraenoic acid, 8-nonatetraenoic acid, 8-nonatetraenoic acid (ECL), AGN 100335, Acide retinoique (French) (DSL), German) (EINECS), Retin A, Retinoic acid, Ro 1-5488, Tretin M, Vitamin A acid, Vitamin A1 acid, all-(E)-Retinoic acid, all-trans-, all-trans-Retinoate, all-trans-Retinoic acid, all-trans-Tretinoin, all-trans-Vitamin A acid, all-trans-b-Retinoic acid, b-Retinoi acid, trans-Retinoic acid, tretinoin (English, tretinoine (French) (EINECS)	C20H27O2	-1	Extracellular
retn	Retinoate	(all-E)-, (all-E)-3, 2, 3, 4, 6, 6-trimethyl-1-cyclohexen-1-yl)-, 6-trimethyl-1-cyclohexen-1-yl)-6-trimethyl-1-cyclohexene-1-yl)-2, 7-Dimethyl-9-(2 7-dimethyl-9-(2, 8-Nonatetraenoic acid, 8-nonatetraenoic acid, 8-nonatetraenoic acid (ECL), AGN 100335, Acide retinoique (French) (DSL), German) (EINECS), Retin A, Retinoic acid, Ro 1-5488, Tretin M, Vitamin A acid, Vitamin A1 acid, all-(E)-Retinoic acid, all-trans-, all-trans-Retinoate, all-trans-Retinoic acid, all-trans-Tretinoin, all-trans-Vitamin A acid, all-trans-b-Retinoic acid, b-Retinoi acid, trans-Retinoic acid, tretinoin (English, tretinoine (French) (EINECS)	C20H27O2	-1	Nucleus

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
retn	Retinoate	(all-E)-, (all-E)-3, 2, 3, 4, 6, 6-trimethyl-1-cyclohexen-1-yl)-, 6-trimethyl-1-cyclohexen-1-yl)-6-trimethyl-1-cyclohexene-1-yl)-2, 7-Dimethyl-9-(2 7-dimethyl-9-(2, 8-Nonatetraenoic acid, 8-nonatetraenoic acid, 8-nonatetraenoic acid (ECL), AGN 100335, Acide retinoique (French) (DSL), German) (EINECS), Retin A, Retinoic acid, Ro 1-5488, Tretin M, Vitamin A acid, Vitamin A1 acid, all-(E)-Retinoic acid, all-trans-, all-trans-Retinoate, all-trans-Retinoic acid, all-trans-Tretinoin, all-trans-Vitamin A acid, all-trans-b-Retinoic acid, b-Retinoi acid, trans-Retinoic acid, tretinoin (English, tretinoine (French) (EINECS)	C20H27O2	-1	Endoplasmic Reticulum
retncoa	retinoyl CoA		C41H58N7O17P3S	-4	Cytosol
retnglc	retinoyl glucuronide	all-trans-Retinoyl-beta-glucuronide, retinoate glucuronide	C26H35O8	-1	Cytosol
retnglc	retinoyl glucuronide	all-trans-Retinoyl-beta-glucuronide, retinoate glucuronide	C26H35O8	-1	Extracellular
retnglc	retinoyl glucuronide	all-trans-Retinoyl-beta-glucuronide, retinoate glucuronide	C26H35O8	-1	Endoplasmic Reticulum
retpalm [deleted 10/09/2005 06:18:49 PM]	Retinyl palminate	Aquasol A (TN), Retinol palmitate;, Retinyl palmitate;, Vitamin A palmitate;, all-trans-Retinyl palmitate;	C36H60O2	0	Extracellular
rib-D	D-Ribose		C5H10O5	0	Cytosol
rib-D	D-Ribose		C5H10O5	0	Extracellular
ribflv	Riboflavin	7,8-Dimethyl-10-ribitylisoalloxazine, Lactoflavin, Vitamin B2	C17H20N4O6	0	Cytosol
ribflv	Riboflavin	7,8-Dimethyl-10-ribitylisoalloxazine, Lactoflavin, Vitamin B2	C17H20N4O6	0	Extracellular
rnam	N-Ribosylnicotinamide		C11H15N2O5	1	Cytosol
Rtotal	R total		CO2FULLR	-1	Cytosol
Rtotal	R total		CO2FULLR	-1	Extracellular
Rtotal	R total		CO2FULLR	-1	Lysosome
Rtotal	R total		CO2FULLR	-1	Peroxisome
Rtotal2	R total 2 position		CO2FULLR2	-1	Cytosol
Rtotal2	R total 2 position		CO2FULLR2	-1	Extracellular
Rtotal2coa	R total 2 coenzyme A		CO2FULLR2C21H31N7O15P3S	-4	Cytosol
Rtotal2coa	R total 2 coenzyme A		CO2FULLR2C21H31N7O15P3S	-4	Mitochondria
Rtotal2crn	R total 2 carnitine		CO2FULLR2C7H14NO2	0	Cytosol
Rtotal2crn	R total 2 carnitine		CO2FULLR2C7H14NO2	0	Mitochondria
Rtotal3	R total 3 position		CO2FULLR3	-1	Cytosol
Rtotal3	R total 3 position		CO2FULLR3	-1	Extracellular
Rtotal3coa	R total 3 Coenzyme A		CO2FULLR3C21H31N7O15P3S	-4	Cytosol
Rtotal3coa	R total 3 Coenzyme A		CO2FULLR3C21H31N7O15P3S	-4	Mitochondria
Rtotal3crn	R total 3 carnitine		CO2FULLR3C7H14NO2	0	Cytosol
Rtotal3crn	R total 3 carnitine		CO2FULLR3C7H14NO2	0	Mitochondria
Rtotalcoa	R total Coenzyme A		CO2FULLRC21H31N7O15P3S	-4	Cytosol
Rtotalcoa	R total Coenzyme A		CO2FULLRC21H31N7O15P3S	-4	Mitochondria
Rtotalcoa	R total Coenzyme A		CO2FULLRC21H31N7O15P3S	-4	Peroxisome
Rtotalcrn	R total carnitine		CO2FULLRC7H14NO2	0	Cytosol
Rtotalcrn	R total carnitine		CO2FULLRC7H14NO2	0	Mitochondria
ru5p-D	D-Ribulose 5-phosphate		C5H9O8P	-2	Cytosol
ru5p-D	D-Ribulose 5-phosphate		C5H9O8P	-2	Endoplasmic Reticulum
s2l2fn2m2masn	PA6	HpxB1	C90H145N6O65X	-2	Extracellular
s2l2fn2m2masn	PA6	HpxB1	C90H145N6O65X	-2	Golgi Apparatus
s2l2fn2m2masn	PA6	HpxB1	C90H145N6O65X	-2	Lysosome
s2l2n2m2m	de-Fuc form of PA6 (w/o peptide linkage)		C84H136N6O62	-2	Cytosol
s2l2n2m2m	de-Fuc form of PA6 (w/o peptide linkage)		C84H136N6O62	-2	Lysosome
s2l2n2m2masn	de-Fuc form of PA6		C84H135N6O61X	-2	Extracellular
s2l2n2m2masn	de-Fuc form of PA6		C84H135N6O61X	-2	Lysosome
s2l2n2m2mn	de-Fuc, reducing GlcNAc removed form of PA6 (w/o peptide linkage)		C76H123N5O57	-2	Cytosol
s2l2n2m2mn	de-Fuc, reducing GlcNAc removed form of PA6 (w/o peptide linkage)		C76H123N5O57	-2	Lysosome
s7p	Sedoheptulose 7-phosphate	altro-Heptulose 7-phosphate	C7H13O10P	-2	Cytosol
saccrp-L	L-Saccharopine	N6-(L-1,3-Dicarboxypropyl)-L-lysine, Saccharopine	C11H19N2O6	-1	Mitochondria
sarcs	Sarcosine	N-Methylglycine	C3H7NO2	0	Cytosol
sarcs	Sarcosine	N-Methylglycine	C3H7NO2	0	Extracellular
sarcs	Sarcosine	N-Methylglycine	C3H7NO2	0	Mitochondria
sarcs	Sarcosine	N-Methylglycine	C3H7NO2	0	Peroxisome
sbt-D	D-Sorbitol	Clucitol, D-Glucitol, D-Sorbit, D-Sorbitol, Glucitol Gulitol, L-gulitol, Sorbite	C6H14O6	0	Cytosol
seahcys	Se-Adenosylselenohomocysteine		C14H20N6O5Se	0	Cytosol
seahcys	Se-Adenosylselenohomocysteine		C14H20N6O5Se	0	Nucleus
seasmet	Se-Adenosylselenomethionine		C15H23N6O5Se	1	Cytosol
seasmet	Se-Adenosylselenomethionine		C15H23N6O5Se	1	Nucleus
sel	Selenate	Selenate, Selenic acid	O4Se	-2	Cytosol
sel	Selenate	Selenate, Selenic acid	O4Se	-2	Extracellular
selcys	Selenocysteine		C3H7NO2Se	0	Cytosol

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
selcyst	Selenocystathionine	Selenocystathionine	C7H14N2O4Se	0	Cytosol
selhcys	Selenohomocysteine		C4H9NO2Se	0	Cytosol
selmeth	Selenomethionine	Selenomethionine	C5H11NO2Se	0	Cytosol
seln	Selenide	Hydrogen selenide, Selenide	HSe	-1	Cytosol
selnp	Selenophosphate	Selenophosphate	H2O3PSe	-1	Cytosol
Ser/Thr	protein-linked serine or threonine residue (O-glycosylation site)		XH	0	Golgi Apparatus
Ser/Thr	protein-linked serine or threonine residue (O-glycosylation site)		XH	0	Lysosome
ser-D	D-Serine	D-2-Amino-3-hydroxypropanoic acid	C3H7NO3	0	Cytosol
ser-D	D-Serine	D-2-Amino-3-hydroxypropanoic acid	C3H7NO3	0	Extracellular
Ser-Gly/Ala-X-Gly	protein-linked serine residue (glycosaminoglycan attachment site)		XH	0	Lysosome
Ser-Gly/Ala-X-Gly	protein-linked serine residue (glycosaminoglycan attachment site)		XH	0	Endoplasmic Reticulum
ser-L	L-Serine	L-2-Amino-3-hydroxypropionic acid, L-3-Hydroxy-alanine, Ser	C3H7NO3	0	Cytosol
ser-L	L-Serine	L-2-Amino-3-hydroxypropionic acid, L-3-Hydroxy-alanine, Ser	C3H7NO3	0	Extracellular
ser-L	L-Serine	L-2-Amino-3-hydroxypropionic acid, L-3-Hydroxy-alanine, Ser	C3H7NO3	0	Mitochondria
ser-L	L-Serine	L-2-Amino-3-hydroxypropionic acid, L-3-Hydroxy-alanine, Ser	C3H7NO3	0	Peroxisome
Sfglutth	S-Formylglutathione		C11H16N3O7S	-1	Cytosol
sgalside_hs	sulfatide galactocerebroside (homo sapiens)	galatocerebroside 3-sulfate	C24H45NO10SFULLRCO	-1	Cytosol
sgalside_hs	sulfatide galactocerebroside (homo sapiens)	galatocerebroside 3-sulfate	C24H45NO10SFULLRCO	-1	Golgi Apparatus
sgalside_hs	sulfatide galactocerebroside (homo sapiens)	galatocerebroside 3-sulfate	C24H45NO10SFULLRCO	-1	Lysosome
sl-L	L-sulfolactate	(S)-3-sulfolactate	C3H4O6S	-2	Cytosol
sl-L	L-sulfolactate	(S)-3-sulfolactate	C3H4O6S	-2	Extracellular
sl-L	L-sulfolactate	(S)-3-sulfolactate	C3H4O6S	-2	Mitochondria
so3	Sulfite	Sulfurous acid	O3S	-2	Cytosol
so3	Sulfite	Sulfurous acid	O3S	-2	Mitochondria
so4	Sulfate	Sulfuric acid	O4S	-2	Cytosol
so4	Sulfate	Sulfuric acid	O4S	-2	Extracellular
so4	Sulfate	Sulfuric acid	O4S	-2	Lysosome
so4	Sulfate	Sulfuric acid	O4S	-2	Mitochondria
so4	Sulfate	Sulfuric acid	O4S	-2	Endoplasmic Reticulum
spc_hs	sphingosylphosphorylcholine (homo sapiens)		C23H50N2O5P	1	Cytosol
spc_hs	sphingosylphosphorylcholine (homo sapiens)		C23H50N2O5P	1	Extracellular
sph1p	Sphinganine 1-phosphate	Dihydrosphingosine 1-phosphate	C18H39NO5P	-1	Cytosol
sph1p	Sphinganine 1-phosphate	Dihydrosphingosine 1-phosphate	C18H39NO5P	-1	Extracellular
sph1p	Sphinganine 1-phosphate	Dihydrosphingosine 1-phosphate	C18H39NO5P	-1	Endoplasmic Reticulum
sphgn	Sphinganine	2-Amino-1, 3-dihydroxyoctadecane, Dihydrosphingosine	C18H40NO2	1	Cytosol
sphgn	Sphinganine	2-Amino-1, 3-dihydroxyoctadecane, Dihydrosphingosine	C18H40NO2	1	Endoplasmic Reticulum
sphings	Sphingosine	Sphingenine, Sphingoid	C18H38NO2	1	Cytosol
sphings	Sphingosine	Sphingenine, Sphingoid	C18H38NO2	1	Lysosome
sphings	Sphingosine	Sphingenine, Sphingoid	C18H38NO2	1	Endoplasmic Reticulum
sphmyln_hs	sphingomyelin (homo sapiens)		C23H48N2O5PFULLRCO	0	Cytosol
sphmyln_hs	sphingomyelin (homo sapiens)		C23H48N2O5PFULLRCO	0	Golgi Apparatus
sphmyln_hs	sphingomyelin (homo sapiens)		C23H48N2O5PFULLRCO	0	Lysosome
sphs1p	Sphingosine 1-phosphate	Sphing-4-enine 1-phosphate, Sphingosine 1-phosphate	C18H37NO5P	-1	Cytosol
sphs1p	Sphingosine 1-phosphate	Sphing-4-enine 1-phosphate, Sphingosine 1-phosphate	C18H37NO5P	-1	Extracellular
sphs1p	Sphingosine 1-phosphate	Sphing-4-enine 1-phosphate, Sphingosine 1-phosphate	C18H37NO5P	-1	Endoplasmic Reticulum
spmd	Spermidine	N-(3-Aminopropyl)-1,4-butane-diamine	C7H22N3	3	Cytosol
sprm	Spermine	4-butanediamine, N, N'-Bis(3-aminopropyl)-1	C10H30N4	4	Cytosol
sql	Squalene	Spinacene, Supraene	C30H50	0	Endoplasmic Reticulum
srtn	Serotonin	3-(2-Aminoethyl)-1H-indol-5-ol, 5-Hydroxytryptamine, Enteramine	C10H13N2O	1	Cytosol
srtn	Serotonin	3-(2-Aminoethyl)-1H-indol-5-ol, 5-Hydroxytryptamine, Enteramine	C10H13N2O	1	Extracellular
Ssq23epx	(S)-Squalene-2,3-epoxide	(S)-2, 3-Epoxysqualene, 3-epoxide, 3-oxide, Squalene 2	C30H50O	0	Endoplasmic Reticulum
sT_antigen	sialyl-T antigen	alpha-N-Acetylneuraminyl-2,3-beta-D-galactosyl-1,3-N-acetyl-alpha-D-galactosaminyl-R	C25H40N2O18X	-1	Golgi Apparatus
stcoa	Stearoyl-CoA (n-C18:0CoA)	Octadecanoyl-CoA, Stearyl-CoA	C39H66N7O17P3S	-4	Cytosol
stcoa	Stearoyl-CoA (n-C18:0CoA)	Octadecanoyl-CoA, Stearyl-CoA	C39H66N7O17P3S	-4	Mitochondria
stcoa	Stearoyl-CoA (n-C18:0CoA)	Octadecanoyl-CoA, Stearyl-CoA	C39H66N7O17P3S	-4	Peroxisome
stcrn	stearoylcarnitine		C25H49NO4	0	Cytosol
stcrn	stearoylcarnitine		C25H49NO4	0	Mitochondria
sTn_antigen	sialyl-Tn antigen	Glycano-(2,6-alpha-N-acetylneuraminyl)-(N-acetyl-D-galactosaminyl)-glycoprotein	C19H30N2O13X	-1	Golgi Apparatus
strch1	starch, structure 1 (1,6-{7[1,4-Glc], 4[1,4-Glc]})		C66H112O56	0	Extracellular
strch2	starch, structure 2 (1,6-{2[1,4-Glc], [1,4-Glc]})		C18H32O16	0	Extracellular
strdnc	stearidonic acid C18:4, n-3	Stearidonic acid, octadeca-6,9,12,15-tetraenoic acid	C18H27O2	-1	Cytosol
strdnc	stearidonic acid C18:4, n-3	Stearidonic acid, octadeca-6,9,12,15-tetraenoic acid	C18H27O2	-1	Extracellular
strdnccoa	stearidonyl coenzyme A	stearidonic acid CoA, stearidonic acid coenzyme A	C39H58N7O17P3S	-4	Cytosol
strdnccoa	stearidonyl coenzyme A	stearidonic acid CoA, stearidonic acid coenzyme A	C39H58N7O17P3S	-4	Mitochondria

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
strdnccoa	stearidonyl coenzyme A	stearidonic acid CoA, stearidonic acid coenzyme A	C39H58N7O17P3S	-4	Peroxisome
strdnccrn	stearidonyl carnitine	stearidonic acid carnitine	C25H41NO4	0	Cytosol
strdnccrn	stearidonyl carnitine	stearidonic acid carnitine	C25H41NO4	0	Mitochondria
succ	Succinate	Butanedionic acid, Ethylenesuccinic acid, Succinic acid	C4H4O4	-2	Cytosol
succ	Succinate	Butanedionic acid, Ethylenesuccinic acid, Succinic acid	C4H4O4	-2	Extracellular
succ	Succinate	Butanedionic acid, Ethylenesuccinic acid, Succinic acid	C4H4O4	-2	Mitochondria
succ	Succinate	Butanedionic acid, Ethylenesuccinic acid, Succinic acid	C4H4O4	-2	Endoplasmic Reticulum
succ	Succinate	Butanedionic acid, Ethylenesuccinic acid, Succinic acid	C4H4O4	-2	Peroxisome
succoa	Succinyl-CoA	Succinyl coenzyme A, succino-1-yl-coenzymeA	C25H35N7O19P3S	-5	Mitochondria
sucr	Sucrose	1-alpha-D-glucopyranosyl-2-beta-D-fructofuranoside, Cane sugar, Saccharose, Sugar	C12H22O11	0	Extracellular
sucsal	Succinic semialdehyde	4-Oxobutanoate, Succinate semialdehyde	C4H5O3	-1	Mitochondria
T_antigen	T antigen (core 1)	Core 1, Glycoprotein D-galactosyl-1,3-N-acetyl-D-galactosamine, beta-D-Galactosyl-1,3-N-acetyl-D-galactosaminyl-R, beta-D-Galactosyl-1,3-N-acetyl-alpha-D-galactosaminyl-R	C14H24NO10X	0	Golgi Apparatus
t2m26dcoa	trans-2-Methyl-5-isopropylhexa-2,5-dienoyl-CoA		C31H46N7O17P3S	-4	Mitochondria
t2m26dcoa	trans-2-Methyl-5-isopropylhexa-2,5-dienoyl-CoA		C31H46N7O17P3S	-4	Peroxisome
T4hcinnm	trans-4-Hydroxycinnamate	4-Coumarate, 4-Hydroxycinnamate, 4-Hydroxycinnamic acid, p-Coumaric acid	C9H7O3	-1	Cytosol
T4hcinnm	trans-4-Hydroxycinnamate	4-Coumarate, 4-Hydroxycinnamate, 4-Hydroxycinnamic acid, p-Coumaric acid	C9H7O3	-1	Mitochondria
tag_hs	triacylglycerol (homo sapiens)		C3H5FULLRCO2FULLR2CO2FULLR3CO2	0	Cytosol
tag_hs	triacylglycerol (homo sapiens)		C3H5FULLRCO2FULLR2CO2FULLR3CO2	0	Extracellular
tag1p-D	D-Tagatose 1-phosphate		C6H11O9P	-2	Cytosol
tagat-D	D-Tagatose	lyxo-Hexulose	C6H12O6	0	Cytosol
tagat-D	D-Tagatose	lyxo-Hexulose	C6H12O6	0	Extracellular
taur	Taurine	2-Aminoethanesulfonic acid	C2H7NO3S	0	Cytosol
taur	Taurine	2-Aminoethanesulfonic acid	C2H7NO3S	0	Extracellular
taur	Taurine	2-Aminoethanesulfonic acid	C2H7NO3S	0	Peroxisome
taxol	paclitaxel	LipoPac, Onxol, Paxceed, TAXOL, Taxol A [MeSH: Paclitaxel], paclitaxel [MeSH: Paclitaxel]	C47H31NO14	0	Cytosol
taxol	paclitaxel	LipoPac, Onxol, Paxceed, TAXOL, Taxol A [MeSH: Paclitaxel], paclitaxel [MeSH: Paclitaxel]	C47H31NO14	0	Extracellular
tchola	taurocholic acid	5-beta-cholanic acid-3-alpha-7-alpha-12-alpha-triol-N-(2-sulphoethyl-amide), Cholyltaurine, Taurocholate, Taurocholic acid, bile acid	C26H45NO7S	0	Cytosol
tchola	taurocholic acid	5-beta-cholanic acid-3-alpha-7-alpha-12-alpha-triol-N-(2-sulphoethyl-amide), Cholyltaurine, Taurocholate, Taurocholic acid, bile acid	C26H45NO7S	0	Extracellular
tchola	taurocholic acid	5-beta-cholanic acid-3-alpha-7-alpha-12-alpha-triol-N-(2-sulphoethyl-amide), Cholyltaurine, Taurocholate, Taurocholic acid, bile acid	C26H45NO7S	0	Peroxisome
tcynt	Thiocyanate	Thiocyanate, Thiocyanic acid	CNS	-1	Cytosol
tcynt	Thiocyanate	Thiocyanate, Thiocyanic acid	CNS	-1	Extracellular
tcynt	Thiocyanate	Thiocyanate, Thiocyanic acid	CNS	-1	Mitochondria
tdchola	taurochenodeoxycholate	Taurochenodeoxycholate, bile acid	C26H45NO6S	0	Cytosol
tdchola	taurochenodeoxycholate	Taurochenodeoxycholate, bile acid	C26H45NO6S	0	Extracellular
tdchola	taurochenodeoxycholate	Taurochenodeoxycholate, bile acid	C26H45NO6S	0	Peroxisome
tdcoa	Tetradecanoyl-CoA (n-C14:0CoA)	Myristoyl-CoA	C35H58N7O17P3S	-4	Cytosol
tdcoa	Tetradecanoyl-CoA (n-C14:0CoA)	Myristoyl-CoA	C35H58N7O17P3S	-4	Mitochondria
tdcoa	Tetradecanoyl-CoA (n-C14:0CoA)	Myristoyl-CoA	C35H58N7O17P3S	-4	Peroxisome
tdeACP	cis-tetradec-7-enoyl-[acyl-carrier protein] (n-C14:1)	Tetradecenoyl-ACP (n-C14:1ACP), cis-myristol-7-eoyl-[acyl-carrier protein] (n-C14:1)	C25H45N2O8PRS	-1	Cytosol
tethex3	tetracosahexaenoic acid, n-3		C24H35O2	-1	Cytosol
tethex3	tetracosahexaenoic acid, n-3		C24H35O2	-1	Extracellular
tethex3coa	tetracosahexaenoyl coenzyme A		C45H66N7O17P3S	-4	Cytosol
tethex3coa	tetracosahexaenoyl coenzyme A		C45H66N7O17P3S	-4	Peroxisome
tetpent3	tetracosapentaenoic acid, n-3		C24H37O2	-1	Cytosol
tetpent3	tetracosapentaenoic acid, n-3		C24H37O2	-1	Extracellular
tetpent3coa	tetracosapentaenoyl coenzyme A, n-3		C45H68N7O17P3S	-4	Cytosol
tetpent3coa	tetracosapentaenoyl coenzyme A, n-3		C45H68N7O17P3S	-4	Mitochondria
tetpent3coa	tetracosapentaenoyl coenzyme A, n-3		C45H68N7O17P3S	-4	Peroxisome
tetpent3crn	tetracosapentaenoyl carnitine		C31H51NO4	0	Cytosol
tetpent3crn	tetracosapentaenoyl carnitine		C31H51NO4	0	Mitochondria
tetpent6	tetracosapentaenoic acid, n-6	tetracosapentaenoate, n-6, tetracosapentaenoic acid n-6	C24H37O2	-1	Cytosol
tetpent6	tetracosapentaenoic acid, n-6	tetracosapentaenoate, n-6, tetracosapentaenoic acid n-6	C24H37O2	-1	Extracellular
tetpent6coa	tetracosapentaenoyl coenzyme A, n-6		C45H68N7O17P3S	-4	Cytosol
tetpent6coa	tetracosapentaenoyl coenzyme A, n-6		C45H68N7O17P3S	-4	Mitochondria
tetpent6coa	tetracosapentaenoyl coenzyme A, n-6		C45H68N7O17P3S	-4	Peroxisome

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
tetpent6crn	tetracosapentaenoyl carnitine		C31H51NO4	0	Cytosol
tetpent6crn	tetracosapentaenoyl carnitine		C31H51NO4	0	Mitochondria
tettet6	tetracosatetraenoic acid n-6		C24H39O2	-1	Cytosol
tettet6	tetracosatetraenoic acid n-6		C24H39O2	-1	Extracellular
tettet6coa	tetracosatetraenoyl coenzyme A		C45H70N7O17P3S	-4	Cytosol
tettet6coa	tetracosatetraenoyl coenzyme A		C45H70N7O17P3S	-4	Mitochondria
tettet6coa	tetracosatetraenoyl coenzyme A		C45H70N7O17P3S	-4	Peroxisome
tettet6crn	Tetracosatetraenoyl carnitine	tetracosatraenoic acid carnitine	C31H53NO4	0	Cytosol
tettet6crn	Tetracosatetraenoyl carnitine	tetracosatraenoic acid carnitine	C31H53NO4	0	Mitochondria
thbpt	Tetrahydrobiopterin	2-Amino-6-(1,2-dihydroxypropyl)-5,6,7,8-tetrahydoro-4(1H)-pteridinone, 5,6,7,8-Tetrahydrobiopterin, Tetrahydrobiopterin	C9H15N5O3	0	Cytosol
thbpt	Tetrahydrobiopterin	2-Amino-6-(1,2-dihydroxypropyl)-5,6,7,8-tetrahydoro-4(1H)-pteridinone, 5,6,7,8-Tetrahydrobiopterin, Tetrahydrobiopterin	C9H15N5O3	0	Nucleus
thbpt4acam	Tetrahydrobiopterin-4a-carbinolamine		C9H15N5O4	0	Cytosol
thcholoylcoa	3alpha,7alpha,24-Trihydroxy-5beta-cholestanoyl-CoA	3alpha,7alpha,24-Trihydroxy-5beta-cholestanoyl-CoA	C48H76N7O20P3S	-4	Peroxisome
thcholst	3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestan-26-al	3-alpha-7-alpha-12-alpha-trihydroxy-5-beta-cholestan-26-al	C27H46O4	0	Mitochondria
thcholstoic	3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestanoate	3-alpha-7-alpha-12-alpha-trihydroxy-5-beta-cholestanoic acid, 3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestan-26-oate, 3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestanoate	C27H45O5	-1	Mitochondria
thcholstoic	3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestanoate	3-alpha-7-alpha-12-alpha-trihydroxy-5-beta-cholestanoic acid, 3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestan-26-oate, 3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestanoate	C27H45O5	-1	Endoplasmic Reticulum
thcholstoic	3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestanoate	3-alpha-7-alpha-12-alpha-trihydroxy-5-beta-cholestanoic acid, 3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestan-26-oate, 3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestanoate	C27H45O5	-1	Peroxisome
thcrm_hs	trihexosyl ceramide (homo sapiens)	Gal(alpha 1->4)-Gal(beta 1->4)-Glc-Cer, Gal-Gal-Glc-Cer, Gal-Gal-Glu-Cer	C36H66NO17FULLRCO	0	Cytosol
thcrm_hs	trihexosyl ceramide (homo sapiens)	Gal(alpha 1->4)-Gal(beta 1->4)-Glc-Cer, Gal-Gal-Glc-Cer, Gal-Gal-Glu-Cer	C36H66NO17FULLRCO	0	Golgi Apparatus
thcys	Thiocysteine	Thiocysteine	C3H7NO2S2	0	Cytosol
thf	5,6,7,8-Tetrahydrofolate	(6S)-THFA, (6S)-Tetrahydrofolate, (6S)-Tetrahydrofolic acid, THF, Tetrahydrofolate, Tetrahydrofolic acid	C19H21N7O6	-2	Cytosol
thf	5,6,7,8-Tetrahydrofolate	(6S)-THFA, (6S)-Tetrahydrofolate, (6S)-Tetrahydrofolic acid, THF, Tetrahydrofolate, Tetrahydrofolic acid	C19H21N7O6	-2	Extracellular
thf	5,6,7,8-Tetrahydrofolate	(6S)-THFA, (6S)-Tetrahydrofolate, (6S)-Tetrahydrofolic acid, THF, Tetrahydrofolate, Tetrahydrofolic acid	C19H21N7O6	-2	Lysosome
thf	5,6,7,8-Tetrahydrofolate	(6S)-THFA, (6S)-Tetrahydrofolate, (6S)-Tetrahydrofolic acid, THF, Tetrahydrofolate, Tetrahydrofolic acid	C19H21N7O6	-2	Mitochondria
thm	Thiamin	Aneurin, Antiberiberi factor, Thiamine, Vitamin B1	C12H17N4OS	1	Cytosol
thm	Thiamin	Aneurin, Antiberiberi factor, Thiamine, Vitamin B1	C12H17N4OS	1	Extracellular
thm	Thiamin	Aneurin, Antiberiberi factor, Thiamine, Vitamin B1	C12H17N4OS	1	Mitochondria
thmmp	Thiamin monophosphate	TMP, Thiamin phosphate, Thiamine monophosphate, Thiamine phosphate	C12H16N4O4PS	-1	Cytosol
thmmp	Thiamin monophosphate	TMP, Thiamin phosphate, Thiamine monophosphate, Thiamine phosphate	C12H16N4O4PS	-1	Extracellular
thmmp	Thiamin monophosphate	TMP, Thiamin phosphate, Thiamine monophosphate, Thiamine phosphate	C12H16N4O4PS	-1	Mitochondria
thmpp	Thiamine diphosphate	TPP, ThPP, Thiamin diphosphate, Thiamin pyrophosphate, cocarboxylase	C12H16N4O7P2S	-2	Cytosol
thmpp	Thiamine diphosphate	TPP, ThPP, Thiamin diphosphate, Thiamin pyrophosphate, cocarboxylase	C12H16N4O7P2S	-2	Mitochondria
thmtp	Thiamin triphosphate	Thiamine triphosphate	C12H16N4O10P3S	-3	Cytosol
thmtp	Thiamin triphosphate	Thiamine triphosphate	C12H16N4O10P3S	-3	Extracellular
thp2c	2,3,4,5-Tetrahydropyridine-2-carboxylate	(R)-2,3,4,5-Tetrahydropyridine-2-carboxylate, delta-6-Piperideine-2-L-carboxylate	C6H8NO2	-1	Cytosol
thp2c	2,3,4,5-Tetrahydropyridine-2-carboxylate	(R)-2,3,4,5-Tetrahydropyridine-2-carboxylate, delta-6-Piperideine-2-L-carboxylate	C6H8NO2	-1	Peroxisome
thr-L	L-Threonine	2-Amino-3-hydroxybutyric acid, Thr	C4H9NO3	0	Cytosol
thr-L	L-Threonine	2-Amino-3-hydroxybutyric acid, Thr	C4H9NO3	0	Extracellular
thrnt	L-Threonate	L-Threonic acid	C4H7O5	-1	Cytosol
thym	Thymine	2,4-Dihydroxy-5-methylpyrimidine, T, Thy	C5H6N2O2	0	Cytosol
thym	Thymine	2,4-Dihydroxy-5-methylpyrimidine, T, Thy	C5H6N2O2	0	Extracellular
thymd	Thymidine	2'-Deoxythymidine, Deoxythymidine, dT	C10H14N2O5	0	Cytosol
thymd	Thymidine	2'-Deoxythymidine, Deoxythymidine, dT	C10H14N2O5	0	Extracellular
thymd	Thymidine	2'-Deoxythymidine, Deoxythymidine, dT	C10H14N2O5	0	Lysosome
thymd	Thymidine	2'-Deoxythymidine, Deoxythymidine, dT	C10H14N2O5	0	Mitochondria

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
thyox-L	L-Thyroxine	3,5,3'5'-Tetraiiodo-L-thyronine, O-(4-Hydroxy-3,5-diidophenyl)-3,5-diiodo-L-tyrosine, T4, Thyroxine, thyroid hormone	C15H11I4NO4	0	Cytosol
thyox-L	L-Thyroxine	3,5,3'5'-Tetraiiodo-L-thyronine, O-(4-Hydroxy-3,5-diidophenyl)-3,5-diiodo-L-tyrosine, T4, Thyroxine, thyroid hormone	C15H11I4NO4	0	Extracellular
tmlys	N6,N6,N6-Trimethyl-L-lysine	N6,N6,N6-Trimethyl-L-lysine	C9H20N2O2	0	Cytosol
tmlys	N6,N6,N6-Trimethyl-L-lysine	N6,N6,N6-Trimethyl-L-lysine	C9H20N2O2	0	Endoplasmic Reticulum
tmndnc	timnodonic acid C20:5, n-3	(5Z,8Z,11Z,14Z,17Z)-Eicosapentaenoate, 5,8,11,14,17-Eicosapentaenoic acid, (5Z,8Z,11Z,14Z,17Z)-, 5,8,11,14,17-Icosapentaenoic acid, Eicosapentaenoic acid, Icosapentaenoic acid, Icosapento, Icosapentum [INN-Latin], Timnodonic acid, cis-5,8,11,14,17-Eicosapentaenoic acid	C20H29O2	-1	Cytosol
tmndnc	timnodonic acid C20:5, n-3	(5Z,8Z,11Z,14Z,17Z)-Eicosapentaenoate, 5,8,11,14,17-Eicosapentaenoic acid, (5Z,8Z,11Z,14Z,17Z)-, 5,8,11,14,17-Icosapentaenoic acid, Eicosapentaenoic acid, Icosapentaenoic acid, Icosapento, Icosapentum [INN-Latin], Timnodonic acid, cis-5,8,11,14,17-Eicosapentaenoic acid	C20H29O2	-1	Extracellular
tmndnccoa	timnodonyl coenzyme A		C41H60N7O17P3S	-4	Cytosol
tmndnccoa	timnodonyl coenzyme A		C41H60N7O17P3S	-4	Mitochondria
tmndnccoa	timnodonyl coenzyme A		C41H60N7O17P3S	-4	Peroxisome
tmndnccrn	Timnodonyl carnitine	timnodonic acid carnitine	C27H43NO4	0	Cytosol
tmndnccrn	Timnodonyl carnitine	timnodonic acid carnitine	C27H43NO4	0	Mitochondria
Tn_antigen	Tn antigen	Glycoprotein N-acetyl-D-galactosamine	C8H14NO5X	0	Golgi Apparatus
Tn_antigen	Tn antigen	Glycoprotein N-acetyl-D-galactosamine	C8H14NO5X	0	Lysosome
tolbutamide	tolbutamide	Aglicid, Arkozal, Artosin, Butamide [MeSH: Tolbutamide], Diabetamid, Diabetol [MeSH: Tolbutamide], Diabuton, Diasulfon, Dirastan, tolbutamide [MeSH: Tolbutamide]	C12H18N2O3S	0	Cytosol
tolbutamide	tolbutamide	Aglicid, Arkozal, Artosin, Butamide [MeSH: Tolbutamide], Diabetamid, Diabetol [MeSH: Tolbutamide], Diabuton, Diasulfon, Dirastan, tolbutamide [MeSH: Tolbutamide]	C12H18N2O3S	0	Extracellular
trdox	Oxidized thioredoxin		X	0	Cytosol
trdox	Oxidized thioredoxin		X	0	Mitochondria
trdrd	Reduced thioredoxin		XH2	0	Cytosol
trdrd	Reduced thioredoxin		XH2	0	Mitochondria
tre	Trehalose	alpha, alpha'-Trehalose;, alpha,alpha-Trehalose	C12H22O11	0	Cytosol
tre	Trehalose	alpha, alpha'-Trehalose;, alpha,alpha-Trehalose	C12H22O11	0	Extracellular
triodthy	Triiodothyronine	3,3'5-Triiodo-L-thyronine, 3,5,3'-L-Triiodo-L-thyronine, 3,5,3'-Triiodothyronine, L-3,5,3'-Triiodothyronine, Liothyronine, T3	C15H12I3NO4	0	Cytosol
triodthy	Triiodothyronine	3,3'5-Triiodo-L-thyronine, 3,5,3'-L-Triiodo-L-thyronine, 3,5,3'-Triiodothyronine, L-3,5,3'-Triiodothyronine, Liothyronine, T3	C15H12I3NO4	0	Extracellular
triodthysuf	Triiodothyronine sulfate	IUPAC Name: 2-amino-3-[3,5-diiodo-4-(3-iodo-4-sulfooxy-phenoxy)-phenyl]-propanoic acid, L-Tyrosine, 3,5-diiodo-O-(3-iodo-4-(sulfooxy)phenyl)-31135-55-4, Triiodothyronine sulfuric ester	C15H11I3NO7S	-1	Cytosol
triodthysuf	Triiodothyronine sulfate	IUPAC Name: 2-amino-3-[3,5-diiodo-4-(3-iodo-4-sulfooxy-phenoxy)-phenyl]-propanoic acid, L-Tyrosine, 3,5-diiodo-O-(3-iodo-4-(sulfooxy)phenyl)-31135-55-4, Triiodothyronine sulfuric ester	C15H11I3NO7S	-1	Extracellular
trp-L	L-Tryptophan	(S)-alpha-amino-beta-(3-indolyl)-propionic acid	C11H12N2O2	0	Cytosol
trp-L	L-Tryptophan	(S)-alpha-amino-beta-(3-indolyl)-propionic acid	C11H12N2O2	0	Extracellular
trypta	Tryptamine	3-(2-Aminoethyl)indole	C10H13N2	1	Cytosol
ts3	Tachysterol 3		C27H44O	0	Cytosol
tststerone	Testosterone	17beta-Hydroxy-4-androsten-3-one	C19H28O2	0	Cytosol
tststerone	Testosterone	17beta-Hydroxy-4-androsten-3-one	C19H28O2	0	Endoplasmic Reticulum
tststeroneglc	testosterone glucuronide		C25H36O8	0	Cytosol
tststeroneglc	testosterone glucuronide		C25H36O8	0	Extracellular
tststeroneglc	testosterone glucuronide		C25H36O8	0	Endoplasmic Reticulum
tststerones	testosterone sulfate	17beta-(Sulfooxy)androst-4-en-3-one, Testosterone 17-sulphate, Testosterone-17-sulfate	C19H27O5S	-1	Cytosol
tststerones	testosterone sulfate	17beta-(Sulfooxy)androst-4-en-3-one, Testosterone 17-sulphate, Testosterone-17-sulfate	C19H27O5S	-1	Extracellular
tsul	Thiosulfate	Hyposulfite	O3S2	-2	Cytosol
tsul	Thiosulfate	Hyposulfite	O3S2	-2	Extracellular
tsul	Thiosulfate	Hyposulfite	O3S2	-2	Mitochondria
ttccoa	tetracosanoyl-CoA (n-C24:0CoA)		C45H78N7O17P3S	-4	Peroxisome

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
ttc-ggdp	trans,trans,cis-Geranylgeranyl diphosphate	trans,trans,cis-Geranylgeranyl pyrophosphate	C20H33O7P2	-3	Cytosol
ttdca	tetradecanoate (n-C14:0)	1-tridecanecarboxylic acid;, Myristate, Myristic Acid;, Myristic acid, Tetradecanoate;, crodacid;, emery 655;, hydrofol acid 1495;, hystrene 9014, myristic acid, n-Tetradecanoic Acid;, n-tetradecoic acid;, neo-fat 14;, univol u 3165;	C14H27O2	-1	Cytosol
ttdca	tetradecanoate (n-C14:0)	1-tridecanecarboxylic acid;, Myristate, Myristic Acid;, Myristic acid, Tetradecanoate;, crodacid;, emery 655;, hydrofol acid 1495;, hystrene 9014, myristic acid, n-Tetradecanoic Acid;, n-tetradecoic acid;, neo-fat 14;, univol u 3165;	C14H27O2	-1	Extracellular
ttdcea	tetradecenoate (n-C14:1)	tetradecenoic acid	C14H25O2	-1	Cytosol
ttdcrn	tetradecanoyl carnitine	myristic acid carnitine	C21H41NO4	0	Cytosol
ttdcrn	tetradecanoyl carnitine	myristic acid carnitine	C21H41NO4	0	Mitochondria
txa2	Thromboxane A2	$5,13-dien-1-oic acid, $dienoate, (5Z,13E)-(15S)-9alpha,11alpha-Epoxy-15-hydroxythromboxa-5,13-, (5Z,9alpha,11alpha,13E,15S)-9,11-Epoxy-15-hydroxythromboxa-, Thromboxane A2	C20H31O5	-1	Cytosol
txa2	Thromboxane A2	$5,13-dien-1-oic acid, $dienoate, (5Z,13E)-(15S)-9alpha,11alpha-Epoxy-15-hydroxythromboxa-5,13-, (5Z,9alpha,11alpha,13E,15S)-9,11-Epoxy-15-hydroxythromboxa-, Thromboxane A2	C20H31O5	-1	Extracellular
txa2	Thromboxane A2	$5,13-dien-1-oic acid, $dienoate, (5Z,13E)-(15S)-9alpha,11alpha-Epoxy-15-hydroxythromboxa-5,13-, (5Z,9alpha,11alpha,13E,15S)-9,11-Epoxy-15-hydroxythromboxa-, Thromboxane A2	C20H31O5	-1	Endoplasmic Reticulum
tym	Tyramine	2-(p-Hydroxyphenyl)ethylamine	C8H12NO	1	Cytosol
tymsf	Tyramine O-sulfate	IUPAC Name: 1-(2-aminoethyl)-4-sulfooxy-benzene, Phenol, 4-(2-aminoethyl)-, hydrogen sulfate (ester)	C8H11NO4S	0	Cytosol
tymsf	Tyramine O-sulfate	IUPAC Name: 1-(2-aminoethyl)-4-sulfooxy-benzene, Phenol, 4-(2-aminoethyl)-, hydrogen sulfate (ester)	C8H11NO4S	0	Extracellular
Tyr-ggn	Tyr-194 of apo-glycogenin protein (primer for glycogen synthesis)		XOH	0	Cytosol
Tyr-ggn	Tyr-194 of apo-glycogenin protein (primer for glycogen synthesis)		XOH	0	Extracellular
tyr-L	L-Tyrosine	(S)-2-Amino-3-(p-hydroxyphenyl)propionic acid, (S)-3-(p-Hydroxyphenyl)alanine	C9H11NO3	0	Cytosol
tyr-L	L-Tyrosine	(S)-2-Amino-3-(p-hydroxyphenyl)propionic acid, (S)-3-(p-Hydroxyphenyl)alanine	C9H11NO3	0	Extracellular
tyr-L	L-Tyrosine	(S)-2-Amino-3-(p-hydroxyphenyl)propionic acid, (S)-3-(p-Hydroxyphenyl)alanine	C9H11NO3	0	Mitochondria
uacgam	UDP-N-acetyl-D-glucosamine	UDP-GlcNAc, UDP-N-acetylglucosamine, common abbr: UDP-NAcGlc	C17H25N3O17P2	-2	Cytosol
uacgam	UDP-N-acetyl-D-glucosamine	UDP-GlcNAc, UDP-N-acetylglucosamine, common abbr: UDP-NAcGlc	C17H25N3O17P2	-2	Golgi Apparatus
udp	UDP	5'-uridylate diphosphate, Uridine 5'-diphosphate, uridine diphosphate	C9H11N2O12P2	-3	Cytosol
udp	UDP	5'-uridylate diphosphate, Uridine 5'-diphosphate, uridine diphosphate	C9H11N2O12P2	-3	Extracellular
udp	UDP	5'-uridylate diphosphate, Uridine 5'-diphosphate, uridine diphosphate	C9H11N2O12P2	-3	Golgi Apparatus
udp	UDP	5'-uridylate diphosphate, Uridine 5'-diphosphate, uridine diphosphate	C9H11N2O12P2	-3	Lysosome
udp	UDP	5'-uridylate diphosphate, Uridine 5'-diphosphate, uridine diphosphate	C9H11N2O12P2	-3	Mitochondria
udp	UDP	5'-uridylate diphosphate, Uridine 5'-diphosphate, uridine diphosphate	C9H11N2O12P2	-3	Nucleus
udp	UDP	5'-uridylate diphosphate, Uridine 5'-diphosphate, uridine diphosphate	C9H11N2O12P2	-3	Endoplasmic Reticulum
udpacgal	UDP-N-acetyl-D-galactosamine	UDP-GalNAc	C17H25N3O17P2	-2	Cytosol
udpacgal	UDP-N-acetyl-D-galactosamine	UDP-GalNAc	C17H25N3O17P2	-2	Golgi Apparatus
udpacgal	UDP-N-acetyl-D-galactosamine	UDP-GalNAc	C17H25N3O17P2	-2	Lysosome
udpacgal	UDP-N-acetyl-D-galactosamine	UDP-GalNAc	C17H25N3O17P2	-2	Endoplasmic Reticulum
udpg	UDPglucose	UDP-D-glucose	C15H22N2O17P2	-2	Cytosol
udpg	UDPglucose	UDP-D-glucose	C15H22N2O17P2	-2	Golgi Apparatus
udpg	UDPglucose	UDP-D-glucose	C15H22N2O17P2	-2	Endoplasmic Reticulum
udpgal	UDPgalactose	UDP-D-galactopyranose, UDP-D-galactose	C15H22N2O17P2	-2	Cytosol
udpgal	UDPgalactose	UDP-D-galactopyranose, UDP-D-galactose	C15H22N2O17P2	-2	Golgi Apparatus
udpglcur	UDP-D-glucuronate	UDP-GlcA, UDPglucuronate	C15H19N2O18P2	-3	Cytosol
udpglcur	UDP-D-glucuronate	UDP-GlcA, UDPglucuronate	C15H19N2O18P2	-3	Golgi Apparatus
udpglcur	UDP-D-glucuronate	UDP-GlcA, UDPglucuronate	C15H19N2O18P2	-3	Endoplasmic Reticulum
udpxyl	UDP-D-xylose	UDP-alpha-D-xylose, UDPxylose	C14H20N2O16P2	-2	Cytosol
udpxyl	UDP-D-xylose	UDP-alpha-D-xylose, UDPxylose	C14H20N2O16P2	-2	Golgi Apparatus
udpxyl	UDP-D-xylose	UDP-alpha-D-xylose, UDPxylose	C14H20N2O16P2	-2	Endoplasmic Reticulum

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
ump	UMP	5'Uridylic acid, Uridine 5'-monophosphate, Uridine monophosphate, Uridylic acid	C9H11N2O9P	-2	Cytosol
ump	UMP	5'Uridylic acid, Uridine 5'-monophosphate, Uridine monophosphate, Uridylic acid	C9H11N2O9P	-2	Extracellular
ump	UMP	5'Uridylic acid, Uridine 5'-monophosphate, Uridine monophosphate, Uridylic acid	C9H11N2O9P	-2	Golgi Apparatus
ump	UMP	5'Uridylic acid, Uridine 5'-monophosphate, Uridine monophosphate, Uridylic acid	C9H11N2O9P	-2	Lysosome
ump	UMP	5'Uridylic acid, Uridine 5'-monophosphate, Uridine monophosphate, Uridylic acid	C9H11N2O9P	-2	Mitochondria
ump	UMP	5'Uridylic acid, Uridine 5'-monophosphate, Uridine monophosphate, Uridylic acid	C9H11N2O9P	-2	Nucleus
ump	UMP	5'Uridylic acid, Uridine 5'-monophosphate, Uridine monophosphate, Uridylic acid	C9H11N2O9P	-2	Endoplasmic Reticulum
uppg3	Uroporphyrinogen III		C40H36N4O16	-8	Cytosol
ura	Uracil	2,4(1H,3H)-Pyrimidinedione, 2,4-Dihydroxypyrimidine, 2,4-dioxy pyrimidine, U	C4H4N2O2	0	Cytosol
ura	Uracil	2,4(1H,3H)-Pyrimidinedione, 2,4-Dihydroxypyrimidine, 2,4-dioxy pyrimidine, U	C4H4N2O2	0	Extracellular
urate	Urate	2,6,8-trioxypurine, 8-Hydroxyxanthine, Lithic acid, Uric acid, Uric oxide	C5H4N4O3	0	Cytosol
urate	Urate	2,6,8-trioxypurine, 8-Hydroxyxanthine, Lithic acid, Uric acid, Uric oxide	C5H4N4O3	0	Extracellular
urate	Urate	2,6,8-trioxypurine, 8-Hydroxyxanthine, Lithic acid, Uric acid, Uric oxide	C5H4N4O3	0	Peroxisome
urcan	Urocanate	2-Propenoic acid, 4-Imidazoleacrylic acid, Urocanic acid	C6H5N2O2	-1	Cytosol
urea	Urea	Carbamide, Carbamimidic acid, Carbonyl diamine, Isourea, aquadrate	CH4N2O	0	Cytosol
urea	Urea	Carbamide, Carbamimidic acid, Carbonyl diamine, Isourea, aquadrate	CH4N2O	0	Extracellular
urea	Urea	Carbamide, Carbamimidic acid, Carbonyl diamine, Isourea, aquadrate	CH4N2O	0	Mitochondria
uri	Uridine		C9H12N2O6	0	Cytosol
uri	Uridine		C9H12N2O6	0	Extracellular
uri	Uridine		C9H12N2O6	0	Lysosome
uri	Uridine		C9H12N2O6	0	Mitochondria
uri	Uridine		C9H12N2O6	0	Nucleus
utp	UTP	5'-uridylate triphosphate, Uridine 5'-triphosphate, Uridine triphosphate, rUTP	C9H11N2O15P3	-4	Cytosol
utp	UTP	5'-uridylate triphosphate, Uridine 5'-triphosphate, Uridine triphosphate, rUTP	C9H11N2O15P3	-4	Extracellular
utp	UTP	5'-uridylate triphosphate, Uridine 5'-triphosphate, Uridine triphosphate, rUTP	C9H11N2O15P3	-4	Mitochondria
utp	UTP	5'-uridylate triphosphate, Uridine 5'-triphosphate, Uridine triphosphate, rUTP	C9H11N2O15P3	-4	Nucleus
vacc	vaccenic acid	(E)-Octadec-11-enoic acid, 11-Octadecenoic acid, (E)-, 11-octadecenoic acid	C18H33O2	-1	Cytosol
vacc	vaccenic acid	(E)-Octadec-11-enoic acid, 11-Octadecenoic acid, (E)-, 11-octadecenoic acid	C18H33O2	-1	Extracellular
vacccoa	vaccenyl coenzyme A	vaccenyl CoA	C39H64N7O17P3S	-4	Cytosol
vacccoa	vaccenyl coenzyme A	vaccenyl CoA	C39H64N7O17P3S	-4	Mitochondria
vacccrn	Vaccenyl carnitine		C25H47NO4	0	Cytosol
vacccrn	Vaccenyl carnitine		C25H47NO4	0	Mitochondria
val-L	L-Valine	2-Amino-3-methylbutyric acid, 2-Aminoisovaleric acid, Val	C5H11NO2	0	Cytosol
val-L	L-Valine	2-Amino-3-methylbutyric acid, 2-Aminoisovaleric acid, Val	C5H11NO2	0	Extracellular
val-L	L-Valine	2-Amino-3-methylbutyric acid, 2-Aminoisovaleric acid, Val	C5H11NO2	0	Mitochondria
vitd2	Vitamin D2	Calciferol (TN);, Drisdol (TN), Ergocalciferol;	C28H44O	0	Cytosol
vitd2	Vitamin D2	Calciferol (TN);, Drisdol (TN), Ergocalciferol;	C28H44O	0	Extracellular
vitd2	Vitamin D2	Calciferol (TN);, Drisdol (TN), Ergocalciferol;	C28H44O	0	Mitochondria
vitd3	Vitamin D3		C27H44O	0	Cytosol
vitd3	Vitamin D3		C27H44O	0	Extracellular
vitd3	Vitamin D3		C27H44O	0	Mitochondria
wharachd	w-hydroxyl arachidonic acid	omega hydroxylated arachidonic acid	C20H31O3	-1	Endoplasmic Reticulum
whddca	omega hydroxy dodecanoate (n-C12:0)	omega hydroxy lauric acid	C12H23O3	-1	Cytosol
whddca	omega hydroxy dodecanoate (n-C12:0)	omega hydroxy lauric acid	C12H23O3	-1	Extracellular
whhdca	omega hydroxy hexadecanoate (n-C16:0)	omega hydroxy palmitic acid	C16H31O3	-1	Cytosol
whhdca	omega hydroxy hexadecanoate (n-C16:0)	omega hydroxy palmitic acid	C16H31O3	-1	Extracellular
whtststerone	w hydroxy testosterone	omega hydroxy testosterone	C19H28O3	0	Cytosol
whtststerone	w hydroxy testosterone	omega hydroxy testosterone	C19H28O3	0	Extracellular
whtststerone	w hydroxy testosterone	omega hydroxy testosterone	C19H28O3	0	Endoplasmic Reticulum
whttdca	omega hydroxy tetradecanoate (n-C14:0)	omega hydroxy myristic acid	C14H27O3	-1	Cytosol

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
whttdca	omega hydroxy tetradecanoate (n-C14:0)	omega hydroxy myristic acid	C14H27O3	-1	Extracellular
xan	Xanthine	2,6-Dioxopurine	C5H4N4O2	0	Cytosol
xan	Xanthine	2,6-Dioxopurine	C5H4N4O2	0	Peroxisome
xmp	Xanthosine 5'-phosphate	(9-D-Ribosylxanthine)-5'-phosphate, XMP, Xanthylic acid	C10H11N4O9P	-2	Cytosol
xol24oh	24-Hydroxycholesterol	Cerebrosterol, Cholest-5-ene-3,24-diol, Cholest-5-ene-3,24-diol, (3beta,24S)-	C27H46O2	0	Endoplasmic Reticulum
xol25oh	25-Hydroxycholesterol	5-Cholestene-3beta,25-diol, Cholest-5-ene-3beta,25-diol	C27H46O2	0	Endoplasmic Reticulum
xol27oh	27-Hydroxycholesterol	27-Hydroxycholesterol, 5-Cholesten-3beta,27-diol	C27H46O2	0	Mitochondria
xol27oh	27-Hydroxycholesterol	27-Hydroxycholesterol, 5-Cholesten-3beta,27-diol	C27H46O2	0	Endoplasmic Reticulum
xol7a	7 alpha-Hydroxycholesterol	7alpha-Hydroxycholesterol, Cholest-5-ene-3beta,7alpha-diol	C27H46O2	0	Endoplasmic Reticulum
xol7ah	7alpha-Hydroxy-5beta-cholestan-3-one	5-beta-cholestan-7-alpha-ol-3-one	C27H46O2	0	Cytosol
xol7ah2	3alpha,7alpha-Dihydroxy-5beta-cholestane	3alpha,7alpha-Dihydroxy-5beta-cholestane, 5-beta-cholestan-3-alpha-7-alpha-diol, 5beta-cholestane-3alpha,7alpha-diol	C27H48O2	0	Cytosol
xol7ah2	3alpha,7alpha-Dihydroxy-5beta-cholestane	3alpha,7alpha-Dihydroxy-5beta-cholestane, 5-beta-cholestan-3-alpha-7-alpha-diol, 5beta-cholestane-3alpha,7alpha-diol	C27H48O2	0	Mitochondria
xol7ah2	3alpha,7alpha-Dihydroxy-5beta-cholestane	3alpha,7alpha-Dihydroxy-5beta-cholestane, 5-beta-cholestan-3-alpha-7-alpha-diol, 5beta-cholestane-3alpha,7alpha-diol	C27H48O2	0	Endoplasmic Reticulum
xol7ah2al	3alpha,7alpha-Dihydroxy-5beta-cholestan-26-al	3alpha,7alpha-Dihydroxy-5beta-cholestan-26-al	C27H46O3	0	Mitochondria
xol7ah3	3alpha,7alpha,26-Trihydroxy-5beta-cholestane	3alpha,7alpha,26-Trihydroxy-5beta-cholestane, 5beta-Cholestane-3alpha,7alpha,26-triol	C27H48O3	0	Mitochondria
xol7aone	7alpha-Hydroxycholest-4-en-3-one	4-cholesten-7-alpha-ol-3-one	C27H44O2	0	Cytosol
xol7aone	7alpha-Hydroxycholest-4-en-3-one	4-cholesten-7-alpha-ol-3-one	C27H44O2	0	Endoplasmic Reticulum
xoldiolone	7alpha,12alpha-Dihydroxycholest-4-en-3-one	4-cholestan-7-alpha-12-alpha-diol-3-one, 7alpha,12alpha-Dihydroxycholest-4-en-3-one	C27H44O3	0	Cytosol
xoldiolone	7alpha,12alpha-Dihydroxycholest-4-en-3-one	4-cholestan-7-alpha-12-alpha-diol-3-one, 7alpha,12alpha-Dihydroxycholest-4-en-3-one	C27H44O3	0	Mitochondria
xoldiolone	7alpha,12alpha-Dihydroxycholest-4-en-3-one	4-cholestan-7-alpha-12-alpha-diol-3-one, 7alpha,12alpha-Dihydroxycholest-4-en-3-one	C27H44O3	0	Endoplasmic Reticulum
xoldioloneh	7alpha,12alpha-Dihydroxy-5beta-cholestan-3-one	5-beta-cholestan-7-alpha-12-alpha-3-one, 7alpha,12alpha-Dihydroxy-5beta-cholestan-3-one	C27H46O3	0	Cytosol
xolest_hs	cholesterol ester	Cholesterol ester	C27H45XCO2	0	Cytosol
xolest_hs	cholesterol ester	Cholesterol ester	C27H45XCO2	0	Extracellular
xolest_hs	cholesterol ester	Cholesterol ester	C27H45XCO2	0	Endoplasmic Reticulum
xolest2_hs	cholesterol ester (from FULLR2)		C27H45FULLR2CO2	0	Cytosol
xolest2_hs	cholesterol ester (from FULLR2)		C27H45FULLR2CO2	0	Extracellular
xoltetrol	3alpha,7alpha,12alpha,26-Tetrahydroxy-5beta-cholestane		C27H48O4	0	Mitochondria
xoltri24	7-alpha,24(S)-Dihydroxycholesterol	5-Cholesten-3-beta, 7 alpha, 24(S)-triol	C27H46O3	0	Cytosol
xoltri24	7-alpha,24(S)-Dihydroxycholesterol	5-Cholesten-3-beta, 7 alpha, 24(S)-triol	C27H46O3	0	Extracellular
xoltri24	7-alpha,24(S)-Dihydroxycholesterol	5-Cholesten-3-beta, 7 alpha, 24(S)-triol	C27H46O3	0	Endoplasmic Reticulum
xoltri25	7-alpha,25-Dihydroxycholesterol	5-Cholesten-3-beta, 7 alpha, 25-triol	C27H46O3	0	Cytosol
xoltri25	7-alpha,25-Dihydroxycholesterol	5-Cholesten-3-beta, 7 alpha, 25-triol	C27H46O3	0	Extracellular
xoltri25	7-alpha,25-Dihydroxycholesterol	5-Cholesten-3-beta, 7 alpha, 25-triol	C27H46O3	0	Endoplasmic Reticulum
xoltri27	7-alpha,27-Dihydroxycholesterol	5-Cholesten-3-beta, 7 alpha, 27-triol	C27H46O3	0	Cytosol
xoltri27	7-alpha,27-Dihydroxycholesterol	5-Cholesten-3-beta, 7 alpha, 27-triol	C27H46O3	0	Extracellular
xoltri27	7-alpha,27-Dihydroxycholesterol	5-Cholesten-3-beta, 7 alpha, 27-triol	C27H46O3	0	Endoplasmic Reticulum
xoltriol	3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestane	3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestane, 5-beta-cholestan-3-alpha-7-alpha-12-alpha-triol	C27H48O3	0	Cytosol
xoltriol	3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestane	3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestane, 5-beta-cholestan-3-alpha-7-alpha-12-alpha-triol	C27H48O3	0	Mitochondria
xoltriol	3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestane	3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestane, 5-beta-cholestan-3-alpha-7-alpha-12-alpha-triol	C27H48O3	0	Endoplasmic Reticulum
xser	Xyl-L-Ser (protein)		C5H9O4X	0	Golgi Apparatus
xser	Xyl-L-Ser (protein)		C5H9O4X	0	Endoplasmic Reticulum
xtp	XTP		C10H11N4O15P3	-4	Cytosol
xtsn	Xanthosine		C10H12N4O6	0	Cytosol
xu1p-D	D-Xylulose 1-phosphate		C5H9O8P	-2	Cytosol
xu5p-D	D-Xylulose 5-phosphate		C5H9O8P	-2	Cytosol
xyl-D	D-Xylose	Wood sugar	C5H10O5	0	Cytosol
xyl-D	D-Xylose	Wood sugar	C5H10O5	0	Extracellular
xyl-D	D-Xylose	Wood sugar	C5H10O5	0	Lysosome
xylnt	L-Xylonate	L-xylonic acid	C5H9O6	-1	Cytosol
xylt	Xylitol		C5H12O5	0	Cytosol
xylt	Xylitol		C5H12O5	0	Extracellular
xylu-D	D-Xylulose	D-Lyxulose, D-threo-Pentulose	C5H10O5	0	Cytosol
xylu-L	L-Xylulose	L-Lyxulose, L-threo-Pentulose	C5H10O5	0	Cytosol
yvite	gamma-Tocopherol	7,8-Dimethyltocol, 7,8-Dimethyltocolo-xylotocopherol, CCRIS 3610, CCRIS 4506, E-MIX 80, Methyltocols, TOCOPHEROL, gamma-Tokoferol, o-Xylotocopherol	C28H48O2	0	Cytosol

Abbreviation	Metabolite Name	Synonyms	Formula	Charge	Compartment
yvite	gamma-Tocopherol	7,8-Dimethyltocol, 7,8-Dimethyltocolo-xylotocopherol, CCRIS 3610, CCRIS 4506, E-MIX 80, Methyltocols, TOCOPHEROL, gamma-Tokoferol, o-Xylotocopherol	C28H48O2	0	Extracellular
zym_int2	zymosterol intermediate 2		C27H42O	0	Endoplasmic Reticulum
zymst	zymosterol	delta8,24-Cholestadien-3beta-ol	C27H44O	0	Endoplasmic Reticulum
zymstnl	Zymostenol	5alpha-Cholest-8-en-3beta-ol, Cholestenol, Lathosterol, Zymostenol	C27H46O	0	Endoplasmic Reticulum

Table 8: *H. sapiens* Recon 1 metabolic genes. List of the 1,496 genes included in the network. Each locus may encode more than one transcript, which is denoted by the suffix ".1", ".2", etc., after the locus number (Entrez Gene ID). Database abbreviations in additional notes field: HUGO – Human Genome Organization, MGD – Mouse Genome Database, MGI – Mouse Genome Index.

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
3162.1	3162	HMOX1	heme oxygenase (decycling) 1	Aliases: bK286B10, HO-1/HUGO ID: 5013/UniProt ID: P09601/
4514.1	4514	MTCO3	cytochrome c oxidase III	HUGO ID: 7422/UniProt ID: P00414/
3421.1	3421	IDH3G	isocitrate dehydrogenase 3 (NAD+) gamma	HUGO ID: 5386/UniProt ID: P51553/
5033.1	5033	P4HA1	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I	HUGO ID: 8546/UniProt ID: P13674/
4907.1	4907	NT5E	5'-nucleotidase, ecto (CD73)	Aliases: CD73, eN, eNT/HUGO ID: 8021/UniProt ID: P21589/
5106.1	5106	PCK2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	Aliases: PEPCK/HUGO ID: 8725/UniProt ID: Q16822/
212.1	212	ALAS2	aminolevulinate, delta-, synthase 2 (sideroblastic/hypochromic anemia)	HUGO ID: 397/UniProt ID: P22557/
9446.1	9446	GSTTLp28	glutathione-S-transferase like; glutathione transferase omega	
51478.1	51478	HSD17B7	hydroxysteroid (17-beta) dehydrogenase 7	
875.1	875	CBS	cystathionine-beta-synthase	Aliases: HIP4/HUGO ID: 1550/UniProt ID: P35520/
7086.1	7086	TKT	transketolase (Wernicke-Korsakoff syndrome)	HUGO ID: 11834/UniProt ID: P29401/
6472.1	6472	SHMT2	serine hydroxymethyltransferase 2 (mitochondrial)	HUGO ID: 10852/UniProt ID: P34897/
3036.1	3036	HAS1	hyaluronan synthase 1	HUGO ID: 4818/UniProt ID: Q92839/
3990.1	3990	LIPC	lipase, hepatic	HUGO ID: 6619/UniProt ID: P11150/
2731.1	2731	GLDC	glycine dehydrogenase (decarboxylating; glycine decarboxylase, glycine cleavage system protein P)	
3615.1	3615	IMPDH2	IMP (inosine monophosphate) dehydrogenase 2	
130.1	130	ADH6	alcohol dehydrogenase 6 (class V)	Locus type: gene with protein product, function known or inferred/Aliases: ADH-5/HUGO ID: 255/UniProt ID: P28332/
9957.1	9957	HS3ST1	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	Locus type: gene with protein product, function known or inferred/Aliases: 3OST1/HUGO ID: 5194/UniProt ID: O14792/
39.1	39	ACAT2	acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase)	HUGO ID: 94/UniProt ID: Q16146/
9488.1	9488	PIGB	phosphatidylinositol glycan, class B	HUGO ID: 8959/UniProt ID: Q8WVN7/
7841.1	7841	GCS1	glucosidase I	transcript: NM_006302
112.1	112	ADCY6	adenylate cyclase 6	HUGO ID: 237/UniProt ID: O43306/
7054.1	7054	TH	tyrosine hydroxylase	HUGO ID: 11782/UniProt ID: P07101/
3037.1	3037	HAS2	hyaluronan synthase 2	Locus type: gene with protein product, function known or inferred/HUGO ID: 4819/UniProt ID: Q92819/
3293.1	3293	HSD17B3	hydroxysteroid (17-beta) dehydrogenase 3	HUGO ID: 5212/UniProt ID: P37058/
1371.1	1371	CPOX	coproporphyrinogen oxidase (coproporphyria, harderoporphyria)	
4126.1	4126	MANBA	mannosidase, beta A, lysosomal	HUGO ID: 6831/UniProt ID: O00462/
8867.1	8867	SYNJ1	synaptojanin 1	transcript: NM_003895
7357.1	7357	UGCG	UDP-glucose ceramide glucosyltransferase	
1585.1	1585	CYP11B2	cytochrome P450, family 11, subfamily B, polypeptide 2	Locus type: gene with protein product, function known or inferred/Aliases: CYP11BL, CPN2, P-450C18, P450aldo, ALDOS/HUGO ID: 2592/UniProt ID: P19099/
5959.1	5959	RDH5	retinol dehydrogenase 5 (11-cis and 9-cis)	
8693.1	8693	GALNT4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4 (GalNAc-T4)	Locus type: gene with protein product, function known or inferred/Aliases: GalNAc-T4/HUGO ID: 4126/UniProt ID: O00208/
1606.1	1606	DGKA	diacylglycerol kinase, alpha 80kDa	*PubMed
2519.1	2519	FUCA2	fucosidase, alpha-L- 2, plasma	Locus type: gene with protein product, function known or inferred/Aliases: MGC1314, dJ20N2.5/HUGO ID: 4008/UniProt ID: Q9BTY2/
23439.1	23439	ATP1B4	ATPase, (Na+)/K+ transporting, beta 4 polypeptide	HUGO ID: 808/UniProt ID: Q9UN42/
4694.1	4694	NDUFA1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa	Locus type: gene with protein product, function known or inferred/Aliases: MWFE, CI-MWFE/HUGO ID: 7683/UniProt ID: O15239/
3614.1	3614	IMPDH1	IMP (inosine monophosphate) dehydrogenase 1	Aliases: sWSS2608/HUGO ID: 6052/UniProt ID: P20839/
4712.1	4712	NDUFB6	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa	
100.1	100	ADA	adenosine deaminase	
223.1	223	ALDH9A1	aldehyde dehydrogenase 9 family, member A1	
3423.1	3423	IDS	iduronate 2-sulfatase (Hunter syndrome)	HUGO ID: 5389/UniProt ID: P22304/
1553.1	1553	CYP2A13	cytochrome P450, family 2, subfamily A, polypeptide 13	
1892.1	1892	ECHS1	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	Aliases: SCEH/HUGO ID: 3151/UniProt ID: P30084/
2984.1	2984	GUCY2C	guanylate cyclase 2C (heat stable enterotoxin receptor)	Aliases: STAR/HUGO ID: 4688/UniProt ID: P25092/
4047.1	4047	LSS	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	
2977.1	2977	GUCY1A2	guanylate cyclase 1, soluble, alpha 2	Aliases: GC-SA2/HUGO ID: 4684/UniProt ID: P33402/
5049.1	5049	PAFAH1B2	platelet-activating factor acetylhydrolase, isoform Ib, beta subunit 30kDa	
10007.1	10007	GNPI	glucosamine-6-phosphate isomerase	
4513.1	4513	MTCO2	cytochrome c oxidase II	
5305.1	5305	PIP5K2A	phosphatidylinositol-4-phosphate 5-kinase, type II, alpha	HUGO ID: 8997/UniProt ID: P48426/
4759.1	4759	NEU2	sialidase 2 (cytosolic sialidase)	HUGO ID: 7759/UniProt ID: Q9Y3R4/
3242.1	3242	HPD	4-hydroxyphenylpyruvate dioxygenase	HUGO ID: 5147/UniProt ID: P32754/

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
4702.1	4702	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 19kDa	Locus type: gene with protein product, function known or inferred/Aliases: PGIV, MGC793/HUGO ID: 7692/UniProt ID: P51970/
6303.1	6303	SAT	spermidine/spermine N1-acetyltransferase	
6489.1	6489	SIAT8A	sialyltransferase 8A (alpha-N-acetylneuraminate: alpha-2,8-sialyltransferase, GD3 synthase)	Aliases: ST8Sia I/HUGO ID: 10869/UniProt ID: Q92185/
3420.1	3420	IDH3B	isocitrate dehydrogenase 3 (NAD+) beta	HUGO ID: 5385/UniProt ID: O43837/
501.1	501	ALDH7A1	aldehyde dehydrogenase 7 family, member A1	HUGO ID: 877/UniProt ID: P49419/
622.1	622	BDH1	3-hydroxybutyrate dehydrogenase (heart, mitochondrial)	HUGO ID: 1027/UniProt ID: Q02338/
8942.1	8942	KYNU	kynureninase (L-kynurenine hydrolase)	
3038.1	3038	HAS3	hyaluronan synthase 3	transcript: NM_005329
4051.1	4051	CYP4F3	cytochrome P450, family 4, subfamily F, polypeptide 3	
9162.1	9162	DGKI	diacylglycerol kinase, iota	HUGO ID: 2855/UniProt ID: O75912/
2730.1	2730	GCLM	glutamate-cysteine ligase, modifier subunit	HUGO ID: 4312/UniProt ID: P48507/
15.1	15	AANAT	arylalkylamine N-acetyltransferase	Aliases: SNAT/HUGO ID: 19/UniProt ID: Q16613/
7381.1	7381	UQCRB	ubiquinol-cytochrome c reductase binding protein	Aliases: QP-C/HUGO ID: 12582/UniProt ID: P14927/
6392.1	6392	SDHD	succinate dehydrogenase complex, subunit D, integral membrane protein	*PubMed
5139.1	5139	PDE3A	phosphodiesterase 3A, cGMP-inhibited	
4728.1	4728	NDUFS8	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)	
4538.1	4538	MTND4	NADH dehydrogenase 4	HUGO ID: 7459/UniProt ID: P03905/
113.1	113	ADCY7	adenylate cyclase 7	Aliases: KIAA0037/HUGO ID: 238/UniProt ID: P51828/
6716.1	6716	SRD5A2	steroid-5-alpha-reductase, alpha polypeptide 2 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 2)	HUGO ID: 11285/UniProt ID: P31213/
4967.1	4967	OGDH	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	transcript: NM_001003941
6185.1	6185	RPN2	ribophorin II	HUGO ID: 10382/UniProt ID: P04844/
4860.1	4860	NP	nucleoside phosphorylase	HUGO ID: 7892/UniProt ID: P00491/
29922.1	29922	NME7	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase)	Locus type: gene with protein product, function known or inferred/HUGO ID: 20461/UniProt ID: Q9Y5B8/MGD ID: MGI:2449121/
211.1	211	ALAS1	aminolevulinate, delta-, synthase 1	HUGO ID: 396/UniProt ID: P13196/
30833.1	30833	NT5C	5', 3'-nucleotidase, cytosolic	Aliases: DNT1, DNT-1, PN-I, cdN, dNT-1, HGNC:12561/HUGO ID: 17144/UniProt ID: Q8TCD5/
5105.1	5105	PCK1	phosphoenolpyruvate carboxykinase 1 (soluble)	HUGO ID: 8724/UniProt ID: P35558/
4129.1	4129	MAOB	monoamine oxidase B	HUGO ID: 6834/UniProt ID: P27338/
9956.1	9956	HS3ST2	heparan sulfate (glucosamine) 3-O-sulfotransferase 2	Locus type: gene with protein product, function known or inferred/Aliases: 3OST2/HUGO ID: 5195/UniProt ID: Q9Y278/
4353.1	4353	MPO	myeloperoxidase	HUGO ID: 7218/UniProt ID: P05164/
56052.1	56052	ALG1	asparagine-linked glycosylation 1 homolog (yeast, beta-1,4-mannosyltransferase)	Locus type: gene with protein product, function known or inferred/Aliases: HMT-1, HMAT1/HUGO ID: 18294/UniProt ID: Q8N5Y4/
23498.1	23498	HAAO	3-hydroxyanthranilate 3,4-dioxygenase	HUGO ID: 4796/UniProt ID: P46952/
7358.1	7358	UGDH	UDP-glucose dehydrogenase	
5048.1	5048	PAFAH1B1	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa	
1632.1	1632	DCI	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)	HUGO ID: 2703/UniProt ID: P42126/
2990.1	2990	GUSB	glucuronidase, beta	HUGO ID: 4696/UniProt ID: P08236/
5167.1	5167	ENPP1	ectonucleotide pyrophosphatase/phosphodiesterase 1	Aliases: PC-1, PCA1/HUGO ID: 3356/UniProt ID: P22413/
4023.1	4023	LPL	lipoprotein lipase	HUGO ID: 6677/UniProt ID: P06858/
4144.1	4144	MAT2A	methionine adenosyltransferase II, alpha	Aliases: SAMS2, MATA2, MATII/HUGO ID: 6904/UniProt ID: P31153/
2937.1	2937	GSS	glutathione synthetase	HUGO ID: 4624/UniProt ID: P48637/
9334.1	9334	B4GALT5	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5	
51733.1	51733	UPB1	ureidopropionase, beta	Aliases: BUP1/HUGO ID: 16297/UniProt ID: Q9UBR1/
3251.1	3251	HPRT1	hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)	Locus type: gene with protein product, function known or inferred/Aliases: HGPRT/HUGO ID: 5157/UniProt ID: P00492/
4669.1	4669	NAGLU	N-acetylglucosaminidase, alpha- (Sanfilippo disease IIIB)	Aliases: NAG/HUGO ID: 7632/UniProt ID: P54802/
4713.1	4713	NDUFB7	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 18kDa	
4537.1	4537	MTND3	NADH dehydrogenase 3	HUGO ID: 7458/UniProt ID: P03897/
7296.1	7296	TXNRD1	thioredoxin reductase 1	Locus type: gene with protein product, function known or inferred/Aliases: TXNR/HUGO ID: 12437/UniProt ID: Q16881/
5831.1	5831	PYCR1	pyrroline-5-carboxylate reductase 1	Aliases: P5C/HUGO ID: 9721/UniProt ID: P32322/
3631.1	3631	INPP4A	inositol polyphosphate-4-phosphatase, type I, 107kDa	transcript: NM_001566
1584.1	1584	CYP11B1	cytochrome P450, family 11, subfamily B, polypeptide 1	Locus type: gene with protein product, function known or inferred/Aliases: P450C11, FHI, CPN1/HUGO ID: 2591/UniProt ID: P15538/
3613.1	3613	IMPA2	inositol(myo)-1(or 4)-monophosphatase 2	HUGO ID: 6051/UniProt ID: O14732/
3795.1	3795	KHK	ketohexokinase (fructokinase)	HUGO ID: 6315/UniProt ID: P50053/
2135.1	2135	EXTL2	exostoses (multiple)-like 2	HUGO ID: 3516/UniProt ID: Q9UBQ6/

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
10380.1	10380	BPNT1	3'(2'), 5'-bisphosphate nucleotidase 1	Locus type: gene with protein product, function known or inferred/HUGO ID: 1096/UniProt ID: Q8WVL5/
224.1	224	ALDH3A2	aldehyde dehydrogenase 3 family, member A2	Aliases: FALDH/HUGO ID: 403/UniProt ID: P51648/
3422.1	3422	IDI1	isopentenyl-diphosphate delta isomerase	Locus type: gene with protein product, function known or inferred/HUGO ID: 5387/UniProt ID: Q13907/
7083.1	7083	TK1	thymidine kinase 1, soluble	HUGO ID: 11830/UniProt ID: P04183/
1160.1	1160	CKMT2	creatine kinase, mitochondrial 2 (sarcomeric)	Aliases: SMTCK/HUGO ID: 1996/UniProt ID: P17540/
4048.1	4048	LTA4H	leukotriene A4 hydrolase	Locus type: gene with protein product, function known or inferred/HUGO ID: 6710/UniProt ID: P09960/
2762.1	2762	GMDS	GDP-mannose 4,6-dehydratase	Aliases: GMD/HUGO ID: 4369/UniProt ID: O60547/
1119.1	1119	CHK	choline kinase	
5730.1	5730	PTGDS	prostaglandin D2 synthase 21kDa (brain)	Locus type: gene with protein product, function known or inferred/HUGO ID: 9592/UniProt ID: P41222/
5149.1	5149	PDE6H	phosphodiesterase 6H, cGMP-specific, cone, gamma	HUGO ID: 8790/UniProt ID: Q13956/
8821.1	8821	INPP4B	inositol polyphosphate-4-phosphatase, type II, 105kDa	Locus type: gene with protein product, function known or inferred/HUGO ID: 6075/UniProt ID: O15327/
3283.1	3283	HSD3B1	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1	Locus type: gene with protein product, function known or inferred/HUGO ID: 5217/UniProt ID: P14060/
3141.1	3141	HLCS	holocarboxylase synthetase (biotin-[proprionyl-Coenzyme A-carboxylase (ATP-hydrolysing)] ligase)	Aliases: HCS/HUGO ID: 4976/UniProt ID: P50747/
8789.1	8789	FBP2	fructose-1,6-bisphosphatase 2	HUGO ID: 3607/UniProt ID: O00757/
1503.1	1503	CTPS	CTP synthase	Locus type: gene with protein product, function known or inferred/HUGO ID: 2519/UniProt ID: P17812/
95.1	95	ACY1	aminoacylase 1	HUGO ID: 177/UniProt ID: Q03154/
23632.1	23632	CA14	carbonic anhydrase XIV	HUGO ID: 1372/UniProt ID: Q9ULX7/
4758.1	4758	NEU1	sialidase 1 (lysosomal sialidase)	HUGO ID: 7758/UniProt ID: Q99519/
1716.1	1716	DGUOK	deoxyguanosine kinase	Aliases: dGK/HUGO ID: 2858/UniProt ID: Q16854/
7167.1	7167	TPI1	triosephosphate isomerase 1	HUGO ID: 12009/UniProt ID: P00938/
1431.1	1431	CS	citrate synthase	HUGO ID: 2422/UniProt ID: O75390/
518.1	518	ATP5G3	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3	HUGO ID: 843/UniProt ID: P48201/Variant 1: This variant represents the longest transcript. Transcript variants 1, 2 and 3 encode the same protein.
4539.1	4539	MTND4L	NADH dehydrogenase 4L	HUGO ID: 7460/UniProt ID: P03901/
2271.1	2271	FH	fumarate hydratase	Locus type: gene with protein product, function known or inferred/HUGO ID: 3700/UniProt ID: P07954/
1594.1	1594	CYP27B1	cytochrome P450, family 27, subfamily B, polypeptide 1	
4697.1	4697	NDUFA4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa	Locus type: gene with protein product, function known or inferred/Aliases: MLRQ/HUGO ID: 7687/UniProt ID: O00483/
760.1	760	CA2	carbonic anhydrase II	HUGO ID: 1373/UniProt ID: P00918/
4128.1	4128	MAOA	monoamine oxidase A	HUGO ID: 6833/UniProt ID: P21397/
6184.1	6184	RPN1	ribophorin I	HUGO ID: 10381/UniProt ID: P04843/
9377.1	9377	COX5A	cytochrome c oxidase subunit Va	
410.1	410	ARSA	arylsulfatase A	HUGO ID: 713/UniProt ID: P15289/
1373.1	1373	CPS1	carbamoyl-phosphate synthetase 1, mitochondrial	HUGO ID: 2323/UniProt ID: P31327/
1565.1	1565	CYP2D6	cytochrome P450, family 2, subfamily D, polypeptide 6	Locus type: gene with protein product, function known or inferred/Aliases: HGNC:2629, CPD6, P450-DB1, CYP2D, P450C2D/HUGO ID: 2625/UniProt ID: P10635/
2651.1	2651	GCNT2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	
18.1	18	ABAT	4-aminobutyrate aminotransferase	Aliases: GABAT/HUGO ID: 23/UniProt ID: P80404/
2131.1	2131	EXT1	exostoses (multiple) 1	HUGO ID: 3512/UniProt ID: Q16394/
5464.1	5464	PP	pyrophosphatase (inorganic)	*PubMed
10157.1	10157	AASS	aminoadipate-semialdehyde synthase	Aliases: LORSDH, LKRSDH, AASS/HUGO ID: 17366/UniProt ID: O95462/
6999.1	6999	TDO2	tryptophan 2,3-dioxygenase	HUGO ID: 11708/UniProt ID: P48775/
3292.1	3292	HSD17B1	hydroxysteroid (17-beta) dehydrogenase 1	Aliases: HSD17/HUGO ID: 5210/UniProt ID: P14061/
2572.1	2572	GAD2	glutamate decarboxylase 2 (pancreatic islets and brain, 65kDa)	Locus type: gene with protein product, function known or inferred/Aliases: GAD65/HUGO ID: 4093/UniProt ID: Q05329/
8833.1	8833	GMPS	guanine monophosphate synthetase	
4729.1	4729	NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa	
5742.1	5742	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	
2597.1	2597	GAPDH	glyceraldehyde-3-phosphate dehydrogenase	Aliases: GAPDH/HUGO ID: 4141/UniProt ID: P04406/
4837.1	4837	NNMT	nicotinamide N-methyltransferase	HUGO ID: 7861/UniProt ID: P40261/
5168.1	5168	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	Aliases: ATX, PD-IALPHA/HUGO ID: 3357/UniProt ID: Q13822/
7359.1	7359	UGP1	UDP-glucose pyrophosphorylase 1	Locus type: gene with protein product, function known or inferred/Aliases: UGPP1/HUGO ID: 12526/
5836.1	5836	PYGL	phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI)	HUGO ID: 9725/UniProt ID: P06737/
5352.1	5352	PLOD2	procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2	Locus type: gene with protein product, function known or inferred/HUGO ID: 9082/UniProt ID: O00469/
2986.1	2986	GUCY2F	guanylate cyclase 2F, retinal	
2517.1	2517	FUCA1	fucosidase, alpha-L- 1, tissue	Locus type: gene with protein product, function known or inferred/HUGO ID: 4006/UniProt ID: P04066/MGD ID: MGI:95593/

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
4200.1	4200	ME2	malic enzyme 2, NAD(+)-dependent, mitochondrial	Locus type: gene with protein product, function known or inferred/HUGO ID: 6984/UniProt ID: P23368/
1551.1	1551	CYP3A7	cytochrome P450, family 3, subfamily A, polypeptide 7	Locus type: gene with protein product, function known or inferred/Aliases: CP37, P450-HFLA/HUGO ID: 2640/UniProt ID: P24462/
64080.1	64080	RBKS	ribokinase	
51268.1	51268	PIPOX	pipecolic acid oxidase	
1583.1	1583	CYP11A1	cytochrome P450, family 11, subfamily A, polypeptide 1	Locus type: gene with protein product, function known or inferred/Aliases: P450SCC/HUGO ID: 2590/UniProt ID: P05108/
5214.1	5214	PFKP	phosphofructokinase, platelet	Locus type: gene with protein product, function known or inferred/Aliases: PFK-C, PFKF/HUGO ID: 8878/UniProt ID: Q01813/
4710.1	4710	NDUFB4	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa	Locus type: gene with protein product, function known or inferred/Aliases: B15/HUGO ID: 7699/UniProt ID: O95168/
8659.1	8659	ALDH4A1	aldehyde dehydrogenase 4 family, member A1	Aliases: P5CDh/HUGO ID: 406/UniProt ID: P30038/
221.1	221	ALDH3B1	aldehyde dehydrogenase 3 family, member B1	
55577.1	55577	NAGK	N-acetylglucosamine kinase	Aliases: GNK/HUGO ID: 17174/UniProt ID: Q9UJ70/
6818.1	6818	SULT1A3	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3	
1572.1	1572	CYP2F1	cytochrome P450, family 2, subfamily F, polypeptide 1	Locus type: gene with protein product, function known or inferred/HUGO ID: 2632/UniProt ID: P24903/
8564.1	8564	KMO	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	HUGO ID: 6381/UniProt ID: O15229/MGD ID: MGI:2138151/
1555.1	1555	CYP2B6	cytochrome P450, family 2, subfamily B, polypeptide 6	
10682.1	10682	EBP	emopamil binding protein (sterol isomerase)	
3632.1	3632	INPP5A	inositol polyphosphate-5-phosphatase, 40kDa	Locus type: gene with protein product, function known or inferred/Aliases: 5PTASE/HUGO ID: 6076/UniProt ID: Q14642/
65220.1	65220	FLJ13052	NAD kinase	transcript: NM_023018
9061.1	9061	PAPSS1	3'-phosphoadenosine 5'-phosphosulfate synthase 1	*PubMed
3425.1	3425	IDUA	iduronidase, alpha-L-	HUGO ID: 5391/UniProt ID: P35475/
5145.1	5145	PDE6A	phosphodiesterase 6A, cGMP-specific, rod, alpha	HUGO ID: 8785/UniProt ID: P16499/
1158.1	1158	CKM	creatine kinase, muscle	HUGO ID: 1994/UniProt ID: P06732/
10606.1	10606	PAICS	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	
7084.1	7084	TK2	thymidine kinase 2, mitochondrial	HUGO ID: 11831/UniProt ID: O00142/
318.1	318	NUDT2	nudix (nucleoside diphosphate linked moiety X)-type motif 2	
54677.1	54677	CROT	carnitine O-octanoyltransferase	Aliases: COT/HUGO ID: 2366/UniProt ID: Q9UKG9/
2950.1	2950	GSTP1	glutathione S-transferase pi	
10026.1	10026	PIGK	phosphatidylinositol glycan, class K	Aliases: hGPI8/HUGO ID: 8965/UniProt ID: Q92643/
7166.1	7166	TPH1	tryptophan hydroxylase 1 (tryptophan 5-monooxygenase)	Locus type: gene with protein product, function known or inferred/HUGO ID: 12008/UniProt ID: P17752/
159.1	159	ADSS	adenylosuccinate synthase	
4121.1	4121	MAN1A1	mannosidase, alpha, class 1A, member 1	HUGO ID: 6821/UniProt ID: P33908/
4594.1	4594	MUT	methylmalonyl Coenzyme A mutase	
8513.1	8513	LIPF	lipase, gastric	
5034.1	5034	P4HB	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55)	HUGO ID: 8548/UniProt ID: P07237/
6487.1	6487	ST3GAL3	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	Locus type: gene with protein product, function known or inferred/Aliases: ST3Gal III/HUGO ID: 10866/UniProt ID: Q11203/
1717.1	1717	DHCR7	7-dehydrocholesterol reductase	
6241.1	6241	RRM2	ribonucleotide reductase M2 polypeptide	HUGO ID: 10452/UniProt ID: P31350/
2683.1	2683	B4GALT1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	Locus type: gene with protein product, function known or inferred/Aliases: beta4Gal-T1/HUGO ID: 924/UniProt ID: P15291/
517.1	517	ATP5G2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2	HUGO ID: 842/UniProt ID: Q06055/Variant 1: This variant represents the longer transcript, and encodes the longer isoform 2a.
26289.1	26289	AK5	adenylate kinase 5	HUGO ID: 365/UniProt ID: Q9Y6K8/
1621.1	1621	DBH	dopamine beta-hydroxylase (dopamine beta-monooxygenase)	HUGO ID: 2689/UniProt ID: P09172/
29880.1	29880	ALG5	asparagine-linked glycosylation 5 homolog (yeast, dolichyl-phosphate beta-glucosyltransferase)	Locus type: gene with protein product, function known or inferred/Aliases: bA421P11.2/HUGO ID: 20266/UniProt ID: Q9Y673/
4696.1	4696	NDUFA3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3, 9kDa	Aliases: B9/HUGO ID: 7686/UniProt ID: O95167/
8802.1	8802	SUCLG1	succinate-CoA ligase, GDP-forming, alpha subunit	Locus type: gene with protein product, function known or inferred/HUGO ID: 11449/UniProt ID: P53597/
481.1	481	ATP1B1	ATPase, Na+/K+ transporting, beta 1 polypeptide	HUGO ID: 804/UniProt ID: P05026/
2132.1	2132	EXT2	exostoses (multiple) 2	NM_000401
4842.1	4842	NOS1	nitric oxide synthase 1 (neuronal)	
11181.1	11181	TREH	trehalase (brush-border membrane glycoprotein)	Aliases: TRE, TREA/HUGO ID: 12266/UniProt ID: O43280/
4700.1	4700	NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa	
5837.1	5837	PYGM	phosphorylase, glycogen; muscle (McArdle syndrome, glycogen storage disease type V)	HUGO ID: 9726/UniProt ID: P11217/

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
111.1	111	ADCY5	adenylate cyclase 5	Locus type: gene with protein product, function known or inferred/HUGO ID: 236/UniProt ID: O95622/
5743.1	5743	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	Aliases: COX2/HUGO ID: 9605/UniProt ID: P35354/
2571.1	2571	GAD1	glutamate decarboxylase 1 (brain, 67kDa)	HUGO ID: 4092/UniProt ID: Q99259/
570.1	570	BAAT	bile acid Coenzyme A: amino acid N-acyltransferase (glycine N-choloyltransferase)	Aliases: BAT/HUGO ID: 932/UniProt ID: Q14032/
3294.1	3294	HSD17B2	hydroxysteroid (17-beta) dehydrogenase 2	Aliases: HSD17/HUGO ID: 5211/UniProt ID: P37059/
4726.1	4726	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase)	HUGO ID: 7713/UniProt ID: O75380/
2940.1	2940	GSTA3	glutathione S-transferase A3	
7915.1	7915	ALDH5A1	aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase)	
1595.1	1595	CYP51A1	cytochrome P450, family 51, subfamily A, polypeptide 1	Locus type: gene with protein product, function known or inferred/Aliases: CP51, CYPL1, P450L1, LDM, P450-14DM/HUGO ID: 2649/UniProt ID: Q16850/
3945.1	3945	LDHB	lactate dehydrogenase B	Locus type: gene with protein product, function known or inferred/HUGO ID: 6541/UniProt ID: P07195/
8694.1	8694	DGAT1	diacylglycerol O-acyltransferase homolog 1 (mouse)	Locus type: gene with protein product, function known or inferred/Aliases: ARGP1, DGAT/HUGO ID: 2843/UniProt ID: O75907/
5634.1	5634	PRPS2	phosphoribosyl pyrophosphate synthetase 2	Aliases: PRS II/HUGO ID: 9465/UniProt ID: P11908/
54363.1	54363	HAO1	hydroxyacid oxidase (glycolate oxidase) 1	Aliases: GOX, HAO1/HUGO ID: 4809/UniProt ID: Q9UJM8/
272.1	272	AMPD3	adenosine monophosphate deaminase (isoform E)	HUGO ID: 470/UniProt ID: Q01432/
55811.1	55811	SAC	testicular soluble adenylyl cyclase	transcript: NM_018417
4548.1	4548	MTR	5-methyltetrahydrofolate-homocysteine methyltransferase	Locus type: gene with protein product, function known or inferred/HUGO ID: 7468/UniProt ID: Q99707/
4351.1	4351	MPI	mannose phosphate isomerase	HUGO ID: 7216/UniProt ID: P34949/
9653.1	9653	HS2ST1	heparan sulfate 2-O-sulfotransferase 1	Aliases: KIAA0448/HUGO ID: 5193/UniProt ID: O75036/
5144.1	5144	PDE4D	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila)	HUGO ID: 8783/UniProt ID: Q08499/
3295.1	3295	HSD17B4	hydroxysteroid (17-beta) dehydrogenase 4	HUGO ID: 5213/UniProt ID: P51659/
5169.1	5169	ENPP3	ectonucleotide pyrophosphatase/phosphodiesterase 3	Aliases: PD-IBETA, gp130RB13-6, B10, CD203C/HUGO ID: 3358/UniProt ID: O14638/
26279.1	26279	PLA2G2D	phospholipase A2, group IID	Aliases: sPLA2S/HUGO ID: 9033/UniProt ID: Q9UNK4/
222.1	222	ALDH3B2	aldehyde dehydrogenase 3 family, member B2	
2983.1	2983	GUCY1B3	guanylate cyclase 1, soluble, beta 3	Aliases: GC-SB3, GC-S-beta-1/HUGO ID: 4687/UniProt ID: Q02153/
2876.1	2876	GPX1	glutathione peroxidase 1	HUGO ID: 4553/UniProt ID: P07203/
4711.1	4711	NDUFB5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa	Locus type: gene with protein product, function known or inferred/Aliases: SGDH, CI-SGDH, MGC12314/HUGO ID: 7700/UniProt ID: O43674/
1159.1	1159	CKMT1B	creatine kinase, mitochondrial 1B (ubiquitous)	Aliases: UMTCK/HUGO ID: 1995/UniProt ID: P12532/
3633.1	3633	INPP5B	inositol polyphosphate-5-phosphatase, 75kDa	Locus type: gene with protein product, function known or inferred/HUGO ID: 6077/UniProt ID: P32019/
2137.1	2137	EXTL3	exostoses (multiple)-like 3	
10858.1	10858	CYP46A1	cytochrome P450, family 46, subfamily A, polypeptide 1	Locus type: gene with protein product, function known or inferred/HUGO ID: 2641/UniProt ID: Q9Y6A2/
1571.1	1571	CYP2E1	cytochrome P450, family 2, subfamily E, polypeptide 1	Locus type: gene with protein product, function known or inferred/HUGO ID: 2631/UniProt ID: P05181/
11226.1	11226	GALNT6	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6)	Locus type: gene with protein product, function known or inferred/HUGO ID: 4128/UniProt ID: Q8NCL4/
384.1	384	ARG2	arginase, type II	HUGO ID: 664/UniProt ID: P78540/
27165.1	27165	GA	liver mitochondrial glutaminase	
8704.1	8704	B4GALT2	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 2	transcript: NM_001005417
9167.1	9167	COX7A2L	cytochrome c oxidase subunit VIIa polypeptide 2 like	Locus type: gene with protein product, function known or inferred/Aliases: EB1, COX7RP, COX7AR, SIG81/HUGO ID: 2289/UniProt ID: O14548/
5321.1	5321	PLA2G4A	phospholipase A2, group IVA (cytosolic, calcium-dependent	Locus type: gene with protein product, function known or inferred/Aliases: cPLA2-alpha/HUGO ID: 9035/UniProt ID: P47712/
1312.1	1312	COMT	catechol-O-methyltransferase	HUGO ID: 2228/UniProt ID: P21964/
5335.1	5335	PLCG1	phospholipase C, gamma 1 (formerly subtype 148)	transcript: NM_002660
239.1	239	ALOX12	arachidonate 12-lipoxygenase	HUGO ID: 429/UniProt ID: P18054/
1337.1	1337	COX6A1	cytochrome c oxidase subunit VIa polypeptide 1	Locus type: gene with protein product, function known or inferred/HUGO ID: 2277/UniProt ID: P12074/
2710.1	2710	GK	glycerol kinase	Locus type: gene with protein product, function known or inferred/HUGO ID: 4289/UniProt ID: P32189/
6240.1	6240	RRM1	ribonucleotide reductase M1 polypeptide	HUGO ID: 10451/UniProt ID: P23921/
158.1	158	ADSL	adenylosuccinate lyase	HUGO ID: 291/UniProt ID: P30566/
9583.1	9583	LYSAL1	lysosomal apyrase-like 1	
51292.1	51292	GMPR2	guanosine monophosphate reductase 2	Locus type: gene with protein product, function known or inferred/HUGO ID: 4377/UniProt ID: Q9P2T1/
8566.1	8566	PDXK	pyridoxal (pyridoxine, vitamin B6) kinase	Aliases: PNK, PKH/HUGO ID: 8819/UniProt ID: O00764/
1375.1	1375	CPT1B	carnitine palmitoyltransferase 1B (muscle)	Aliases: M-CPT1, CPT1-M/HUGO ID: 2329/UniProt ID: Q92523/
533.1	533	ATP6V0B	ATPase, H+ transporting, lysosomal 21kDa, V0 subunit c"	Locus type: gene with protein product, function known or inferred/Aliases: VMA16, HATPL/HUGO ID: 861/UniProt ID: Q99437/MGD ID: MGI:1890510/

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
10632.1	10632	ATP5L	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g	
3074.1	3074	HEXB	hexosaminidase B (beta polypeptide)	HUGO ID: 4879/UniProt ID: P07686/
56913.1	56913	C1GALT1	core 1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-galactosyltransferase	transcript: NM_020156
8382.1	8382	NME5	non-metastatic cells 5, protein expressed in (nucleoside-diphosphate kinase)	Aliases: nm23-H5/HUGO ID: 7853/UniProt ID: P56597/
10455.1	10455	PECI	peroxisomal D3,D2-enoyl-CoA isomerase	Locus type: gene with protein product, function known or inferred/Aliases: ACBD2, DRS1, HCA88/HUGO ID: 14601/UniProt ID: O75521/
8803.1	8803	SUCLA2	succinate-CoA ligase, ADP-forming, beta subunit	HUGO ID: 11448/UniProt ID: Q9P2R7/
2235.1	2235	FECH	ferrochelatase (protoporphyria)	HUGO ID: 3647/UniProt ID: P22830/
1841.1	1841	DTYMK	deoxythymidylate kinase (thymidylate kinase)	
2618.1	2618	GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase	HUGO ID: 4163/UniProt ID: P22102/
9517.1	9517	SPTLC2	serine palmitoyltransferase, long chain base subunit 2	
216.1	216	ALDH1A1	aldehyde dehydrogenase 1 family, member A1	Aliases: RALDH1/HUGO ID: 402/UniProt ID: P00352/
2632.1	2632	GBE1	glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV)	HUGO ID: 4180/UniProt ID: Q04446/
29925.1	29925	GMPPB	GDP-mannose pyrophosphorylase B	transcript: NM_013334
29968.1	29968	PSAT1	phosphoserine aminotransferase 1	
1635.1	1635	DCTD	dCMP deaminase	HUGO ID: 2710/UniProt ID: P32321/
1040.1	1040	CDS1	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 1	
51477.1	51477	ISYNA1	myo-inositol 1-phosphate synthase A1	transcript: NM_016368
669.1	669	BPGM	2,3-bisphosphoglycerate mutase	Locus type: gene with protein product, function known or inferred/HUGO ID: 1093/UniProt ID: P07738/
6888.1	6888	TALDO1	transaldolase 1	HUGO ID: 11559/UniProt ID: P37837/
1650.1	1650	DDOST	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	Aliases: OST, KIAA0115/HUGO ID: 2728/UniProt ID: P39656/
271.1	271	AMPD2	adenosine monophosphate deaminase 2 (isoform L)	HUGO ID: 469/UniProt ID: Q01433/
3290.1	3290	HSD11B1	hydroxysteroid (11-beta) dehydrogenase 1	Locus type: gene with protein product, function known or inferred/HUGO ID: 5208/UniProt ID: P28845/
4716.1	4716	NDUFB10	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa	
5224.1	5224	PGAM2	phosphoglycerate mutase 2 (muscle)	HUGO ID: 8889/UniProt ID: P15259/
1347.1	1347	COX7A2	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)	
11238.1	11238	CA5B	carbonic anhydrase VB, mitochondrial	Locus type: gene with protein product, function known or inferred/HUGO ID: 1378/UniProt ID: Q9Y2D0/
9945.1	9945	GFPT2	glutamine-fructose-6-phosphate transaminase 2	Aliases: GFAT2/HUGO ID: 4242/UniProt ID: O94808/
2589.1	2589	GALNT1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)	Aliases: GalNAc-T1/HUGO ID: 4123/UniProt ID: Q10472/
762.1	762	CA4	carbonic anhydrase IV	Aliases: CAIV/HUGO ID: 1375/UniProt ID: P22748/
4698.1	4698	NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kDa	
4831.1	4831	NME2	non-metastatic cells 2, protein (NM23B) expressed in	Aliases: NM23-H2/HUGO ID: 7850/UniProt ID: P22392/
8613.1	8613	PPAP2B	phosphatidic acid phosphatase type 2B	Aliases: PAP-2b/HUGO ID: 9229/UniProt ID: O14495/
23761.1	23761	PISD	phosphatidylserine decarboxylase	Aliases: dJ858B16.2/HUGO ID: 8999/UniProt ID: Q9UG56/
847.1	847	CAT	catalase	HUGO ID: 1516/UniProt ID: P04040/
2952.1	2952	GSTT1	glutathione S-transferase theta 1	HUGO ID: 4641/UniProt ID: P30711/
3098.1	3098	HK1	hexokinase 1	Locus type: gene with protein product, function known or inferred/HUGO ID: 4922/UniProt ID: P19367/
2583.1	2583	GALGT	UDP-N-acetyl-alpha-D-galactosamine:(N-acetylneuraminyl)-galactosylglucosylceramide N-acetylgalactosaminyltransferase (GalNAc-T)	Aliases: beta1-4GalNAc-T/HUGO ID: 4117/UniProt ID: Q00973/
4143.1	4143	MAT1A	methionine adenosyltransferase I, alpha	Aliases: MAT, SAMS, MATA1, SAMS1/HUGO ID: 6903/UniProt ID: Q00266/
1589.1	1589	CYP21A2	cytochrome P450, family 21, subfamily A, polypeptide 2	Locus type: gene with protein product, function known or inferred/Aliases: P450c21B, CA21H, CPS1, CAH1/HUGO ID: 2600/UniProt ID: P08686/
3067.1	3067	HDC	histidine decarboxylase	HUGO ID: 4855/UniProt ID: P19113/
10588.1	10588	MTHFS	5,10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase)	Locus type: gene with protein product, function known or inferred/Aliases: HsT19268/HUGO ID: 7437/UniProt ID: P49914/
5320.1	5320	PLA2G2A	phospholipase A2, group IIA (platelets, synovial fluid)	Locus type: gene with protein product, function known or inferred/HUGO ID: 9031/UniProt ID: P14555/
26290.1	26290	GALNT8	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8 (GalNAc-T8)	Locus type: gene with protein product, function known or inferred/Aliases: GALNAC-T8/HUGO ID: 4130/UniProt ID: Q9NY28/
116285.1	116285	BUCS1	butyryl Coenzyme A synthetase 1	Aliases: MACS1/HUGO ID: 18049/UniProt ID: Q96A20/MGD ID: MGI:2152200/
8703.1	8703	B4GALT3	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 3	
483.1	483	ATP1B3	ATPase, Na+/K+ transporting, beta 3 polypeptide	
593.1	593	BCKDHA	branched chain keto acid dehydrogenase E1, alpha polypeptide (maple syrup urine disease)	HUGO ID: 986/UniProt ID: P12694/

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
1374.1	1374	CPT1A	carnitine palmitoyltransferase 1A (liver)	
3101.1	3101	HK3	hexokinase 3 (white cell)	HUGO ID: 4925/UniProt ID: P52790/
9348.1	9348	NDST3	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3	Locus type: gene with protein product, function known or inferred/HUGO ID: 7682/UniProt ID: Q9UP21/
1152.1	1152	CKB	creatine kinase, brain	HUGO ID: 1991/UniProt ID: P12277/
48.1	48	ACO1	aconitase 1, soluble	
27115.1	27115	PDE7B	phosphodiesterase 7B	HUGO ID: 8792/UniProt ID: Q9NP56/
3073.1	3073	HEXA	hexosaminidase A (alpha polypeptide)	HUGO ID: 4878/UniProt ID: P06865/
8972.1	8972	MGAM	maltase-glucoamylase (alpha-glucosidase)	Aliases: MGA/HUGO ID: 7043/UniProt ID: O43451/
3291.1	3291	HSD11B2	hydroxysteroid (11-beta) dehydrogenase 2	HUGO ID: 5209/UniProt ID: P80365/
10195.1	10195	ALG3	asparagine-linked glycosylation 3 homolog (yeast, alpha-1,3-mannosyltransferase)	Locus type: gene with protein product, function known or inferred/Aliases: NOT56L, Not56, CDGS4, D16Ertd36e/HUGO ID: 23056/UniProt ID: Q92685/MGD ID: MGI:1098592/
2939.1	2939	GSTA2	glutathione S-transferase A2	Locus type: gene with protein product, function known or inferred/HUGO ID: 4627/UniProt ID: P09210/
4668.1	4668	NAGA	N-acetylgalactosaminidase, alpha-	Aliases: D22S674/HUGO ID: 7631/UniProt ID: P17050/
1609.1	1609	DGKQ	diacylglycerol kinase, theta 110kDa	
5207.1	5207	PFKFB1	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1	HUGO ID: 8872/UniProt ID: P16118/
411.1	411	ARSB	arylsulfatase B	HUGO ID: 714/UniProt ID: P15848/
6652.1	6652	SORD	sorbitol dehydrogenase	HUGO ID: 11184/UniProt ID: Q00796/
29926.1	29926	GMPPA	GDP-mannose pyrophosphorylase A	transcript: NM_013335
8394.1	8394	PIP5K1A	phosphatidylinositol-4-phosphate 5-kinase, type I, alpha	
7385.1	7385	UQCRC2	ubiquinol-cytochrome c reductase core protein II	HUGO ID: 12586/UniProt ID: P22695/
10312.1	10312	TCIRG1	T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 protein a isoform 3	transcript: NM_006019
496.1	496	ATP4B	ATPase, H+/K+ exchanging, beta polypeptide	Aliases: ATP6B/HUGO ID: 820/UniProt ID: P51164/
56895.1	56895	AGPAT4	1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta)	Locus type: gene with protein product, function known or inferred/Aliases: LPAAT-delta, dJ473J16.2/HUGO ID: 20885/UniProt ID: Q9NRZ5/MGD ID: MGI:1915512/
270.1	270	AMPD1	adenosine monophosphate deaminase 1 (isoform M)	Aliases: MAD, MADA/HUGO ID: 468/UniProt ID: P23109/
2938.1	2938	GSTA1	glutathione S-transferase A1	HUGO ID: 4626/UniProt ID: P08263/
4717.1	4717	NDUFC1	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown 1, 6kDa	
249.1	249	ALPL	alkaline phosphatase, liver/bone/kidney	Locus type: gene with protein product, function known or inferred/Aliases: HOPS, TNSALP/HUGO ID: 438/UniProt ID: P05186/
2026.1	2026	ENO2	enolase 2 (gamma, neuronal)	HUGO ID: 3353/UniProt ID: P09104/
3099.1	3099	HK2	hexokinase 2	HUGO ID: 4923/UniProt ID: P52789/
1588.1	1588	CYP19A1	cytochrome P450, family 19, subfamily A, polypeptide 1	Locus type: gene with protein product, function known or inferred/Aliases: ARO, P-450AROM, CPV1, ARO1, CYAR/HUGO ID: 2594/UniProt ID: P11511/
6783.1	6783	SULT1E1	sulfotransferase family 1E, estrogen-preferring, member 1	Aliases: EST/HUGO ID: 11377/UniProt ID: P49888/
26301.1	26301	FS	Forssman glycolipid synthetase	
4123.1	4123	MAN2C1	mannosidase, alpha, class 2C, member 1	
587.1	587	BCAT2	branched chain aminotransferase 2, mitochondrial	Aliases: BCAM/HUGO ID: 977/UniProt ID: O15382/
8813.1	8813	DPM1	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit	
189.1	189	AGXT	alanine-glyoxylate aminotransferase (oxalosis I; hyperoxaluria I; glycolicaciduria; serine-pyruvate aminotransferase)	Aliases: AGXT1/HUGO ID: 341/UniProt ID: P21549/
2194.1	2194	FASN	fatty acid synthase	HUGO ID: 3594/UniProt ID: P49327/
4540.1	4540	MTND5	NADH dehydrogenase 5	HUGO ID: 7461/UniProt ID: P03915/
2946.1	2946	GSTM2	glutathione S-transferase M2 (muscle)	
2953.1	2953	GSTT2	glutathione S-transferase theta 2	HUGO ID: 4642/UniProt ID: P30712/
1346.1	1346	COX7A1	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)	
205.1	205	AK3	adenylate kinase 3	Locus type: gene with protein product, function known or inferred/HUGO ID: 363/UniProt ID: P27144/
47.1	47	ACLY	ATP citrate lyase	HUGO ID: 115/UniProt ID: P53396/
7498.1	7498	XDH	xanthine dehydrogenase	HUGO ID: 12805/UniProt ID: P47989/
1384.1	1384	CRAT	carnitine acetyltransferase	Aliases: CAT1/HUGO ID: 2342/UniProt ID: P43155/
11253.1	11253	MAN1B1	mannosidase, alpha, class 1B, member 1	
6822.1	6822	SULT2A1	sulfotransferase family, cytosolic, 2A, dehydroepiandrosterone (DHEA) -preferring, member 1	
7363.1	7363	UGT2B4	UDP glycosyltransferase 2 family, polypeptide B4	
2356.1	2356	FPGS	folylpolyglutamate synthase	HUGO ID: 3824/UniProt ID: Q05932/
23483.1	23483	TGDS	TDP-glucose 4,6-dehydratase	Locus type: gene with protein product, function known or inferred/Aliases: TDPGD/HUGO ID: 20324/UniProt ID: O95455/MGD ID: MGI:1923605/
8654.1	8654	PDE5A	phosphodiesterase 5A, cGMP-specific	
114.1	114	ADCY8	adenylate cyclase 8 (brain)	Aliases: HBAC1/HUGO ID: 239/UniProt ID: P40145/
6799.1	6799	SULT1A2	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 2	
635.1	635	BHMT	betaine-homocysteine methyltransferase	

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
8424.1	8424	BBOX1	butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1	Aliases: gamma-BBH, G-BBH, BBH/HUGO ID: 964/UniProt ID: O75936/
9955.1	9955	HS3ST3A1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1	Locus type: gene with protein product, function known or inferred/Aliases: 3OST3A1, 30ST3A1/HUGO ID: 5196/UniProt ID: Q9Y663/
435.1	435	ASL	argininosuccinate lyase	Locus type: gene with protein product, function known or inferred/HUGO ID: 746/UniProt ID: P04424/
7372.1	7372	UMPS	uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase)	HUGO ID: 12563/UniProt ID: P11172/
314.1	314	AOC2	amine oxidase, copper containing 2 (retina-specific)	
1633.1	1633	DCK	deoxycytidine kinase	HUGO ID: 2704/UniProt ID: P27707/
55276.1	55276	PGM2	phosphoglucomutase 2	Locus type: gene with protein product, function known or inferred/Aliases: FLJ10983/HUGO ID: 8906/UniProt ID: Q9H0P9/MGD ID: MGI:1913931/
5138.1	5138	PDE2A	phosphodiesterase 2A, cGMP-stimulated	HUGO ID: 8777/UniProt ID: O00408/
210.1	210	ALAD	aminolevulinate, delta-, dehydratase	HUGO ID: 395/UniProt ID: P13716/
4701.1	4701	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7, 14.5kDa	Aliases: B14.5a/HUGO ID: 7691/UniProt ID: O95182/
2941.1	2941	GSTA4	glutathione S-transferase A4	HUGO ID: 4629/UniProt ID: O15217/
7384.1	7384	UQCRC1	ubiquinol-cytochrome c reductase core protein I	Aliases: D3S3191/HUGO ID: 12585/UniProt ID: P31930/
4714.1	4714	NDUFB8	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa	Aliases: ASHI/HUGO ID: 7703/UniProt ID: O95169/
5289.1	5289	PIK3C3	phosphoinositide-3-kinase, class 3	Aliases: Vps34/HUGO ID: 8974/UniProt ID: Q15134/
5291.1	5291	PIK3CB	phosphoinositide-3-kinase, catalytic, beta polypeptide	HUGO ID: 8976/UniProt ID: P42338/
645.1	645	BLVRB	biliverdin reductase B (flavin reductase (NADPH))	HUGO ID: 1063/UniProt ID: P30043/
5498.1	5498	PPOX	protoporphyrinogen oxidase	Locus type: gene with protein product, function known or inferred/Aliases: PPO/HUGO ID: 9280/UniProt ID: P50336/MGD ID: MGI:104968/
5095.1	5095	PCCA	propionyl Coenzyme A carboxylase, alpha polypeptide	Locus type: gene with protein product, function known or inferred/HUGO ID: 8653/UniProt ID: P05165/
43.1	43	ACHE	acetylcholinesterase (YT blood group)	Locus type: gene with protein product, function known or inferred/HUGO ID: 108/UniProt ID: P22303/
2820.1	2820	GPD2	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	HUGO ID: 4456/UniProt ID: P43304/
2720.1	2720	GLB1	galactosidase, beta 1	HUGO ID: 4298/UniProt ID: P16278/
5210.1	5210	PFKFB4	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	
248.1	248	ALPI	alkaline phosphatase, intestinal	HUGO ID: 437/UniProt ID: P09923/
2023.1	2023	ENO1	enolase 1, (alpha)	
7298.1	7298	TYMS	thymidylate synthetase	Locus type: gene with protein product, function known or inferred/Aliases: Tsase, TMS, HsT422/HUGO ID: 12441/UniProt ID: P04818/
3628.1	3628	INPP1	inositol polyphosphate-1-phosphatase	HUGO ID: 6071/UniProt ID: P49441/
2729.1	2729	GCLC	glutamate-cysteine ligase, catalytic subunit	Aliases: GCS/HUGO ID: 4311/UniProt ID: P48506/
2936.1	2936	GSR	glutathione reductase (mitochondrial precursor)	HUGO ID: 4623/UniProt ID: P00390/
93034.1	93034	NT5C1B	5'-nucleotidase, cytosolic IB	Aliases: AIRP, CN-IB/HUGO ID: 17818/UniProt ID: Q96P26/
953.1	953	ENTPD1	ectonucleoside triphosphate diphosphohydrolase 1	Locus type: gene with protein product, function known or inferred/Aliases: NTPDase-1, ATPDase/HUGO ID: 3363/UniProt ID: P49961/
30.1	30	ACAA1	acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase)	HUGO ID: 82/UniProt ID: P09110/
9296.1	9296	ATP6V1F	ATPase, H+ transporting, lysosomal 14kDa, V1 subunit F	
4833.1	4833	NME4	non-metastatic cells 4, protein expressed in	Locus type: gene with protein product, function known or inferred/Aliases: nm23-H4, NM23H4/HUGO ID: 7852/UniProt ID: O00746/
250.1	250	ALPP	alkaline phosphatase, placental (Regan isozyme)	HUGO ID: 439/UniProt ID: P05187/
4122.1	4122	MAN2A2	mannosidase, alpha, class 2A, member 2	Locus type: gene with protein product, function known or inferred/Aliases: MANA2X, HsT19662/HUGO ID: 6825/UniProt ID: P49641/
6898.1	6898	TAT	tyrosine aminotransferase	HUGO ID: 11573/UniProt ID: P17735/
586.1	586	BCAT1	branched chain aminotransferase 1, cytosolic	HUGO ID: 976/UniProt ID: P54687/
509.1	509	ATP5C1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	Variant 1: This variant represents the longer transcript, and encodes the longer isoform (L), also known as a liver type isoform.
2954.1	2954	GSTZ1	glutathione transferase zeta 1 (maleylacetoacetate isomerase)	
56894.1	56894	AGPAT3	1-acylglycerol-3-phosphate O-acyltransferase 3	Aliases: LPAAT-gamma/HUGO ID: 326/UniProt ID: Q9NRZ7/
22928.1	22928	SEPHS2	selenophosphate synthetase 2	Locus type: gene with protein product, function known or inferred/Aliases: SPS2/HUGO ID: 19686/UniProt ID: Q99611/MGD ID: MGI:108388/
2982.1	2982	GUCY1A3	guanylate cyclase 1, soluble, alpha 3	Aliases: GC-SA3/HUGO ID: 4685/UniProt ID: Q02108/
53630.1	53630	BCDO1	beta-carotene 15, 15'-dioxygenase	
4245.1	4245	MGAT1	mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	Aliases: GNT-1, GLCNAC-TI/HUGO ID: 7044/UniProt ID: P26572/
4704.1	4704	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9, 39kDa	Locus type: gene with protein product, function known or inferred/HUGO ID: 7693/UniProt ID: Q16795/
5198.1	5198	PFAS	phosphoribosylformylglycinamidine synthase (FGAR amidotransferase)	Aliases: PURL, FGARAT, KIAA0361/HUGO ID: 8863/UniProt ID: O15067/

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
8050.1	8050	PDHX	pyruvate dehydrogenase complex, component X	
1644.1	1644	DDC	dopa decarboxylase (aromatic L-amino acid decarboxylase)	Aliases: AADC/HUGO ID: 2719/UniProt ID: P20711/
115.1	115	ADCY9	adenylate cyclase 9	HUGO ID: 240/UniProt ID: O60503/
8705.1	8705	B3GALT4	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4	Aliases: beta3Gal-T4, GalT4/HUGO ID: 919/UniProt ID: O96024/
1120.1	1120	CHKL	choline/ethanolamine kinase	*PubMed
6821.1	6821	SUOX	sulfite oxidase	Locus type: gene with protein product, function known or inferred/HUGO ID: 11460/UniProt ID: P51687/
2974.1	2974	GUCY1B2	guanylate cyclase 1, soluble, beta 2	
1562.1	1562	CYP2C18	cytochrome P450, family 2, subfamily C, polypeptide 18	
5322.1	5322	PLA2G5	phospholipase A2, group V	
5236.1	5236	PGM1	phosphoglucomutase 1	
4125.1	4125	MAN2B1	mannosidase, alpha, class 2B, member 1	Aliases: LAMAN/HUGO ID: 6826/UniProt ID: O00754/
11185.1	11185	INMT	indolethylamine N-methyltransferase	HUGO ID: 6069/UniProt ID: O95050/
7371.1	7371	UCK2	uridine-cytidine kinase 2	Locus type: gene with protein product, function known or inferred/HUGO ID: 12562/UniProt ID: Q9BZX2/MGD ID: MGI:98904/
2687.1	2687	GGTLA1	gamma-glutamyltransferase-like activity 1	Aliases: GGT-REL/HUGO ID: 4260/UniProt ID: P36269/
4519.1	4519	MTCYB	cytochrome b	HUGO ID: 7427/UniProt ID: P00156/
7360.1	7360	UGP2	UDP-glucose pyrophosphorylase 2	HUGO ID: 12527/UniProt ID: Q16851/
64132.1	64132	XYLT2	xylosyltransferase II	Aliases: XT-II/HUGO ID: 15517/UniProt ID: Q86V00/
8876.1	8876	VNN1	vanin 1	Aliases: Tiff66/HUGO ID: 12705/UniProt ID: O95497/
31.1	31	ACACA	acetyl-Coenzyme A carboxylase alpha	Aliases: ACC1/HUGO ID: 84/UniProt ID: Q13085/
383.1	383	ARG1	arginase, liver	HUGO ID: 663/UniProt ID: P05089/
2944.1	2944	GSTM1	glutathione S-transferase M1	Locus type: gene with protein product, function known or inferred/Aliases: MU, H-B, GST1/HUGO ID: 4632/UniProt ID: P09488/
6120.1	6120	RPE	ribulose-5-phosphate-3-epimerase	HUGO ID: 10293/UniProt ID: Q96AT9/
9563.1	9563	H6PD	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	Aliases: HGNC:4225/HUGO ID: 4795/UniProt ID: O95479/
7173.1	7173	TPO	thyroid peroxidase	HUGO ID: 12015/UniProt ID: P07202/
2821.1	2821	GPI	glucose phosphate isomerase	
10840.1	10840	FTHFD	formyltetrahydrofolate dehydrogenase	HUGO ID: 3978/UniProt ID: O75891/
8525.1	8525	DGKZ	diacylglycerol kinase, zeta 104kDa	Aliases: DAGK5, hDGKzeta/HUGO ID: 2857/UniProt ID: Q13574/
5240.1	5240	PGP	phosphoglycolate phosphatase	HUGO ID: 8909/
10331.1	10331	B3GNT3	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3	
217.1	217	ALDH2	aldehyde dehydrogenase 2 family (mitochondrial)	HUGO ID: 404/UniProt ID: P05091/
6483.1	6483	SIAT4B	sialyltransferase 4B (beta-galactoside alpha-2,3-sialyltransferase)	
2655.1	2655	GCTG	gamma-glutamylcyclotransferase	Locus type: gene with protein product, function known or inferred/Aliases: Ggc/HUGO ID: 4210/MGD ID: MGI:95700/
7299.1	7299	TYR	tyrosinase (oculocutaneous albinism IA)	Aliases: OCAIA/HUGO ID: 12442/UniProt ID: P14679/
5290.1	5290	PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	HUGO ID: 8975/UniProt ID: P42336/
5148.1	5148	PDE6G	phosphodiesterase 6G, cGMP-specific, rod, gamma	HUGO ID: 8789/UniProt ID: P18545/
126.1	126	ADH1C	alcohol dehydrogenase 1C (class I), gamma polypeptide	Locus type: gene with protein product, function known or inferred/HUGO ID: 251/UniProt ID: P00326/
4715.1	4715	NDUFB9	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa	Locus type: gene with protein product, function known or inferred/Aliases: B22, UQOR22/HUGO ID: 7704/UniProt ID: Q9Y6M9/
763.1	763	CA5A	carbonic anhydrase VA, mitochondrial	
56922.1	56922	MCCC1	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)	Aliases: MCCA/HUGO ID: 6936/UniProt ID: Q96RQ3/
1610.1	1610	DAO	D-amino-acid oxidase	
6482.1	6482	SIAT4A	sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase)	transcript: NM_003033
5223.1	5223	PGAM1	phosphoglycerate mutase 1 (brain)	Locus type: gene with protein product, function known or inferred/HUGO ID: 8888/UniProt ID: P18669/
8612.1	8612	PPAP2C	phosphatidic acid phosphatase type 2C	
1376.1	1376	CPT2	carnitine palmitoyltransferase II	Locus type: gene with protein product, function known or inferred/Aliases: CPTASE/HUGO ID: 2330/UniProt ID: P23786/
2678.1	2678	GGT1	gamma-glutamyltransferase 1	Aliases: D22S672, D22S732, CD224/HUGO ID: 4250/UniProt ID: P19440/
445.1	445	ASS	argininosuccinate synthetase	
4199.1	4199	ME1	malic enzyme 1, NADP(+)-dependent, cytosolic	HUGO ID: 6983/UniProt ID: P48163/
56474.1	56474	CTPS2	CTP synthase II	Locus type: gene with protein product, function known or inferred/HUGO ID: 2520/UniProt ID: Q9H809/
2224.1	2224	FDPS	farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase)	Locus type: gene with protein product, function known or inferred/HUGO ID: 3631/UniProt ID: P14324/
2643.1	2643	GCH1	GTP cyclohydrolase 1 (dopa-responsive dystonia)	
8879.1	8879	SGPL1	sphingosine-1-phosphate lyase 1	Aliases: SPL/HUGO ID: 10817/UniProt ID: Q9ULG8/
226.1	226	ALDOA	aldolase A, fructose-bisphosphate	HUGO ID: 414/UniProt ID: P04075/
6476.1	6476	SI	sucrase-isomaltase	

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
6817.1	6817	SULT1A1	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1	
22929.1	22929	SEPHS1	selenophosphate synthetase 1	Locus type: gene with protein product, function known or inferred/Aliases: SPS, SPS1/HUGO ID: 19685/UniProt ID: P49903/
427.1	427	ASAH1	N-acylsphingosine amidohydrolase (acid ceramidase) 1	
2645.1	2645	GCK	glucokinase (hexokinase 4, maturity onset diabetes of the young 2)	transcript: NM_000162
5331.1	5331	PLCB3	phospholipase C, beta 3 (phosphatidylinositol-specific)	HUGO ID: 9056/UniProt ID: Q01970/
4597.1	4597	MVD	mevalonate (diphospho) decarboxylase	Locus type: gene with protein product, function known or inferred/Aliases: MPD/HUGO ID: 7529/UniProt ID: P53602/
3418.1	3418	IDH2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	HUGO ID: 5383/UniProt ID: P48735/
5740.1	5740	PTGIS	prostaglandin I2 (prostacyclin) synthase	Aliases: PGIS, CYP8/HUGO ID: 9603/UniProt ID: Q16647/
32.1	32	ACACB	acetyl-Coenzyme A carboxylase beta	Locus type: gene with protein product, function known or inferred/Aliases: HACC275, ACC2, ACCB/HUGO ID: 85/UniProt ID: O00763/
4124.1	4124	MAN2A1	mannosidase, alpha, class 2A, member 1	HUGO ID: 6824/UniProt ID: Q16706/
23236.1	23236	PLCB1	phospholipase C, beta 1 (phosphoinositide-specific)	transcript: NM_015192
5631.1	5631	PRPS1	phosphoribosyl pyrophosphate synthetase 1	Aliases: PRS I/HUGO ID: 9462/UniProt ID: P09329/
3706.1	3706	ITPKA	inositol 1,4,5-trisphosphate 3-kinase A	HUGO ID: 6178/UniProt ID: P23677/
2184.1	2184	FAH	fumarylacetoacetate hydrolase (fumarylacetoacetase)	
26227.1	26227	PHGDH	phosphoglycerate dehydrogenase	Locus type: gene with protein product, function known or inferred/Aliases: SERA, PGDH, PDG/HUGO ID: 8923/UniProt ID: O43175/
5315.1	5315	PKM2	pyruvate kinase, muscle	Aliases: THBP1, OIP3/HUGO ID: 9021/UniProt ID: P14618/
5152.1	5152	PDE9A	phosphodiesterase 9A	HUGO ID: 8795/UniProt ID: O76083/
10678.1	10678	B3GNT1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1	transcript info: NM_006577
2819.1	2819	GPD1	glycerol-3-phosphate dehydrogenase 1 (soluble)	HUGO ID: 4455/UniProt ID: P21695/
5019.1	5019	OXCT1	3-oxoacid CoA transferase 1	Locus type: gene with protein product, function known or inferred/Aliases: SCOT/HUGO ID: 8527/UniProt ID: P55809/
7386.1	7386	UQCRFS1	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	Aliases: RIS1/HUGO ID: 12587/UniProt ID: P47985/
2717.1	2717	GLA	galactosidase, alpha	Aliases: GALA/HUGO ID: 4296/UniProt ID: P06280/
9953.1	9953	HS3ST3B1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	Locus type: gene with protein product, function known or inferred/Aliases: 3OST3B1, 30ST3B1/HUGO ID: 5198/UniProt ID: Q9Y662/
1807.1	1807	DPYS	dihydropyrimidinase	Locus type: gene with protein product, function known or inferred/Aliases: DHPase/HUGO ID: 3013/UniProt ID: Q14117/
275.1	275	AMT	aminomethyltransferase (glycine cleavage system protein T)	HUGO ID: 473/UniProt ID: P48728/
5406.1	5406	PNLIP	pancreatic lipase	Locus type: gene with protein product, function known or inferred/HUGO ID: 9155/UniProt ID: P16233/
476.1	476	ATP1A1	ATPase, Na+/K+ transporting, alpha 1 polypeptide	HUGO ID: 799/UniProt ID: P05023/
125.1	125	ADH1B	alcohol dehydrogenase IB (class I), beta polypeptide	Locus type: gene with protein product, function known or inferred/HUGO ID: 250/UniProt ID: P00325/
27232.1	27232	GNMT	glycine N-methyltransferase	
4190.1	4190	MDH1	malate dehydrogenase 1, NAD (soluble)	HUGO ID: 6970/UniProt ID: P40925/
4723.1	4723	NDUFV1	NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa	HUGO ID: 7716/UniProt ID: P49821/
766.1	766	CA7	carbonic anhydrase VII	HUGO ID: 1381/UniProt ID: P43166/
6697.1	6697	SPR	sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase)	HUGO ID: 11257/UniProt ID: P35270/
2998.1	2998	GYS2	glycogen synthase 2 (liver)	HUGO ID: 4707/UniProt ID: P54840/
11285.1	11285	B4GALT7	xylosylprotein beta 1,4-galactosyltransferase, polypeptide 7 (galactosyltransferase I)	*PubMed
8528.1	8528	DDO	D-aspartate oxidase	Locus type: gene with protein product, function known or inferred/HUGO ID: 2727/UniProt ID: Q99489/
5143.1	5143	PDE4C	phosphodiesterase 4C, cAMP-specific (phosphodiesterase E1 dunce homolog, Drosophila)	HUGO ID: 8782/UniProt ID: Q08493/
2806.1	2806	GOT2	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartat aminotransferase 2)	HUGO ID: 4433/UniProt ID: P00505/
3707.1	3707	ITPKB	inositol 1,4,5-trisphosphate 3-kinase B	
8509.1	8509	NDST2	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2	Aliases: NST2, HSST2/HUGO ID: 7681/UniProt ID: P52849/
5287.1	5287	PIK3C2B	phosphoinositide-3-kinase, class 2, beta polypeptide	
2679.1	2679	GGT2	gamma-glutamyltransferase 2	Locus type: gene with protein product, function known or inferred/HUGO ID: 4251/UniProt ID: P36268/
1329.1	1329	COX5B	cytochrome c oxidase subunit Vb	HUGO ID: 2269/UniProt ID: P10606/
55907.1	55907	CMAS	cytidine monophosphate N-acetylneuraminic acid synthetase	*PubMed
10020.1	10020	GNE	UDP-N-acetylglucosamine-2-epimerase/N-acetylmannosamine kinase	
2947.1	2947	GSTM3	glutathione S-transferase M3 (brain)	Locus type: gene with protein product, function known or inferred/Aliases: GST5/HUGO ID: 4635/UniProt ID: P21266/
276.1	276	AMY1A	amylase, alpha 1A; salivary	HUGO ID: 474/UniProt ID: P04745/
5373.1	5373	PMM2	phosphomannomutase 2	Locus type: gene with protein product, function known or inferred/Aliases: CDGS/HUGO ID: 9115/UniProt ID: O15305/

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
4259.1	4259	MGST3	microsomal glutathione S-transferase 3	HUGO ID: 7064/UniProt ID: O14880/
51703.1	51703	ACSL5	acyl-CoA synthetase long-chain family member 5	Locus type: gene with protein product, function known or inferred/Aliases: ACS5, ACS2/HUGO ID: 16526/UniProt ID: Q9ULC5/MGD ID: MGI:1919129/
108.1	108	ADCY2	adenylate cyclase 2 (brain)	Locus type: gene with protein product, function known or inferred/Aliases: HBAC2, KIAA1060/HUGO ID: 233/UniProt ID: Q08462/
2879.1	2879	GPX4	glutathione peroxidase 4 (phospholipid hydroperoxidase)	HUGO ID: 4556/UniProt ID: P36969/
3636.1	3636	INPPL1	inositol polyphosphate phosphatase-like 1	HUGO ID: 6080/UniProt ID: O15357/
5293.1	5293	PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide	*PubMed
53947.1	53947	A4GALT	alpha 1,4-galactosyltransferase	Locus type: gene with protein product, function known or inferred/Aliases: A14GALT, HGNC:8531/HUGO ID: 18149/UniProt ID: Q9NPC4/
5330.1	5330	PLCB2	phospholipase C, beta 2	
10558.1	10558	SPTLC1	serine palmitoyltransferase, long chain base subunit 1	Aliases: LCB1, SPTI, HGNC:5230, HSAN1/HUGO ID: 11277/UniProt ID: O15269/
5230.1	5230	PGK1	phosphoglycerate kinase 1	
1339.1	1339	COX6A2	cytochrome c oxidase subunit VIa polypeptide 2	HUGO ID: 2279/UniProt ID: Q02221/
2739.1	2739	GLO1	glyoxalase I	
2548.1	2548	GAA	glucosidase, alpha; acid (Pompe disease, glycogen storage disease type II)	HUGO ID: 4065/UniProt ID: P10253/
4357.1	4357	MPST	mercaptopyruvate sulfurtransferase	Aliases: MST/HUGO ID: 7223/UniProt ID: P25325/
33.1	33	ACADL	acyl-Coenzyme A dehydrogenase, long chain	Locus type: gene with protein product, function known or inferred/Aliases: LCAD, ACAD4/HUGO ID: 88/UniProt ID: P28330/
8398.1	8398	PLA2G6	phospholipase A2, group VI (cytosolic, calcium-independent)	Aliases: iPLA2/HUGO ID: 9039/UniProt ID: O60733/
2523.1	2523	FUT1	fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase)	HUGO ID: 4012/UniProt ID: P19526/
3419.1	3419	IDH3A	isocitrate dehydrogenase 3 (NAD+) alpha	HUGO ID: 5384/UniProt ID: P50213/
4830.1	4830	NME1	non-metastatic cells 1, protein (NM23A) expressed in	Aliases: NM23, NM23-H1/HUGO ID: 7849/UniProt ID: P15531/
219.1	219	ALDH1B1	aldehyde dehydrogenase 1 family, member B1	Aliases: ALDHX/HUGO ID: 407/UniProt ID: P30837/
7389.1	7389	UROD	uroporphyrinogen decarboxylase	
5351.1	5351	PLOD	procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI)	transcript: NM_000302
5153.1	5153	PDE1B	phosphodiesterase 1B, calmodulin-dependent	
5860.1	5860	QDPR	quinoid dihydropteridine reductase	Aliases: DHPR/HUGO ID: 9752/UniProt ID: P09417/
5338.1	5338	PLD2	phospholipase D2	
5096.1	5096	PCCB	propionyl Coenzyme A carboxylase, beta polypeptide	HUGO ID: 8654/UniProt ID: P05166/
178.1	178	AGL	amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycoge debranching enzyme, glycogen storage disease type III)	Locus type: gene with protein product, function known or inferred/HUGO ID: 321/UniProt ID: P35573/MGD ID: MGI:1924809/
10841.1	10841	FTCD	formiminotransferase cyclodeaminase	*PubMed
2590.1	2590	GALNT2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2)	
3029.1	3029	HAGH	hydroxyacyl glutathione hydrolase	
10400.1	10400	PEMT	phosphatidylethanolamine N-methyltransferase	Aliases: PEMPT, PEMT2/HUGO ID: 8830/UniProt ID: Q9UBM1/
2530.1	2530	FUT8	fucosyltransferase 8 (alpha (1,6) fucosyltransferase)	HUGO ID: 4019/UniProt ID: Q9BYC5/
644.1	644	BLVRA	biliverdin reductase A	Locus type: gene with protein product, function known or inferred/HUGO ID: 1062/UniProt ID: P53004/
1103.1	1103	CHAT	choline acetyltransferase	Locus type: gene with protein product, function known or inferred/HUGO ID: 1912/UniProt ID: P28329/
4508.1	4508	MTATP6	ATP synthase 6	HUGO ID: 7414/UniProt ID: P00846/
686.1	686	BTD	biotinidase	HUGO ID: 1122/UniProt ID: P43251/
1719.1	1719	DHFR	dihydrofolate reductase	HUGO ID: 2861/UniProt ID: P00374/
523.1	523	ATP6V1A	ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A	Aliases: Vma1, VA68/HUGO ID: 851/UniProt ID: P38606/
6480.1	6480	SIAT1	sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase)	Aliases: CD75, ST6Gal I/HUGO ID: 10860/UniProt ID: P15907/
5407.1	5407	PNLIPRP1	pancreatic lipase-related protein 1	Locus type: gene with protein product, function known or inferred/Aliases: PLRP1/HUGO ID: 9156/UniProt ID: P54315/
4707.1	4707	NDUFB1	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7kDa	Aliases: MNLL/HUGO ID: 7695/UniProt ID: O75438/
443.1	443	ASPA	aspartoacylase (aminoacylase 2, Canavan disease)	Aliases: ASP/HUGO ID: 756/UniProt ID: P45381/
8527.1	8527	DGKD	diacylglycerol kinase, delta 130kDa	Aliases: KIAA0145, DGKdelta/HUGO ID: 2851/UniProt ID: Q16760/
5286.1	5286	PIK3C2A	phosphoinositide-3-kinase, class 2, alpha polypeptide	Aliases: PI3K-C2alpha/HUGO ID: 8971/UniProt ID: O00443/
8733.1	8733	GPAA1	GPAA1P anchor attachment protein 1 homolog (yeast)	Aliases: GAA1, hGAA1/HUGO ID: 4446/UniProt ID: O43292/
3158.1	3158	HMGCS2	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial)	
10975.1	10975	UQCR	ubiquinol-cytochrome c reductase (6.4kD) subunit	transcript: NM_006830
109.1	109	ADCY3	adenylate cyclase 3	HUGO ID: 234/UniProt ID: O60266/

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
5142.1	5142	PDE4B	phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)	Locus type: gene with protein product, function known or inferred/HUGO ID: 8781/UniProt ID: Q07343/
2584.1	2584	GALK1	galactokinase 1	HUGO ID: 4118/UniProt ID: P51570/
5372.1	5372	PMM1	phosphomannomutase 1	HUGO ID: 9114/UniProt ID: Q92871/
128.1	128	ADH5	alcohol dehydrogenase 5 (class III), chi polypeptide	Locus type: gene with protein product, function known or inferred/Aliases: ADH-3, HGNC:3630, ADHX/HUGO ID: 253/UniProt ID: P11766/MGD ID: MGI:87929/
2203.1	2203	FBP1	fructose-1,6-bisphosphatase 1	HUGO ID: 3606/UniProt ID: P09467/
1629.1	1629	DBT	dihydrolipoamide branched chain transacylase (E2 componen of branched chain keto acid dehydrogenase complex; maple syrup urine disease)	
1577.1	1577	CYP3A5	cytochrome P450, family 3, subfamily A, polypeptide 5	Locus type: gene with protein product, function known or inferred/Aliases: PCN3, P450PCN3, CP35/HUGO ID: 2638/UniProt ID: P20815/
1786.1	1786	DNMT1	DNA (cytosine-5-)-methyltransferase 1	Locus type: gene with protein product, function known or inferred/Aliases: MCMT, CXXC9/HUGO ID: 2976/UniProt ID: P26358/MGD ID: MGI:94912/
1582.1	1582	CYP8B1	cytochrome P450, family 8, subfamily B, polypeptide 1	Locus type: gene with protein product, function known or inferred/Aliases: CYP12/HUGO ID: 2653/UniProt ID: Q9UNU6/
10993.1	10993	SDS	serine dehydratase	Locus type: gene with protein product, function known or inferred/Aliases: SDH/HUGO ID: 10691/UniProt ID: P20132/
10317.1	10317	B3GALT5	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5	Aliases: beta3Gal-T5/HUGO ID: 920/UniProt ID: Q9Y2C3/
4258.1	4258	MGST2	microsomal glutathione S-transferase 2	Aliases: MGST-II/HUGO ID: 7063/UniProt ID: Q99735/
539.1	539	ATP5O	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein)	Aliases: OSCP, ATPO/HUGO ID: 850/UniProt ID: P48047/
10476.1	10476	ATP5H	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d	Locus type: gene with protein product, function known or inferred/Aliases: ATPQ, ATP5JD/HUGO ID: 845/UniProt ID: O75947/MGD ID: MGI:1918929/
132.1	132	ADK	adenosine kinase	Locus type: gene with protein product, function known or inferred/Aliases: AK/HUGO ID: 257/UniProt ID: P55263/
4705.1	4705	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa	
5333.1	5333	PLCD1	phospholipase C, delta 1	HUGO ID: 9060/UniProt ID: P51178/
6391.1	6391	SDHC	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa	
3030.1	3030	HADHA	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	
23556.1	23556	PIGN	phosphatidylinositol glycan, class N	transcript: NM_012327
768.1	768	CA9	carbonic anhydrase IX	
6723.1	6723	SRM	spermidine synthase	Locus type: gene with protein product, function known or inferred/Aliases: SPS1/HUGO ID: 11296/UniProt ID: P19623/
8985.1	8985	PLOD3	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	
53.1	53	ACP2	acid phosphatase 2, lysosomal	HUGO ID: 123/UniProt ID: P11117/
2182.1	2182	ACSL4	acyl-CoA synthetase long-chain family member 4	Locus type: gene with protein product, function known or inferred/Aliases: ACS4, MRX63, LACS4/HUGO ID: 3571/UniProt ID: O60488/MGD ID: MGI:1354713/
6484.1	6484	SIAT4C	sialyltransferase 4C (beta-galactoside alpha-2,3-sialyltransferase)	
506.1	506	ATP5B	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide	HUGO ID: 830/UniProt ID: P06576/
7367.1	7367	UGT2B17	UDP glycosyltransferase 2 family, polypeptide B17	Locus type: gene with protein product, function known or inferred/HUGO ID: 12547/UniProt ID: O75795/
7388.1	7388	UQCRH	ubiquinol-cytochrome c reductase hinge protein	Locus type: gene with protein product, function known or inferred/HUGO ID: 12590/UniProt ID: P07919/
4952.1	4952	OCRL	oculocerebrorenal syndrome of Lowe	HUGO ID: 8108/UniProt ID: Q01968/
5471.1	5471	PPAT	phosphoribosyl pyrophosphate amidotransferase	Aliases: GPAT/HUGO ID: 9238/UniProt ID: Q06203/
1608.1	1608	DGKG	diacylglycerol kinase, gamma 90kDa	HUGO ID: 2853/UniProt ID: P49619/
51606.1	51606	ATP6V1H	ATPase, H+ transporting, lysosomal 50/57kDa, V1 subunit H	
3704.1	3704	ITPA	inosine triphosphatase (nucleoside triphosphate pyrophosphatase)	Aliases: HGNC:15883, HLC14-06-P, dJ794I6.3/HUGO ID: 6176/UniProt ID: Q9BY32/
26229.1	26229	B3GAT3	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I)	Locus type: gene with protein product, function known or inferred/Aliases: GlcAT-I/HUGO ID: 923/UniProt ID: O94766/
9394.1	9394	HS6ST1	heparan sulfate 6-O-sulfotransferase 1	HUGO ID: 5201/UniProt ID: O60243/
2591.1	2591	GALNT3	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3 (GalNAc-T3)	Aliases: GalNAc-T3/HUGO ID: 4125/UniProt ID: Q14435/
482.1	482	ATP1B2	ATPase, Na+/K+ transporting, beta 2 polypeptide	Aliases: AMOG/HUGO ID: 805/UniProt ID: P14415/
280.1	280	AMY2B	amylase, alpha 2B; pancreatic	HUGO ID: 478/UniProt ID: P19961/
5091.1	5091	PC	pyruvate carboxylase	Aliases: PCB/HUGO ID: 8636/UniProt ID: P11498/
4248.1	4248	MGAT3	mannosyl (beta-1,4-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase	Aliases: GNT-III/HUGO ID: 7046/UniProt ID: Q09327/
1738.1	1738	DLD	dihydrolipoamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex)	Aliases: DLDH/HUGO ID: 2898/UniProt ID: P09622/
23464.1	23464	GCAT	glycine C-acetyltransferase (2-amino-3-ketobutyrate coenzyme A ligase)	Aliases: KBL/HUGO ID: 4188/UniProt ID: O75600/

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
127.1	127	ADH4	alcohol dehydrogenase 4 (class II), pi polypeptide	Locus type: gene with protein product, function known or inferred/Aliases: ADH-2/HUGO ID: 252/UniProt ID: P08319/
5209.1	5209	PFKFB3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	
51251.1	51251	NT5C3	5'-nucleotidase, cytosolic III	*PubMed
1327.1	1327	COX4I1	cytochrome c oxidase subunit IV isoform 1	
27306.1	27306	PGDS	prostaglandin D2 synthase, hematopoietic	transcript: NM_014485
5053.1	5053	PAH	phenylalanine hydroxylase	HUGO ID: 8582/UniProt ID: P00439/
522.1	522	ATP5J	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6	Variant 1: This variant (1) represents the longest transcript. Variants 1, 2, 3 and 4 encode the same isoform (a). transcript: NM_001003703
5137.1	5137	PDE1C	phosphodiesterase 1C, calmodulin-dependent 70kDa	Aliases: Hcam3/HUGO ID: 8776/UniProt ID: Q14123/
4718.1	4718	NDUFC2	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown 2, 14.5kDa	Aliases: B14.5b/HUGO ID: 7706/UniProt ID: O95298/
471.1	471	ATIC	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	Aliases: PURH, AICARFT, IMPCHASE/HUGO ID: 794/UniProt ID: P31939/
10555.1	10555	AGPAT2	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)	
25796.1	25796	PGLS	6-phosphogluconolactonase	Aliases: 6PGL/HUGO ID: 8903/UniProt ID: O95336/
84129.1	84129	FLJ12592	hypothetical protein FLJ12592	transcript: NM_032169
978.1	978	CDA	cytidine deaminase	
6611.1	6611	SMS	spermine synthase	
4541.1	4541	MTND6	NADH dehydrogenase 6	HUGO ID: 7462/UniProt ID: P03923/
4706.1	4706	NDUFAB1	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa	
5160.1	5160	PDHA1	pyruvate dehydrogenase (lipoamide) alpha 1	HUGO ID: 8806/UniProt ID: P08559/
229.1	229	ALDOB	aldolase B, fructose-bisphosphate	HUGO ID: 417/UniProt ID: P05062/
204.1	204	AK2	adenylate kinase 2	Locus type: gene with protein product, function known or inferred/HUGO ID: 362/UniProt ID: P54819/
2585.1	2585	GALK2	galactokinase 2	Aliases: GK2/HUGO ID: 4119/UniProt ID: Q01415/
1345.1	1345	COX6C	cytochrome c oxidase subunit VIc	HUGO ID: 2285/UniProt ID: P09669/
51004.1	51004	COQ6	coenzyme Q6 homolog (yeast)	Locus type: gene with protein product, function unknown/Aliases: CGI-10/HUGO ID: 20233/UniProt ID: Q9Y2Z9/
8639.1	8639	AOC3	amine oxidase, copper containing 3 (vascular adhesion protein 1)	
52.1	52	ACP1	acid phosphatase 1, soluble	HUGO ID: 122/UniProt ID: P24666/
10654.1	10654	PMVK	phosphomevalonate kinase	
1581.1	1581	CYP7A1	cytochrome P450, family 7, subfamily A, polypeptide 1	Locus type: gene with protein product, function known or inferred/HUGO ID: 2651/UniProt ID: P22680/
9380.1	9380	GRHPR	glyoxylate reductase/hydroxypyruvate reductase	HUGO ID: 4570/UniProt ID: Q9UBQ7/
26237.1	26237	ENO1B	enolase alpha, lung-specific	
4942.1	4942	OAT	ornithine aminotransferase (gyrate atrophy)	Locus type: gene with protein product, function known or inferred/Aliases: HOGA/HUGO ID: 8091/UniProt ID: P04181/
8396.1	8396	PIP5K2B	phosphatidylinositol-4-phosphate 5-kinase, type II, beta	transcript: NM_003559
1576.1	1576	CYP3A4	cytochrome P450, family 3, subfamily A, polypeptide 4	
5332.1	5332	PLCB4	phospholipase C, beta 4	HUGO ID: 9059/UniProt ID: Q15147/
4708.1	4708	NDUFB2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2, 8kDa	
50614.1	50614	GALNT9	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 9 (GalNAc-T9)	Aliases: GALNAC-T9/HUGO ID: 4131/UniProt ID: Q9HCQ5/
4953.1	4953	ODC1	ornithine decarboxylase 1	HUGO ID: 8109/UniProt ID: P11926/
9551.1	9551	ATP5J2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2	Aliases: F1Fo-ATPase/HUGO ID: 848/UniProt ID: P56134/Variant 1: This variant represents the longest transcript, and it encodes the longest isoform 2a.
34.1	34	ACADM	acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain	Locus type: gene with protein product, function known or inferred/Aliases: MCAD, MCADH, ACAD1/HUGO ID: 89/UniProt ID: P11310/
2525.1	2525	FUT3	fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood group included)	
4509.1	4509	MTATP8	ATP synthase 8	HUGO ID: 7415/UniProt ID: P03928/
6390.1	6390	SDHB	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	HUGO ID: 10681/UniProt ID: P21912/MGD ID: MGI:1914930/
2592.1	2592	GALT	galactose-1-phosphate uridylyltransferase	HUGO ID: 4135/UniProt ID: P07902/
7364.1	7364	UGT2B7	UDP glycosyltransferase 2 family, polypeptide B7	
262.1	262	AMD1	adenosylmethionine decarboxylase 1	HUGO ID: 457/UniProt ID: P17707/
1806.1	1806	DPYD	dihydropyrimidine dehydrogenase	HUGO ID: 3012/UniProt ID: Q12882/
8526.1	8526	DGKE	diacylglycerol kinase, epsilon 64kDa	
5294.1	5294	PIK3CG	phosphoinositide-3-kinase, catalytic, gamma polypeptide	HUGO ID: 8978/UniProt ID: P48736/
528.1	528	ATP6V1C1	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C, isoform 1	Aliases: ATP6D, VATC, Vma5/HUGO ID: 856/UniProt ID: P21283/
3157.1	3157	HMGCS1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	HUGO ID: 5007/UniProt ID: Q01581/
2948.1	2948	GSTM4	glutathione S-transferase M4	Locus type: gene with protein product, function known or inferred/HUGO ID: 4636/UniProt ID: Q03013/
1737.1	1737	DLAT	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	Aliases: PDC-E2/HUGO ID: 2896/UniProt ID: P10515/

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
1798.1	1798	DPAGT1	dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminephosphotransferase 1 (GlcNAc-1-P transferase)	Aliases: GPT, D11S366, DGPT, ALG7, CDG-Ij/HUGO ID: 2995/UniProt ID: Q9H3H5/
8875.1	8875	VNN2	vanin 2	
5723.1	5723	PSPH	phosphoserine phosphatase	HUGO ID: 9577/UniProt ID: P78330/
4257.1	4257	MGST1	microsomal glutathione S-transferase 1	Aliases: MGST-I/HUGO ID: 7061/UniProt ID: P10620/
2997.1	2997	GYS1	glycogen synthase 1 (muscle)	Aliases: GSY/HUGO ID: 4706/UniProt ID: P13807/
6675.1	6675	UAP1	UDP-N-acteylglucosamine pyrophosphorylase 1	
1548.1	1548	CYP2A6	cytochrome P450, family 2, subfamily A, polypeptide 6	
5136.1	5136	PDE1A	phosphodiesterase 1A, calmodulin-dependent	
23545.1	23545	ATP6V0A2	ATPase, H+ transporting, lysosomal V0 subunit a isoform 2	Aliases: TJ6, a2, TJ6s, TJ6M, ATP6a2, J6B7, ATP6N1D, Vph1, Stv1/HUGO ID: 18481/UniProt ID: Q9Y487/
5208.1	5208	PFKFB2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	HUGO ID: 8873/UniProt ID: O60825/
2588.1	2588	GALNS	galactosamine (N-acetyl)-6-sulfate sulfatase (Morquio syndrome, mucopolysaccharidosis type IVA)	Aliases: GAS, GALNAC6S/HUGO ID: 4122/UniProt ID: P34059/
4719.1	4719	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	HUGO ID: 7707/UniProt ID: P28331/
521.1	521	ATP5I	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e	HUGO ID: 846/UniProt ID: P56385/
2799.1	2799	GNS	glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID)	HUGO ID: 4422/UniProt ID: P15586/
107.1	107	ADCY1	adenylate cyclase 1 (brain)	Locus type: gene with protein product, function known or inferred/HUGO ID: 232/UniProt ID: Q08828/
2805.1	2805	GOT1	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)	Locus type: gene with protein product, function known or inferred/HUGO ID: 4432/UniProt ID: P17174/
6713.1	6713	SQLE	squalene epoxidase	Locus type: gene with protein product, function known or inferred/HUGO ID: 11279/UniProt ID: Q14534/
4832.1	4832	NME3	non-metastatic cells 3, protein expressed in	Locus type: gene with protein product, function known or inferred/Aliases: DI nm23/HUGO ID: 7851/UniProt ID: Q13232/
2582.1	2582	GALE	UDP-galactose-4-epimerase	Locus type: gene with protein product, function known or inferred/HUGO ID: 4116/UniProt ID: Q14376/
5161.1	5161	PDHA2	pyruvate dehydrogenase (lipoamide) alpha 2	HUGO ID: 8807/UniProt ID: P29803/
203.1	203	AK1	adenylate kinase 1	HUGO ID: 361/UniProt ID: P00568/
10423.1	10423	CDIPT	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)	Locus type: gene with protein product, function known or inferred/Aliases: PIS1, PIS/HUGO ID: 1769/UniProt ID: O14735/
8790.1	8790	FPGT	fucose-1-phosphate guanylyltransferase	Aliases: GFPP/HUGO ID: 3825/UniProt ID: O14772/
23478.1	23478	SPC18	signal peptidase complex (18kD)	transcript: NM_014300
10327.1	10327	AKR1A1	aldo-keto reductase family 1, member A1 (aldehyde reductase)	transcript: NM_006066
242.1	242	ALOX12B	arachidonate 12-lipoxygenase, 12R type	HUGO ID: 430/UniProt ID: O75342/
8443.1	8443	GNPAT	glyceronephosphate O-acyltransferase	
1558.1	1558	CYP2C8	cytochrome P450, family 2, subfamily C, polypeptide 8	Locus type: gene with protein product, function known or inferred/Aliases: CPC8/HUGO ID: 2622/UniProt ID: P10632/
2593.1	2593	GAMT	guanidinoacetate N-methyltransferase	
55350.1	55350	VNN3	vanin 3	Locus type: gene with protein product, function known or inferred/Aliases: HSA238982/HUGO ID: 16431/UniProt ID: Q9NY84/
50617.1	50617	ATP6V0A4	ATPase, H+ transporting, lysosomal V0 subunit a isoform 4	*PubMed
2629.1	2629	GBA	glucosidase, beta; acid (includes glucosylceramidase)	Aliases: GLUC, GBA1/HUGO ID: 4177/UniProt ID: P04062/
30814.1	30814	PLA2G2E	phospholipase A2, group IIE	
9420.1	9420	CYP7B1	cytochrome P450, family 7, subfamily B, polypeptide 1	Locus type: gene with protein product, function known or inferred/HUGO ID: 2652/UniProt ID: O75881/
498.1	498	ATP5A1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle	Locus type: gene with protein product, function known or inferred/Aliases: ATP5A, hATP1, ATPM, OMR, ORM, HGNC:826/HUGO ID: 823/UniProt ID: P25705/
10846.1	10846	PDE10A	phosphodiesterase 10A	HUGO ID: 8772/UniProt ID: Q9Y233/
4843.1	4843	NOS2A	nitric oxide synthase 2A (inducible, hepatocytes)	Locus type: gene with protein product, function known or inferred/Aliases: INOS, NOS, HEP-NOS/HUGO ID: 7873/UniProt ID: P35228/
35.1	35	ACADS	acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain	Locus type: gene with protein product, function known or inferred/Aliases: SCAD, ACAD3/HUGO ID: 90/UniProt ID: P16219/
64579.1	64579	NDST4	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4	Locus type: gene with protein product, function known or inferred/HUGO ID: 20779/UniProt ID: Q9H3R1/
51.1	51	ACOX1	acyl-Coenzyme A oxidase 1, palmitoyl	Aliases: PALMCOX/HUGO ID: 119/UniProt ID: Q15067/
3906.1	3906	LALBA	lactalbumin, alpha-	Locus type: gene with protein product, function known or inferred/Aliases: LYZL7/HUGO ID: 6480/UniProt ID: P00709/
22978.1	22978	NT5C2	5'-nucleotidase, cytosolic II	Aliases: PNT5, GMP, cN-II/HUGO ID: 8022/UniProt ID: P49902/
316.1	316	AOX1	aldehyde oxidase 1	Aliases: AO, AOH1/HUGO ID: 553/UniProt ID: Q06278/
1579.1	1579	CYP4A11	cytochrome P450, family 4, subfamily A, polypeptide 11	Locus type: gene with protein product, function known or inferred/Aliases: CYP4AII/HUGO ID: 2642/UniProt ID: Q02928/
97.1	97	ACYP1	acylphosphatase 1, erythrocyte (common) type	transcript: NM_001107
2180.1	2180	ACSL1	acyl-CoA synthetase long-chain family member	
4247.1	4247	MGAT2	mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	Aliases: GNT-II/HUGO ID: 7045/UniProt ID: Q10469/

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
9550.1	9550	ATP6V1G1	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G isoform 1	Aliases: ATP6GL, Vma10/HUGO ID: 864/UniProt ID: O75348/
8854.1	8854	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	Locus type: gene with protein product, function known or inferred/Aliases: RALDH2/HUGO ID: 15472/UniProt ID: O94788/
5319.1	5319	PLA2G1B	phospholipase A2, group IB (pancreas)	HUGO ID: 9030/UniProt ID: P04054/
4329.1	4329	ALDH6A1	aldehyde dehydrogenase 6 family, member A1	HUGO ID: 7179/UniProt ID: Q02252/
23533.1	23533	P101-PI3K	phosphoinositide-3-kinase, regulatory subunit, polypeptide p101	
3156.1	3156	HMGCR	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	HUGO ID: 5006/UniProt ID: P04035/
5297.1	5297	PIK4CA	phosphatidylinositol 4-kinase, catalytic, alpha polypeptide	
5051.1	5051	PAFAH2	platelet-activating factor acetylhydrolase 2, 40kDa	
529.1	529	ATP6V1E1	ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E isoform 1	
5834.1	5834	PYGB	phosphorylase, glycogen; brain	HUGO ID: 9723/UniProt ID: P11216/
50808.1	50808	AK3L1	adenylate kinase 3 like 1	Locus type: gene with protein product, function unknown/Aliases: AKL3L1, HGNC:366/HUGO ID: 17376/UniProt ID: Q9UIJ7/MGD ID: MGI:1860835/
412.1	412	STS	steroid sulfatase (microsomal), arylsulfatase C, isozyme S	Aliases: ARSC/HUGO ID: 11425/UniProt ID: P08842/
1543.1	1543	CYP1A1	cytochrome P450, family 1, subfamily A, polypeptide 1	Locus type: gene with protein product, function known or inferred/Aliases: AHRR, AHH, P450DX, P1-450, P450-C, CP11/HUGO ID: 2595/UniProt ID: P04798/MGD ID: 88588/
5973.1	5973	RENBP	renin binding protein	Aliases: RNBP/HUGO ID: 9959/UniProt ID: P51606/
2752.1	2752	GLUL	glutamate-ammonia ligase (glutamine synthase)	
231.1	231	AKR1B1	aldo-keto reductase family 1, member B1 (aldose reductase)	Aliases: AR/HUGO ID: 381/UniProt ID: P15121/
2538.1	2538	G6PC	glucose-6-phosphatase, catalytic (glycogen storage disease type I, von Gierke disease)	Locus type: gene with protein product, function known or inferred/Aliases: GSD1a/HUGO ID: 4056/UniProt ID: P35575/
7378.1	7378	UPP1	uridine phosphorylase	
4522.1	4522	MTHFD1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase	
516.1	516	ATP5G1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1	HUGO ID: 841/UniProt ID: P05496/Variant 1: This variant represents the longer transcript. Variants 1 and 2 encode the same protein.
2875.1	2875	GPT1	glutamic-pyruvate transaminase (alanine aminotransferase)	Aliases: ALT1, GPT1/HUGO ID: 4552/UniProt ID: P24298/
594.1	594	BCKDHB	branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease)	Locus type: gene with protein product, function known or inferred/HUGO ID: 987/UniProt ID: P21953/
1743.1	1743	DLST	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	HUGO ID: 2911/UniProt ID: P36957/
3032.1	3032	HADHB	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	HUGO ID: 4803/UniProt ID: P55084/
23475.1	23475	QPRT	quinolinate phosphoribosyltransferase (nicotinate-nucleotide pyrophosphorylase (carboxylating))	Locus type: gene with protein product, function known or inferred/Aliases: QPRTase/HUGO ID: 9755/UniProt ID: Q15274/
4882.1	4882	NPR2	natriuretic peptide receptor B/guanylate cyclase B (atrionatriuretic peptide receptor B)	Aliases: GUC2B/HUGO ID: 7944/UniProt ID: P20594/
1557.1	1557	CYP2C19	cytochrome P450, family 2, subfamily C, polypeptide 19	
771.1	771	CA12	carbonic anhydrase XII	Locus type: gene with protein product, function known or inferred/Aliases: HsT18816/HUGO ID: 1371/UniProt ID: O43570/
5162.1	5162	PDHB	pyruvate dehydrogenase (lipoamide) beta	HUGO ID: 8808/UniProt ID: P11177/
6916.1	6916	TBXAS1	thromboxane A synthase 1 (platelet, cytochrome P450, famil 5, subfamily A)	
5147.1	5147	PDE6D	phosphodiesterase 6D, cGMP-specific, rod, delta	
3033.1	3033	HADHSC	L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain	Locus type: gene with protein product, function known or inferred/Aliases: SCHAD/HUGO ID: 4804/UniProt ID: Q16836/
220.1	220	ALDH1A3	aldehyde dehydrogenase 1 family, member A3	Aliases: RALDH3/HUGO ID: 409/UniProt ID: P47895/
9060.1	9060	PAPSS2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	Aliases: ATPSK2/HUGO ID: 8604/UniProt ID: O95340/
5226.1	5226	PGD	phosphogluconate dehydrogenase	Locus type: gene with protein product, function known or inferred/HUGO ID: 8891/UniProt ID: P52209/MGD ID: MGI:97553/
5009.1	5009	OTC	ornithine carbamoyltransferase	HUGO ID: 8512/UniProt ID: P00480/
51809.1	51809	GALNT7	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7)	Locus type: gene with protein product, function known or inferred/Aliases: GALNAC-T7/HUGO ID: 4129/UniProt ID: Q9UJ28/
3712.1	3712	IVD	isovaleryl Coenzyme A dehydrogenase	Locus type: gene with protein product, function known or inferred/Aliases: ACAD2/HUGO ID: 6186/UniProt ID: P26440/
51382.1	51382	ATP6V1D	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	Aliases: VATD, VMA8/HUGO ID: 13527/UniProt ID: Q9Y5K8/
36.1	36	ACADSB	acyl-Coenzyme A dehydrogenase, short/branched chain	
5130.1	5130	PCYT1A	phosphate cytidylyltransferase 1, choline, alpha isoform	Aliases: CT, CTPCT/HUGO ID: 8754/UniProt ID: P49585/
11164.1	11164	NUDT5	nudix (nucleoside diphosphate linked moiety X)-type motif 5	Aliases: hYSAH1, YSA1H/HUGO ID: 8052/UniProt ID: Q9UKK9/
1854.1	1854	DUT	dUTP pyrophosphatase	
8836.1	8836	GGH	gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase)	

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
761.1	761	CA3	carbonic anhydrase III, muscle specific	HUGO ID: 1374/UniProt ID: P07451/
2134.1	2134	EXTL1	exostoses (multiple)-like 1	Aliases: EXTL/HUGO ID: 3515/UniProt ID: Q92935/
9514.1	9514	CST	cerebroside (3'-phosphoadenylylsulfate:galactosylceramide 3 sulfotransferase	
50.1	50	ACO2	aconitase 2, mitochondrial	HUGO ID: 118/UniProt ID: Q99798/
2746.1	2746	GLUD1	glutamate dehydrogenase 1	Locus type: gene with protein product, function known or inferred/Aliases: GDH/HUGO ID: 4335/UniProt ID: P00367/
527.1	527	ATP6V0C	ATPase, H+ transporting, lysosomal 16kDa, V0 subunit c	
175.1	175	AGA	aspartylglucosaminidase	HUGO ID: 318/UniProt ID: P20933/
9791.1	9791	PTDSS1	phosphatidylserine synthase 1	Aliases: KIAA0024, PSSA/HUGO ID: 9587/UniProt ID: P48651/
7390.1	7390	UROS	uroporphyrinogen III synthase (congenital erythropoietic porphyria)	Locus type: gene with protein product, function known or inferred/HUGO ID: 12592/UniProt ID: P10746/
2181.1	2181	ACSL3	acyl-CoA synthetase long-chain family member 3	Locus type: gene with protein product, function known or inferred/Aliases: ACS3, PRO2194/HUGO ID: 3570/UniProt ID: O95573/MGD ID: MGI:1921455/
1491.1	1491	CTH	cystathionase (cystathionine gamma-lyase)	Locus type: gene with protein product, function known or inferred/HUGO ID: 2501/UniProt ID: P32929/
6389.1	6389	SDHA	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	Locus type: gene with protein product, function known or inferred/Aliases: FP SDHF/HUGO ID: 10680/UniProt ID: P31040/
1593.1	1593	CYP27A1	cytochrome P450, family 27, subfamily A, polypeptide 1	Locus type: gene with protein product, function known or inferred/Aliases: CTX, CP27/HUGO ID: 2605/UniProt ID: Q02318/
6309.1	6309	SC5DL	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, fungal)-like	HUGO ID: 10547/UniProt ID: O75845/
251.1	251	ALPPL2	alkaline phosphatase, placental-like 2	HUGO ID: 441/UniProt ID: P10696/
1962.1	1962	EHHADH	enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	HUGO ID: 3247/UniProt ID: Q08426/
3081.1	3081	HGD	homogentisate 1,2-dioxygenase (homogentisate oxidase)	Aliases: HGO/HUGO ID: 4892/UniProt ID: Q93099/
5050.1	5050	PAFAH1B3	platelet-activating factor acetylhydrolase, isoform Ib, gamma subunit 29kDa	HUGO ID: 8576/UniProt ID: Q15102/
279.1	279	AMY2A	amylase, alpha 2A; pancreatic	HUGO ID: 477/UniProt ID: P04746/
1350.1	1350	COX7C	cytochrome c oxidase subunit VIIc	HUGO ID: 2292/UniProt ID: P15954/
4724.1	4724	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase)	
5146.1	5146	PDE6C	phosphodiesterase 6C, cGMP-specific, cone, alpha prime	Locus type: gene with protein product, function known or inferred/Aliases: PDEA2/HUGO ID: 8787/UniProt ID: P51160/
8540.1	8540	AGPS	alkylglycerone phosphate synthase	
3155.1	3155	HMGCL	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaricaciduria)	
23417.1	23417	MLYCD	malonyl-CoA decarboxylase	
27087.1	27087	B3GAT1	beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P)	Locus type: gene with protein product, function known or inferred/Aliases: GlcAT-P/HUGO ID: 921/UniProt ID: Q9P2W7/
3176.1	3176	HNMT	histamine N-methyltransferase	HUGO ID: 5028/UniProt ID: P50135/
10554.1	10554	AGPAT1	1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha)	
4731.1	4731	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa	HUGO ID: 7719/UniProt ID: P56181/
440.1	440	ASNS	asparagine synthetase	Locus type: gene with protein product, function known or inferred/HUGO ID: 753/UniProt ID: P08243/
438.1	438	ASMT	acetylserotonin O-methyltransferase	
2539.1	2539	G6PD	glucose-6-phosphate dehydrogenase	Aliases: G6PD1/HUGO ID: 4057/UniProt ID: P11413/
5313.1	5313	PKLR	pyruvate kinase, liver and RBC	Locus type: gene with protein product, function known or inferred/HUGO ID: 9020/UniProt ID: P30613/
26.1	26	ABP1	amiloride binding protein 1 (amine oxidase (copper-containing))	Locus type: gene with protein product, function known or inferred/Aliases: AOC1, DAO/HUGO ID: 80/UniProt ID: P19801/
2222.1	2222	FDFT1	farnesyl-diphosphate farnesyltransferase 1	HUGO ID: 3629/UniProt ID: P37268/
3948.1	3948	LDHC	lactate dehydrogenase C	HUGO ID: 6544/UniProt ID: P07864/
84701.1	84701	COX4I2	cytochrome c oxidase subunit IV isoform 2 (lung)	Aliases: COXIV-2, COX4B, dJ857M17.2/HUGO ID: 16232/UniProt ID: Q96KJ9/
515.1	515	ATP5F1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1	HUGO ID: 840/UniProt ID: P24539/Variant 1: This variant represents the longest transcript, and encodes the longest isoform (1).
6470.1	6470	SHMT1	serine hydroxymethyltransferase 1 (soluble)	HUGO ID: 10850/UniProt ID: P34896/
5213.1	5213	PFKM	phosphofructokinase, muscle	HUGO ID: 8877/UniProt ID: P08237/
124.1	124	ADH1A	alcohol dehydrogenase 1A (class I), alpha polypeptide	Locus type: gene with protein product, function known or inferred/HUGO ID: 249/UniProt ID: P07327/
8992.1	8992	ATP6V0E	ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e	Aliases: M9.2, Vma21p, VMA21/HUGO ID: 863/UniProt ID: O15342/
2949.1	2949	GSTM5	glutathione S-transferase M5	Locus type: gene with protein product, function known or inferred/HUGO ID: 4637/UniProt ID: P46439/
2878.1	2878	GPX3	glutathione peroxidase 3 (plasma)	
4881.1	4881	NPR1	natriuretic peptide receptor A/guanylate cyclase A (atrionatriuretic peptide receptor A)	Locus type: gene with protein product, function known or inferred/Aliases: GUC2A, ANPa/HUGO ID: 7943/UniProt ID: P16066/
4056.1	4056	LTC4S	leukotriene C4 synthase	Locus type: gene with protein product, function known or inferred/Aliases: MGC33147/HUGO ID: 6719/UniProt ID: Q16873/
240.1	240	ALOX5	arachidonate 5-lipoxygenase	HUGO ID: 435/UniProt ID: P09917/

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
3000.1	3000	GUCY2D	guanylate cyclase 2D, membrane (retina-specific)	Aliases: retGC, RETGC-1, ROS-GC1/HUGO ID: 4689/UniProt ID: Q02846/
3034.1	3034	HAL	histidine ammonia-lyase	HUGO ID: 4806/UniProt ID: P42357/
8399.1	8399	PLA2G10	phospholipase A2, group X	Locus type: gene with protein product, function known or inferred/Aliases: GXPLA2/HUGO ID: 9029/UniProt ID: O15496/
4512.1	4512	MTCO1	cytochrome c oxidase I	HUGO ID: 7419/UniProt ID: P00395/
3340.1	3340	NDST1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	*PubMed
514.1	514	ATP5E	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit	HUGO ID: 838/UniProt ID: P56381/
8529.1	8529	CYP4F2	cytochrome P450, family 4, subfamily F, polypeptide 2	
9615.1	9615	GDA	guanine deaminase	
5140.1	5140	PDE3B	phosphodiesterase 3B, cGMP-inhibited	HUGO ID: 8779/UniProt ID: Q13370/
1891.1	1891	ECH1	enoyl Coenzyme A hydratase 1, peroxisomal	Locus type: gene with protein product, function unknown/Aliases: HPXEL/HUGO ID: 3149/UniProt ID: Q13011/
2766.1	2766	GMPR	guanosine monophosphate reductase	HUGO ID: 4376/UniProt ID: P36959/
1036.1	1036	CDO1	cysteine dioxygenase, type I	Locus type: gene with protein product, function known or inferred/HUGO ID: 1795/UniProt ID: Q16878/
2595.1	2595	GANC	glucosidase, alpha; neutral C	*PubMed
1340.1	1340	COX6B1	cytochrome c oxidase subunit Vib polypeptide 1 (ubiquitous)	Locus type: gene with protein product, function known or inferred/Aliases: COXG/HUGO ID: 2280/UniProt ID: P14854/
218.1	218	ALDH3A1	aldehyde dehydrogenase 3 family, memberA1	
4709.1	4709	NDUFB3	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa	Aliases: B12/HUGO ID: 7698/UniProt ID: O43676/
5337.1	5337	PLD1	phospholipase D1, phophatidylcholine-specific	
3938.1	3938	LCT	lactase	HUGO ID: 6530/UniProt ID: P09848/
6715.1	6715	SRD5A1	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha steroid delta 4-dehydrogenase alpha 1)	HUGO ID: 11284/UniProt ID: P18405/
4720.1	4720	NDUFS2	NADH dehydrogenase (ubiquinone) Fe-S protein 2, 49kDa (NADH-coenzyme Q reductase)	
51727.1	51727	UMP-CMPK	UMP-CMP kinase	transcript: NM_016308
526.1	526	ATP6V1B2	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B, isoform 2	Aliases: VATB, Vma2, HO57/HUGO ID: 854/UniProt ID: P21281/
5277.1	5277	PIGA	phosphatidylinositol glycan, class A (paroxysmal nocturnal hemoglobinuria)	Aliases: GPI3/HUGO ID: 8957/UniProt ID: P37287/
55500.1	55500	EKI1	ethanolamine kinase	
26330.1	26330	GAPDS	glyceraldehyde-3-phosphate dehydrogenase, testis-specific	
5158.1	5158	PDE6B	phosphodiesterase 6B, cGMP-specific, rod, beta (congenital stationary night blindness 3, autosomal dominant)	Locus type: gene with protein product, function known or inferred/Aliases: CSNB3/HUGO ID: 8786/UniProt ID: P35913/
2027.1	2027	ENO3	enolase 3 (beta, muscle)	HUGO ID: 3354/UniProt ID: P13929/
3145.1	3145	HMBS	hydroxymethylbilane synthase	HUGO ID: 4982/UniProt ID: P08397/
23530.1	23530	NNT	nicotinamide nucleotide transhydrogenase	
4535.1	4535	MTND1	NADH dehydrogenase 1	HUGO ID: 7455/UniProt ID: P03886/
3028.1	3028	HADH2	hydroxyacyl-Coenzyme A dehydrogenase, type II	Locus type: gene with protein product, function known or inferred/Aliases: ERAB, MHBD, 17b-HSD10, ABAD, HSD17B10/HUGO ID: 4800/UniProt ID: Q99714/
4725.1	4725	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase)	
5408.1	5408	PNLIPRP2	pancreatic lipase-related protein 2	Locus type: gene with protein product, function known or inferred/Aliases: PLRP2/HUGO ID: 9157/UniProt ID: P54317/
1351.1	1351	COX8	cytochrome c oxidase subunit VIII	
5238.1	5238	PGM3	phosphoglucomutase 3	
2744.1	2744	GLS	glutaminase	Aliases: KIAA0838, GLS1/HUGO ID: 4331/UniProt ID: O94925/
873.1	873	CBR1	carbonyl reductase 1	HUGO ID: 1548/UniProt ID: P16152/
1178.1	1178	CLC	Charcot-Leyden crystal protein	Aliases: LGALS10/HUGO ID: 2014/UniProt ID: Q05315/
4846.1	4846	NOS3	nitric oxide synthase 3 (endothelial cell)	Aliases: ECNOS/HUGO ID: 7876/UniProt ID: P29474/
535.1	535	ATP6V0A1	ATPase, H+ transporting, lysosomal V0 subunit a isoform 1	Aliases: a1, Vph1, Stv1/HUGO ID: 865/UniProt ID: Q93050/
51179.1	51179	HAO2	hydroxyacid oxidase 2 (long chain)	Aliases: HAOX2/HUGO ID: 4810/UniProt ID: Q9NYQ3/
353.1	353	APRT	adenine phosphoribosyltransferase	HUGO ID: 626/UniProt ID: P07741/
278.1	278	AMY1C	amylase, alpha 1C; salivary	Locus type: unknown/HUGO ID: 476/
191.1	191	AHCY	S-adenosylhomocysteine hydrolase	HUGO ID: 343/UniProt ID: P23526/
1545.1	1545	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	
11283.1	11283	CYP4F8	cytochrome P450, family 4, subfamily F, polypeptide 8	Locus type: gene with protein product, function known or inferred/HUGO ID: 2648/UniProt ID: P98187/
5832.1	5832	ALDH18A1	aldehyde dehydrogenase 18 family, member A1	Locus type: gene with protein product, function known or inferred/Aliases: P5CS/HUGO ID: 9722/UniProt ID: P54886/
2877.1	2877	GPX2	glutathione peroxidase 2 (gastrointestinal)	
3612.1	3612	IMPA1	inositol(myo)-1(or 4)-monophosphatase 1	HUGO ID: 6050/UniProt ID: P29218/
1559.1	1559	CYP2C9	cytochrome P450, family 2, subfamily C, polypeptide 9	*PubMed
3163.1	3163	HMOX2	heme oxygenase (decycling) 2	Aliases: HO-2/HUGO ID: 5014/UniProt ID: P30519/
5281.1	5281	PIGF	phosphatidylinositol glycan, class F	HUGO ID: 8962/UniProt ID: Q07326/
3284.1	3284	HSD3B2	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2	HUGO ID: 5218/UniProt ID: P26439/

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
5141.1	5141	PDE4A	phosphodiesterase 4A, cAMP-specific (phosphodiesterase E2 dunce homolog, Drosophila)	HUGO ID: 8780/UniProt ID: P27815/
10873.1	10873	ME3	malic enzyme 3, NADP(+)-dependent, mitochondrial	HUGO ID: 6985/UniProt ID: Q16798/
13.1	13	AADAC	arylacetamide deacetylase (esterase)	Locus type: gene with protein product, function known or inferred/Aliases: DAC/HUGO ID: 17/UniProt ID: P22760/
4598.1	4598	MVK	mevalonate kinase (mevalonic aciduria)	HUGO ID: 7530/UniProt ID: Q03426/
513.1	513	ATP5D	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	HUGO ID: 837/UniProt ID: P30049/
246.1	246	ALOX15	arachidonate 15-lipoxygenase	HUGO ID: 433/UniProt ID: P16050/
2628.1	2628	GATM	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	HUGO ID: 4175/UniProt ID: P50440/
1890.1	1890	ECGF1	endothelial cell growth factor 1 (platelet-derived)	HUGO ID: 3148/UniProt ID: P19971/
8277.1	8277	TKTL1	transketolase-like 1	Locus type: gene with protein product, function known or inferred/Aliases: TKR, TKT2/HUGO ID: 11835/UniProt ID: P51854/
9487.1	9487	PIGL	phosphatidylinositol glycan, class L	HUGO ID: 8966/UniProt ID: Q9Y2B2/
9453.1	9453	GGPS1	geranylgeranyl diphosphate synthase 1	
1591.1	1591	CYP24A1	cytochrome P450, family 24, subfamily A, polypeptide 1	Locus type: gene with protein product, function known or inferred/Aliases: CP24, P450-CC24/HUGO ID: 2602/UniProt ID: Q07973/
3939.1	3939	LDHA	lactate dehydrogenase A	HUGO ID: 6535/UniProt ID: P00338/
2650.1	2650	GCNT1	glucosaminyl (N-acetyl) transferase 1, core 2 (beta-1,6-N-acetylglucosaminyltransferase)	
10797.1	10797	MTHFD2	methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase	
131.1	131	ADH7	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide	Locus type: gene with protein product, function known or inferred/Aliases: ADH-4/HUGO ID: 256/UniProt ID: P40394/
6718.1	6718	AKR1D1	aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase)	
1537.1	1537	CYC1	cytochrome c-1	Locus type: gene with protein product, function known or inferred/HUGO ID: 2579/UniProt ID: P08574/
3620.1	3620	INDO	indoleamine-pyrrole 2,3 dioxygenase	
2673.1	2673	GFPT1	glutamine-fructose-6-phosphate transaminase 1	Aliases: GFAT, GFA, GFAT1/HUGO ID: 4241/UniProt ID: Q06210/
3417.1	3417	IDH1	isocitrate dehydrogenase 1 (NADP+), soluble	HUGO ID: 5382/UniProt ID: O75874/
55967.1	55967	DAP13	13kDa differentiation-associated protein	transcript: NM_018838
4536.1	4536	MTND2	NADH dehydrogenase 2	HUGO ID: 7456/UniProt ID: P03891/
5336.1	5336	PLCG2	phospholipase C, gamma 2 (phosphatidylinositol-specific)	HUGO ID: 9066/UniProt ID: P16885/
1723.1	1723	DHODH	dihydroorotate dehydrogenase	HUGO ID: 2867/UniProt ID: Q02127/
38.1	38	ACAT1	acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase)	Aliases: THIL/HUGO ID: 93/UniProt ID: P24752/
98.1	98	ACYP2	acylphosphatase 2, muscle type	HUGO ID: 180/UniProt ID: P14621/trancscipt: NM_138448.2
1586.1	1586	CYP17A1	cytochrome P450, family 17, subfamily A, polypeptide 1	Locus type: gene with protein product, function known or inferred/Aliases: P450C17, CPT7, S17AH/HUGO ID: 2593/UniProt ID: P05093/
1349.1	1349	COX7B	cytochrome c oxidase subunit VIIb	HUGO ID: 2291/UniProt ID: P24311/
230.1	230	ALDOC	aldolase C, fructose-bisphosphate	HUGO ID: 418/UniProt ID: P09972/
6646.1	6646	SOAT1	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1	Aliases: ACAT/HUGO ID: 11177/UniProt ID: P35610/
4722.1	4722	NDUFS3	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase)	HUGO ID: 7710/UniProt ID: O75489/
5409.1	5409	PNMT	phenylethanolamine N-methyltransferase	HUGO ID: 9160/UniProt ID: P11086/
277.1	277	AMY1B	amylase, alpha 1B; salivary	Locus type: unknown/HUGO ID: 475/
5211.1	5211	PFKL	phosphofructokinase, liver	HUGO ID: 8876/UniProt ID: P17858/
5833.1	5833	PCYT2	phosphate cytidylyltransferase 2, ethanolamine	Aliases: ET/HUGO ID: 8756/UniProt ID: Q99447/
8288.1	8288	EPX	eosinophil peroxidase	
27089.1	27089	QP-C	low molecular mass ubiquinone-binding protein (9.5kD)	transcript: NM_014402
7941.1	7941	PLA2G7	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	
10090.1	10090	UST	uronyl-2-sulfotransferase	HUGO ID: 17223/UniProt ID: Q9Y2C2/
759.1	759	CA1	carbonic anhydrase I	HUGO ID: 1368/UniProt ID: P00915/
10768.1	10768	AHCYL1	S-adenosylhomocysteine hydrolase-like 1	Aliases: XPVKONA/HUGO ID: 344/UniProt ID: O43865/
4695.1	4695	NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa	
5288.1	5288	PIK3C2G	phosphoinositide-3-kinase, class 2, gamma polypeptide	Locus type: gene with protein product, function known or inferred/HUGO ID: 8973/UniProt ID: O75747/
29958.1	29958	DMGDH	dimethylglycine dehydrogenase precursor	*PubMed
2639.1	2639	GCDH	glutaryl-Coenzyme A dehydrogenase	
1544.1	1544	CYP1A2	cytochrome P450, family 1, subfamily A, polypeptide 2	Locus type: gene with protein product, function known or inferred/Aliases: P3-450, CP12/HUGO ID: 2596/UniProt ID: P05177/MGD ID: 88589/
4191.1	4191	MDH2	malate dehydrogenase 2, NAD (mitochondrial)	HUGO ID: 6971/UniProt ID: P40926/
2987.1	2987	GUK1	guanylate kinase 1	Locus type: gene with protein product, function known or inferred/HUGO ID: 4693/UniProt ID: Q16774/
247.1	247	ALOX15B	arachidonate 15-lipoxygenase, second type	HUGO ID: 434/UniProt ID: O15296/

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
525.1	525	ATP6V1B1	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B, isoform 1 (Renal tubular acidosis with deafness)	
55512.1	55512	SMPD3	sphingomyelin phosphodiesterase 3, neutral membrane (neutral sphingomyelinase II)	Locus type: gene with protein product, function known or inferred/Aliases: NSMASE2/HUGO ID: 14240/UniProt ID: Q9NY59/
28.1	28	ABO	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase)	HUGO ID: 79/UniProt ID: P16442/
790.1	790	CAD1	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	
5805.1	5805	PTS	6-pyruvoyltetrahydropterin synthase	HUGO ID: 9689/UniProt ID: Q03393/
952.1	952	CD38	CD38 antigen (p45)	HUGO ID: 1667/UniProt ID: P28907/
8604.1	8604	SLC25A12	solute carrier family 25 (mitochondrial carrier, Aralar), member 12	
8402.1	8402	SLC25A11	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11	
6576.1	6576	SLC25A1	solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1	Aliases: CTP/HUGO ID: 10979/UniProt ID: P53007/
83884.1	83884	SLC25A2	solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 2	Locus type: gene with protein product, function known or inferred/Aliases: ORNT2/HUGO ID: 22921/UniProt ID: Q9BXI2/
9016.1	9016	UCP5	solute carrier family 25 (mitochondrial carrier, brain), member 14	Locus type: gene with protein product, function known or inferred/Aliases: BMCP1, UCP5/HUGO ID: 10984/UniProt ID: O95258/
1468.1	1468	SLC25A10	solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10	
57678.1	57678	KIAA1560	glycerol 3-phosphate acyltransferase, mitochondrial	
5250.1	5250	SLC25A3	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3	Locus type: gene with protein product, function known or inferred/HUGO ID: 10989/UniProt ID: Q00325/
6648.1	6648	SOD2	superoxide dismutase 2, mitochondrial	Locus type: gene with protein product, function known or inferred/HUGO ID: 11180/UniProt ID: P04179/
7350.1	7350	UCP1	uncoupling protein 1 (mitochondrial, proton carrier)	Aliases: SLC25A7/HUGO ID: 12517/UniProt ID: P25874/
7351.1	7351	UCP2	uncoupling protein 2 (mitochondrial, proton carrier)	Aliases: SLC25A8/HUGO ID: 12518/UniProt ID: P55851/
89874.1	89874	SLC25A21	solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21	Aliases: ODC1/HUGO ID: 14411/UniProt ID: Q9BQT8/
7352.1	7352	UCP3	uncoupling protein 3 (mitochondrial, proton carrier)	
291.1	291	SLC25A4	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4	Locus type: gene with protein product, function known or inferred/Aliases: T1/HUGO ID: 10990/UniProt ID: P12235/
10166.1	10166	SLC25A15	solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15	Aliases: D13S327, HHH/HUGO ID: 10985/UniProt ID: Q9Y619/
292.1	292	SLC25A5	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	
293.1	293	SLC25A6	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	Locus type: gene with protein product, function known or inferred/Aliases: ANT3Y, MGC17525/HUGO ID: 10992/UniProt ID: P12236/
83733.1	83733	SLC25A18	solute carrier family 25 (mitochondrial carrier), member 18	HUGO ID: 10988/UniProt ID: Q9H1K4/
56953.1	56953	NT5M	5',3'-nucleotidase, mitochondrial	Aliases: dNT-2, dNT2, mdN/HUGO ID: 15769/UniProt ID: Q9NPB1/
79751.1	79751	SLC25A22	solute carrier family 25 (mitochondrial carrier: glutamate), member 22	Locus type: gene with protein product, function known or inferred/Aliases: GC1, FLJ13044/HUGO ID: 19954/UniProt ID: Q9H936/
60386.1	60386	SLC25A19	solute carrier family 25 (mitochondrial deoxynucleotide carrier), member 19	
8034.1	8034	SLC25A16	solute carrier family 25 (mitochondrial carrier; Graves diseas autoantigen), member 16	
51079.1	51079	GRIM19	cell death-regulatory protein GRIM19	transcript: NM_015965
10587.1	10587	TXNRD2	thioredoxin reductase 2	
10935.1	10935	PRDX3	peroxiredoxin 3	
64087.1	64087	MCCC2	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	Aliases: MCCB/HUGO ID: 6937/UniProt ID: Q9HCC0/
2653.1	2653	GCSH	glycine cleavage system protein H (aminomethyl carrier)	HUGO ID: 4208/UniProt ID: P23434/
9481.1	9481	UCP4	uncoupling protein 4	
27034.1	27034	ACAD8	acyl-Coenzyme A dehydrogenase family, member 8	HUGO ID: 87/UniProt ID: Q9UKU7/
64902.1	64902	AGXT2	alanine-glyoxylate aminotransferase 2	HUGO ID: 14412/UniProt ID: Q9BYV1/
788.1	788	SLC25A20	solute carrier family 25 (carnitine/acylcarnitine translocase), member 20	
51805.1	51805	COQ3	coenzyme Q3 homolog, methyltransferase (yeast)	Locus type: gene with protein product, function known or inferred/Aliases: bA9819.1/HUGO ID: 18175/UniProt ID: Q9NZJ6/MGD ID: MGI:101813/
23600.1	23600	AMACR	alpha-methylacyl-CoA racemase	Aliases: RACE/HUGO ID: 451/UniProt ID: Q9UHK6/
2747.1	2747	GLUD2	glutamate dehydrogenase 2	
2110.1	2110	ETFDH	electron-transferring-flavoprotein dehydrogenase	Aliases: ETFQO/HUGO ID: 3483/UniProt ID: Q16134/
6342.1	6342	SCP2	sterol carrier protein 2	
10165.1	10165	SLC25A13	solute carrier family 25, member 13 (citrin)	HUGO ID: 10983/UniProt ID: Q9UJS0/
10229.1	10229	COQ7	coenzyme Q7 homolog, ubiquinone (yeast)	
79814.1	79814	AGMAT	agmatine ureohydrolase (agmatinase)	Aliases: FLJ23384/HUGO ID: 18407/UniProt ID: Q9BSE5/
11112.1	11112	HIBADH	3-hydroxyisobutyrate dehydrogenase	HUGO ID: 4907/UniProt ID: P31937/
5232.1	5232	PGK2	phosphoglycerate kinase 2	
92579.1	92579	G6PC3	glucose 6 phosphatase, catalytic, 3	

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
85365.1	85365	ALG2	asparagine-linked glycosylation 2 homolog (yeast, alpha-1,3-mannosyltransferase)	Locus type: gene with protein product, function known or inferred/Aliases: CDGIi, FLJ14511, hALPG2/HUGO ID: 23159/UniProt ID: Q8NBX2/
8818.1	8818	DPM2	dolichyl-phosphate mannosyltransferase polypeptide 2, regulatory subunit	Locus type: gene with protein product, function known or inferred/HUGO ID: 3006/UniProt ID: O94777/
54344.1	54344	DPM3	dolichyl-phosphate mannosyltransferase polypeptide 3	Locus type: gene with protein product, function known or inferred/HUGO ID: 3007/UniProt ID: Q9P2X0/
79087.1	79087	ALG12	asparagine-linked glycosylation 12 homolog (yeast, alpha-1,6-mannosyltransferase)	Locus type: gene with protein product, function known or inferred/Aliases: ECM39/HUGO ID: 19358/UniProt ID: Q96AA4/MGD ID: MGI:2385025/
29929.1	29929	ALG6	asparagine-linked glycosylation 6 homolog (yeast, alpha-1,3-glucosyltransferase)	
79053.1	79053	ALG8	asparagine-linked glycosylation 8 homolog (yeast, alpha-1,3-glucosyltransferase)	Locus type: gene with protein product, function known or inferred/Aliases: MGC2840/HUGO ID: 23161/UniProt ID: Q9BVK2/
84920.1	84920	ALG10	asparagine-linked glycosylation 10 homolog (yeast, alpha-1,2-glucosyltransferase)	Locus type: gene with protein product, function known or inferred/Aliases: FLJ14751/HUGO ID: 23162/UniProt ID: Q96DU0/
8801.1	8801	SUCLG2	succinate-CoA ligase, GDP-forming, beta subunit	Locus type: gene with protein product, function known or inferred/HUGO ID: 11450/UniProt ID: Q96I99/
22934.1	22934	RPIA	ribose 5-phosphate isomerase A (ribose 5-phosphate epimerase)	HUGO ID: 10297/UniProt ID: P49247/
84076.1	84076	DKFZP434L1717	similar to transketolase	transcript: NM_032136
126328.1	126328	NDUFA11	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 11, 14.7kDa	Locus type: gene with protein product, function known or inferred/Aliases: B14.7/HUGO ID: 20371/UniProt ID: Q86Y39/
29796.1	29796	HSPC051	ubiquinol-cytochrome c reductase complex (7.2 kD)	transcript: NM_013387
10905.1	10905	MAN1A2	mannosidase, alpha, class 1A, member 2	Aliases: MAN1B/HUGO ID: 6822/UniProt ID: O60476/
57134.1	57134	MAN1C1	mannosidase, alpha, class 1C, member 1	Aliases: HMIC/HUGO ID: 19080/UniProt ID: Q9NR34/MGD ID: MGI:2446214/
11320.1	11320	MGAT4A	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isoenzyme A	Aliases: GnT-Iva/HUGO ID: 7047/UniProt ID: Q9UM21/
11282.1	11282	MGAT4B	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isoenzyme B	Locus type: gene with protein product, function known or inferred/Aliases: GnT-Ivb/HUGO ID: 7048/UniProt ID: Q9UQ53/
4249.1	4249	MGAT5	mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase	Aliases: GNT-V/HUGO ID: 7049/UniProt ID: Q09328/
1603.1	1603	DAD1	defender against cell death 1	HUGO ID: 2664/UniProt ID: P46966/
64772.1	64772	FLJ21865	endo-beta-N-acetylglucosaminidase	transcript: NM_022759
5476.1	5476	PPGB	protective protein for beta-galactosidase (galactosialidosis)	HUGO ID: 9251/UniProt ID: P10619/
129807.1	129807	NEU4	sialidase 4	Locus type: gene with protein product, function known or inferred/Aliases: NEU4/HUGO ID: 21328/UniProt ID: Q8WWR8/MGD ID: MGI:2661364/
55568.1	55568	GALNT10	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (GalNAc-T10)	Locus type: gene with protein product, function known or inferred/Aliases: DKFZp586H0623/HUGO ID: 19873/UniProt ID: Q86SR1/
63917.1	63917	GALNT11	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 11 (GalNAc-T11)	Locus type: gene with protein product, function known or inferred/Aliases: FLJ21634/HUGO ID: 19875/UniProt ID: Q8NCW6/
79695.1	79695	GALNT12	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 12 (GalNAc-T12)	Locus type: gene with protein product, function known or inferred/Aliases: FLJ21212/HUGO ID: 19877/UniProt ID: Q8IXK2/
114805.1	114805	GALNT13	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13 (GalNAc-T13)	
79623.1	79623	GALNT14	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14)	Locus type: gene with protein product, function known or inferred/Aliases: GalNac-T10, FLJ12691, GalNac-T14/HUGO ID: 22946/UniProt ID: Q9H9J8/MGD ID: MGI:1918935/
11227.1	11227	GALNT5	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 5 (GalNAc-T5)	HUGO ID: 4127/
117248.1	117248	GALNTL2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 2	
55808.1	55808	SIAT7A	sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltransferase) A	Locus type: gene with protein product, function known or inferred/Aliases: ST6GalNAcI/HUGO ID: 23614/UniProt ID: Q9NSC7/
192134.1	192134	IMAGE:4907098	beta-1,3-N-acetylglucosaminyltransferase protein	transcript: NM_138706
9245.1	9245	GCNT3	glucosaminyl (N-acetyl) transferase 3, mucin type	
51301.1	51301	C2GNT3	core 2 beta 1,6-N-acetylglucosaminyltransferase 3	transcript: NM_016591
51146.1	51146	A4GNT	alpha-1,4-N-acetylglucosaminyltransferase	Locus type: gene with protein product, function unknown/Aliases: LOC51146 alpha4GnT/HUGO ID: 17968/
57171.1	57171	DOLPP1	dolichyl pyrophosphate phosphatase 1	
80201.1	80201	FLJ22761	hypothetical protein FLJ22761	transcript: NM_025130
113452.1	113452	BCLP	beta-casein-like protein	transcript: NM_033504
348477.1	348477	FLJ39207	C219-reactive peptide	transcript: XM_371369
1645.1	1645	AKR1C1	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	Aliases: DDH, MBAB, DD1, HAKRC/HUGO ID: 384/UniProt ID: Q04828/
55217.1	55217	TMLHE	trimethyllysine hydroxylase, epsilon	Aliases: TMLH, FLJ10727/HUGO ID: 18308/UniProt ID: Q9NVH6/

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
145226.1	145226	RDH12	retinol dehydrogenase 12 (all-trans and 9-cis)	Locus type: gene with protein product, function known or inferred/Aliases: FLJ30273/HUGO ID: 19977/UniProt ID: Q8TAW6/
6511.1	6511	SLC1A6	solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6	Locus type: gene with protein product, function known or inferred/Aliases: EAAT4/HUGO ID: 10944/UniProt ID: P48664/
84889.1	84889	SLC7A3	solute carrier family 7 (cationic amino acid transporter, y+ system), member 3	Locus type: gene with protein product, function known or inferred/Aliases: CAT-3, ATRC3, FLJ14541/HUGO ID: 11061/UniProt ID: Q8N185/
65985.1	65985	AACS	acetoacetyl-CoA synthetase	Locus type: gene with protein product, function known or inferred/Aliases: FLJ12389/HUGO ID: 21298/UniProt ID: Q8IWD2/
29906.1	29906	SIAT8E	sialyltransferase 8E (alpha-2, 8-polysialyltransferase)	Aliases: ST8Sia V/HUGO ID: 17827/UniProt ID: O15466/
6550.1	6550	SLC9A3	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3	HUGO ID: 11073/UniProt ID: P48764/
157506.1	157506	RDH10	retinol dehydrogenase 10 (all-trans)	Locus type: gene with protein product, function known or inferred/HUGO ID: 19975/UniProt ID: Q8IZV5/
6005.1	6005	RHAG	Rhesus blood group-associated glycoprotein	Aliases: RH50A/HUGO ID: 10006/UniProt ID: Q02094/
56548.1	56548	CHST7	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	Aliases: C6ST-2, C6ST2/HUGO ID: 13817/UniProt ID: O75667/
3931.1	3931	LCAT	lecithin-cholesterol acyltransferase	HUGO ID: 6522/UniProt ID: P04180/
11309.1	11309	SLCO2B1	solute carrier organic anion transporter family, member 2B1	Locus type: gene with protein product, function known or inferred/Aliases: OATP-B, OATP2B1/HUGO ID: 10962/UniProt ID: O94956/
284273.1	284273	ZADH2	zinc binding alcohol dehydrogenase, domain containing 2	Locus type: gene with protein product, function unknown/Aliases: MGC45594/HUGO ID: 28697/MGD ID: MGI:2444835/
6515.1	6515	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	HUGO ID: 11007/UniProt ID: P11169/
114134.1	114134	SLC2A13	solute carrier family 2 (facilitated glucose transporter), member 13	Aliases: HMIT/HUGO ID: 15956/UniProt ID: Q96QE2/
2348.1	2348	FOLR1	folate receptor 1 (adult)	HUGO ID: 3791/UniProt ID: P15328/
93183.1	93183	PIGM	phosphatidylinositol glycan, class M	HUGO ID: 18858/UniProt ID: Q9H3S5/MGD ID: MGI:1914806/
54575.1	54575	UGT1A10	UDP glycosyltransferase 1 family, polypeptide A10	Aliases: UGT1J/HUGO ID: 12531/UniProt ID: Q9HAW8/
6785.1	6785	ELOVL4	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4	HUGO ID: 14415/UniProt ID: Q9GZR5/
66002.1	66002	CYP4F12	cytochrome P450, family 4, subfamily F, polypeptide 12	Locus type: gene with protein product, function known or inferred/HUGO ID: 18857/UniProt ID: Q9HCS2/
4905.1	4905	NSF	N-ethylmaleimide-sensitive factor	Aliases: SKD2/HUGO ID: 8016/UniProt ID: P46459/
142680.1	142680	SLC34A3	solute carrier family 34 (sodium phosphate), member 3	Locus type: gene with protein product, function known or inferred/Aliases: NPTIIc, FLJ38680/HUGO ID: 20305/UniProt ID: Q8N130/
6529.1	6529	SLC6A1	solute carrier family 6 (neurotransmitter transporter, GABA), member 1	Aliases: GAT1/HUGO ID: 11042/UniProt ID: P30531/
126129.1	126129	CPT1C	carnitine palmitoyltransferase 1C	Locus type: gene with protein product, function known or inferred/Aliases: FLJ23809, CPTIC/HUGO ID: 18540/UniProt ID: Q8TCG5/
490.1	490	ATP2B1	ATPase, Ca++ transporting, plasma membrane 1	Aliases: PMCA1/HUGO ID: 814/UniProt ID: P20020/
11254.1	11254	SLC6A14	solute carrier family 6 (neurotransmitter transporter), member 14	HUGO ID: 11047/UniProt ID: Q9UN76/
57419.1	57419	SLC24A3	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	Locus type: gene with protein product, function known or inferred/HUGO ID: 10977/UniProt ID: Q9HC58/
54675.1	54675	C20orf155	chromosome 20 open reading frame 155	Aliases: dJ967N21.6/HUGO ID: 16148/
6542.1	6542	SLC7A2	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	Locus type: gene with protein product, function known or inferred/Aliases: CAT-2, HCAT2/HUGO ID: 11060/UniProt ID: P52569/
257202.1	257202	GPX6	glutathione peroxidase 6 (olfactory)	HUGO ID: 4558/UniProt ID: P59796/
79723.1	79723	SUV39H2	suppressor of variegation 3-9 homolog 2 (Drosophila)	Locus type: gene with protein product, function known or inferred/Aliases: FLJ23414/HUGO ID: 17287/UniProt ID: Q9H5I1/MGD ID: MGI:1890396/
84912.1	84912	SLC35B4	solute carrier family 35, member B4	Locus type: gene with protein product, function known or inferred/Aliases: FLJ14697, YEA4/HUGO ID: 20584/UniProt ID: Q969S0/
245972.1	245972	ATP6V0D2	ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d isoform 2	Locus type: gene with protein product, function known or inferred/Aliases: FLJ38708, VMA6, ATP6D2/HUGO ID: 18266/UniProt ID: Q8N8Y2/
22856.1	22856	CHSY1	carbohydrate (chondroitin) synthase 1	Aliases: KIAA0990/HUGO ID: 17198/UniProt ID: Q86X52/
160851.1	160851	DGKH	diacylglycerol kinase, eta	Locus type: gene with protein product, function known or inferred/Aliases: DGKeta/HUGO ID: 2854/UniProt ID: Q9BX34/
51302.1	51302	CYP39A1	cytochrome P450, family 39, subfamily A, polypeptide 1	Locus type: gene with protein product, function known or inferred/HUGO ID: 17449/UniProt ID: Q9NYL5/MGD ID: MGI:1927096/
2544.1	2544	G6PT2	glucose-6-phosphatase, transport (phosphate/pyrophosphate) protein 2	Locus type: unknown/Aliases: GSD1c/HUGO ID: 4062/
374291.1	374291	NDUFS7	NADH dehydrogenase (ubiquinone) Fe-S protein 7, 20kDa (NADH-coenzyme Q reductase)	Locus type: gene with protein product, function known or inferred/Aliases: PSST, FLJ46880, FLJ45860/HUGO ID: 7714/UniProt ID: O75251/
27010.1	27010	TPK1	thiamin pyrophosphokinase 1	Aliases: HTPK1/HUGO ID: 17358/UniProt ID: Q9H3S4/
2531.1	2531	FVT1	follicular lymphoma variant translocation 1	HUGO ID: 4021/UniProt ID: Q06136/
222537.1	222537	HS3ST5	heparan sulfate (glucosamine) 3-O-sulfotransferase 5	Locus type: gene with protein product, function known or inferred/Aliases: 3-OST-5/HUGO ID: 19419/UniProt ID: Q8IZT8/

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
122481.1	122481	AK7	adenylate kinase 7	Locus type: gene with protein product, function known or inferred/Aliases: FLJ32864/HUGO ID: 20091/UniProt ID: Q96M32/
6568.1	6568	SLC17A1	solute carrier family 17 (sodium phosphate), member 1	Aliases: NAPI-1/HUGO ID: 10929/UniProt ID: Q14916/
171425.1	171425	CLYBL	citrate lyase beta like	Locus type: gene with protein product, function known or inferred/Aliases: CLB/HUGO ID: 18355/UniProt ID: Q8N0X4/MGD ID: MGI:1916884/
80142.1	80142	PTGES2	prostaglandin E synthase 2	Aliases: FLJ14038/HUGO ID: 17822/UniProt ID: Q9H7Z7/
127124.1	127124	ATP6V1G3	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G isoform 3	Locus type: gene with protein product, function known or inferred/Aliases: ATP6G3, Vma10/HUGO ID: 18265/UniProt ID: Q96LB4/MGD ID: MGI:2450548/
50515.1	50515	CHST11	carbohydrate (chondroitin 4) sulfotransferase 11	Locus type: gene with protein product, function known or inferred/Aliases: C4ST1, C4St-1, C4ST, HSA269537/HUGO ID: 17422/UniProt ID: Q9NPF2/MGD ID: MGI:1927166/
26062.1	26062	HYALP1	hyaluronoglucosaminidase pseudogene 1	Locus type: pseudogene/HUGO ID: 5324/
9154.1	9154	SLC28A1	solute carrier family 28 (sodium-coupled nucleoside transporter), member 1	Aliases: CNT1/HUGO ID: 11001/UniProt ID: O00337/
79896.1	79896	THNSL1	threonine synthase-like 1 (bacterial)	Locus type: gene with protein product, function unknown/Aliases: FLJ22002/HUGO ID: 26160/
11041.1	11041	B3GNT6	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6	Aliases: iGNT, iGAT/HUGO ID: 15685/UniProt ID: O43505/
6546.1	6546	SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member	HUGO ID: 11068/UniProt ID: P32418/
140838.1	140838	HDHD4	haloacid dehalogenase-like hydrolase domain containing 4	Locus type: gene with protein product, function known or inferred/Aliases: dJ694B14.3, MGC26833/HUGO ID: 16140/UniProt ID: Q8TBE9/
10050.1	10050	SLC17A4	solute carrier family 17 (sodium phosphate), member 4	Aliases: KAIA2138/HUGO ID: 10932/UniProt ID: Q9Y2C5/
56848.1	56848	SPHK2	sphingosine kinase 2	HUGO ID: 18859/UniProt ID: Q9NRA0/MGD ID: MGI:1861380/
246213.1	246213	SLC17A8	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 8	Locus type: gene with protein product, function known or inferred/Aliases: VGLUT3/HUGO ID: 20151/UniProt ID: Q8NDX2/
2745.1	2745	GLRX	glutaredoxin (thioltransferase)	Aliases: GRX/HUGO ID: 4330/UniProt ID: P35754/
6533.1	6533	SLC6A6	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	Aliases: TAUT/HUGO ID: 11052/UniProt ID: P31641/
91734.1	91734	IDI2	isopentenyl-diphosphate delta isomerase 2	Locus type: gene with protein product, function known or inferred/Aliases: IPPI2/HUGO ID: 23487/UniProt ID: Q9BXS1/
5295.1	5295	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	Locus type: gene with protein product, function known or inferred/Aliases: GRB1, p85-ALPHA/HUGO ID: 8979/UniProt ID: P27986/
6507.1	6507	SLC1A3	solute carrier family 1 (glial high affinity glutamate transporter), member 3	Aliases: GLAST, EAAT1/HUGO ID: 10941/UniProt ID: P43003/
80271.1	80271	ITPKC	inositol 1,4,5-trisphosphate 3-kinase C	HUGO ID: 14897/UniProt ID: Q96DU7/
80724.1	80724	ACAD10	acyl-Coenzyme A dehydrogenase family, member 10	Locus type: gene with protein product, function unknown/Aliases: MGC5601/HUGO ID: 21597/
84264.1	84264	HAGHL	hydroxyacylglutathione hydrolase-like	Locus type: gene with protein product, function known or inferred/Aliases: MGC2605/HUGO ID: 14177/UniProt ID: Q9BT45/
65263.1	65263	PYCRL	pyrroline-5-carboxylate reductase-like	Locus type: gene with protein product, function unknown/Aliases: FLJ13852/HUGO ID: 25846/
123041.1	123041	SLC24A4	solute carrier family 24 (sodium/potassium/calcium exchanger), member 4	Locus type: gene with protein product, function known or inferred/Aliases: NCKX4/HUGO ID: 10978/UniProt ID: Q8NFF2/
6572.1	6572	SLC18A3	solute carrier family 18 (vesicular acetylcholine), member 3	Locus type: gene with protein product, function known or inferred/Aliases: VACHT/HUGO ID: 10936/UniProt ID: Q16572/
5728.1	5728	PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	Locus type: gene with protein product, function known or inferred/Aliases: MMAC1, TEP1, PTEN1/HUGO ID: 9588/UniProt ID: O00633/
6537.1	6537	SLC6A10	solute carrier family 6 (neurotransmitter transporter, creatine), member 10	Aliases: CT-2/HUGO ID: 11043/UniProt ID: P53796/
5283.1	5283	PIGH	phosphatidylinositol glycan, class H	Aliases: GPI-H/HUGO ID: 8964/UniProt ID: Q14442/
5092.1	5092	PCBD	6-pyruvoyl-tetrahydropterin synthase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1)	Locus type: gene with protein product, function known or inferred/Aliases: PCD/HUGO ID: 8646/UniProt ID: P80095/
124935.1	124935	SLC43A2	solute carrier family 43, member 2	Locus type: gene with protein product, function known or inferred/Aliases: MGC34680/HUGO ID: 23087/MGD ID: MGI:2442746/
55501.1	55501	CHST12	carbohydrate (chondroitin 4) sulfotransferase 12	Locus type: gene with protein product, function known or inferred/Aliases: C4S-2, C4ST2/HUGO ID: 17423/UniProt ID: Q9NRB3/MGD ID: MGI:1929064/
6559.1	6559	SLC12A3	solute carrier family 12 (sodium/chloride transporters), member 3	HUGO ID: 10912/UniProt ID: P55017/
6520.1	6520	SLC3A2	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	Aliases: 4T2HC, 4F2, NACAE/HUGO ID: 11026/UniProt ID: P08195/
6563.1	6563	SLC14A1	solute carrier family 14 (urea transporter), member 1 (Kidd blood group)	Locus type: gene with protein product, function known or inferred/Aliases: HsT1341/HUGO ID: 10918/UniProt ID: Q13336/
28976.1	28976	ACAD9	acyl-Coenzyme A dehydrogenase family, member 9	Locus type: gene with protein product, function known or inferred/Aliases: NPD002, MGC14452/HUGO ID: 21497/UniProt ID: Q9H845/
883.1	883	CCBL1	cysteine conjugate-beta lyase; cytoplasmic (glutamine transaminase K, kyneurenine aminotransferase)	HUGO ID: 1564/UniProt ID: Q16773/

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
10919.1	10919	BAT8	HLA-B associated transcript 8	Locus type: gene with protein product, function unknown/Aliases: G9A, Em:AF134726.3, HGNC:13942/HUGO ID: 14129/UniProt ID: Q96KQ7/
221823.1	221823	PRPS1L1	phosphoribosyl pyrophosphate synthetase 1-like 1	Locus type: gene with protein product, function known or inferred/Aliases: PRPS3/HUGO ID: 9463/UniProt ID: P21108/
89869.1	89869	PLCZ1	phospholipase C, zeta 1	Aliases: NYD-SP27/HUGO ID: 19218/UniProt ID: Q86YW0/
6524.1	6524	SLC5A2	solute carrier family 5 (sodium/glucose cotransporter), member 2	HUGO ID: 11037/UniProt ID: P31639/
9869.1	9869	SETDB1	SET domain, bifurcated 1	Aliases: KG1T, KIAA0067, ESET/HUGO ID: 10761/UniProt ID: Q15047/
11001.1	11001	SLC27A2	solute carrier family 27 (fatty acid transporter), member 2	Locus type: gene with protein product, function known or inferred/Aliases: FATP2, HGNC:3572, hFACVL1, VLACS, VLCS, HsT17226/HUGO ID: 10996/UniProt ID: O14975/MGD ID: MGI:1347099/
23657.1	23657	SLC7A11	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	Aliases: xCT/HUGO ID: 11059/UniProt ID: Q9UPY5/
6839.1	6839	SUV39H1	suppressor of variegation 3-9 homolog 1 (Drosophila)	Locus type: gene with protein product, function known or inferred/HUGO ID: 11479/UniProt ID: O43463/
4845.1	4845	NOS2C	nitric oxide synthase 2C	Locus type: gene with protein product, function known or inferred/HUGO ID: 7875/UniProt ID: Q14961/
53919.1	53919	SLCO1C1	solute carrier organic anion transporter family, member 1C1	Locus type: gene with protein product, function known or inferred/Aliases: OATP-F, OATP1C1, OATP1/HUGO ID: 13819/UniProt ID: Q9NYB5/
6555.1	6555	SLC10A2	solute carrier family 10 (sodium/bile acid cotransporter family), member 2	Locus type: gene with protein product, function known or inferred/HUGO ID: 10906/UniProt ID: Q12908/
80168.1	80168	MOGAT2	monoacylglycerol O-acyltransferase 2	Locus type: gene with protein product, function known or inferred/Aliases: MGAT2, DGAT2L5, FLJ22644/HUGO ID: 23248/
155184.1	155184	SLC2A7	solute carrier family 2 (facilitated glucose transporter), member 7	HUGO ID: 13445/
9197.1	9197	SLC33A1	solute carrier family 33 (acetyl-CoA transporter), member 1	Aliases: AT-1/HUGO ID: 95/UniProt ID: O00400/
9056.1	9056	SLC7A7	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	Aliases: y+LAT-1/HUGO ID: 11065/UniProt ID: Q9UM01/
26873.1	26873	OPLAH	5-oxoprolinase (ATP-hydrolysing)	Aliases: OPLA, 5-Opase/HUGO ID: 8149/UniProt ID: O14841/
28234.1	28234	SLCO1B3	solute carrier organic anion transporter family, member 1B3	Locus type: gene with protein product, function known or inferred/Aliases: OATP8, OATP1B3/HUGO ID: 10961/UniProt ID: Q9NPD5/
50700.1	50700	RDH8	retinol dehydrogenase 8 (all-trans)	Locus type: gene with protein product, function known or inferred/Aliases: PRRDH/HUGO ID: 14423/UniProt ID: Q9NYR8/
57665.1	57665	RDH14	retinol dehydrogenase 14 (all-trans and 9-cis)	Locus type: gene with protein product, function known or inferred/Aliases: PAN2/HUGO ID: 19979/UniProt ID: Q9HBH5/
57282.1	57282	SLC4A10	solute carrier family 4, sodium bicarbonate transporter-like, member 10	HUGO ID: 13811/UniProt ID: Q9HCQ6/
374907.1	374907	B3GALT7	UDP-Gal:betaGal beta 1,3-galactosyltransferase polypeptide 7	Locus type: gene with protein product, function known or inferred/Aliases: BGALT15/HUGO ID: 24139/
119391.1	119391	GSTO2	glutathione S-transferase omega 2	Locus type: gene with protein product, function known or inferred/HUGO ID: 23064/
8869.1	8869	SIAT9	sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase)	Aliases: ST3GalV, SIATGM3S/HUGO ID: 10872/UniProt ID: Q9UNP4/
55229.1	55229	PANK4	pantothenate kinase 4	Locus type: gene with protein product, function known or inferred/Aliases: FLJ10782/HUGO ID: 19366/UniProt ID: Q9NVE7/
23539.1	23539	SLC16A8	solute carrier 16 (monocarboxylic acid transporters), member 8	Aliases: MCT3/HUGO ID: 16270/UniProt ID: O95907/
140679.1	140679	SLC32A1	solute carrier family 32 (GABA vesicular transporter), member 1	Locus type: gene with protein product, function known or inferred/Aliases: VGAT, bA122O1.1, HGNC:15800/HUGO ID: 11018/
6528.1	6528	SLC5A5	solute carrier family 5 (sodium iodide symporter), member 5	Aliases: NIS/HUGO ID: 11040/UniProt ID: Q92911/
57127.1	57127	RHBG	Rhesus blood group, B glycoprotein	HUGO ID: 14572/UniProt ID: Q9H310/
122622.1	122622	ADSSL1	adenylosuccinate synthase like 1	Locus type: gene with protein product, function unknown/Aliases: FLJ38602/HUGO ID: 20093/UniProt ID: Q8N714/
160287.1	160287	LDHAL6A	lactate dehydrogenase A-like 6A	Locus type: gene with protein product, function unknown/Aliases: MGC23940/HUGO ID: 28335/
284111.1	284111	SLC13A5	solute carrier family 13 (sodium-dependent citrate transporter), member 5	Locus type: gene with protein product, function known or inferred/Aliases: NACT/HUGO ID: 23089/UniProt ID: Q86YT5/
29920.1	29920	PYCR2	pyrroline-5-carboxylate reductase family, member 2	Locus type: gene with protein product, function known or inferred/Aliases: P5CR2/HUGO ID: 30262/
80146.1	80146	UXS1	UDP-glucuronate decarboxylase 1	Aliases: FLJ23591/HUGO ID: 17729/UniProt ID: Q8NBX3/
51540.1	51540	SCLY	selenocysteine lyase	Locus type: gene with protein product, function known or inferred/Aliases: SCLY, SCL/HUGO ID: 18161/MGD ID: MGI:1355310/
257068.1	257068	PLCXD2	phosphatidylinositol-specific phospholipase C, X domain containing 2	Locus type: gene with protein product, function unknown/Aliases: FLJ31579/HUGO ID: 26462/
54981.1	54981	C9orf95	chromosome 9 open reading frame 95	Locus type: gene with protein product, function unknown/Aliases: FLJ20559, NRK1, bA235O14.2/HUGO ID: 26057/
130752.1	130752	MDH1B	malate dehydrogenase 1B, NAD (soluble)	Aliases: FLJ25341, RP11-95H11/HUGO ID: 17836/UniProt ID: Q8IV51/
112611.1	112611	RWDD2	RWD domain containing 2	Locus type: gene with protein product, function unknown/Aliases: MGC13523, dJ747H23.2/HUGO ID: 21385/UniProt ID: Q9UIY3/MGD ID: MGI:1916769/

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
81537.1	81537	SGPP1	sphingosine-1-phosphate phosphatase 1	Locus type: gene with protein product, function known or inferred/HUGO ID: 17720/UniProt ID: Q9BX95/MGD ID: MGI:2135760/
5334.1	5334	PLCL1	phospholipase C-like 1	Aliases: PLC-L, PLCL/HUGO ID: 9063/UniProt ID: Q15111/
8706.1	8706	B3GALT3	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 3	Locus type: gene with protein product, function known or inferred/Aliases: beta3Gal-T3, galT3, P1/HUGO ID: 918/UniProt ID: O75752/
23443.1	23443	SLC35A3	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member A3	HUGO ID: 11023/UniProt ID: Q9Y2D2/
534.1	534	ATP6V1G2	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G isoform 2	Aliases: Vma10, NG38, Em:AC004181.3/HUGO ID: 862/UniProt ID: O95670/
19.1	19	ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1	Aliases: TGD, Tangier disease/HUGO ID: 29/UniProt ID: O95477/
92483.1	92483	LDHAL6B	lactate dehydrogenase A-like 6B	Locus type: gene with protein product, function unknown/Aliases: LDHL/HUGO ID: 21481/
8503.1	8503	PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (p55, gamma)	HUGO ID: 8981/UniProt ID: Q92569/
55315.1	55315	SLC29A3	solute carrier family 29 (nucleoside transporters), member 3	Locus type: gene with protein product, function known or inferred/Aliases: ENT3, FLJ11160/HUGO ID: 23096/UniProt ID: Q9BZD2/
9152.1	9152	SLC6A5	solute carrier family 6 (neurotransmitter transporter, glycine), member 5	Aliases: GLYT2/HUGO ID: 11051/UniProt ID: Q9Y345/
90161.1	90161	HS6ST2	heparan sulfate 6-O-sulfotransferase 2	Locus type: gene with protein product, function known or inferred/HUGO ID: 19133/UniProt ID: Q96MM7/
27124.1	27124	PIB5PA	phosphatidylinositol (4,5) bisphosphate 5-phosphatase, A	HUGO ID: 8956/UniProt ID: Q15735/
55301.1	55301	THEDC1	thioesterase domain containing 1	Locus type: gene with protein product, function unknown/Aliases: FLJ11106/HUGO ID: 25625/
491.1	491	ATP2B2	ATPase, Ca++ transporting, plasma membrane 2	Aliases: PMCA2/HUGO ID: 815/UniProt ID: Q01814/
91703.1	91703	ACY3	aspartoacylase (aminocyclase) 3	Locus type: gene with protein product, function known or inferred/Aliases: HCBP1, MGC9740, ACY-3/HUGO ID: 24104/MGD ID: MGI:1918920/
6506.1	6506	SLC1A2	solute carrier family 1 (glial high affinity glutamate transporter), member 2	Aliases: GLT-1, EAAT2/HUGO ID: 10940/UniProt ID: P43004/
284129.1	284129	SLC26A11	solute carrier family 26, member 11	HUGO ID: 14471/UniProt ID: Q86YX7/
10861.1	10861	SLC26A1	solute carrier family 26 (sulfate transporter), member 1	Locus type: gene with protein product, function known or inferred/Aliases: SAT-1, EDM4/HUGO ID: 10993/UniProt ID: Q9H2B4/
26002.1	26002	MOXD1	monooxygenase, DBH-like 1	Locus type: gene with protein product, function unknown/Aliases: DKFZP564G202, MOX, dJ248E1.1/HUGO ID: 21063/UniProt ID: Q9H4M6/
5264.1	5264	PHYH	phytanoyl-CoA hydroxylase (Refsum disease)	Aliases: PAHX/HUGO ID: 8940/UniProt ID: O14832/
2108.1	2108	ETFA	electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II)	Locus type: gene with protein product, function known or inferred/Aliases: GA2, EMA, MADD/HUGO ID: 3481/UniProt ID: P13804/
6558.1	6558	SLC12A2	solute carrier family 12 (sodium/potassium/chloride transporters), member 2	Aliases: NKCC1/HUGO ID: 10911/UniProt ID: P55011/
53354.1	53354	PANK1	pantothenate kinase 1	Locus type: gene with protein product, function known or inferred/Aliases: MGC24596, PANK1a, PANK1b/HUGO ID: 8598/UniProt ID: Q8TE04/
79901.1	79901	CYBRD1	cytochrome b reductase 1	Locus type: gene with protein product, function known or inferred/Aliases: DCYTB, FLJ23462/HUGO ID: 20797/UniProt ID: Q9H0Q8/MGD ID: MGI:2654575/
6541.1	6541	SLC7A1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	Aliases: CAT-1, HCAT1, REC1L/HUGO ID: 11057/UniProt ID: P30825/
80270.1	80270	HSD3B7	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	Locus type: gene with protein product, function known or inferred/Aliases: C(27)-3BETA-HSD/HUGO ID: 18324/UniProt ID: Q9BSN9/
58510.1	58510	PRODH2	proline dehydrogenase (oxidase) 2	Locus type: gene with protein product, function known or inferred/Aliases: HSPOX1/HUGO ID: 17325/UniProt ID: O00420/
477.1	477	ATP1A2	ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide	HUGO ID: 800/UniProt ID: P50993/
121278.1	121278	TPH2	tryptophan hydroxylase 2	Locus type: gene with protein product, function known or inferred/Aliases: NTPH, FLJ37295/HUGO ID: 20692/UniProt ID: Q8IWU9/MGD ID: MGI:2651811/
51557.1	51557	GLULD1	glutamate-ammonia ligase (glutamine synthase) domain containing 1	Locus type: gene with protein product, function known or inferred/Aliases: lengsin, LGS/HUGO ID: 21016/UniProt ID: Q9NYJ0/
956.1	956	ENTPD3	ectonucleoside triphosphate diphosphohydrolase 3	Locus type: gene with protein product, function known or inferred/Aliases: NTPDase-3, HB6/HUGO ID: 3365/UniProt ID: O75355/
8781.1	8781	PSPHL	phosphoserine phosphatase-like	Aliases: CO9/HUGO ID: 9578/UniProt ID: O15172/
10164.1	10164	CHST4	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 4	Aliases: HEC-GLCNAC-6-ST, LSST/HUGO ID: 1972/UniProt ID: Q8NCG5/MGD ID: MGI:1349479/
57733.1	57733	GBA3	glucosidase, beta, acid 3 (cytosolic)	Locus type: gene with protein product, function known or inferred/Aliases: GLUC/HUGO ID: 19069/UniProt ID: Q9H227/
6549.1	6549	SLC9A2	solute carrier family 9 (sodium/hydrogen exchanger), isoform 2	HUGO ID: 11072/UniProt ID: Q9UBY0/
83852.1	83852	SETDB2	SET domain, bifurcated 2	Locus type: gene with protein product, function unknown/Aliases: CLLD8, CLLL8/HUGO ID: 20263/UniProt ID: Q96T68/
25769.1	25769	SLC24A2	solute carrier family 24 (sodium/potassium/calcium exchanger), member 2	Locus type: gene with protein product, function known or inferred/Aliases: NCKX2/HUGO ID: 10976/UniProt ID: Q9UI40/

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
6647.1	6647	SOD1	superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))	HUGO ID: 11179/UniProt ID: P00441/
9114.1	9114	ATP6V0D1	ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d isoform 1	Aliases: ATP6DV, VATX, VPATPD, P39, Vma6/HUGO ID: 13724/UniProt ID: P12953/
50940.1	50940	PDE11A	phosphodiesterase 11A	HUGO ID: 8773/UniProt ID: Q9HCR9/
166012.1	166012	CHST13	carbohydrate (chondroitin 4) sulfotransferase 13	Locus type: gene with protein product, function known or inferred/Aliases: C4ST3/HUGO ID: 21755/UniProt ID: Q8NET6/
9227.1	9227	LRAT	lecithin retinol acyltransferase (phosphatidylcholine--retinol O-acyltransferase)	HUGO ID: 6685/UniProt ID: O95237/
132789.1	132789	GNPDA2	glucosamine-6-phosphate deaminase 2	Locus type: gene with protein product, function known or inferred/Aliases: 4921523I18Rik, SB52/HUGO ID: 21526/UniProt ID: Q8TDQ7/MGD ID: MGI:1915230/
94005.1	94005	PIGS	phosphatidylinositol glycan, class S	HUGO ID: 14937/UniProt ID: Q96S52/
11212.1	11212	PROSC	proline synthetase co-transcribed homolog (bacterial)	Locus type: gene with protein product, function known or inferred/HUGO ID: 9457/UniProt ID: O94903/
1836.1	1836	SLC26A2	solute carrier family 26 (sulfate transporter), member 2	Locus type: gene with protein product, function known or inferred/HUGO ID: 10994/UniProt ID: P50443/
495.1	495	ATP4A	ATPase, H+/K+ exchanging, alpha polypeptide	Aliases: ATP6A/HUGO ID: 819/UniProt ID: P20648/
5052.1	5052	PRDX1	peroxiredoxin 1	Locus type: gene with protein product, function known or inferred/Aliases: NKEFA/HUGO ID: 9352/UniProt ID: Q06830/
9153.1	9153	SLC28A2	solute carrier family 28 (sodium-coupled nucleoside transporter), member 2	Locus type: gene with protein product, function known or inferred/Aliases: CNT2, SPNT1, HCNT2, HsT17153/HUGO ID: 11002/UniProt ID: O43868/
84720.1	84720	PIGO	phosphatidylinositol glycan, class O	Locus type: gene with protein product, function known or inferred/Aliases: DKFZp434M222, FLJ00135/HUGO ID: 23215/UniProt ID: Q8TEQ8/
6523.1	6523	SLC5A1	solute carrier family 5 (sodium/glucose cotransporter), member 1	Aliases: D22S675/HUGO ID: 11036/UniProt ID: P13866/
10723.1	10723	SLC12A7	solute carrier family 12 (potassium/chloride transporters), member 7	Locus type: gene with protein product, function known or inferred/Aliases: KCC4, DKFZP434F076/HUGO ID: 10915/UniProt ID: Q9Y666/
66035.1	66035	SLC2A11	solute carrier family 2 (facilitated glucose transporter), member 11	Aliases: GLUT11, GLUT10/HUGO ID: 14239/UniProt ID: Q9BYW1/
56606.1	56606	SLC2A9	solute carrier family 2 (facilitated glucose transporter), member 9	Aliases: Glut9, GLUTX/HUGO ID: 13446/UniProt ID: Q9NRM0/
11343.1	11343	MGLL	monoglyceride lipase	Locus type: gene with protein product, function known or inferred/Aliases: HU K5, MGL/HUGO ID: 17038/UniProt ID: Q99685/
6820.1	6820	SULT2B1	sulfotransferase family, cytosolic, 2B, member 1	Aliases: HSST2/HUGO ID: 11459/UniProt ID: O00205/
51380.1	51380	CSAD	cysteine sulfinic acid decarboxylase	Aliases: PCAP, CSD/HUGO ID: 18966/UniProt ID: Q9Y600/MGD ID: MGI:2180098/
6554.1	6554	SLC10A1	solute carrier family 10 (sodium/bile acid cotransporter family), member 1	Aliases: NTCP/HUGO ID: 10905/UniProt ID: Q14973/
6532.1	6532	SLC6A4	solute carrier family 6 (neurotransmitter transporter, serotonin), member 4	HUGO ID: 11050/UniProt ID: P31645/
6514.1	6514	SLC2A2	solute carrier family 2 (facilitated glucose transporter), member 2	HUGO ID: 11006/UniProt ID: P11168/
8622.1	8622	PDE8B	phosphodiesterase 8B	Locus type: gene with protein product, function known or inferred/HUGO ID: 8794/UniProt ID: O95263/
5296.1	5296	PIK3R2	phosphoinositide-3-kinase, regulatory subunit 2 (p85 beta)	Aliases: P85B/HUGO ID: 8980/UniProt ID: O00459/
6505.1	6505	SLC1A1	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	Aliases: EAAC1, EAAT3/HUGO ID: 10939/UniProt ID: P43005/
6571.1	6571	SLC18A2	solute carrier family 18 (vesicular monoamine), member 2	Locus type: gene with protein product, function known or inferred/Aliases: SVMT, SVAT/HUGO ID: 10935/UniProt ID: Q05940/
23743.1	23743	BHMT2	betaine-homocysteine methyltransferase 2	HUGO ID: 1048/UniProt ID: Q9H2M3/
11000.1	11000	SLC27A3	solute carrier family 27 (fatty acid transporter), member 3	Locus type: gene with protein product, function known or inferred/Aliases: FATP3, MGC4365/HUGO ID: 10997/UniProt ID: Q9BTY5/MGD ID: MGI:1347358/
366.1	366	AQP9	aquaporin 9	Locus type: gene with protein product, function known or inferred/Aliases: SSC1, HsT17287/HUGO ID: 643/UniProt ID: O43315/
3635.1	3635	INPP5D	inositol polyphosphate-5-phosphatase, 145kDa	Aliases: SHIP, hp51CN/HUGO ID: 6079/UniProt ID: O00145/
2581.1	2581	GALC	galactosylceramidase (Krabbe disease)	HUGO ID: 4115/UniProt ID: P54803/
30815.1	30815	SIAT7F	sialytransferase 7 ((alpha-N-acetylneuraminyl 2,3-betagalactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialytransferase) F	Locus type: gene with protein product, function known or inferred/Aliases: ST6GALNAC6, ST6GALNACVI/HUGO ID: 23364/MGD ID: MGI:1355316/
10610.1	10610	SIAT7B	sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltransferase) B	Locus type: gene with protein product, function known or inferred/Aliases: ST6GalNA II, III, IV, STHM/HUGO ID: 10867/UniProt ID: Q9UJ37/
6519.1	6519	SLC3A1	solute carrier family 3 (cystine, dibasic and neutral amino acid transporters, activator of cystine, dibasic and neutral amino acid transport), member 1	Aliases: CSNU1, D2H, RBAT/HUGO ID: 11025/UniProt ID: Q07837/
2992.1	2992	GYG	glycogenin	Locus type: gene with protein product, function known or inferred/HUGO ID: 4699/UniProt ID: P46976/
9057.1	9057	SLC7A6	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	Locus type: gene with protein product, function known or inferred/Aliases: y+LAT-2, KIAA0245, LAT3, LAT-2/HUGO ID: 11064/UniProt ID: Q92536/
7923.1	7923	HSD17B8	hydroxysteroid (17-beta) dehydrogenase 8	Aliases: HKE6, RING2, HKE6, D6S2245E, RING2, KE6, H2-KE6/HUGO ID: 3554/UniProt ID: Q92506/

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
137872.1	137872	ADHFE1	alcohol dehydrogenase, iron containing, 1	Locus type: gene with protein product, function known or inferred/Aliases: ADHFe1, FLJ32430/HUGO ID: 16354/UniProt ID: Q8IWW8/MGD ID: MGI:1923437/
57084.1	57084	SLC17A6	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 6	Aliases: DNPI/HUGO ID: 16703/UniProt ID: Q9P2U8/
6579.1	6579	SLCO1A2	solute carrier organic anion transporter family, member 1A2	Locus type: gene with protein product, function known or inferred/Aliases: OATP, OATP1A2, OATP-A/HUGO ID: 10956/UniProt ID: P46721/
6535.1	6535	SLC6A8	solute carrier family 6 (neurotransmitter transporter, creatine) member 8	Aliases: CRTR, CT1/HUGO ID: 11055/UniProt ID: P48029/
9435.1	9435	CHST2	carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2	Locus type: gene with protein product, function known or inferred/Aliases: C6ST/HUGO ID: 1970/UniProt ID: Q9Y4C5/
6448.1	6448	SGSH	N-sulfoglucosamine sulfohydrolase (sulfamidase)	Locus type: gene with protein product, function known or inferred/Aliases: HSS, MPS3A, SFMD/HUGO ID: 10818/UniProt ID: P51688/
7001.1	7001	PRDX2	peroxiredoxin 2	Aliases: PRP, NKEFB/HUGO ID: 9353/UniProt ID: P32119/
90423.1	90423	ATP6V1E2	ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E isoform 2	Locus type: gene with protein product, function known or inferred/Aliases: MGC9341, VMA4, ATP6E1/HUGO ID: 18125/UniProt ID: Q96A05/
349565.1	349565	NMNAT3	nicotinamide nucleotide adenylyltransferase 3	Locus type: gene with protein product, function known or inferred/Aliases: PNAT3/HUGO ID: 20989/UniProt ID: Q96T66/
11182.1	11182	SLC2A6	solute carrier family 2 (facilitated glucose transporter), member 6	Aliases: GLUT9, GLUT6/HUGO ID: 11011/UniProt ID: Q9UGQ3/
84706.1	84706	GPT2	glutamic pyruvate transaminase (alanine aminotransferase) 2	Aliases: ALT2/HUGO ID: 18062/UniProt ID: Q8TD30/
197257.1	197257	LDHD	lactate dehydrogenase D	Locus type: gene with protein product, function known or inferred/HUGO ID: 19708/UniProt ID: Q8IZK5/
6575.1	6575	SLC20A2	solute carrier family 20 (phosphate transporter), member 2	Aliases: PiT-2, Glvr-2/HUGO ID: 10947/UniProt ID: Q08357/
56623.1	56623	INPP5E	inositol polyphosphate-5-phosphatase, 72 kDa	Locus type: gene with protein product, function known or inferred/Aliases: PPI5PIV/HUGO ID: 21474/UniProt ID: Q9NRR6/MGD ID: MGI:1927753/
128869.1	128869	CDC91L1	CDC91 cell division cycle 91-like 1 (S. cerevisiae)	Aliases: bA346K17.2/HUGO ID: 15791/UniProt ID: Q9H490/
7295.1	7295	TXN	thioredoxin	Aliases: TRX/HUGO ID: 12435/UniProt ID: P10599/
10948.1	10948	STARD3	START domain containing 3	Aliases: es64, MLN64/HUGO ID: 17579/UniProt ID: Q14849/MGD ID: MGI:1929618/
1638.1	1638	DCT	dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2)	HUGO ID: 2709/UniProt ID: P40126/
5244.1	5244	ABCB4	ATP-binding cassette, sub-family B (MDR/TAP), member 4	Locus type: gene with protein product, function known or inferred/Aliases: MDR2/3, PFIC-3/HUGO ID: 45/UniProt ID: P21439/
60482.1	60482	SLC5A7	solute carrier family 5 (choline transporter), member 7	Aliases: hCHT, CHT1/HUGO ID: 14025/UniProt ID: Q9GZV3/
144195.1	144195	SLC2A14	solute carrier family 2 (facilitated glucose transporter), member 14	Locus type: gene with protein product, function known or inferred/Aliases: GLUT14/HUGO ID: 18301/UniProt ID: Q8TDB8/
1718.1	1718	DHCR24	24-dehydrocholesterol reductase	Aliases: KIAA0018, seladin-1/HUGO ID: 2859/UniProt ID: Q15392/
53905.1	53905	DUOX1	dual oxidase 1	Aliases: NOXEF1, THOX1/HUGO ID: 3062/UniProt ID: Q9NRD9/
10246.1	10246	SLC17A2	solute carrier family 17 (sodium phosphate), member 2	Aliases: NPT3/HUGO ID: 10930/UniProt ID: O00624/
6580.1	6580	SLC22A1	solute carrier family 22 (organic cation transporter), member 1	Aliases: 38261/HUGO ID: 10963/UniProt ID: O15245/
124583.1	124583	CANT1	calcium activated nucleotidase 1	Locus type: gene with protein product, function known or inferred/Aliases: SHAPY, SCAN-1/HUGO ID: 19721/MGD ID: MGI:1923275/
284208.1	284208	B3GNTL1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-like 1	Locus type: gene with protein product, function known or inferred/HUGO ID: 21727/ transcript: NM_001009905
162466.1	162466	PHOSPHO1	phosphatase, orphan 1	HUGO ID: 16815/UniProt ID: Q8TCT1/
266722.1	266722	HS6ST3	heparan sulfate 6-O-sulfotransferase 3	HUGO ID: 19134/UniProt ID: Q8IZP7/
2351.1	2351	FOLR2L	folate receptor 2 (fetal) like	HUGO ID: 3794/
92745.1	92745	SLC38A5	solute carrier family 38, member 5	Locus type: gene with protein product, function known or inferred/Aliases: SN2, JM24/HUGO ID: 18070/UniProt ID: Q9UJU8/
91373.1	91373	UAP1L1	UDP-N-acteylglucosamine pyrophosphorylase 1-like 1	Locus type: gene with protein product, function unknown/HUGO ID: 28082/
10201.1	10201	NME6	non-metastatic cells 6, protein expressed in (nucleoside-diphosphate kinase)	Locus type: gene with protein product, function known or inferred/Aliases: NM23-H6, IPIA-ALPHA/HUGO ID: 20567/UniProt ID: O75414/MGD ID: MGI:1861676/
9187.1	9187	SLC24A1	solute carrier family 24 (sodium/potassium/calcium exchanger), member 1	Locus type: gene with protein product, function known or inferred/Aliases: NCKX1, NCKX, RODX, KIAA0702, HsT17412/HUGO ID: 10975/UniProt ID: O60721/
492.1	492	ATP2B3	ATPase, Ca++ transporting, plasma membrane 3	Aliases: PMCA3/HUGO ID: 816/UniProt ID: Q16720/
8611.1	8611	PPAP2A	phosphatidic acid phosphatase type 2A	Aliases: PAP-2a/HUGO ID: 9228/UniProt ID: O60463/
8310.1	8310	ACOX3	acyl-Coenzyme A oxidase 3, pristanoyl	HUGO ID: 121/UniProt ID: O15254/
55224.1	55224	ETNK2	ethanolamine kinase 2	Locus type: gene with protein product, function unknown/Aliases: FLJ10761, EKI2/HUGO ID: 25575/MGD ID: MGI:2443760/
28231.1	28231	SLCO4A1	solute carrier organic anion transporter family, member 4A1	Locus type: gene with protein product, function known or inferred/Aliases: OATP-E, OATP4A1/HUGO ID: 10953/UniProt ID: Q96BD0/

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
10402.1	10402	SIAT10	sialyltransferase 10 (alpha-2,3-sialyltransferase VI)	Locus type: gene with protein product, function known or inferred/Aliases: ST3GALVI/HUGO ID: 18080/UniProt ID: Q9Y274/
2109.1	2109	ETFB	electron-transfer-flavoprotein, beta polypeptide	Locus type: gene with protein product, function known or inferred/HUGO ID: 3482/UniProt ID: P38117/
64078.1	64078	SLC28A3	solute carrier family 28 (sodium-coupled nucleoside transporter), member 3	Aliases: CNT3/HUGO ID: 16484/UniProt ID: Q9HAS3/
80704.1	80704	SLC19A3	solute carrier family 19, member 3	HUGO ID: 16266/UniProt ID: Q9BZV2/
10999.1	10999	SLC27A4	solute carrier family 27 (fatty acid transporter), member 4	Locus type: gene with protein product, function known or inferred/Aliases: FATP4/HUGO ID: 10998/UniProt ID: O95186/MGD ID: MGI:1347347/
80150.1	80150	ASRGL1	asparaginase like 1	Aliases: FLJ22316, ALP1/HUGO ID: 16448/UniProt ID: Q8NI34/
6518.1	6518	SLC2A5	solute carrier family 2 (facilitated glucose/fructose transporter), member 5	Locus type: gene with protein product, function known or inferred/HUGO ID: 11010/UniProt ID: P22732/MGD ID: MGI:1928369/
478.1	478	ATP1A3	ATPase, Na+/K+ transporting, alpha 3 polypeptide	HUGO ID: 801/UniProt ID: P13637/
9194.1	9194	SLC16A7	solute carrier family 16 (monocarboxylic acid transporters), member 7	Locus type: gene with protein product, function known or inferred/Aliases: MCT2/HUGO ID: 10928/UniProt ID: O60669/
6509.1	6509	SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	Aliases: SATT, ASCT1/HUGO ID: 10942/UniProt ID: P43007/
1808.1	1808	DPYSL2	dihydropyrimidinase-like 2	Locus type: gene with protein product, function known or inferred/Aliases: DRP-2, DHPRP2, CRMP2, DRP2/HUGO ID: 3014/UniProt ID: Q16555/
57379.1	57379	AICDA	activation-induced cytidine deaminase	Aliases: CDA2, AID/HUGO ID: 13203/UniProt ID: Q9GZX7/
9952.1	9952	HS3ST3B2	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B2	Aliases: 3OST3B2/HUGO ID: 5199/
159963.1	159963	SLC5A12	solute carrier family 5 (sodium/glucose cotransporter), member 12	Locus type: gene with protein product, function unknown/Aliases: MGC52019/HUGO ID: 28750/MGD ID: MGI:2138890/
56994.1	56994	CHPT1	choline phosphotransferase 1	Aliases: CPT1/HUGO ID: 17852/UniProt ID: Q8WUD6/
84002.1	84002	B3GNT5	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5	Aliases: B3GN-T5, beta3Gn-T5/HUGO ID: 15684/UniProt ID: Q9BYG0/
6540.1	6540	SLC6A13	solute carrier family 6 (neurotransmitter transporter, GABA), member 13	Locus type: gene with protein product, function known or inferred/Aliases: GAT2/HUGO ID: 11046/UniProt ID: Q9NSD5/
6574.1	6574	SLC20A1	solute carrier family 20 (phosphate transporter), member 1	Aliases: PiT-1, Glvr-1/HUGO ID: 10946/UniProt ID: Q08344/
7263.1	7263	TST	thiosulfate sulfurtransferase (rhodanese)	Aliases: RDS/HUGO ID: 12388/UniProt ID: Q16762/
1607.1	1607	DGKB	diacylglycerol kinase, beta 90kDa	Locus type: gene with protein product, function known or inferred/Aliases: KIAA0718, DGK, DGK-BETA/HUGO ID: 2850/UniProt ID: Q9Y6T7/
10087.1	10087	COL4A3BP	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	Aliases: GPBP, STARD11/HUGO ID: 2205/UniProt ID: Q9Y5P4/
9807.1	9807	IHPK1	inositol hexaphosphate kinase 1	Locus type: gene with protein product, function known or inferred/Aliases: KIAA0263, IP6K1/HUGO ID: 18360/UniProt ID: Q92551/
54490.1	54490	UGT2B28	UDP glycosyltransferase 2 family, polypeptide B28	Locus type: gene with protein product, function known or inferred/HUGO ID: 13479/UniProt ID: Q9BY64/
2712.1	2712	GK2	glycerol kinase 2	Aliases: GKTA/HUGO ID: 4291/UniProt ID: Q14410/
6522.1	6522	SLC4A2	solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein band 3-like 1)	Aliases: HKB3/HUGO ID: 11028/UniProt ID: P04920/
955.1	955	ENTPD6	ectonucleoside triphosphate diphosphohydrolase 6 (putative function)	Locus type: gene with protein product, function known or inferred/Aliases: NTPDase-6, HGNC:16241, dJ738P15.3/HUGO ID: 3368/UniProt ID: O75354/
7306.1	7306	TYRP1	tyrosinase-related protein 1	HUGO ID: 12450/UniProt ID: P17643/
6548.1	6548	SLC9A1	solute carrier family 9 (sodium/hydrogen exchanger), isoform 1 (antiporter, Na+/H+, amiloride sensitive)	Locus type: gene with protein product, function known or inferred/HUGO ID: 11071/UniProt ID: P19634/MGD ID: MGI:102462/
6557.1	6557	SLC12A1	solute carrier family 12 (sodium/potassium/chloride transporters), member 1	Aliases: NKCC2/HUGO ID: 10910/UniProt ID: Q13621/
6561.1	6561	SLC13A1	solute carrier family 13 (sodium/sulfate symporters), member 1	Aliases: NaSi-1/HUGO ID: 10916/UniProt ID: Q9BZW2/
6513.1	6513	SLC2A1	solute carrier family 2 (facilitated glucose transporter), member 1	HUGO ID: 11005/UniProt ID: P11166/
51227.1	51227	DSCR5	Down syndrome critical region gene 5	Aliases: DCRC, DSRC/HUGO ID: 3046/UniProt ID: P57054/
6531.1	6531	SLC6A3	solute carrier family 6 (neurotransmitter transporter, dopamine), member 3	HUGO ID: 11049/UniProt ID: Q01959/
51604.1	51604	PIGT	phosphatidylinositol glycan, class T	Locus type: gene with protein product, function known or inferred/HUGO ID: 14938/UniProt ID: Q969N2/
117283.1	117283	IHPK3	inositol hexaphosphate kinase 3	Locus type: gene with protein product, function known or inferred/Aliases: INSP6K3, IP6K3/HUGO ID: 17269/UniProt ID: Q96PC2/
151531.1	151531	UPP2	uridine phosphorylase 2	Locus type: gene with protein product, function known or inferred/Aliases: UPASE2, UP2, UDRPASE2/HUGO ID: 23061/UniProt ID: O95045/
10786.1	10786	SLC17A3	solute carrier family 17 (sodium phosphate), member 3	Aliases: NPT4/HUGO ID: 10931/UniProt ID: O00476/
6583.1	6583	SLC22A4	solute carrier family 22 (organic cation transporter), member 4	Locus type: gene with protein product, function known or inferred/Aliases: OCTN1, MGC34546/HUGO ID: 10968/UniProt ID: O14546/
51447.1	51447	IHPK2	inositol hexaphosphate kinase 2	Aliases: IP6K2/HUGO ID: 17313/UniProt ID: Q9H4P7/
6526.1	6526	SLC5A3	solute carrier family 5 (inositol transporters), member 3	Aliases: SMIT/HUGO ID: 11038/UniProt ID: P53794/

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
55349.1	55349	CHDH	choline dehydrogenase	Locus type: gene with protein product, function known or inferred/HUGO ID: 24288/MGD ID: MGI:1860776/
11136.1	11136	SLC7A9	solute carrier family 7 (cationic amino acid transporter, y+ system), member 9	HUGO ID: 11067/UniProt ID: P82251/
3992.1	3992	FADS1	fatty acid desaturase 1	Locus type: gene with protein product, function known or inferred/Aliases: D5D, FADSD5, TU12, FADS6/HUGO ID: 3574/UniProt ID: Q8NCC7/
7355.1	7355	SLC35A2	solute carrier family 35 (UDP-galactose transporter), member A2	Locus type: gene with protein product, function known or inferred/Aliases: UGAT, UGT, UGT1, UGT2, UGTL/HUGO ID: 11022/UniProt ID: P78381/
4524.1	4524	MTHFR	5,10-methylenetetrahydrofolate reductase (NADPH)	Locus type: gene with protein product, function known or inferred/HUGO ID: 7436/UniProt ID: P42898/
341947.1	341947	COX8C	cytochrome c oxidase subunit 8C	Locus type: gene with protein product, function known or inferred/Aliases: COX8-3/HUGO ID: 24382/MGD ID: MGI:1922733/
55586.1	55586	ALDRL6	aldehyde reductase (aldose reductase) like 6	HUGO ID: 14522/UniProt ID: Q9UGB7/
8871.1	8871	SYNJ2	synaptojanin 2	Aliases: INPP5H/HUGO ID: 11504/UniProt ID: O15056/
1109.1	1109	AKR1C4	aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihydrodiol dehydrogenase 4)	Locus type: gene with protein product, function known or inferred/Aliases: DD4, HAKRA, C11, 3-alpha-HSD, CDR, MGC22581/HUGO ID: 387/UniProt ID: P17516/
3658.1	3658	IREB2	iron-responsive element binding protein 2	Locus type: gene with protein product, function known or inferred/Aliases: IRP2/HUGO ID: 6115/UniProt ID: P48200/
6565.1	6565	SLC15A2	solute carrier family 15 (H+/peptide transporter), member 2	Locus type: gene with protein product, function known or inferred/Aliases: PEPT2/HUGO ID: 10921/UniProt ID: Q16348/
9498.1	9498	SLC4A8	solute carrier family 4, sodium bicarbonate cotransporter, member 8	Locus type: gene with protein product, function known or inferred/Aliases: NBC3/HUGO ID: 11034/UniProt ID: O94843/
549.1	549	AUH	AU RNA binding protein/enoyl-Coenzyme A hydratase	HUGO ID: 890/UniProt ID: Q13825/
6512.1	6512	SLC1A7	solute carrier family 1 (glutamate transporter), member 7	Aliases: EAAT5/HUGO ID: 10945/UniProt ID: O00341/MGD ID: MGI:2444087/
377677.1	377677	CA13	carbonic anhydrase XIII	Locus type: gene with protein product, function known or inferred/Aliases: CAXIII, FLJ37995, MGC59868/HUGO ID: 14914/
9468.1	9468	PCYT1B	phosphate cytidylyltransferase 1, choline, beta isoform	Locus type: gene with protein product, function known or inferred/Aliases: CCT-beta, CTB/HUGO ID: 8755/UniProt ID: Q9Y5K3/
8170.1	8170	SLC14A2	solute carrier family 14 (urea transporter), member 2	Aliases: HUT2, UT2/HUGO ID: 10919/UniProt ID: Q15849/
54576.1	54576	UGT1A8	UDP glycosyltransferase 1 family, polypeptide A8	Aliases: UGT1H/HUGO ID: 12540/UniProt ID: Q9HAW9/
6538.1	6538	SLC6A11	solute carrier family 6 (neurotransmitter transporter, GABA), member 11	Locus type: gene with protein product, function known or inferred/Aliases: GAT3/HUGO ID: 11044/UniProt ID: P48066/
376497.1	376497	SLC27A1	solute carrier family 27 (fatty acid transporter), member 1	Locus type: gene with protein product, function known or inferred/Aliases: FATP1, FATP, MGC71751, FLJ00336/HUGO ID: 10995/UniProt ID: Q96DY3/MGD ID: MGI:1347098/
6539.1	6539	SLC6A12	solute carrier family 6 (neurotransmitter transporter, betaine/GABA), member 12	Locus type: gene with protein product, function known or inferred/Aliases: BGT-1/HUGO ID: 11045/UniProt ID: P48065/
245973.1	245973	ATP6V1C2	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C isoform 2	Locus type: gene with protein product, function known or inferred/Aliases: VMA5, ATP6C2/HUGO ID: 18264/UniProt ID: Q8NEY4/
6543.1	6543	SLC8A2	solute carrier family 8 (sodium-calcium exchanger), member 2	Aliases: NCX2, KIAA1087/HUGO ID: 11069/UniProt ID: Q9UPR5/
50487.1	50487	PLA2G3	phospholipase A2, group III	Aliases: GIII-SPLA2/HUGO ID: 17934/UniProt ID: Q9NZ20/
57468.1	57468	SLC12A5	solute carrier family 12, (potassium-chloride transporter) member 5	Aliases: KIAA1176/HUGO ID: 13818/UniProt ID: Q9H2X9/
112724.1	112724	RDH13	retinol dehydrogenase 13 (all-trans and 9-cis)	Locus type: gene with protein product, function known or inferred/HUGO ID: 19978/UniProt ID: Q8NBN7/
2098.1	2098	ESD	esterase D/formylglutathione hydrolase	HUGO ID: 3465/UniProt ID: P10768/
64711.1	64711	HS3ST6	heparan sulfate (glucosamine) 3-O-sulfotransferase 6	HUGO ID: 14178/UniProt ID: Q96QI5/transcript: NM_001009606
84532.1	84532	ACAS2L	acetyl-Coenzyme A synthetase 2 (AMP forming)-like	Aliases: dJ568C11.3/HUGO ID: 16091/UniProt ID: Q9NUB1/
115286.1	115286	SLC25A26	solute carrier family 25, member 26	Locus type: gene with protein product, function known or inferred/HUGO ID: 20661/UniProt ID: Q96E68/
126792.1	126792	B3GALT6	UDP-Gal:betaGal beta 1,3-galactosyltransferase polypeptide 6	Aliases: beta3GalT6/HUGO ID: 17978/UniProt ID: Q96L58/
81579.1	81579	PLA2G12A	phospholipase A2, group XIIA	HUGO ID: 18554/UniProt ID: Q9BZM1/
79178.1	79178	THTPA	thiamine triphosphatase	Aliases: THTPASE/HUGO ID: 18987/UniProt ID: Q9BU02/
83697.1	83697	SLC4A9	solute carrier family 4, sodium bicarbonate cotransporter, member 9	Locus type: gene with protein product, function known or inferred/Aliases: AE4/HUGO ID: 11035/UniProt ID: Q96Q91/
28232.1	28232	SLCO3A1	solute carrier organic anion transporter family, member 3A1	Locus type: gene with protein product, function known or inferred/Aliases: OATP-D, OATP3A1/HUGO ID: 10952/UniProt ID: Q9UIG8/
196883.1	196883	ADCY4	adenylate cyclase 4	HUGO ID: 235/UniProt ID: Q8NFM4/
93010.1	93010	B3GNT7	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7	HUGO ID: 18811/UniProt ID: Q8NFL0/
8647.1	8647	ABCB11	ATP-binding cassette, sub-family B (MDR/TAP), member 11	Aliases: ABC16, SPGP, PFIC-2, PFIC2, PGY4/HUGO ID: 42/UniProt ID: O95342/
54407.1	54407	SLC38A2	solute carrier family 38, member 2	Aliases: SAT2, ATA2, KIAA1382/HUGO ID: 13448/UniProt ID: Q96QD8/
6570.1	6570	SLC18A1	solute carrier family 18 (vesicular monoamine), member 1	Aliases: CGAT/HUGO ID: 10934/UniProt ID: P54219/
2352.1	2352	FOLR3	folate receptor 3 (gamma)	Aliases: FR-G/HUGO ID: 3795/UniProt ID: P41439/

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
64131.1	64131	XYLT1	xylosyltransferase I	Aliases: XT-I/HUGO ID: 15516/UniProt ID: Q86Y38/
64600.1	64600	PLA2G2F	phospholipase A2, group IIF	Locus type: gene with protein product, function known or inferred/HUGO ID: 30040/UniProt ID: Q9BZM2/
8574.1	8574	AKR7A2	aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase)	Aliases: AFAR/HUGO ID: 389/UniProt ID: O43488/
51022.1	51022	GLRX2	glutaredoxin 2	Aliases: GRX2/HUGO ID: 16065/UniProt ID: Q96JC0/
81031.1	81031	SLC2A10	solute carrier family 2 (facilitated glucose transporter), member 10	Aliases: GLUT10/HUGO ID: 13444/UniProt ID: O95528/
51181.1	51181	DCXR	dicarbonyl/L-xylulose reductase	Aliases: KIDCR, DCR/HUGO ID: 18985/MGD ID: MGI:1915130/
55821.1	55821	ALLC	allantoicase	Aliases: ALC/HUGO ID: 17377/UniProt ID: Q8N6M5/MGD ID: MGI:2136971/
9023.1	9023	CH25H	cholesterol 25-hydroxylase	Locus type: gene with protein product, function known or inferred/HUGO ID: 1907/UniProt ID: O95992/
79646.1	79646	PANK3	pantothenate kinase 3	Aliases: FLJ12899/HUGO ID: 19365/UniProt ID: Q9H999/
23315.1	23315	SLC9A8	solute carrier family 9 (sodium/hydrogen exchanger), isoform 8	Locus type: gene with protein product, function known or inferred/Aliases: KIAA0939, NHE8/HUGO ID: 20728/UniProt ID: Q9Y2E8/
9954.1	9954	HS3ST3A2	heparan sulfate (glucosamine) 3-O-sulfotransferase 3A2	Aliases: 3OST3A2/HUGO ID: 5197/
1757.1	1757	SARDH	sarcosine dehydrogenase	Aliases: SDH/HUGO ID: 10536/UniProt ID: Q9UL12/
79837.1	79837	PIP5K2C	phosphatidylinositol-4-phosphate 5-kinase, type II, gamma	Locus type: gene with protein product, function known or inferred/Aliases: FLJ22055/HUGO ID: 23786/UniProt ID: Q8TBX8/
26275.1	26275	HIBCH	3-hydroxyisobutyryl-Coenzyme A hydrolase	HUGO ID: 4908/UniProt ID: Q92931/
9123.1	9123	SLC16A3	solute carrier family 16 (monocarboxylic acid transporters), member 3	Locus type: gene with protein product, function known or inferred/Aliases: MCT3/HUGO ID: 10924/UniProt ID: O15427/
6517.1	6517	SLC2A4	solute carrier family 2 (facilitated glucose transporter), member 4	HUGO ID: 11009/UniProt ID: P14672/
6530.1	6530	SLC6A2	solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2	HUGO ID: 11048/UniProt ID: P23975/
6547.1	6547	SLC8A3	solute carrier family 8 (sodium-calcium exchanger), member 3	Aliases: NCX3/HUGO ID: 11070/UniProt ID: P57103/
53343.1	53343	NUDT9	nudix (nucleoside diphosphate linked moiety X)-type motif 9	Aliases: MGC3037/HUGO ID: 8056/UniProt ID: Q9BW91/
5151.1	5151	PDE8A	phosphodiesterase 8A	Locus type: gene with protein product, function known or inferred/Aliases: HsT19550/HUGO ID: 8793/UniProt ID: O60658/
79369.1	79369	B3GNT4	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 4	Aliases: B3GN-T4, beta3Gn-T4/HUGO ID: 15683/UniProt ID: Q8ND21/
10599.1	10599	SLCO1B1	solute carrier organic anion transporter family, member 1B1	Locus type: gene with protein product, function known or inferred/Aliases: OATP-C, LST-1, OATP1B1/HUGO ID: 10959/UniProt ID: Q9Y6L6/
26266.1	26266	SLC13A4	solute carrier family 13 (sodium/sulfate symporters), member 4	Aliases: SUT-1/HUGO ID: 15827/UniProt ID: Q9UKG4/
166785.1	166785	MMAA	methylmalonic aciduria (cobalamin deficiency) type A	Locus type: gene with protein product, function known or inferred/HUGO ID: 18871/UniProt ID: Q8IVH4/
54187.1	54187	NANS	N-acetylneuraminic acid synthase (sialic acid synthase)	Locus type: gene with protein product, function known or inferred/Aliases: SAS/HUGO ID: 19237/UniProt ID: Q9NR45/
493.1	493	ATP2B4	ATPase, Ca++ transporting, plasma membrane 4	Aliases: PMCA4/HUGO ID: 817/UniProt ID: P23634/
954.1	954	ENTPD2	ectonucleoside triphosphate diphosphohydrolase 2	Aliases: NTPDase-2/HUGO ID: 3364/UniProt ID: Q9Y5L3/
55089.1	55089	SLC38A4	solute carrier family 38, member 4	Aliases: PAAT, NAT3, ATA3/HUGO ID: 14679/UniProt ID: Q969I6/
135152.1	135152	B3GAT2	beta-1,3-glucuronyltransferase 2 (glucuronosyltransferase S)	Locus type: gene with protein product, function known or inferred/Aliases: GlcAT-S/HUGO ID: 922/UniProt ID: Q9NPZ5/
6582.1	6582	SLC22A2	solute carrier family 22 (organic cation transporter), member 2	Aliases: 38262/HUGO ID: 10966/UniProt ID: O15244/
81539.1	81539	SLC38A1	solute carrier family 38, member 1	Aliases: ATA1, NAT2, SAT1/HUGO ID: 13447/UniProt ID: Q9H2Q2/
9951.1	9951	HS3ST4	heparan sulfate (glucosamine) 3-O-sulfotransferase 4	Locus type: gene with protein product, function known or inferred/Aliases: 3OST4/HUGO ID: 5200/UniProt ID: Q8NDC2/
117247.1	117247	SLC16A10	solute carrier family 16 (monocarboxylic acid transporters), member 10	Aliases: TAT1/HUGO ID: 17027/UniProt ID: Q8TF71/
23169.1	23169	SLC35D1	solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1	Locus type: gene with protein product, function known or inferred/Aliases: UGTREL7, KIAA0260/HUGO ID: 20800/UniProt ID: Q9NTN3/
6534.1	6534	SLC6A7	solute carrier family 6 (neurotransmitter transporter, L-proline), member 7	Aliases: PROT/HUGO ID: 11054/UniProt ID: Q99884/
8908.1	8908	GYG2	glycogenin 2	Locus type: gene with protein product, function unknown/Aliases: GN-2/HUGO ID: 4700/UniProt ID: O15488/
6573.1	6573	SLC19A1	solute carrier family 19 (folate transporter), member 1	Aliases: FOLT/HUGO ID: 10937/UniProt ID: P41440/
2713.1	2713	GKP3	glycerol kinase pseudogene 3	Locus type: pseudogene/HUGO ID: 4292/UniProt ID: Q14409/
9942.1	9942	XYLB	xylulokinase homolog (H. influenzae)	Locus type: gene with protein product, function known or inferred/Aliases: FLJ10343, FLJ22075, FLJ12539/HUGO ID: 12839/UniProt ID: O75191/
200010.1	200010	SLC5A9	solute carrier family 5 (sodium/glucose cotransporter), member 9	Locus type: gene with protein product, function known or inferred/Aliases: SGLT4/HUGO ID: 22146/
84679.1	84679	SLC9A7	solute carrier family 9 (sodium/hydrogen exchanger), isoform 7	Aliases: NHE7/HUGO ID: 17123/UniProt ID: Q96T83/
55326.1	55326	AGPAT5	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon)	Locus type: gene with protein product, function known or inferred/Aliases: FLJ11210, LPAAT-e/HUGO ID: 20886/MGD ID: MGI:1196345/

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
125206.1	125206	SLC5A10	solute carrier family 5 (sodium/glucose cotransporter), member 10	Locus type: gene with protein product, function known or inferred/Aliases: SGLT5/HUGO ID: 23155/
130013.1	130013	ACMSD	aminocarboxymuconate semialdehyde decarboxylase	HUGO ID: 19288/UniProt ID: Q8TDX5/
389015.1	389015	SLC9A4	solute carrier family 9 (sodium/hydrogen exchanger), isoform 4	Locus type: gene with protein product, function known or inferred/Aliases: NHE4/HUGO ID: 11077/transcript: NM_001011552
58508.1	58508	MLL3	myeloid/lymphoid or mixed-lineage leukemia 3	Aliases: KIAA1506, HALR/HUGO ID: 13726/UniProt ID: Q8NEZ4/
4507.1	4507	MTAP	methylthioadenosine phosphorylase	Locus type: gene with protein product, function known or inferred/Aliases: MSAP, c86fus/HUGO ID: 7413/UniProt ID: Q13126/
64850.1	64850	AGXT2L1	alanine-glyoxylate aminotransferase 2-like 1	HUGO ID: 14404/UniProt ID: Q8TBG4/
84693.1	84693	MCEE	methylmalonyl CoA epimerase	HUGO ID: 16732/UniProt ID: Q8WW63/
115019.1	115019	SLC26A9	solute carrier family 26, member 9	HUGO ID: 14469/UniProt ID: Q96PK9/
81490.1	81490	PTDSS2	phosphatidylserine synthase 2	Aliases: PSS2/HUGO ID: 15463/UniProt ID: Q9BVG9/
4844.1	4844	NOS2B	nitric oxide synthase 2B	Locus type: gene with protein product, function known or inferred/HUGO ID: 7874/UniProt ID: P81272/
6649.1	6649	SOD3	superoxide dismutase 3, extracellular	HUGO ID: 11181/UniProt ID: P08294/
11046.1	11046	SLC35D2	solute carrier family 35, member D2	Locus type: gene with protein product, function unknown/Aliases: UGTrel8, SQV7L/HUGO ID: 20799/UniProt ID: O95454/
23396.1	23396	PIP5K1C	phosphatidylinositol-4-phosphate 5-kinase, type I, gamma	Aliases: PIP5Kgamma, KIAA0589 gene/HUGO ID: 8996/UniProt ID: O60331/
6508.1	6508	SLC4A3	solute carrier family 4, anion exchanger, member 3	Aliases: AE3, SLC2C/HUGO ID: 11029/UniProt ID: P48751/
347734.1	347734	SLC35B2	solute carrier family 35, member B2	Locus type: gene with protein product, function known or inferred/Aliases: UGTrel4/HUGO ID: 16872/UniProt ID: Q8TB61/
112483.1	112483	SAT2	spermidine/spermine N1-acetyltransferase 2	Locus type: gene with protein product, function known or inferred/Aliases: SSAT2/HUGO ID: 23160/UniProt ID: Q96F10/
256435.1	256435	SIAT7C	sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltransferase) C	Locus type: gene with protein product, function known or inferred/Aliases: ST6GALNAC III/HUGO ID: 19343/UniProt ID: Q8N259/
116255.1	116255	MOGAT1	monoacylglycerol O-acyltransferase 1	Locus type: gene with protein product, function known or inferred/Aliases: DGAT2L, MGAT1/HUGO ID: 18210/UniProt ID: Q96PD6/MGD ID: MGI:1915643/
6521.1	6521	SLC4A1	solute carrier family 4, anion exchanger, member 1 (erythrocyte membrane protein band 3, Diego blood group)	Locus type: gene with protein product, function known or inferred/Aliases: RTA1A, HGNC:12753, CD233/HUGO ID: 11027/UniProt ID: P02730/
6560.1	6560	SLC12A4	solute carrier family 12 (potassium/chloride transporters), member 4	Locus type: gene with protein product, function known or inferred/Aliases: KCC1/HUGO ID: 10913/UniProt ID: Q9UP95/
9415.1	9415	FADS2	fatty acid desaturase 2	Aliases: FADSD6, D6D, TU13, DES6, SLL0262/HUGO ID: 3575/UniProt ID: O95864/
64841.1	64841	GNPNAT1	glucosamine-phosphate N-acetyltransferase 1	Locus type: gene with protein product, function known or inferred/Aliases: Gpnat1, FLJ10607/HUGO ID: 19980/UniProt ID: Q96EK6/
55902.1	55902	ACAS2	acetyl-Coenzyme A synthetase 2 (ADP forming)	Aliases: LOC55902, ACS, dJ1161H23.1/HUGO ID: 15814/UniProt ID: Q9NR19/
2530.2	2530	FUT8	fucosyltransferase 8 (alpha (1,6) fucosyltransferase)	HUGO ID: 4019/UniProt ID: Q9BYC5/
440.3	440	ASNS	asparagine synthetase	Locus type: gene with protein product, function known or inferred/HUGO ID: 753/UniProt ID: P08243/
5332.2	5332	PLCB4	phospholipase C, beta 4	HUGO ID: 9059/UniProt ID: Q15147/
5831.2	5831	PYCR1	pyrroline-5-carboxylate reductase 1	Aliases: P5C/HUGO ID: 9721/UniProt ID: P32322/
5152.15	5152	PDE9A	phosphodiesterase 9A	HUGO ID: 8795/UniProt ID: O76083/
6547.5	6547	SLC8A3	solute carrier family 8 (sodium-calcium exchanger), member 3	Aliases: NCX3/HUGO ID: 11070/UniProt ID: P57103/
1716.3	1716	DGUOK	deoxyguanosine kinase	Aliases: dGK/HUGO ID: 2858/UniProt ID: Q16854/
3098.4	3098	HK1	hexokinase 1	Locus type: gene with protein product, function known or inferred/HUGO ID: 4922/UniProt ID: P19367/
11282.2	11282	MGAT4B	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isoenzyme B	Locus type: gene with protein product, function known or inferred/Aliases: GnT-Ivb/HUGO ID: 7048/UniProt ID: Q9UQ53/
5152.5	5152	PDE9A	phosphodiesterase 9A	HUGO ID: 8795/UniProt ID: O76083/
7296.4	7296	TXNRD1	thioredoxin reductase 1	Locus type: gene with protein product, function known or inferred/Aliases: TXNR/HUGO ID: 12437/UniProt ID: Q16881/
10861.3	10861	SLC26A1	solute carrier family 26 (sulfate transporter), member 1	Locus type: gene with protein product, function known or inferred/Aliases: SAT-1, EDM4/HUGO ID: 10993/UniProt ID: Q9H2B4/
2944.2	2944	GSTM1	glutathione S-transferase M1	Locus type: gene with protein product, function known or inferred/Aliases: MU, H-B, GST1/HUGO ID: 4632/UniProt ID: P09488/
115019.2	115019	SLC26A9	solute carrier family 26, member 9	HUGO ID: 14469/UniProt ID: Q96PK9/
2592.3	2592	GALT	galactose-1-phosphate uridylyltransferase	HUGO ID: 4135/UniProt ID: P07902/
7173.2	7173	TPO	thyroid peroxidase	HUGO ID: 12015/UniProt ID: P07202/
10317.3	10317	B3GALT5	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5	Aliases: beta3Gal-T5/HUGO ID: 920/UniProt ID: Q9Y2C3/
374907.2	374907	B3GALT7	UDP-Gal:betaGal beta 1,3-galactosyltransferase polypeptide 7	Locus type: gene with protein product, function known or inferred/Aliases: BGALT15/HUGO ID: 24139/
204.3	204	AK2	adenylate kinase 2	Locus type: gene with protein product, function known or inferred/HUGO ID: 362/UniProt ID: P54819/
122622.2	122622	ADSSL1	adenylosuccinate synthase like 1	Locus type: gene with protein product, function unknown/Aliases: FLJ38602/HUGO ID: 20093/UniProt ID: Q8N714/
6487.10	6487	SIAT6	sialyltransferase 6 (N-acetyllacosaminide alpha 2,3-sialyltransferase)	Locus type: gene with protein product, function known or inferred/Aliases: ST3Gal III/HUGO ID: 10866/UniProt ID: Q11203/

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
622.3	622	BDH1	3-hydroxybutyrate dehydrogenase (heart, mitochondrial)	HUGO ID: 1027/UniProt ID: Q02338/
6487.2	6487	SIAT6	sialyltransferase 6 (N-acetyllacosaminide alpha 2,3-sialyltransferase)	Locus type: gene with protein product, function known or inferred/Aliases: ST3Gal III/HUGO ID: 10866/UniProt ID: Q11203/
9551.2	9551	ATP5J2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2	Aliases: F1Fo-ATPase/HUGO ID: 848/UniProt ID: P56134/
7001.2	7001	PRDX2	peroxiredoxin 2	Aliases: PRP, NKEFB/HUGO ID: 9353/UniProt ID: P32119/
4952.2	4952	OCRL	oculocerebrorenal syndrome of Lowe	HUGO ID: 8108/UniProt ID: Q01968/
84720.2	84720	PIGO	phosphatidylinositol glycan, class O	Locus type: gene with protein product, function known or inferred/Aliases: DKFZp434M222, FLJ00135/HUGO ID: 23215/UniProt ID: Q8TEQ8/
80142.3	80142	PTGES2	prostaglandin E synthase 2	Aliases: FLJ14038/HUGO ID: 17822/UniProt ID: Q9H7Z7/
10423.2	10423	CDIPT	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)	Locus type: gene with protein product, function known or inferred/Aliases: PIS1, PIS/HUGO ID: 1769/UniProt ID: O14735/
5224.2	5224	PGAM2	phosphoglycerate mutase 2 (muscle)	HUGO ID: 8889/UniProt ID: P15259/
3948.2	3948	LDHC	lactate dehydrogenase C	HUGO ID: 6544/UniProt ID: P07864/
6547.4	6547	SLC8A3	solute carrier family 8 (sodium-calcium exchanger), member 3	Aliases: NCX3/HUGO ID: 11070/UniProt ID: P57103/
5211.2	5211	PFKL	phosphofructokinase, liver	HUGO ID: 8876/UniProt ID: P17858/
5250.2	5250	SLC25A3	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3	Locus type: gene with protein product, function known or inferred/HUGO ID: 10989/UniProt ID: Q00325/
226.2	226	ALDOA	aldolase A, fructose-bisphosphate	HUGO ID: 414/UniProt ID: P04075/
5152.16	5152	PDE9A	phosphodiesterase 9A	HUGO ID: 8795/UniProt ID: O76083/
2027.2	2027	ENO3	enolase 3 (beta, muscle)	HUGO ID: 3354/UniProt ID: P13929/
8659.2	8659	ALDH4A1	aldehyde dehydrogenase 4 family, member A1	Aliases: P5CDh/HUGO ID: 406/UniProt ID: P30038/
53343.2	53343	NUDT9	nudix (nucleoside diphosphate linked moiety X)-type motif 9	Aliases: MGC3037/HUGO ID: 8056/UniProt ID: Q9BW91/
58508.2	58508	MLL3	myeloid/lymphoid or mixed-lineage leukemia 3	Aliases: KIAA1506, HALR/HUGO ID: 13726/UniProt ID: Q8NEZ4/
127124.2	127124	ATP6V1G3	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G isoform 3	Locus type: gene with protein product, function known or inferred/Aliases: ATP6G3, Vma10/HUGO ID: 18265/UniProt ID: Q96LB4/MGD ID: MGI:2450548/
669.2	669	BPGM	2,3-bisphosphoglycerate mutase	Locus type: gene with protein product, function known or inferred/HUGO ID: 1093/UniProt ID: P07738/
1716.4	1716	DGUOK	deoxyguanosine kinase	Aliases: dGK/HUGO ID: 2858/UniProt ID: Q16854/
2629.5	2629	GBA	glucosidase, beta; acid (includes glucosylceramidase)	Aliases: GLUC, GBA1/HUGO ID: 4177/UniProt ID: P04062/
47.2	47	ACLY	ATP citrate lyase	HUGO ID: 115/UniProt ID: P53396/
51703.3	51703	ACSL5	acyl-CoA synthetase long-chain family member 5	Locus type: gene with protein product, function known or inferred/Aliases: ACS5, ACS2/HUGO ID: 16526/UniProt ID: Q9ULC5/MGD ID: MGI:1919129/
3098.3	3098	HK1	hexokinase 1	Locus type: gene with protein product, function known or inferred/HUGO ID: 4922/UniProt ID: P19367/
1491.2	1491	CTH	cystathionase (cystathionine gamma-lyase)	Locus type: gene with protein product, function known or inferred/HUGO ID: 2501/UniProt ID: P32929/
5313.2	5313	PKLR	pyruvate kinase, liver and RBC	Locus type: gene with protein product, function known or inferred/HUGO ID: 9020/UniProt ID: P30613/
5152.2	5152	PDE9A	phosphodiesterase 9A	HUGO ID: 8795/UniProt ID: O76083/
132.2	132	ADK	adenosine kinase	Locus type: gene with protein product, function known or inferred/Aliases: AK/HUGO ID: 257/UniProt ID: P55263/
93034.2	93034	NT5C1B	5'-nucleotidase, cytosolic IB	Aliases: AIRP, CN-IB/HUGO ID: 17818/UniProt ID: Q96P26/
7173.5	7173	TPO	thyroid peroxidase	HUGO ID: 12015/UniProt ID: P07202/
4882.2	4882	NPR2	natriuretic peptide receptor B/guanylate cyclase B (atrionatriuretic peptide receptor B)	Aliases: GUC2B/HUGO ID: 7944/UniProt ID: P20594/
8398.2	8398	PLA2G6	phospholipase A2, group VI (cytosolic, calcium-independent)	Aliases: iPLA2/HUGO ID: 9039/UniProt ID: O60733/
7054.3	7054	TH	tyrosine hydroxylase	HUGO ID: 11782/UniProt ID: P07101/
2592.2	2592	GALT	galactose-1-phosphate uridylyltransferase	HUGO ID: 4135/UniProt ID: P07902/
518.3	518	ATP5G3	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3	HUGO ID: 843/UniProt ID: P48201/Variant 3: This variant (3) differs in the 5' UTR, compared to variant 1. Transcript variants 1, 2 and 3 encode the same protein.
8525.2	8525	DGKZ	diacylglycerol kinase, zeta 104kDa	Aliases: DAGK5, hDGKzeta/HUGO ID: 2857/UniProt ID: Q13574/
56606.2	56606	SLC2A9	solute carrier family 2 (facilitated glucose transporter), member 9	Aliases: Glut9, GLUTX/HUGO ID: 13446/UniProt ID: Q9NRM0/
8527.2	8527	DGKD	diacylglycerol kinase, delta 130kDa	Aliases: KIAA0145, DGKdelta/HUGO ID: 2851/UniProt ID: Q16760/
6487.11	6487	SIAT6	sialyltransferase 6 (N-acetyllacosaminide alpha 2,3-sialyltransferase)	Locus type: gene with protein product, function known or inferred/Aliases: ST3Gal III/HUGO ID: 10866/UniProt ID: Q11203/
5277.2	5277	PIGA	phosphatidylinositol glycan, class A (paroxysmal nocturnal hemoglobinuria)	Aliases: GPI3/HUGO ID: 8957/UniProt ID: P37287/
6480.2	6480	SIAT1	sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase)	Aliases: CD75, ST6Gal I/HUGO ID: 10860/UniProt ID: P15907/
204.2	204	AK2	adenylate kinase 2	Locus type: gene with protein product, function known or inferred/HUGO ID: 362/UniProt ID: P54819/
51227.2	51227	DSCR5	Down syndrome critical region gene 5	Aliases: DCRC, DSRC/HUGO ID: 3046/UniProt ID: P57054/
5151.2	5151	PDE8A	phosphodiesterase 8A	Locus type: gene with protein product, function known or inferred/Aliases: HsT19550/HUGO ID: 8793/UniProt ID: O60658/
3614.2	3614	IMPDH1	IMP (inosine monophosphate) dehydrogenase 1	Aliases: sWSS2608/HUGO ID: 6052/UniProt ID: P20839/

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
7001.3	7001	PRDX2	peroxiredoxin 2	Aliases: PRP, NKEFB/HUGO ID: 9353/UniProt ID: P32119/
276.2	276	AMY1A	amylase, alpha 1A; salivary	HUGO ID: 474/UniProt ID: P04745/
5152.17	5152	PDE9A	phosphodiesterase 9A	HUGO ID: 8795/UniProt ID: O76083/
5052.3	5052	PRDX1	peroxiredoxin 1	Locus type: gene with protein product, function known or inferred/Aliases: NKEFA/HUGO ID: 9352/UniProt ID: Q06830/
6487.9	6487	SIAT6	sialyltransferase 6 (N-acetyllacosaminide alpha 2,3-sialyltransferase)	Locus type: gene with protein product, function known or inferred/Aliases: ST3Gal III/HUGO ID: 10866/UniProt ID: Q11203/
80142.2	80142	PTGES2	prostaglandin E synthase 2	Aliases: FLJ14038/HUGO ID: 17822/UniProt ID: Q9H7Z7/
2678.3	2678	GGT1	gamma-glutamyltransferase 1	Aliases: D22S672, D22S732, CD224/HUGO ID: 4250/UniProt ID: P19440/
9551.3	9551	ATP5J2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2	Aliases: F1Fo-ATPase/HUGO ID: 848/UniProt ID: P56134/
53343.3	53343	NUDT9	nudix (nucleoside diphosphate linked moiety X)-type motif 9	Aliases: MGC3037/HUGO ID: 8056/UniProt ID: Q9BW91/
8706.4	8706	B3GALT3	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 3	Locus type: gene with protein product, function known or inferred/Aliases: beta3Gal-T3, galT3, P1/HUGO ID: 918/UniProt ID: O75752/
515.2	515	ATP5F1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1	HUGO ID: 840/UniProt ID: P24539/
226.3	226	ALDOA	aldolase A, fructose-bisphosphate	HUGO ID: 414/UniProt ID: P04075/
5140.2	5140	PDE3B	phosphodiesterase 3B, cGMP-inhibited	HUGO ID: 8779/UniProt ID: Q13370/
1716.5	1716	DGUOK	deoxyguanosine kinase	Aliases: dGK/HUGO ID: 2858/UniProt ID: Q16854/
43.2	43	ACHE	acetylcholinesterase (YT blood group)	Locus type: gene with protein product, function known or inferred/HUGO ID: 108/UniProt ID: P22303/
8818.2	8818	DPM2	dolichyl-phosphate mannosyltransferase polypeptide 2, regulatory subunit	Locus type: gene with protein product, function known or inferred/HUGO ID: 3006/UniProt ID: O94777/
2530.4	2530	FUT8	fucosyltransferase 8 (alpha (1,6) fucosyltransferase)	HUGO ID: 4019/UniProt ID: Q9BYC5/
5092.2	5092	PCBD	6-pyruvoyl-tetrahydropterin synthase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1)	Locus type: gene with protein product, function known or inferred/Aliases: PCD/HUGO ID: 8646/UniProt ID: P80095/
5315.2	5315	PKM2	pyruvate kinase, muscle	Aliases: THBP1, OIP3/HUGO ID: 9021/UniProt ID: P14618/
53354.2	53354	PANK1	pantothenate kinase 1	Locus type: gene with protein product, function known or inferred/Aliases: MGC24596, PANK1a, PANK1b/HUGO ID: 8598/UniProt ID: Q8TE04/
3420.2	3420	IDH3B	isocitrate dehydrogenase 3 (NAD+) beta	HUGO ID: 5385/UniProt ID: O43837/
1558.2	1558	CYP2C8	cytochrome P450, family 2, subfamily C, polypeptide 8	Locus type: gene with protein product, function known or inferred/Aliases: CPC8/HUGO ID: 2622/UniProt ID: P10632/
51703.2	51703	ACSL5	acyl-CoA synthetase long-chain family member 5	Locus type: gene with protein product, function known or inferred/Aliases: ACS5, ACS2/HUGO ID: 16526/UniProt ID: Q9ULC5/MGD ID: MGI:1919129/
4731.2	4731	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa	HUGO ID: 7719/UniProt ID: P56181/
284273.2	284273	ZADH2	zinc binding alcohol dehydrogenase, domain containing 2	Locus type: gene with protein product, function unknown/Aliases: MGC45594/HUGO ID: 28697/MGD ID: MGI:2444835/
498.3	498	ATP5A1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle	Locus type: gene with protein product, function known or inferred/Aliases: ATP5A, hATP1, ATPM, OMR, ORM, HGNC:826/HUGO ID: 823/UniProt ID: P25705/
51.2	51	ACOX1	acyl-Coenzyme A oxidase 1, palmitoyl	Aliases: PALMCOX/HUGO ID: 119/UniProt ID: Q15067/
84264.2	84264	HAGHL	hydroxyacylglutathione hydrolase-like	Locus type: gene with protein product, function known or inferred/Aliases: MGC2605/HUGO ID: 14177/UniProt ID: Q9BT45/
29922.2	29922	NME7	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase)	Locus type: gene with protein product, function known or inferred/HUGO ID: 20461/UniProt ID: Q9Y5B8/MGD ID: MGI:2449121/
3704.2	3704	ITPA	inosine triphosphatase (nucleoside triphosphate pyrophosphatase)	Aliases: HGNC:15883, HLC14-06-P, dJ794I6.3/HUGO ID: 6176/UniProt ID: Q9BY32/
7173.4	7173	TPO	thyroid peroxidase	HUGO ID: 12015/UniProt ID: P07202/
178.6	178	AGL	amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycoge debranching enzyme, glycogen storage disease type III)	Locus type: gene with protein product, function known or inferred/HUGO ID: 321/UniProt ID: P35573/MGD ID: MGI:1924809/
518.2	518	ATP5G3	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3	HUGO ID: 843/UniProt ID: P48201/Variant 2: This variant differs in the 5' UTR, compared to variant 1. Transcript variants 1, 2 and 3 encode the same protein.
51004.2	51004	COQ6	coenzyme Q6 homolog (yeast)	Locus type: gene with protein product, function unknown/Aliases: CGI-10/HUGO ID: 20233/UniProt ID: Q9Y2Z9/
7054.2	7054	TH	tyrosine hydroxylase	HUGO ID: 11782/UniProt ID: P07101/
51227.3	51227	DSCR5	Down syndrome critical region gene 5	Aliases: DCRC, DSRC/HUGO ID: 3046/UniProt ID: P57054/
52.2	52	ACP1	acid phosphatase 1, soluble	HUGO ID: 122/UniProt ID: P24666/
10195.4	10195	ALG3	asparagine-linked glycosylation 3 homolog (yeast, alpha-1,3-mannosyltransferase)	Locus type: gene with protein product, function known or inferred/Aliases: NOT56L, Not56, CDGS4, D16Ertd36e/HUGO ID: 23056/UniProt ID: Q92685/MGD ID: MGI:1098592/
5152.18	5152	PDE9A	phosphodiesterase 9A	HUGO ID: 8795/UniProt ID: O76083/
6120.2	6120	RPE	ribulose-5-phosphate-3-epimerase	HUGO ID: 10293/UniProt ID: Q96AT9/
528.2	528	ATP6V1C1	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C, isoform 1	Aliases: ATP6D, VATC, Vma5/HUGO ID: 856/UniProt ID: P21283/
517.2	517	ATP5G2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2	HUGO ID: 842/UniProt ID: Q06055/Variant 2: This variant differs in the 5' UTR and the 5' coding region, and uses a downstream start codon, compared to variant 1. The resulting isoform (2b) has a shorter N-terminus when compared to isoform 2a.
5152.6	5152	PDE9A	phosphodiesterase 9A	HUGO ID: 8795/UniProt ID: O76083/

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
10768.2	10768	AHCYL1	S-adenosylhomocysteine hydrolase-like 1	Aliases: XPVKONA/HUGO ID: 344/UniProt ID: O43865/
90161.2	90161	HS6ST2	heparan sulfate 6-O-sulfotransferase 2	Locus type: gene with protein product, function known or inferred/HUGO ID: 19133/UniProt ID: Q96MM7/
6547.3	6547	SLC8A3	solute carrier family 8 (sodium-calcium exchanger), member 3	Aliases: NCX3/HUGO ID: 11070/UniProt ID: P57103/
51447.3	51447	IHPK2	inositol hexaphosphate kinase 2	Aliases: IP6K2/HUGO ID: 17313/UniProt ID: Q9H4P7/
6487.4	6487	SIAT6	sialyltransferase 6 (N-acetyllacosaminide alpha 2,3-sialyltransferase)	Locus type: gene with protein product, function known or inferred/Aliases: ST3Gal III/HUGO ID: 10866/UniProt ID: Q11203/
515.3	515	ATP5F1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1	HUGO ID: 840/UniProt ID: P24539/
3098.5	3098	HK1	hexokinase 1	Locus type: gene with protein product, function known or inferred/HUGO ID: 4922/UniProt ID: P19367/
3157.2	3157	HMGCS1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	HUGO ID: 5007/UniProt ID: Q01581/
2948.2	2948	GSTM4	glutathione S-transferase M4	Locus type: gene with protein product, function known or inferred/HUGO ID: 4636/UniProt ID: Q03013/
55821.2	55821	ALLC	allantoicase	Aliases: ALC/HUGO ID: 17377/UniProt ID: Q8N6M5/MGD ID: MGI:2136971/
2530.3	2530	FUT8	fucosyltransferase 8 (alpha (1,6) fucosyltransferase)	HUGO ID: 4019/UniProt ID: Q9BYC5/
5052.2	5052	PRDX1	peroxiredoxin 1	Locus type: gene with protein product, function known or inferred/Aliases: NKEFA/HUGO ID: 9352/UniProt ID: Q06830/
498.2	498	ATP5A1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle	Locus type: gene with protein product, function known or inferred/Aliases: ATP5A, hATP1, ATPM, OMR, ORM, HGNC:826/HUGO ID: 823/UniProt ID: P25705/
5315.3	5315	PKM2	pyruvate kinase, muscle	Aliases: THBP1, OIP3/HUGO ID: 9021/UniProt ID: P14618/
2629.3	2629	GBA	glucosidase, beta; acid (includes glucosylceramidase)	Aliases: GLUC, GBA1/HUGO ID: 4177/UniProt ID: P04062/
5152.10	5152	PDE9A	phosphodiesterase 9A	HUGO ID: 8795/UniProt ID: O76083/
4257.4	4257	MGST1	microsomal glutathione S-transferase 1	Aliases: MGST-I/HUGO ID: 7061/UniProt ID: P10620/
2348.3	2348	FOLR1	folate receptor 1 (adult)	HUGO ID: 3791/UniProt ID: P15328/
53354.3	53354	PANK1	pantothenate kinase 1	Locus type: gene with protein product, function known or inferred/Aliases: MGC24596, PANK1a, PANK1b/HUGO ID: 8598/UniProt ID: Q8TE04/
2582.2	2582	GALE	UDP-galactose-4-epimerase	Locus type: gene with protein product, function known or inferred/HUGO ID: 4116/UniProt ID: Q14376/
5244.3	5244	ABCB4	ATP-binding cassette, sub-family B (MDR/TAP), member 4	Locus type: gene with protein product, function known or inferred/Aliases: MDR2/3, PFIC-3/HUGO ID: 45/UniProt ID: P21439/
5152.4	5152	PDE9A	phosphodiesterase 9A	HUGO ID: 8795/UniProt ID: O76083/
6547.2	6547	SLC8A3	solute carrier family 8 (sodium-calcium exchanger), member 3	Aliases: NCX3/HUGO ID: 11070/UniProt ID: P57103/
10317.2	10317	B3GALT5	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5	Aliases: beta3Gal-T5/HUGO ID: 920/UniProt ID: Q9Y2C3/
171425.2	171425	CLYBL	citrate lyase beta like	Locus type: gene with protein product, function known or inferred/Aliases: CLB/HUGO ID: 18355/UniProt ID: Q8N0X4/MGD ID: MGI:1916884/
622.2	622	BDH1	3-hydroxybutyrate dehydrogenase (heart, mitochondrial)	HUGO ID: 1027/UniProt ID: Q02338/
5152.7	5152	PDE9A	phosphodiesterase 9A	HUGO ID: 8795/UniProt ID: O76083/
51179.2	51179	HAO2	hydroxyacid oxidase 2 (long chain)	Aliases: HAOX2/HUGO ID: 4810/UniProt ID: Q9NYQ3/
10195.3	10195	ALG3	asparagine-linked glycosylation 3 homolog (yeast, alpha-1,3-mannosyltransferase)	Locus type: gene with protein product, function known or inferred/Aliases: NOT56L, Not56, CDGS4, D16Ertd36e/HUGO ID: 23056/UniProt ID: Q92685/MGD ID: MGI:1098592/
10400.2	10400	PEMT	phosphatidylethanolamine N-methyltransferase	Aliases: PEMPT, PEMT2/HUGO ID: 8830/UniProt ID: Q9UBM1/
178.5	178	AGL	amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycoge debranching enzyme, glycogen storage disease type III)	Locus type: gene with protein product, function known or inferred/HUGO ID: 321/UniProt ID: P35573/MGD ID: MGI:1924809/
55350.2	55350	VNN3	vanin 3	Locus type: gene with protein product, function known or inferred/Aliases: HSA238982/HUGO ID: 16431/UniProt ID: Q9NY84/
10476.2	10476	ATP5H	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d	Locus type: gene with protein product, function known or inferred/Aliases: ATPQ, ATP5JD/HUGO ID: 845/UniProt ID: O75947/MGD ID: MGI:1918929/
26275.2	26275	HIBCH	3-hydroxyisobutyryl-Coenzyme A hydrolase	HUGO ID: 4908/UniProt ID: Q92931/
53905.2	53905	DUOX1	dual oxidase 1	Aliases: NOXEF1, THOX1/HUGO ID: 3062/UniProt ID: Q9NRD9/
5152.19	5152	PDE9A	phosphodiesterase 9A	HUGO ID: 8795/UniProt ID: O76083/
6487.3	6487	SIAT6	sialyltransferase 6 (N-acetyllacosaminide alpha 2,3-sialyltransferase)	Locus type: gene with protein product, function known or inferred/Aliases: ST3Gal III/HUGO ID: 10866/UniProt ID: Q11203/
51447.2	51447	IHPK2	inositol hexaphosphate kinase 2	Aliases: IP6K2/HUGO ID: 17313/UniProt ID: Q9H4P7/
2629.4	2629	GBA	glucosidase, beta; acid (includes glucosylceramidase)	Aliases: GLUC, GBA1/HUGO ID: 4177/UniProt ID: P04062/
6487.6	6487	SIAT6	sialyltransferase 6 (N-acetyllacosaminide alpha 2,3-sialyltransferase)	Locus type: gene with protein product, function known or inferred/Aliases: ST3Gal III/HUGO ID: 10866/UniProt ID: Q11203/
197257.2	197257	LDHD	lactate dehydrogenase D	Locus type: gene with protein product, function known or inferred/HUGO ID: 19708/UniProt ID: Q8IZK5/
6508.2	6508	SLC4A3	solute carrier family 4, anion exchanger, member 3	Aliases: AE3, SLC2C/HUGO ID: 11029/UniProt ID: P48751/
178.4	178	AGL	amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycoge debranching enzyme, glycogen storage disease type III)	Locus type: gene with protein product, function known or inferred/HUGO ID: 321/UniProt ID: P35573/MGD ID: MGI:1924809/

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
8706.2	8706	B3GALT3	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 3	Locus type: gene with protein product, function known or inferred/Aliases: beta3Gal-T3, galT3, P1/HUGO ID: 918/UniProt ID: O75752/
51447.5	51447	IHPK2	inositol hexaphosphate kinase 2	Aliases: IP6K2/HUGO ID: 17313/UniProt ID: Q9H4P7/
55568.2	55568	GALNT10	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (GalNAc-T10)	Locus type: gene with protein product, function known or inferred/Aliases: DKFZp586H0623/HUGO ID: 19873/UniProt ID: Q86SR1/
4843.2	4843	NOS2A	nitric oxide synthase 2A (inducible, hepatocytes)	Locus type: gene with protein product, function known or inferred/Aliases: INOS, NOS, HEP-NOS/HUGO ID: 7873/UniProt ID: P35228/
2710.2	2710	GK	glycerol kinase	Locus type: gene with protein product, function known or inferred/HUGO ID: 4289/UniProt ID: P32189/
2348.2	2348	FOLR1	folate receptor 1 (adult)	HUGO ID: 3791/UniProt ID: P15328/
10195.2	10195	ALG3	asparagine-linked glycosylation 3 homolog (yeast, alpha-1,3-mannosyltransferase)	Locus type: gene with protein product, function known or inferred/Aliases: NOT56L, Not56, CDGS4, D16Ertd36e/HUGO ID: 23056/UniProt ID: Q92685/MGD ID: MGI:1098592/
54344.2	54344	DPM3	dolichyl-phosphate mannosyltransferase polypeptide 3	Locus type: gene with protein product, function known or inferred/HUGO ID: 3007/UniProt ID: Q9P2X0/
51292.3	51292	GMPR2	guanosine monophosphate reductase 2	Locus type: gene with protein product, function known or inferred/HUGO ID: 4377/UniProt ID: Q9P2T1/
26289.2	26289	AK5	adenylate kinase 5	HUGO ID: 365/UniProt ID: Q9Y6K8/
1103.4	1103	CHAT	choline acetyltransferase	Locus type: gene with protein product, function known or inferred/HUGO ID: 1912/UniProt ID: P28329/
210.2	210	ALAD	aminolevulinate, delta-, dehydratase	HUGO ID: 395/UniProt ID: P13716/
5295.2	5295	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	Locus type: gene with protein product, function known or inferred/Aliases: GRB1, p85-ALPHA/HUGO ID: 8979/UniProt ID: P27986/
5152.11	5152	PDE9A	phosphodiesterase 9A	HUGO ID: 8795/UniProt ID: O76083/
2948.3	2948	GSTM4	glutathione S-transferase M4	Locus type: gene with protein product, function known or inferred/HUGO ID: 4636/UniProt ID: Q03013/
5151.3	5151	PDE8A	phosphodiesterase 8A	Locus type: gene with protein product, function known or inferred/Aliases: HsT19550/HUGO ID: 8793/UniProt ID: O60658/
7296.2	7296	TXNRD1	thioredoxin reductase 1	Locus type: gene with protein product, function known or inferred/Aliases: TXNR/HUGO ID: 12437/UniProt ID: Q16881/
4257.3	4257	MGST1	microsomal glutathione S-transferase 1	Aliases: MGST-I/HUGO ID: 7061/UniProt ID: P10620/
205.3	205	AK3	adenylate kinase 3	Locus type: gene with protein product, function known or inferred/HUGO ID: 363/UniProt ID: P27144/
1312.2	1312	COMT	catechol-O-methyltransferase	HUGO ID: 2228/UniProt ID: P21964/
31.2	31	ACACA	acetyl-Coenzyme A carboxylase alpha	Aliases: ACC1/HUGO ID: 84/UniProt ID: Q13085/
11343.2	11343	MGLL	monoglyceride lipase	Locus type: gene with protein product, function known or inferred/Aliases: HU K5, MGL/HUGO ID: 17038/UniProt ID: Q99685/
2876.2	2876	GPX1	glutathione peroxidase 1	HUGO ID: 4553/UniProt ID: P07203/
51022.2	51022	GLRX2	glutaredoxin 2	Aliases: GRX2/HUGO ID: 16065/UniProt ID: Q96JC0/
3290.2	3290	HSD11B1	hydroxysteroid (11-beta) dehydrogenase 1	Locus type: gene with protein product, function known or inferred/HUGO ID: 5208/UniProt ID: P28845/
5250.3	5250	SLC25A3	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3	Locus type: gene with protein product, function known or inferred/HUGO ID: 10989/UniProt ID: Q00325/
1375.2	1375	CPT1B	carnitine palmitoyltransferase 1B (muscle)	Aliases: M-CPT1, CPT1-M/HUGO ID: 2329/UniProt ID: Q92523/
9016.2	9016	SLC25A14	solute carrier family 25 (mitochondrial carrier, brain), member 14	Locus type: gene with protein product, function known or inferred/Aliases: BMCP1, UCP5/HUGO ID: 10984/UniProt ID: O95258/
18.2	18	ABAT	4-aminobutyrate aminotransferase	Aliases: GABAT/HUGO ID: 23/UniProt ID: P80404/
79053.2	79053	ALG8	asparagine-linked glycosylation 8 homolog (yeast, alpha-1,3-glucosyltransferase)	Locus type: gene with protein product, function known or inferred/Aliases: MGC2840/HUGO ID: 23161/UniProt ID: Q9BVK2/
1431.2	1431	CS	citrate synthase	HUGO ID: 2422/UniProt ID: O75390/
10919.2	10919	BAT8	HLA-B associated transcript 8	Locus type: gene with protein product, function unknown/Aliases: G9A, Em:AF134726.3, HGNC:13942/HUGO ID: 14129/UniProt ID: Q96KQ7/
376497.2	376497	SLC27A1	solute carrier family 27 (fatty acid transporter), member 1	Locus type: gene with protein product, function known or inferred/Aliases: FATP1, FATP, MGC71751, FLJ00336/HUGO ID: 10995/UniProt ID: Q96DY3/MGD ID: MGI:1347098/
6582.2	6582	SLC22A2	solute carrier family 22 (organic cation transporter), member 2	Aliases: 38262/HUGO ID: 10966/UniProt ID: O15244/
6470.2	6470	SHMT1	serine hydroxymethyltransferase 1 (soluble)	HUGO ID: 10850/UniProt ID: P34896/
2182.2	2182	ACSL4	acyl-CoA synthetase long-chain family member 4	Locus type: gene with protein product, function known or inferred/Aliases: ACS4, MRX63, LACS4/HUGO ID: 3571/UniProt ID: O60488/MGD ID: MGI:1354713/
2530.5	2530	FUT8	fucosyltransferase 8 (alpha (1,6) fucosyltransferase)	HUGO ID: 4019/UniProt ID: Q9BYC5/
51292.2	51292	GMPR2	guanosine monophosphate reductase 2	Locus type: gene with protein product, function known or inferred/HUGO ID: 4377/UniProt ID: Q9P2T1/
178.3	178	AGL	amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycoge debranching enzyme, glycogen storage disease type III)	Locus type: gene with protein product, function known or inferred/HUGO ID: 321/UniProt ID: P35573/MGD ID: MGI:1924809/
10400.3	10400	PEMT	phosphatidylethanolamine N-methyltransferase	Aliases: PEMPT, PEMT2/HUGO ID: 8830/UniProt ID: Q9UBM1/
5152.12	5152	PDE9A	phosphodiesterase 9A	HUGO ID: 8795/UniProt ID: O76083/
4257.2	4257	MGST1	microsomal glutathione S-transferase 1	Aliases: MGST-I/HUGO ID: 7061/UniProt ID: P10620/
5244.2	5244	ABCB4	ATP-binding cassette, sub-family B (MDR/TAP), member 4	Locus type: gene with protein product, function known or inferred/Aliases: MDR2/3, PFIC-3/HUGO ID: 45/UniProt ID: P21439/

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
211.2	211	ALAS1	aminolevulinate, delta-, synthase 1	HUGO ID: 396/UniProt ID: P13196/
2348.5	2348	FOLR1	folate receptor 1 (adult)	HUGO ID: 3791/UniProt ID: P15328/
5295.3	5295	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	Locus type: gene with protein product, function known or inferred/Aliases: GRB1, p85-ALPHA/HUGO ID: 8979/UniProt ID: P27986/
8528.2	8528	DDO	D-aspartate oxidase	Locus type: gene with protein product, function known or inferred/HUGO ID: 2727/UniProt ID: Q99489/
7296.3	7296	TXNRD1	thioredoxin reductase 1	Locus type: gene with protein product, function known or inferred/Aliases: TXNR/HUGO ID: 12437/UniProt ID: Q16881/
31.3	31	ACACA	acetyl-Coenzyme A carboxylase alpha	Aliases: ACC1/HUGO ID: 84/UniProt ID: Q13085/
6487.5	6487	SIAT6	sialyltransferase 6 (N-acetyllacosaminide alpha 2,3-sialyltransferase)	Locus type: gene with protein product, function known or inferred/Aliases: ST3Gal III/HUGO ID: 10866/UniProt ID: Q11203/
3098.2	3098	HK1	hexokinase 1	Locus type: gene with protein product, function known or inferred/HUGO ID: 4922/UniProt ID: P19367/
56474.2	56474	CTPS2	CTP synthase II	Locus type: gene with protein product, function known or inferred/HUGO ID: 2520/UniProt ID: Q9H809/
5152.20	5152	PDE9A	phosphodiesterase 9A	HUGO ID: 8795/UniProt ID: O76083/
5281.2	5281	PIGF	phosphatidylinositol glycan, class F	HUGO ID: 8962/UniProt ID: Q07326/
52.3	52	ACP1	acid phosphatase 1, soluble	HUGO ID: 122/UniProt ID: P24666/
1375.3	1375	CPT1B	carnitine palmitoyltransferase 1B (muscle)	Aliases: M-CPT1, CPT1-M/HUGO ID: 2329/UniProt ID: Q92523/
123041.2	123041	SLC24A4	solute carrier family 24 (sodium/potassium/calcium exchanger), member 4	Locus type: gene with protein product, function known or inferred/Aliases: NCKX4/HUGO ID: 10978/UniProt ID: Q8NFF2/
51447.4	51447	IHPK2	inositol hexaphosphate kinase 2	Aliases: IP6K2/HUGO ID: 17313/UniProt ID: Q9H4P7/
5151.5	5151	PDE8A	phosphodiesterase 8A	Locus type: gene with protein product, function known or inferred/Aliases: HsT19550/HUGO ID: 8793/UniProt ID: O60658/
2585.2	2585	GALK2	galactokinase 2	Aliases: GK2/HUGO ID: 4119/UniProt ID: Q01415/
9154.2	9154	SLC28A1	solute carrier family 28 (sodium-coupled nucleoside transporter), member 1	Aliases: CNT1/HUGO ID: 11001/UniProt ID: O00337/
80142.4	80142	PTGES2	prostaglandin E synthase 2	Aliases: FLJ14038/HUGO ID: 17822/UniProt ID: Q9H7Z7/
5152.13	5152	PDE9A	phosphodiesterase 9A	HUGO ID: 8795/UniProt ID: O76083/
160851.2	160851	DGKH	diacylglycerol kinase, eta	Locus type: gene with protein product, function known or inferred/Aliases: DGKeta/HUGO ID: 2854/UniProt ID: Q9BX34/
6487.8	6487	SIAT6	sialyltransferase 6 (N-acetyllacosaminide alpha 2,3-sialyltransferase)	Locus type: gene with protein product, function known or inferred/Aliases: ST3Gal III/HUGO ID: 10866/UniProt ID: Q11203/
411.2	411	ARSB	arylsulfatase B	HUGO ID: 714/UniProt ID: P15848/
3421.2	3421	IDH3G	isocitrate dehydrogenase 3 (NAD+) gamma	HUGO ID: 5386/UniProt ID: P51553/
56894.2	56894	AGPAT3	1-acylglycerol-3-phosphate O-acyltransferase 3	Aliases: LPAAT-gamma/HUGO ID: 326/UniProt ID: Q9NRZ7/
123041.3	123041	SLC24A4	solute carrier family 24 (sodium/potassium/calcium exchanger), member 4	Locus type: gene with protein product, function known or inferred/Aliases: NCKX4/HUGO ID: 10978/UniProt ID: Q8NFF2/
178.2	178	AGL	amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycoge debranching enzyme, glycogen storage disease type III)	Locus type: gene with protein product, function known or inferred/HUGO ID: 321/UniProt ID: P35573/MGD ID: MGI:1924809/
5152.3	5152	PDE9A	phosphodiesterase 9A	HUGO ID: 8795/UniProt ID: O76083/
1607.2	1607	DGKB	diacylglycerol kinase, beta 90kDa	Locus type: gene with protein product, function known or inferred/Aliases: KIAA0718, DGK, DGK-BETA/HUGO ID: 2850/UniProt ID: Q9Y6T7/
8611.2	8611	PPAP2A	phosphatidic acid phosphatase type 2A	Aliases: PAP-2a/HUGO ID: 9228/UniProt ID: O60463/
516.2	516	ATP5G1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1	HUGO ID: 841/UniProt ID: P05496/Variant 2: This variant differs in the 5' UTR, compared to variant 1. Variants 1 and 2 encode the same protein.
513.2	513	ATP5D	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	HUGO ID: 837/UniProt ID: P30049/
55902.2	55902	ACAS2	acetyl-Coenzyme A synthetase 2 (ADP forming)	Aliases: LOC55902, ACS, dJ1161H23.1/HUGO ID: 15814/UniProt ID: Q9NR19/
2348.4	2348	FOLR1	folate receptor 1 (adult)	HUGO ID: 3791/UniProt ID: P15328/
2629.2	2629	GBA	glucosidase, beta; acid (includes glucosylceramidase)	Aliases: GLUC, GBA1/HUGO ID: 4177/UniProt ID: P04062/
1588.2	1588	CYP19A1	cytochrome P450, family 19, subfamily A, polypeptide 1	Locus type: gene with protein product, function known or inferred/Aliases: ARO, P-450AROM, CPV1, ARO1, CYAR/HUGO ID: 2594/UniProt ID: P11511/
10317.4	10317	B3GALT5	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5	Aliases: beta3Gal-T5/HUGO ID: 920/UniProt ID: Q9Y2C3/
1375.4	1375	CPT1B	carnitine palmitoyltransferase 1B (muscle)	Aliases: M-CPT1, CPT1-M/HUGO ID: 2329/UniProt ID: Q92523/
8854.3	8854	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	Locus type: gene with protein product, function known or inferred/Aliases: RALDH2/HUGO ID: 15472/UniProt ID: O94788/
1103.2	1103	CHAT	choline acetyltransferase	Locus type: gene with protein product, function known or inferred/HUGO ID: 1912/UniProt ID: P28329/
3423.2	3423	IDS	iduronate 2-sulfatase (Hunter syndrome)	HUGO ID: 5389/UniProt ID: P22304/
1384.2	1384	CRAT	carnitine acetyltransferase	Aliases: CAT1/HUGO ID: 2342/UniProt ID: P43155/
594.2	594	BCKDHB	branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease)	Locus type: gene with protein product, function known or inferred/HUGO ID: 987/UniProt ID: P21953/
31.4	31	ACACA	acetyl-Coenzyme A carboxylase alpha	Aliases: ACC1/HUGO ID: 84/UniProt ID: Q13085/
8854.2	8854	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	Locus type: gene with protein product, function known or inferred/Aliases: RALDH2/HUGO ID: 15472/UniProt ID: O94788/
85365.2	85365	ALG2	asparagine-linked glycosylation 2 homolog (yeast, alpha-1,3-mannosyltransferase)	Locus type: gene with protein product, function known or inferred/Aliases: CDGIi, FLJ14511, hALPG2/HUGO ID: 23159/UniProt ID: Q8NBX2/
6480.3	6480	SIAT1	sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase)	Aliases: CD75, ST6Gal I/HUGO ID: 10860/UniProt ID: P15907/

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
514.2	514	ATP5E	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit	HUGO ID: 838/UniProt ID: P56381/
6573.2	6573	SLC19A1	solute carrier family 19 (folate transporter), member 1	Aliases: FOLT/HUGO ID: 10937/UniProt ID: P41440/
5352.2	5352	PLOD2	procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2	Locus type: gene with protein product, function known or inferred/HUGO ID: 9082/UniProt ID: O00469/
271.2	271	AMPD2	adenosine monophosphate deaminase 2 (isoform L)	HUGO ID: 469/UniProt ID: Q01433/
3420.3	3420	IDH3B	isocitrate dehydrogenase 3 (NAD+) beta	HUGO ID: 5385/UniProt ID: O43837/
55512.2	55512	SMPD3	sphingomyelin phosphodiesterase 3, neutral membrane (neutral sphingomyelinase II)	Locus type: gene with protein product, function known or inferred/Aliases: NSMASE2/HUGO ID: 14240/UniProt ID: Q9NY59/
5277.3	5277	PIGA	phosphatidylinositol glycan, class A (paroxysmal nocturnal hemoglobinuria)	Aliases: GPI3/HUGO ID: 8957/UniProt ID: P37287/
2678.2	2678	GGT1	gamma-glutamyltransferase 1	Aliases: D22S672, D22S732, CD224/HUGO ID: 4250/UniProt ID: P19440/
27124.2	27124	PIB5PA	phosphatidylinositol (4,5) bisphosphate 5-phosphatase, A	HUGO ID: 8956/UniProt ID: Q15735/
2571.2	2571	GAD1	glutamate decarboxylase 1 (brain, 67kDa)	HUGO ID: 4092/UniProt ID: Q99259/
5152.14	5152	PDE9A	phosphodiesterase 9A	HUGO ID: 8795/UniProt ID: O76083/
6820.2	6820	SULT2B1	sulfotransferase family, cytosolic, 2B, member 1	Aliases: HSST2/HUGO ID: 11459/UniProt ID: O00205/
1798.2	1798	DPAGT1	dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminephosphotransferase 1 (GlcNAc-1-P transferase)	Aliases: GPT, D11S366, DGPT, ALG7, CDG-Ij/HUGO ID: 2995/UniProt ID: Q9H3H5/
112.2	112	ADCY6	adenylate cyclase 6	HUGO ID: 237/UniProt ID: O43306/
51447.6	51447	IHPK2	inositol hexaphosphate kinase 2	Aliases: IP6K2/HUGO ID: 17313/UniProt ID: Q9H4P7/
8706.3	8706	B3GALT3	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 3	Locus type: gene with protein product, function known or inferred/Aliases: beta3Gal-T3, galT3, P1/HUGO ID: 918/UniProt ID: O75752/
6487.7	6487	SIAT6	sialyltransferase 6 (N-acetyllacosaminide alpha 2,3-sialyltransferase)	Locus type: gene with protein product, function known or inferred/Aliases: ST3Gal III/HUGO ID: 10866/UniProt ID: Q11203/
5250.4	5250	SLC25A3	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3	Locus type: gene with protein product, function known or inferred/HUGO ID: 10989/UniProt ID: Q00325/
9807.2	9807	IHPK1	inositol hexaphosphate kinase 1	Locus type: gene with protein product, function known or inferred/Aliases: KIAA0263, IP6K1/HUGO ID: 18360/UniProt ID: Q92551/
8525.3	8525	DGKZ	diacylglycerol kinase, zeta 104kDa	Aliases: DAGK5, hDGKzeta/HUGO ID: 2857/UniProt ID: Q13574/
4056.2	4056	LTC4S	leukotriene C4 synthase	Locus type: gene with protein product, function known or inferred/Aliases: MGC33147/HUGO ID: 6719/UniProt ID: Q16873/
771.2	771	CA12	carbonic anhydrase XII	Locus type: gene with protein product, function known or inferred/Aliases: HsT18816/HUGO ID: 1371/UniProt ID: O43570/
7360.2	7360	UGP2	UDP-glucose pyrophosphorylase 2	HUGO ID: 12527/UniProt ID: Q16851/
440.2	440	ASNS	asparagine synthetase	Locus type: gene with protein product, function known or inferred/HUGO ID: 753/UniProt ID: P08243/
1103.3	1103	CHAT	choline acetyltransferase	Locus type: gene with protein product, function known or inferred/HUGO ID: 1912/UniProt ID: P28329/
3795.2	3795	KHK	ketohexokinase (fructokinase)	HUGO ID: 6315/UniProt ID: P50053/
5091.2	5091	PC	pyruvate carboxylase	Aliases: PCB/HUGO ID: 8636/UniProt ID: P11498/
1716.2	1716	DGUOK	deoxyguanosine kinase	Aliases: dGK/HUGO ID: 2858/UniProt ID: Q16854/
10861.2	10861	SLC26A1	solute carrier family 26 (sulfate transporter), member 1	Locus type: gene with protein product, function known or inferred/Aliases: SAT-1, EDM4/HUGO ID: 10993/UniProt ID: Q9H2B4/
10317.5	10317	B3GALT5	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5	Aliases: beta3Gal-T5/HUGO ID: 920/UniProt ID: Q9Y2C3/
2348.6	2348	FOLR1	folate receptor 1 (adult)	HUGO ID: 3791/UniProt ID: P15328/
2181.2	2181	ACSL3	acyl-CoA synthetase long-chain family member 3	Locus type: gene with protein product, function known or inferred/Aliases: ACS3, PRO2194/HUGO ID: 3570/UniProt ID: O95573/MGD ID: MGI:1921455/
31.5	31	ACACA	acetyl-Coenzyme A carboxylase alpha	Aliases: ACC1/HUGO ID: 84/UniProt ID: Q13085/
271.3	271	AMPD2	adenosine monophosphate deaminase 2 (isoform L)	HUGO ID: 469/UniProt ID: Q01433/
23600.2	23600	AMACR	alpha-methylacyl-CoA racemase	Aliases: RACE/HUGO ID: 451/UniProt ID: Q9UHK6/
1384.3	1384	CRAT	carnitine acetyltransferase	Aliases: CAT1/HUGO ID: 2342/UniProt ID: P43155/
4830.2	4830	NME1	non-metastatic cells 1, protein (NM23A) expressed in	Aliases: NM23, NM23-H1/HUGO ID: 7849/UniProt ID: P15531/
5151.4	5151	PDE8A	phosphodiesterase 8A	Locus type: gene with protein product, function known or inferred/Aliases: HsT19550/HUGO ID: 8793/UniProt ID: O60658/
2618.2	2618	GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase	HUGO ID: 4163/UniProt ID: P22102/
7173.3	7173	TPO	thyroid peroxidase	HUGO ID: 12015/UniProt ID: P07202/
221823.2	221823	PRPS1L1	phosphoribosyl pyrophosphate synthetase 1-like 1	Locus type: gene with protein product, function known or inferred/Aliases: PRPS3/HUGO ID: 9463/UniProt ID: P21108/
205.2	205	AK3	adenylate kinase 3	Locus type: gene with protein product, function known or inferred/HUGO ID: 363/UniProt ID: P27144/
954.2	954	ENTPD2	ectonucleoside triphosphate diphosphohydrolase 2	Aliases: NTPDase-2/HUGO ID: 3364/UniProt ID: Q9Y5L3/
534.2	534	ATP6V1G2	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G isoform 2	Aliases: Vma10, NG38, Em:AC004181.3/HUGO ID: 862/UniProt ID: O95670/
6547.6	6547	SLC8A3	solute carrier family 8 (sodium-calcium exchanger), member 3	Aliases: NCX3/HUGO ID: 11070/UniProt ID: P57103/

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
27087.2	27087	B3GAT1	beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P)	Locus type: gene with protein product, function known or inferred/Aliases: GlcAT-P/HUGO ID: 921/UniProt ID: Q9P2W7/
131669.1	131669	FLJ31300	urocanate hydratase	transcript: NM_144639
10841.2	10841	FTCD	formiminotransferase cyclodeaminase	
314.2	314	AOC2	amine oxidase, copper containing 2 (retina-specific)	
27165.2	27165	GA	liver mitochondrial glutaminase	
84735.1	84735	CNDP1	carnosine dipeptidase 1 (metallopeptidase M20 family)	
7915.2	7915	ALDH5A1	aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase)	
55191.1	55191	NADSYN1	NAD synthetase 1 (glutamine-dependent)	transcript: NM_018161
1373.2	1373	CPS1	carbamoyl-phosphate synthetase 1, mitochondrial	transcript: NM_001875
2954.2	2954	GSTZ1	glutathione transferase zeta 1 (maleylacetoacetate isomerase)	
2954.3	2954	GSTZ1	glutathione transferase zeta 1 (maleylacetoacetate isomerase)	
158.2	158	ADSL	adenylosuccinate lyase	transcript: NM_000026
445.2	445	ASS	argininosuccinate synthetase	
80347.1	80347	KDTB/COAE	Phosphopantetheine adenylyltransferase/dephospho-CoA kinase	
60490.1	60490	PPCDC	Phosphopantothenoylcysteine decarboxylase	
2645.2	2645	GCK	glucokinase (hexokinase 4, maturity onset diabetes of the young 2)	transcript: NM_033507
79717.1	79717	PPCS	Phosphopantothenate-cysteine ligase	transcript: NM_024664
80025.1	80025	PANK2	Pantothenate kinase 2	
80025.2	80025	PANK2	Pantothenate kinase 2	
80025.3	80025	PANK2	Pantothenate kinase 2	
80025.4	80025	PANK2	Pantothenate kinase 2	
80025.5	80025	PANK2	Pantothenate kinase 2	
8884.1	8884	SMVT	sodium-dependent vitamin transporter	
10560.1	10560	SLC19A2	thiamine transporter	
286016.1	286016	LOC286016	hypothetical protein LOC286016	transcript: NR_002187
55293.1	55293	UEV3	ubiquitin-conjugating enzyme E2-like	transcript: NM_018314
2639.2	2639	GCDH	glutaryl-Coenzyme A dehydrogenase	
51166.1	51166	AADAT	aminoadipate aminotransferase	
51166.2	51166	AADAT	aminoadipate aminotransferase	
97.2	97	ACYP1	acylphosphatase 1, erythrocyte (common) type	
55312.1	55312	RFK	Riboflavin kinase	
80308.1	80308	FADS	FAD-synthetase	transcript: NM_025207
80308.2	80308	FADS	FAD-synthetase	transcript: NM_201398
10327.2	10327	AKR1A1	aldo-keto reductase family 1, member iA (aldehyde reductase)	
522.2	522	ATP5J	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6	Variant 2
522.3	522	ATP5J	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6	Variant 3
522.4	522	ATP5J	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6	Variant 4: This variant (4) differs in the 5' UTR, compared to variant 1. Variants 1, 2, 3 and 4 encode the same isoform (a).
509.2	509	ATP5C1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	Variant 2: This variant lacks a segment in the coding region compared to variant 1. The resulting isoform (H), also known as a heart type isoform, contains a shorter and distinct C-terminus compared to isoform L.
4967.2	4967	OGDH	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	transcript: NM_002541
27349.1	27349	MT	malonyl-CoA:acyl carrier protein transacylase, mitochondrial	transcript: NM_173467
27349.2	27349	MT	malonyl-CoA:acyl carrier protein transacylase, mitochondrial	transcript: NM_014507
29968.2	29968	PSAT1	phosphoserine aminotransferase 1	
50617.2	50617	ATP6V0A4	ATPase, H+ transporting, lysosomal V0 subunit a isoform 4	
50617.3	50617	ATP6V0A4	ATPase, H+ transporting, lysosomal V0 subunit a isoform 4	
51606.2	51606	ATP6V1H	ATPase, H+ transporting, lysosomal 50/57kDa, V1 subunit H isoform 1	
51606.3	51606	ATP6V1H	ATPase, H+ transporting, lysosomal 50/57kDa, V1 subunit H isoform 2	
23057.1	23057	NMNAT2	Nicotinamide nucleotide adenylyltransferase 2	
23057.2	23057	NMNAT2	Nicotinamide nucleotide adenylyltransferase 2	
8704.2	8704	B4GALT2	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 2	transcript: NM_003780
64802.1	64802	NMNAT1	Nicotinamide nucleotide adenylyltransferase 1	
79053.3	79053	ALG8	asparagine-linked glycosylation 8 homolog (yeast, alpha-1,3-glucosyltransferase)	transcript: NM_001007027
6482.2	6482	SIAT4A	sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase)	transcript: NM_173344
29796.2	29796	HSPC051	ubiquinol-cytochrome c reductase complex	
125965.1	125965	COX6B2	cytochrome c oxidase subunit VIb polypeptide 2 (testis)	

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
170712.1	170712	COX7B2	cytochrome c oxidase subunit VIIb2	
134526.1	134526	CACH-1	cytosolic acetyl-CoA hydrolase	transcript: NM_130767
124637.1	124637	FLJ32499	hypothetical protein FLJ32499	transcript: NM_144607
162417.1	162417	NAGS	N-acetylglutamate synthase	
2593.2	2593	GAMT	guanidinoacetate N-methyltransferase	
29925.2	29925	GMPPB	GDP-mannose pyrophosphorylase B	transcript: NM_021971
29926.2	29926	GMPPA	GDP-mannose pyrophosphorylase A	transcript: NM_205847
7264.1	7264	TSTA3	tissue specific transplantation antigen P35B	transcript: NM_003313
197258.1	197258	FUK	fucokinase	transcript: NM_145059
2645.3	2645	GCK	glucokinase (hexokinase 4, maturity onset diabetes of the young 2)	transcript: NM_033508
4712.2	4712	NDUFB6	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa	
7991.1	7991	TUSC3	tumor suppressor candidate 3	
7991.2	7991	TUSC3	tumor suppressor candidate 3	
8309.1	8309	ACOX2	acyl-Coenzyme A oxidase 2, branched chain	
113451.1	113451	ODC-p	ornithine decarboxylase-like	transcript: NM_052998
1809.1	1809	DPYSL3	dihydropyrimidinase-like 3	
7108.1	7108	TM7SF2	transmembrane 7 superfamily member 2	
6307.1	6307	SC4MOL	sterol-C4-methyl oxidase-like	
1119.2	1119	CHK	choline kinase	
1120.2	1120	CHKL	choline/ethanolamine kinase	
8760.1	8760	CDS2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	
9489.1	9489	PGS1	phosphatidylglycerophosphate synthase	
5136.2	5136	PDE1A	phosphodiesterase 1A, calmodulin-dependent	
27430.1	27430	MAT2B	methionine adenosyltransferase II, beta	
27430.2	27430	MAT2B	methionine adenosyltransferase II, beta	
23382.1	23382	AHCYL2	S-adenosylhomocysteine hydrolase-like 2	
5150.1	5150	PDE7A	phosphodiesterase 7A isoform a	
5150.2	5150	PDE7A	phosphodiesterase 7A isoform b	
80162.1	80162	FLJ22635	hypothetical protein FLJ22635	
9536.1	9536	PTGES	prostaglandin E synthase	
9536.2	9536	PTGES	prostaglandin E synthase	
2542.1	2542	SLC37A4	solute carrier family 37 (glycerol-6-phosphate transporter), member 4	transcript: NM_001467
7352.2	7352	UCP3	uncoupling protein 3 (mitochondrial, proton carrier)	
318.2	318	NUDT2	nucleoside diphosphatase	
318.3	318	NUDT2	nucleoside diphosphatase	
57818.1	57818	G6PC2	glucose-6-phosphatase, catalytic, 2	transcript: NM_021176
83549.1	83549	UCK1	uridine-cytidine kinase 1	
7378.2	7378	UPP1	uridine phosphorylase 1	
10587.2	10587	TXNRD2	thioredoxin reductase 2	
10587.3	10587	TXNRD2	thioredoxin reductase 2	
5625.1	5625	PRODH	proline dehydrogenase (oxidase) 1	aliases: PIG6; HSPOX2; PRODH1; PRODH2; TP53I6
8974.1	8974	P4HA2	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide II	
1789.1	1789	DNMT3B	DNA (cytosine-5-)-methyltransferase 3 beta	
1789.2	1789	DNMT3B	DNA (cytosine-5-)-methyltransferase 3 beta	
1789.3	1789	DNMT3B	DNA (cytosine-5-)-methyltransferase 3 beta	
1789.4	1789	DNMT3B	DNA (cytosine-5-)-methyltransferase 3 beta	
1788.1	1788	DNMT3A	DNA (cytosine-5-)-methyltransferase 3	
1788.2	1788	DNMT3A	DNA (cytosine-5-)-methyltransferase 3	
1788.3	1788	DNMT3A	DNA (cytosine-5-)-methyltransferase 3	
1788.4	1788	DNMT3A	DNA (cytosine-5-)-methyltransferase 3	
1787.1	1787	DNMT2	DNA (cytosine-5-)-methyltransferase 2	
1787.2	1787	DNMT2	DNA (cytosine-5-)-methyltransferase 2	
1787.3	1787	DNMT2	DNA (cytosine-5-)-methyltransferase 2	
1787.4	1787	DNMT2	DNA (cytosine-5-)-methyltransferase 2	
1787.5	1787	DNMT2	DNA (cytosine-5-)-methyltransferase 2	
1787.6	1787	DNMT2	DNA (cytosine-5-)-methyltransferase 2	
6319.1	6319	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	
64064.1	64064	OXCT2	3-oxoacid CoA transferase 2	
54511.1	54511	HMGCLL1	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase-like 1	
957.1	957	ENTPD5	ectonucleoside triphosphate diphosphohydrolase 5	
23530.2	23530	NNT	Nicotinamide nucleotide transhydrogenase	
27235.1	27235	COQ2	para-hydroxybenzoate - polyprenyltransferase, mitochondrial	transcript: NM_015697
25902.1	25902	MTHFD1L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	transcript: NM_015440
286297.1	286297	LOC286297	hypothetical protein LOC286297	transcript: XM_372099
80068.1	80068	FLJ13105	hypothetical protein FLJ13105	transcript: NM_001004346
285216.1	285216	LOC285216	hypothetical protein LOC285216	transcript: XM_496652
10390.1	10390	CEPT1	choline/ethanolamine phosphotransferase 1	

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
51005.1	51005	CGI-14	CGI-14 protein	transcript: NM_015944
27159.1	27159	CHIA	eosinophil chemotactic cytokine	transcript: NM_021797
27159.2	27159	CHIA	eosinophil chemotactic cytokine	transcript: NM_201653
54682.1	54682	MANSC1	MANSC domain containing 1	transcript: NM_018050
1118.1	1118	CHIT1	chitinase 1 (chitotriosidase)	transcript: NM_003465
200576.1	200576	PIP5K3	phosphatidylinositol-3-phosphate/phosphatidylinositol 5-kinase, type III	
200576.2	200576	PIP5K3	phosphatidylinositol-3-phosphate/phosphatidylinositol 5-kinase, type III	
200576.3	200576	PIP5K3	phosphatidylinositol-3-phosphate/phosphatidylinositol 5-kinase, type III	
5298.1	5298	PIK4CB	phosphatidylinositol 4-kinase, catalytic, beta polypeptide	
55361.1	55361	PI4KII	phosphatidylinositol 4-kinase type II	transcript: NM_018425
55268.1	55268	ECHDC2	enoyl Coenzyme A hydratase domain containing 2	transcript: NM_018281
8395.1	8395	PIP5K1B	phosphatidylinositol-4-phosphate 5-kinase, type I, beta	transcript: NM_003558
8396.2	8396	PIP5K2B	phosphatidylinositol-4-phosphate 5-kinase, type II, beta	transcript: NM_138687
8867.2	8867	SYNJ1	synaptojanin 1	transcript: NM_203446
290.1	290	ANPEP	alanyl (membrane) aminopeptidase	
10870.1	10870	HCST	hematopoietic cell signal transducer	transcript: NM_001007469
29124.1	29124	LGALS13	lectin, galactoside-binding, soluble, 13 (galectin 13)	
8560.1	8560	DEGS1	degenerative spermatocyte homolog 1, lipid desaturase (Drosophila)	transcript: NM_003676
8560.2	8560	DEGS1	degenerative spermatocyte homolog 1, lipid desaturase (Drosophila)	transcript: NM_144780
55163.1	55163	PNPO	Pyridoxine-5'-phosphate oxidase	
3631.2	3631	INPP4A	inositol polyphosphate-4-phosphatase, type I, 107kDa	transcript: NM_004027
57026.1	57026	PDXP	Pyridoxal Phosphatase	
253430.1	253430	IPMK	inositol polyphosphate multikinase	transcript: NM_152230
51109.1	51109	RDH11	retinol dehydrogenase 11 (all-trans and 9-cis)	
195814.1	195814	RDHE2	epidermal retinal dehydrogenase 2	transcript: NM_138969
84812.1	84812	PLCD4	phospholipase C, delta 4	transcript: NM_032726
23007.1	23007	PLCL3	phospholipase C-like 3	transcript: NM_014996
51196.1	51196	PLCE1	phospholipase C, epsilon 1	transcript: NM_016341
23236.2	23236	PLCB1	phospholipase C, beta 1 (phosphoinositide-specific)	transcript: NM_182734
113026.1	113026	PLCD3	phospholipase C, delta 3	transcript: NM_133373
84444.1	84444	DOT1L	DOT1-like, histone H3 methyltransferase (S. cerevisiae)	
80854.1	80854	SET7	SET domain-containing protein 7	
5335.2	5335	PLCG1	phospholipase C, gamma 1	
9651.1	9651	PLCL4	phospholipase C-like 4	transcript: XM_371214
27068.2	27068	PPA2	Inorganic pyrophosphatase 2	
27068.1	27068	PPA2	Inorganic pyrophosphatase 2	
27068.3	27068	PPA2	Inorganic pyrophosphatase 2	
27068.4	27068	PPA2	Inorganic pyrophosphatase 2	
79813.1	79813	EHMT1	euchromatic histone methyltransferase 1	
387893.1	387893	SET8	PR/SET domain containing protein 8	
5279.1	5279	PIGC	phosphatidylinositol glycan, class C	transcript: NM_002642
5279.2	5279	PIGC	phosphatidylinositol glycan, class C	transcript: NM_153747
2235.2	2235	FECH	ferrochelatase (protoporphyria)	
9091.1	9091	PIGQ	phosphatidylinositol glycan, class Q	transcript: NM_004204
9091.2	9091	PIGQ	phosphatidylinositol glycan, class Q	transcript: NM_148920
8824.1	8824	CES2	carboxylesterase 2 (intestine, liver)	
8824.2	8824	CES2	carboxylesterase 2 (intestine, liver)	
259230.1	259230	TMEM23	transmembrane protein 23	
64781.1	64781	CERK	ceramide kinase	
64781.2	64781	CERK	ceramide kinase	
284098.1	284098	PIGW	phosphatidylinositol glycan, class W	transcript: NM_178517
81849.1	81849	ST6GALNAC5	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 5	
54965.1	54965	PIGX	phosphatidylinositol glycan, class X	transcript: NM_017861
55650.1	55650	PIGV	phosphatidylinositol glycan, class V	transcipt: NM_017837
23556.2	23556	PIGN	phosphatidylinositol glycan, class N	transcript: NM_176787
54872.1	54872	GPI7	GPI7 protein	transcript: NM_017733
343.1	343	AQP8	Aquaporin 8	
80055.1	80055	PGAP1	GPI deacylase	transcript: NM_024989
80235.1	80235	SMP3	SMP3 mannosyltransferase	transcript: NM_025163
22305.1	22305	ACSL6	acyl-CoA synthetase long-chain family member 6	
22305.2	22305	ACSL6	acyl-CoA synthetase long-chain family member 6	
427.2	427	ASAH1	N-acylsphingosine amidohydrolase (acid ceramidase) 1	

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
10678.2	10678	B3GNT1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1	transcript: NM_033252
60559.1	60559	SPCS3	signal peptidase complex subunit 3 homolog (S. cerevisiae)	
28972.1	28972	SPCS1	signal peptidase complex subunit 1 homolog	
9789.1	9789	SPCS2	signal peptidase complex subunit 2 homolog	
90701.1	90701	SEC11L3	SEC11-like 3 (S. cerevisiae)	
50814.1	50814	NSDHL	NAD(P) dependent steroid dehydrogenase-like	
8654.2	8654	PDE5A	phosphodiesterase 5A, cGMP-specific	
8654.3	8654	PDE5A	phosphodiesterase 5A, cGMP-specific	
114112.1	114112	TXNRD3	thioredoxin reductase 3	
8534.1	8534	CHST1	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	transcript: NM_003654
9469.1	9469	CHST3	carbohydrate (chondroitin 6) sulfotransferase 3	transcript: NM_004273
23563.1	23563	CHST5	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 5	transcript: NM_012126
23563.2	23563	CHST5	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 5	transcript: NM_024533
4166.1	4166	CHST6	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 6	transcript: NM_021615
6566.1	6566	SLC16A1	solute carrier family 16 (monocarboxylic acid transporters), member 1	1 - 1p12 NM_003051
373156.1	373156	GSTK1	glutathione S-transferase kappa 1	
55454.1	55454	GALNACT-2	chondroitin sulfate GalNAcT-2	transcript: NM_018590
55790.1	55790	ChGn	chondroitin beta1,4 N-acetylgalactosaminyltransferase	transcript: NM_018371
113189.1	113189	D4ST1	dermatan 4 sulfotransferase 1	transcript: NM_130468
54480.1	54480	CSGlcA-T	chondroitin sulfate glucuronyltransferase	transcript: NM_019015
79586.1	79586	CHPF	chondroitin polymerizing factor	transcript: NM_024536
337876.1	337876	CSS3	chondroitin sulfate synthase 3	transcript: NM_175856
2109.2	2109	ETFB	Electron-transfer-flavoprotein, beta polypeptide	
2132.2	2132	EXT2	exostoses (multiple) 2	transcript: NM_207122
64816.1	64816	CYP3A43	cytochrome P450, family 3, subfamily A, polypeptide	
64816.2	64816	CYP3A43	cytochrome P450, family 3, subfamily A, polypeptide	
64816.3	64816	CYP3A43	cytochrome P450, family 3, subfamily A, polypeptide	
26035.1	26035	GLCE	glucuronyl C5-epimerase	transcript: NM_015554
10991.1	10991	SLC38A3	solute carrier family 38, member 3	
206358.1	206358	SLC36A1	solute carrier family 36 (proton/amino acid symporter), member 1	
23428.1	23428	SLC7A8	solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	
23428.2	23428	SLC7A8	solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	
56301.1	56301	SLC7A10	solute carrier family 7, (neutral amino acid transporter, y+ system) member 10	
6510.1	6510	SLC1A5	solute carrier family 1 (neutral amino acid transporter), member 5	
8140.1	8140	SLC7A5	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	
84649.1	84649	DGAT2	diacylglycerol O-acyltransferase homolog 2 (mouse)	
57030.1	57030	SLC17A7	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7	
29988.1	29988	SLC2A8	solute carrier family 2, (facilitated glucose transporter) member 8	transcript: NM_014580
154091.1	154091	SLC2A12	solute carrier family 2 (facilitated glucose transporter), member 12	transcript: NM_145176
118881.1	118881	COMTD1	catechol-O-methyltransferase domain containing 1	
766.2	766	CA7	Carbonic anhydrase VII	HUGO ID: 1381/UniProt ID: P43166/
8501.1	8501	SLC43A1	solute carrier family 43, member 1	
6536.1	6536	SLC6A9	solute carrier family 6 (neurotransmitter transporter, glycine) member 9	
6536.2	6536	SLC6A9	solute carrier family 6 (neurotransmitter transporter, glycine) member 9	
8671.1	8671	SLC4A4	solute carrier family 4, sodium bicarbonate cotransporter, member 4	
57835.1	57835	SLC4A5	solute carrier family 4, sodium bicarbonate cotransporter, member 5	
57835.2	57835	SLC4A5	solute carrier family 4, sodium bicarbonate cotransporter, member 5	
57835.3	57835	SLC4A5	solute carrier family 4, sodium bicarbonate cotransporter, member 5	
57835.4	57835	SLC4A5	solute carrier family 4, sodium bicarbonate cotransporter, member 5	
9497.1	9497	SLC4A7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	
10935.2	10935	PRDX3	Peroxiredoxin 3	

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
6817.2	6817	SULT1A1	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1	
6817.3	6817	SULT1A1	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1	
6817.4	6817	SULT1A1	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1	
6817.5	6817	SULT1A1	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1	
6799.2	6799	SULT1A2	Sulfotransferase family, cytosolic, 1A, phenol-preferring, member 2	
6818.2	6818	SULT1A3	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3	
6818.3	6818	SULT1A3	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3	
480.1	480	ATP1A4	ATPase, Na+/K+ transporting, alpha 4 polypeptide	
115286.2	115286	SLC25A26	solute carrier family 25, member 26	UniGene Hs.379386
115286.3	115286	SLC25A26	solute carrier family 25, member 26	UniGene Hs.379386
160728.1	160728	SLC5A8	solute carrier family 5 (iodide transporter), member 8	transcript: NM_145913
115584.1	115584	SLC5A11	solute carrier family 5 (sodium/glucose cotransporter), member 11	transcript: NM_052944
9963.1	9963	SLC23A1	solute carrier family 23 (nucleobase transporters), member 1	transcript: NM_005847
9963.2	9963	SLC23A1	solute carrier family 23 (nucleobase transporters), member 1	transcript: NM_152685
9962.1	9962	SLC23A2	solute carrier family 23 (nucleobase transporters), member 2	transcript: NM_005116
9962.2	9962	SLC23A2	solute carrier family 23 (nucleobase transporters), member 2	transcript: NM_203327
10559.1	10559	SLC35A1	solute carrier family 35 (CMP-sialic acid transporter), member A1	transcript: NM_006416
2030.1	2030	SLC29A1	solute carrier family 29 (nucleoside transporters), member 1	
55343.1	55343	SLC35C1	solute carrier family 35, member C1	transcript: NM_018389
9058.1	9058	SLC13A2	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2	transcript: NM_003984
64849.1	64849	SLC13A3	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3	transcript: NM_001011554
64849.2	64849	SLC13A3	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3	transcript: NM_022829
6581.1	6581	SLC22A3	solute carrier family 22 (extraneuronal monoamine transporter), member 3	
6584.1	6584	SLC22A5	solute carrier family 22 (organic cation transporter), member 5	
6578.1	6578	SLCO2A1	solute carrier organic anion transporter family, member 2A1	
6569.1	6569	SLC34A1	solute carrier family 34 (sodium phosphate), member 1	
10568.1	10568	SLC34A2	solute carrier family 34 (sodium phosphate), member 2	
1811.1	1811	SLC26A3	solute carrier family 26, member 3	
5172.1	5172	SLC26A4	solute carrier family 26, member 4	
65010.1	65010	SLC26A6	solute carrier family 26, member 6	
65010.2	65010	SLC26A6	solute carrier family 26, member 6	
65010.3	65010	SLC26A6	solute carrier family 26, member 6	
115111.1	115111	SLC26A7	solute carrier family 26, member 7	
115111.2	115111	SLC26A7	solute carrier family 26, member 7	
116369.1	116369	SLC26A8	solute carrier family 26, member 8	
116369.2	116369	SLC26A8	solute carrier family 26, member 8	
6567.1	6567	SLC16A2	solute carrier family 16 (monocarboxylic acid transporters), member 2	transcript: NM_006517
3177.1	3177	SLC29A2	solute carrier family 29 (nucleoside transporters), member 2	IT
10998.1	10998	SLC27A5	solute carrier family 27 (fatty acid transporter), member 5	
10257.1	10257	ABCC4	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	IT
10057.1	10057	ABCC5	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	IT
10057.2	10057	ABCC5	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	IT
8714.1	8714	ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	
8714.2	8714	ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	
6553.1	6553	SLC9A5	solute carrier family 9 (sodium/hydrogen exchanger), isoform 5	transcript: NM_004594
8714.3	8714	ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	
137964.1	137964	AGPAT6	1-acylglycerol-3-phosphate O-acyltransferase 6	transcript: NM_178819

Abbreviation	Entrez Gene ID	Gene Symbol	Putative Function	Additional notes
9990.1	9990	SLC12A6	solute carrier family 12 (potassium/chloride transporters), member 6	transcript: NM_005135
50506.1	50506	DUOX2	dual oxidase 2	
26503.1	26503	SLC17A5	solute carrier family 17 (anion/sugar transporter), member 5	
10005.1	10005	PTE1	peroxisomal acyl-CoA thioesterase	
10005.2	10005	PTE1	peroxisomal acyl-CoA thioesterase	
10005.3	10005	PTE1	peroxisomal acyl-CoA thioesterase	
10965.1	10965	ZAP128	peroxisomal long-chain acyl-coA thioesterase	transcript: NM_006821
3038.2	3038	HAS3	hyaluronan synthase 3	
8875.2	8875	VNN2	vanin 2	IT
55350.3	55350	VNN3	vanin 3	IT
113235.1	113235	MGC9564	similar to RIKEN cDNA 1110002C08 gene	transcript: NM_080669
10690.1	10690	FUT9	fucosyltransferase 9 (alpha (1,3) fucosyltransferase)	
9388.1	9388	LIPG	lipase, endothelial	
10396.1	10396	ATP8A1	ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1	
57194.1	57194	ATP10A	ATPase, Class V, type 10A	
8228.1	8228	PNPLA4	keratinocyte retinyl ester hydrolase	IT
8608.1	8608	RDH16	retinol dehydrogenase 16 (all-trans and 13-cis)	IT
8897.1	8897	MTMR3	myotubularin related protein 3	transcript: NM_021090
8897.2	8897	MTMR3	myotubularin related protein 3	transcript: NM_153050
8897.3	8897	MTMR3	myotubularin related protein 3	transcript: NM_153051
4363.1	4363	ABCC1.1	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	
522.5	522	Atp5j.5-m	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6	Transcript Variant: This variant (5) differs in the 5' UTR and the 5' coding region, compared to variant 1. The predicted isoform (b) is longer, and it contains a distinct N-terminus, compared to isoform a. The existence of a translated product from this transcript needs to be experimentally confirmed.
10312.2	10312	TCIRG1	T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 protein A3	

Table 9: *H. sapiens* Recon 1 network gaps. Final list of network gaps in Recon 1. Gaps are defined as metabolites that can only be produced or consumed and are compartment-specific. Note that the gap may arise from more than one reaction; only one has been shown here for demonstrative purposes. Each gap was carefully reviewed and classified as either model-scope (i.e., reactions which produce/consume the metabolite are part of pathways which are beyond the scope of this reaction) or knowledge-base (i.e., gap cannot be resolved due to lack of knowledge of how a particular metabolite is produced or consumed).

Reviewer initials
ND: Natalie C. Duarte SAB: Scott A. Becker
NJ: Neema Jamshidi MM: Monica L. Mo
IT: Ines Thiele

Metabolite Abbreviation	Metabolite Name	Gap Type	Compartment	Reaction Abbreviation	Notes	Reviewer
2mcit	2-Methylcitrate	Produced only	Cytosol	2MCITt	added transport rxn 2MCITt; methycitrate is excreted in urine of patients who suffer from propionic acidaemia (Weidman et al. 1979)	MM
42A3HP24DB	4-(2-Amino-3-hydroxyphenyl)-2,4-dioxobutanoate	Produced only	Cytosol	3HKYNAKGAT	knowledge-base gap	SAB
3hpcoa	3-Hydroxypropionyl-CoA	Consumed only	Cytosol	3HPCOAHYD	model-scope gap	SAB
msa	Malonate semialdehyde	Produced only	Cytosol	3HPPD	knowledge-based gap: this rxn has been described and studied in mammalians, but not in humans; gap could be filled since msa is metabolized in mitochondria, but there is no evidence for msa mitochondrial transport activity	MM
48dhoxquin	4,8-Dihydroxyquinoline	Produced only	Cytosol	3HXKYNOXDA	model-scope gap	SAB
5hoxnfkyn	5-Hydroxy-N-formylkynurenine	Produced only	Cytosol	5HTRPDOX	knowledge-base gap: not enough evidence to include reaction before this in line	SAB
5hxkyn	5-Hydroxykynurenine	Consumed only	Cytosol	5HXKYNDCL	knowledge-base gap: not enough evidence to include reaction before this in line	SAB
46dhoxquin	4,6-Dihydroxyquinoline	Produced only	Cytosol	5HXKYNOXDA	model-scope gap	SAB
thcrm_hs	trihexosyl ceramide (homo sapiens)	Produced only	Cytosol	A4GALTc	pathway complete in Golgi - knowledge gap about extent of cytosolic metabolism of thcrm_hs	NJ
4abut	4-Aminobutanoate	Consumed only	Lysosome	ABUTt2rL	knowledge-base gap	SAB
ppa	Propionate (n-C3:0)	Consumed only	Cytosol	ACCOAL	gap removed; added rxn for extracellular -> cytosolic transport based on ref in thuy's mito model	ND
acgbgbside_hs	beta GalNAc globoside (homo sapiens)	Produced only	Lysosome	ACGBGBSIDEtl	gap removed by single reaction addition: NAGAIby added in analogy to NAGAIy (no real evidence that this occurs in vivo)	NJ
acACP	Acetyl-ACP	Produced only	Cytosol	ACOATA	FA synthesis is lumped, so activation w/ ACP will not be utilized at this point, this may be useful in a future version of the reconstruction if FAS is 'unlumped'	NJ
acorn	N2-Acetyl-L-ornithine	Consumed only	Cytosol	ACODA	knowledge-base gap	SAB
ppa	Propionate (n-C3:0)	Consumed only	Cytosol	ACS2	gap removed; added rxn for extracellular -> cytosolic transport based on ref in thuy's mito model	ND
5moxact	5-Methoxyindoleacetate	Produced only	Cytosol	ACSOMT	model-scope gap: end of the line in KEGG	SAB
ade	Adenine	Consumed only	Lysosome	ADEtl	leave gap; knowledge gap: at least i have no idea of the function of adenine in lysosome but uptake was studied by PMID: 2925670	IT
adpglc	ADPglucose	Consumed only	Cytosol	ADPGLC	leave gap: ADPglucose is an important precursor bacterial glycogen and plant starch synthesis, whereas ADP-mannose has no known physiological function, although the commercially available synthetic compound can replace ADP-heptoses in bacterial outer-membrane lipopolysaccharide synthesis in vitro . ADP-ribose might therefore also be the most important substrate for human in vivo (from discussion of Gasmi et al, 1999)	IT
adpman	ADPmannose	Consumed only	Cytosol	ADPMAN	leave gap: ADPglucose is an important precursor bacterial glycogen and plant starch synthesis, whereas ADP-mannose has no known physiological function, although the commercially available synthetic compound can replace ADP-heptoses in bacterial outer-membrane lipopolysaccharide synthesis in vitro . ADP-ribose might therefore also be the most important substrate for human in vivo (from discussion of Gasmi et al, 1999)	IT
3padsel	3'-Phosphoadenylylselenate	Produced only	Cytosol	ADSELK	knowledge-base gap	SAB
dak2gpe_hs	1-alkenyl 2-acylglycerol 3-phosphoethanolamine plasmalogen (homo sapiens)	Produced only	Cytosol	AGLPED	knowledge gap and model scope limitations - rxns included up to extent of biochem texts (Voet and Voet/Murray's Biochem), further details may be gleanable from lit, will require more time investment	NJ
ahcys	S-Adenosyl-L-homocysteine	Produced only	Endoplasmic Reticulum	AHCYStr	gap filled, added AHCYStr	NJ
ala-L	L-Alanine	Consumed only	Lysosome	ALAt2rL	model-scope gap	SAB
ind3ac	Indole-3-acetate	Produced only	Cytosol	ALDD20x	model-scope gap	SAB
dha	Dihydroxyacetone	Produced only	Cytosol	ALKP	model scope limitations in addition to knowledge gaps: PMID 9370313, 9370314	NJ
12HPET	12-Hydroperoxyeicosa-5,8,10,14-tetraenoate	Produced only	Cytosol	ALOX12	12HPETte, unknown mechanism, needs to get into EC space, inflamm mediator, knowledge gap area (subsequent metabolism, etc)	NJ
12RHPET	12R-Hydroperoxyeicosatetraenoate	Produced only	Cytosol	ALOX12R	12RHPETte, unknown mechanism, needs to get into EC space, inflamm mediator, knowledge gap area (subsequent metabolism, etc)	NJ
15HPET	15-Hydroperoxyeicosatetraenoic acid	Produced only	Cytosol	ALOX15	15HPETte, unknown mechanism, needs to get into EC space, inflamm mediator, knowledge gap area (subsequent metabolism, etc)	NJ
amet	S-Adenosyl-L-methionine	Consumed only	Endoplasmic Reticulum	AMETr	gap filled, added AMETr	NJ
andrstrnglc	androsterone glucuronide	Consumed only	Cytosol	ANDRSTRNGLCte	ANDRSTRNGLCtr, ANDRSTRNGLCte	NJ
ap4a	P1,P4-Bis(5'-adenosyl) tetraphosphate	Consumed only	Cytosol	AP4AH1	leave gap; for explanation read not of reaction	IT

Metabolite Abbreviation	Metabolite Name	Gap Type	Compartment	Reaction Abbreviation	Notes	Reviewer
m2mn	(alpha-D-mannosyl)2-beta-D-mannosyl-N-acetylglucosamine	Consumed only	Cytosol	A_MANASE	leave reaction even though it causes gap; it's a redundant reaction since the primary rxn is in lysosome, but there's evidence it might be in cytosol	ND
mn	beta-1,4-mannose-N-acetylglucosamine	Produced only	Cytosol	A_MANASE	leave reaction even though it causes gap; it's a redundant reaction since the primary rxn is in lysosome, but there's evidence it might be in cytosol	ND
bdg2hc	cis-beta-D-Glucosyl-2-hydroxycinnamate	Consumed only	Cytosol	BDG2HCGHD	model-scope gap: unimportant	SAB
2coum	cis-2-Hydroxy cinnamate	Produced only	Cytosol	BDG2HCGHD	model-scope gap: unimportant	SAB
betald	Betaine aldehyde	Consumed only	Cytosol	BETALDHx	knowledge-based gap	MM
bhb	(R)-3-Hydroxybutanoate	Consumed only	Cytosol	BHBt	gap removed; added extracellular transport rxn	ND
bhb	(R)-3-Hydroxybutanoate	Consumed only	Cytosol	BHBtm	gap removed; added extracellular transport rxn	ND
bz	Benzoate	Consumed only	Cytosol	BZt	gap filled, added BZt	NJ
bz	Benzoate	Consumed only	Cytosol	BZtr	gap filled, added BZt	NJ
cbl2	Cob(II)alamin	Produced only	Mitochondria	CBL2tm	leave for the moment --> unfinished PW	IT
prostg1	(13E)-11alpha-Hydroxy-9,15-dioxoprost-13-enoate	Consumed only	Cytosol	CBR1	principally a knowledge gap problem - further metabolism, etc unknown, since at the 'fringes' partial model scope gap also - see Goodman and Gilman, Murray Biochem for overall pathway	NJ
cca_d3	Calcitroic acid (D3)	Consumed only	Mitochondria	CCA_D3tm	knowledge gap; reactions as well as enzymes for vit D degradation are unknown	IT
chsterol	Cholesterol	Consumed only	Golgi Apparatus	CHSTEROLtg	By IT shows transport between golgi and plasma membrane	NJ
chtn	chitin	Consumed only	Cytosol	CHTNASE	leave gap; function has only been characterized in vitro, no physiologically known function	ND
clpn_hs	cardiolipin (homo sapiens)	Produced only	Cytosol	CLS_hs	cardiolipin is a biomass constituent, should be made part of biomass, in future can also update metabolic interconversions	NJ
co2	CO2	Consumed only	Nucleus	CO2tn	gap is due to transporter rxn in nucleus (not needed now, but ok to leave in)	ND
ntm2amep	N-Trimethyl-2-aminoethylphosphonate	Consumed only	Cytosol	CPCTDTX	knowledge gap - strong evidence for the presence of these metabolites in humans lacking, although the enzyme can carry out this conversion (in addition to others more relevant to human metabolism	NJ
cmpntm2amep	CMP-N-trimethyl-2-aminoethylphosphonate	Produced only	Cytosol	CPCTDTX	knowledge gap - strong evidence for the presence of these metabolites in humans lacking, although the enzyme can carry out this conversion (in addition to others more relevant to human metabolism	NJ
crtn	Creatinine	Produced only	Cytosol	CRTNsyn	model-scope gap: a transporter could be added to get this out of the cell, but relatively unimportant	SAB
crtstrn	Corticosterone	Produced only	Endoplasmic Reticulum	CRTSTRNtr	CRTSTRNtr, CRTSTRNtm	NJ
thcys	Thiocysteine	Produced only	Cytosol	CYSLYSL	knowledge-based gap	MM
ala-D	D-Alanine	Consumed only	Lysosome	DALAt2rL	knowledge-base gap: how does alanine get into the lysosome--good evidence for inclusion regardless of gap	SAB
dmpp	Dimethylallyl diphosphate	Consumed only	Cytosol	DMATT	DMATTx version is complete - w/out gaps - was in original copy of gaps list	NJ
ipdp	Isopentenyl diphosphate	Consumed only	Cytosol	DMATT	GRTTx version is complete - w/out gaps - was not in this list but was in original list as gap	NJ
dmhptcoa	2,6 dimethylheptanoyl-CoA	Consumed only	Cytosol	DMHPTCRNCPT1	DMHPTCRNCPT1 added (although the metabolism of this metabolite has not been well characterized, it should be transportable on the sam carnitine shuttle as other FA)	NJ
lyxnt	L-lyxonate	Produced only	Cytosol	DOGULND1	known gap; could not find any specific info as to how this is metabolized in humans	ND
xylnt	L-Xylonate	Produced only	Cytosol	DOGULND2	known gap; could not find any specific info as to how this is metabolized in humans	ND
thrnt	L-Threonate	Produced only	Cytosol	DOGULNO1	known gap; could not find any specific info as to how this is metabolized in humans	ND
eryth	L-Erythrulose	Produced only	Cytosol	DOGULNO2	known gap; could not find any specific info as to how this is metabolized in humans	ND
e4hglu	L-erythro-4-Hydroxyglutamate	Consumed only	Cytosol	EHGLAT	knowledge-base gap: cytosolic enzyme found for a reaction that is not a gap in the mitochondria	SAB
4h2oglt	4-Hydroxy-2-oxoglutarate	Produced only	Cytosol	EHGLAT	gap OK--cytosolic localized enzyme found for reaction	SAB
s2l2n2m2m	de-Fuc form of PA6 (w/o peptide linkage)	Consumed only	Cytosol	ENGASE	leave reaction even though it causes gap; it's a redundant reaction since the primary rxn is in lysosome, but there's evidence it might be in cytosol	ND
n2m2nm	n2m2nmasn (w/o peptide linkage)	Consumed only	Cytosol	ENGASE2	leave reaction even though it causes gap; it's a redundant reaction since the primary rxn is in lysosome, but there's evidence it might be in cytosol	ND
n2m2nmn	reducing GlcNAc removed form of n2m2nmasn (w/o peptide)	Produced only	Cytosol	ENGASE2	leave reaction even though it causes gap; it's a redundant reaction since the primary rxn is in lysosome, but there's evidence it might be in cytosol	ND
2ameph	(2-Aminoethyl)phosphonate	Consumed only	Cytosol	EPCTX	knowledge gap - strong evidence for the presence of these metabolites in humans lacking, although the enzyme can carry out this conversion (in addition to others more relevant to human metabolism	NJ
cmp2amep	CMP-2-aminoethylphosphonate	Produced only	Cytosol	EPCTX	knowledge gap - strong evidence for the presence of these metabolites in humans lacking, although the enzyme can carry out this conversion (in addition to others more relevant to human metabolism	NJ

Metabolite Abbreviation	Metabolite Name	Gap Type	Compartment	Reaction Abbreviation	Notes	Reviewer
m2mn	(alpha-D-mannosyl)2-beta-D-mannosyl-N-acetylglucosamine	Consumed only	Cytosol	A_MANASE	leave reaction even though it causes gap; it's a redundant reaction since the primary rxn is in lysosome, but there's evidence it might be in cytosol	ND
mn	beta-1,4-mannose-N-acetylglucosamine	Produced only	Cytosol	A_MANASE	leave reaction even though it causes gap; it's a redundant reaction since the primary rxn is in lysosome, but there's evidence it might be in cytosol	ND
bdg2hc	cis-beta-D-Glucosyl-2-hydroxycinnamate	Consumed only	Cytosol	BDG2HCGHD	model-scope gap: unimportant	SAB
2coum	cis-2-Hydroxy cinnamate	Produced only	Cytosol	BDG2HCGHD	model-scope gap: unimportant	SAB
betald	Betaine aldehyde	Consumed only	Cytosol	BETALDHx	knowledge-based gap	MM
bhb	(R)-3-Hydroxybutanoate	Consumed only	Cytosol	BHBt	gap removed; added extracellular transport rxn	ND
bhb	(R)-3-Hydroxybutanoate	Consumed only	Cytosol	BHBtm	gap removed; added extracellular transport rxn	ND
bz	Benzoate	Consumed only	Cytosol	BZt	gap filled, added BZt	NJ
bz	Benzoate	Consumed only	Cytosol	BZtr	gap filled, added BZt	NJ
cbl2	Cob(II)alamin	Produced only	Mitochondria	CBL2tm	leave for the moment --> unfinished PW	IT
prostg1	(13E)-11alpha-Hydroxy-9,15-dioxoprost-13-enoate	Consumed only	Cytosol	CBR1	principally a knowledge gap problem - further metabolism, etc unknown, since at the 'fringes' partial model scope gap also - see Goodman and Gilman, Murray Biochem for overall pathway	NJ
cca_d3	Calcitroic acid (D3)	Consumed only	Mitochondria	CCA_D3tm	knowledge gap; reactions as well as enzymes for vit D degradation are unknown	IT
chsterol	Cholesterol	Consumed only	Golgi Apparatus	CHSTEROLtg	By IT shows transport between golgi and plasma membrane	NJ
chtn	chitin	Consumed only	Cytosol	CHTNASE	leave gap; function has only been characterized in vitro, no physiologically known function	ND
clpn_hs	cardiolipin (homo sapiens)	Produced only	Cytosol	CLS_hs	cardiolipin is a biomass constituent, should be made part of biomass, in future can also update metabolic interconversions	NJ
co2	CO2	Consumed only	Nucleus	CO2tn	gap is due to transporter rxn in nucleus (not needed now, but ok to leave in)	ND
ntm2amep	N-Trimethyl-2-aminoethylphosphonate	Consumed only	Cytosol	CPCTDTX	knowledge gap - strong evidence for the presence of these metabolites in humans lacking, although the enzyme can carry out this conversion (in addition to others more relevant to human metabolism	NJ
cmpntm2amep	CMP-N-trimethyl-2-aminoethylphosphonate	Produced only	Cytosol	CPCTDTX	knowledge gap - strong evidence for the presence of these metabolites in humans lacking, although the enzyme can carry out this conversion (in addition to others more relevant to human metabolism	NJ
crtn	Creatinine	Produced only	Cytosol	CRTNsyn	model-scope gap: a transporter could be added to get this out of the cell, but relatively unimportant	SAB
crtstrn	Corticosterone	Produced only	Endoplasmic Reticulum	CRTSTRNtr	CRTSTRNtr, CRTSTRNtm	NJ
thcys	Thiocysteine	Produced only	Cytosol	CYSLYSL	knowledge-based gap	MM
ala-D	D-Alanine	Consumed only	Lysosome	DALAt2rL	knowledge-base gap: how does alanine get into the lysosome--good evidence for inclusion regardless of gap	SAB
dmpp	Dimethylallyl diphosphate	Consumed only	Cytosol	DMATT	DMATTx version is complete - w/out gaps - was in original copy of gaps list	NJ
ipdp	Isopentenyl diphosphate	Consumed only	Cytosol	DMATT	GRTTx version is complete - w/out gaps - was not in this list but was in original list as gap	NJ
dmhptcoa	2,6 dimethylheptanoyl-CoA	Consumed only	Cytosol	DMHPTCRNCPT1	DMHPTCRNCPT1 added (although the metabolism of this metabolite has not been well characterized, it should be transportable on the sam carnitine shuttle as other FA)	NJ
lyxnt	L-lyxonate	Produced only	Cytosol	DOGULND1	known gap; could not find any specific info as to how this is metabolized in humans	ND
xylnt	L-Xylonate	Produced only	Cytosol	DOGULND2	known gap; could not find any specific info as to how this is metabolized in humans	ND
thrnt	L-Threonate	Produced only	Cytosol	DOGULNO1	known gap; could not find any specific info as to how this is metabolized in humans	ND
eryth	L-Erythrulose	Produced only	Cytosol	DOGULNO2	known gap; could not find any specific info as to how this is metabolized in humans	ND
e4hglu	L-erythro-4-Hydroxyglutamate	Consumed only	Cytosol	EHGLAT	knowledge-base gap: cytosolic enzyme found for a reaction that is not a gap in the mitochondria	SAB
4h2oglt	4-Hydroxy-2-oxoglutarate	Produced only	Cytosol	EHGLAT	gap OK--cytosolic localized enzyme found for reaction	SAB
s2l2n2m2m	de-Fuc form of PA6 (w/o peptide linkage)	Consumed only	Cytosol	ENGASE	leave reaction even though it causes gap; it's a redundant reaction since the primary rxn is in lysosome, but there's evidence it might be in cytosol	ND
n2m2nm	n2m2nmasn (w/o peptide linkage)	Consumed only	Cytosol	ENGASE2	leave reaction even though it causes gap; it's a redundant reaction since the primary rxn is in lysosome, but there's evidence it might be in cytosol	ND
n2m2nmn	reducing GlcNAc removed form of n2m2nmasn (w/o peptide)	Produced only	Cytosol	ENGASE2	leave reaction even though it causes gap; it's a redundant reaction since the primary rxn is in lysosome, but there's evidence it might be in cytosol	ND
2ameph	(2-Aminoethyl)phosphonate	Consumed only	Cytosol	EPCTX	knowledge gap - strong evidence for the presence of these metabolites in humans lacking, although the enzyme can carry out this conversion (in addition to others more relevant to human metabolism	NJ
cmp2amep	CMP-2-aminoethylphosphonate	Produced only	Cytosol	EPCTX	knowledge gap - strong evidence for the presence of these metabolites in humans lacking, although the enzyme can carry out this conversion (in addition to others more relevant to human metabolism	NJ

Metabolite Abbreviation	Metabolite Name	Gap Type	Compartment	Reaction Abbreviation	Notes	Reviewer
lcts	Lactose	Consumed only	Cytosol	LCTStl	gap removed; have decided to remove this reaction since it probably doesn't exist in the cytosol -- I don't want to associate it with the lysosomal complex until it has been experimentally verified	ND
nformanth	N-Formylanthranilate	Produced only	Cytosol	LFORKYNHYD	reaction based on KEGG--probably OK	SAB
lipoate	Lipoate	Produced only	Cytosol	LIPOti	leave gap for the moment; lipoate gets imported in cell, converted to dihydrolipoate and this compounds is the active form and gets directly exported again - unknown mechanism. Concrete reaction from lipoate to dihydrolipoate is not really clear to me	IT
lanost	Lanosterol	Consumed only	Cytosol	LNS14DM	was stated to occur in cyt and ER -> ER has the completed pathway	NJ
44mctr	4,4-dimethylcholesta-8,14,24-trienol	Produced only	Cytosol	LNS14DM	was stated to occur in cyt and ER -> ER has the completed pathway	NJ
lum3	Lumisterol 3	Produced only	Cytosol	LS3	is not really a gap; conversion takes place when sufficient Vit D has been produced in skin cell - this mechanism avoids toxicity by Vit D - I included this reaction for completeness	IT
2mcit	2-Methylcitrate	Produced only	Cytosol	MCITS	added transport rxn 2MCITt; methycitrate is excreted in urine of patients who suffer from propionic acidaemia (Weidman et al. 1979)	MM
malACP	Malonyl-[acyl-carrier protein]	Produced only	Cytosol	MCOATA	FA synthesis is lumped, so activation w/ ACP will not be utilized at this point, this may be useful in a future version of the reconstruction if FAS is 'unlumped'	NJ
fna5moxam	Formyl-N-acetyl-5-methoxykynurenamine	Produced only	Cytosol	MELATN23DOX	citation describes reaction but unknown where product goes	SAB
6hoxmelatn	6-Hydroxymelatonin	Produced only	Cytosol	MELATNOX	model-scope gap: end of the line in KEGG	SAB
meoh	Methanol	Consumed only	Lysosome	MEOHtly	gap removed; added transporter for lysosome transport	ND
mi3456p	1D-myo-Inositol 3,4,5,6-tetrakisphosphate	Consumed only	Cytosol	MI3456PK	cannot remove gap; this molecule is currently a dead end	ND
2mcacn	cis-2-Methylaconitate	Consumed only	Cytosol	MICITDr	leave as gap; rxn is low confidence (physiological data from rat), model scope gap for now	ND
micit	methylisocitrate	Produced only	Cytosol	MICITDr	rxn has been removed (since it is incorrect) unfortunately it has been replaced with another (MICITDr) which does NOT remove the gap; this is a knowledge-base gap, not sure if methyl-cis-aconitate or methylisocitrate are physiologically relevant cpds, but	ND
malttr	Maltotriose	Consumed only	Cytosol	MLTG1	leave gap; protein has been functionally verified but could not find any information on its localization	ND
mmcoa-S	(S)-Methylmalonyl-CoA	Consumed only	Cytosol	MMCD	knowledge-based gap	MM
4aabutn	4-Acetamidobutanoate	Produced only	Cytosol	NABTNO	knowledge-base gap: not entirely clear how these metabolites are metabolized	SAB
adprbp	ADPribose 2'-phosphate	Produced only	Cytosol	NADPN	leave gap; exceeds model	IT
na1	Sodium	Produced only	Golgi Apparatus	NAt3_1g	gap is due to transport reaction in Golgi (not needed now, but ok to leave in)	ND
carn	L-Carnosine	Consumed only	Cytosol	NBAHH_ir	model-scope gap: carnosine metabolism not in current model	SAB
nmptrc	N-Methylputrescine	Consumed only	Cytosol	NMPTRCOX	modeling-gap: these compounds are found in mam. cells according to reference, but not in our model	SAB
1mpyr	1-Methylpyrrolinium	Produced only	Cytosol	NMPTRCOX	modeling-gap: these compounds are found in mam. cells according to reference, but not in our model	SAB
no	Nitric oxide	Produced only	Cytosol	NOt	added diffusive transporter	SAB
xtp	XTP	Consumed only	Cytosol	NTPP11	leave gap; knowledge gap	IT
o2s	Superoxide anion	Consumed only	Cytosol	O2St	gap removed; added rxn for diffusion of o2s	ND
o2s	Superoxide anion	Consumed only	Cytosol	O2Stm	gap removed; added rxn for diffusion of o2s	ND
o2s	Superoxide anion	Consumed only	Cytosol	O2Stn	gap removed; added rxn for diffusion of o2s	ND
o2s	Superoxide anion	Consumed only	Nucleus	O2Stn	gap removed; added rxn for diffusion of o2s	ND
o2s	Superoxide anion	Consumed only	Cytosol	O2Stx	gap removed; added rxn for diffusion of o2s	ND
o2s	Superoxide anion	Consumed only	Peroxisome	O2Stx	gap removed; added rxn for diffusion of o2s	ND
hnifedipine	hydroxy nifedipine	Produced only	Cytosol	P4503A4	HNIFEDIPINEte	NJ
pcollglys	Procollagen L-lysine	Consumed only	Cytosol	PCLYSOX	model-scope gap	MM
pcollg5hlys	Procollagen 5-hydroxy-L-lysine	Produced only	Cytosol	PCLYSOX	model-scope gap	MM
pcrn	propionyl-carnitine	Produced only	Mitochondria	PCRNtm	CSNAT3m removed and replaced with CSNAT2m, CSNAT3x made reversible	NJ
pe_hs	phosphatidylethanolamine (homo sapiens)	Produced only	Golgi Apparatus	PE_HStg	pe_hs not used in any Golgi rxns right now	NJ
2pglyc	2-Phosphoglycolate	Consumed only	Cytosol	PGLYCP	appears to be a knowledge base gap (INCOMPLETE!!)	ND
phyQ	Phylloquinone	Produced only	Cytosol	PHYQt	leave gap; knowledge gap	IT
ppa	Propionate (n-C3:0)	Consumed only	Cytosol	PPAt	gap removed; added rxn for extracellular -> cytosolic transport based on ref in thuy's mito model	ND
ppa	Propionate (n-C3:0)	Consumed only	Cytosol	PPAtm	gap removed; added rxn for extracellular -> cytosolic transport based on ref in thuy's mito model	ND
2hyoxplac	2-Hydroxyphenylacetate	Produced only	Cytosol	PPOR	reaction based on KEGG	SAB
pro-D	D-Proline	Consumed only	Lysosome	PRODt2rL	knowledge-base gap: good evidence for inclusion regardless of gap	SAB
pro-L	L-Proline	Consumed only	Lysosome	PROt2rL	knowledge-base gap: good evidence for inclusion regardless of gap	SAB

Metabolite Abbreviation	Metabolite Name	Gap Type	Compartment	Reaction Abbreviation	Notes	Reviewer
ps_hs	phosphatidylserine (homo sapiens)	Produced only	Endoplasmic Reticulum	PS_HSter	ps_hs not used in any ER reactions currently	NJ
ps_hs	phosphatidylserine (homo sapiens)	Produced only	Golgi Apparatus	PS_HStg	ps_hs not used in any Golgi rxns right now	NJ
pyam5p	Pyridoxamine 5'-phosphate	Produced only	Mitochondria	PYAM5Ptm	leave gap; excedds model	IT
pydx5p	Pyridoxal 5'-phosphate	Produced only	Mitochondria	PYDX5Ptm	leave gap; excedds model	IT
pylald	Perillyl aldehyde	Consumed only	Cytosol	PYLALDOX	knowledge-base gap: unknown where this metabolite goes in humans; low priority subsystem also	SAB
peracd	Perillic acid	Produced only	Cytosol	PYLALDOX	knowledge-base gap: unknown where this metabolite goes in humans; low priority subsystem also	SAB
retn	Retinoate	Produced only	Nucleus	RAtn	leave gap; excedds model	IT
rbl-D	D-Ribulose	Consumed only	Cytosol	RBK_D	gap removed; physiologial evidence that D-ribulose can be taken up by cultured human fibroblasts	ND
rbt	Ribitol	Consumed only	Cytosol	RBTt	gap is due to extracellular transport reaction (not needed now, but ok to leave in)	ND
retncoa	retinoyl CoA	Produced only	Cytosol	RETNCOA	Retinoyl-CoA is used in cell to retinoylate proteins --> I created demand function	IT
dmnoncoa	4,8 dimethylnonanoyl-CoA	Consumed only	Cytosol	SCP22x	Will leave gap at present time, sterol carrier protein can move fatty acid derivatives (usually steroid precursors) into different compartments, details about specific substrates and mechanisms not known	NJ
dtt	Dithiothreitol	Consumed only	Cytosol	SELCYSLY	modeling gap: selenoamino acid metabolism is a low priority	SAB
dttOX	Oxidized dithiothreitol	Produced only	Cytosol	SELCYSLY	modeling gap: selenoamino acid metabolism is a low priority	SAB
selmeth	Selenomethionine	Consumed only	Cytosol	SELMETAT	knowledge-base gap: unknown where selmeth comes from in humans; modeling evidence only, need a source of selenomethionine	SAB
selnp	Selenophosphate	Produced only	Cytosol	SELNPS	model-scope gap: although there is not a great deal of information about selenoamino acid metabolism, this area is not particularly important to the initial model	SAB
l2n2m2mn	de-Fuc, reducing GlcNAc removed, de-Sia form of PA6 (w/o peptide linkage)	Produced only	Cytosol	SIAASE	leave reaction even though it causes gap; it's a redundant reaction since the primary rxn is in lysosome, but there's evidence it might be in cytosol	ND
spc_hs	sphingosylphosphorylcholine (homo sapiens)	Produced only	Cytosol	SMPD4	filled with SMPD4 and SPC_HSt - note that each one individually could have resolved the gap, however the evidence for both reactions was approximately the same	NJ
spc_hs	sphingosylphosphorylcholine (homo sapiens)	Produced only	Cytosol	SPC_HSt	filled with SMPD4 and SPC_HSt - note that each one individually could have resolved the gap, however the evidence for both reactions was approximately the same	NJ
spc_hs	sphingosylphosphorylcholine (homo sapiens)	Produced only	Cytosol	SPHMDAc	filled with SMPD4 and SPC_HSt - note that each one individually could have resolved the gap, however the evidence for both reactions was approximately the same	NJ
f5hoxkyn	Formyl-5-hydroxykynurenamine	Produced only	Cytosol	SRTN23OX	model-scope gap	SAB
nmthsrtn	N-Methylserotonin	Produced only	Cytosol	SRTNMTX	knowledge-base gap: KEGG is the only evidence for this reaction	SAB
dtdprmn	dTDP-L-rhamnose	Produced only	Cytosol	TDPDRR	leave gap; according to Devlin, dTDP leads to UDP-GalNAc biosynthesis in mammals, but I can't find any evidence how this might occur	ND
thm	Thiamin	Produced only	Mitochondria	THMt2m	leave gap; knowledge based: It is thought that this SLC19A2 is also reponsible for the mitochondrial transport since cells of TRMA patients (thiamine-responive megaloblastic anemia) in this gene show no mitochondrial transport of thiamine. Role of thiamine in mitochondria is not clear (therefore will be a gap) since there is no mitochondrial thiamine diphosphokinase)	IT
phom	O-Phospho-L-homoserine	Consumed only	Cytosol	THRS	knowledge-based gap	MM
q10	Ubiquinone-10	Consumed only	Cytosol	TRDR2	leave gap knowledge gap: q10h2 Ubiquinol-10 Produced only Cytosol TRDR2 Miscellaneous [c]:h+nadph+q10-->nadp+q10h2 IT leave gap; knowledge gap:	IT
q10	Ubiquinone-10	Consumed only	Cytosol	TRDR3	leave gap knowledge gap: q10h2 Ubiquinol-10 Produced only Cytosol TRDR3 Miscellaneous [c]:h+nadh+q10-->nad+q10h2 IT leave gap; knowledge gap:	IT
tre	Trehalose	Consumed only	Cytosol	TREH	leave gap; rxn only based on sequence annotation	ND
ts3	Tachysterol 3	Produced only	Cytosol	TS3	is not really a gap; conversion takes place when sufficient Vit D has been produced in skin cell - this mechanism avoids toxicity by Vit D - I included this reaction for completeness	IT
txa2	Thromboxane A2	Consumed only	Cytosol	TXA2te	removed gap, replaced TXA2te	NJ
txa2	Thromboxane A2	Consumed only	Cytosol	TXA2tr	removed gap, replaced TXA2te	NJ
udpg	UDPglucose	Produced only	Golgi Apparatus	UDPGLCtg	gap is due to transporter rxn in Golgi (not needed now, but ok to leave in)	ND
udpacgal	UDP-N-acetyl-D-galactosamine	Produced only	Endoplasmic Reticulum	UGALNACter	udpacgal is not used in any ER reactions currently	NJ
whtststerone	w hydroxy testosterone	Consumed only	Cytosol	WHTSTSTERONEte	WHTSTSTERONEte - unkown transporter and metabolism	NJ

Metabolite Abbreviation	Metabolite Name	Gap Type	Compartment	Reaction Abbreviation	Notes	Reviewer
xol7ah2	3alpha,7alpha-Dihydroxy-5beta-cholestane	Produced only	Endoplasmic Reticulum	XOL7AH2tr	no xol7ah2 reactions in ER right now	NJ
xolest2_hs	cholesterol ester (from FULLR2)	Produced only	Cytosol	XOLEST2te	xolest2_hs produced extracellularly, currently no intracellular reaction in model w/ xol from R2	NJ
xoltriol	3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestane	Produced only	Endoplasmic Reticulum	XOLTRIOLtr	no xoltriol reactions in ER right now	NJ
2mcit	2-Methylcitrate	Produced only	Cytosol	2MCITt	added transport rxn 2MCITt; methycitrate is excreted in urine of patients who suffer from propionic acidaemia (Weidman et al. 1979)	MM
andrstrnglc	androsterone glucuronide	Consumed only	Cytosol	ANDRSTRNGLCte	ANDRSTRNGLCtr, ANDRSTRNGLCte	NJ
bhb	(R)-3-Hydroxybutanoate	Consumed only	Cytosol	BHBt	gap removed; added extracellular transport rxn	ND
bz	Benzoate	Consumed only	Cytosol	BZt	gap filled, added BZt	NJ
hom-L	L-Homoserine	Produced only	Cytosol	HOMt4	knowledge-based gap; insufficient evidence to show that homoserine i an intermediate of the cystathione g-lyase rxn, which would have removed gap	MM
lipoate	Lipoate	Produced only	Cytosol	LIPOti	leave gap for the moment; lipoate gets imported in cell, converted to dihydrolipoate and this compounds is the active form and gets directly exported again - unknown mechanism. Concrete reaction from lipoate to dihydrolipoate is not really clear to me	IT
no	Nitric oxide	Produced only	Cytosol	NOt	added diffusive transporter	SAB
o2s	Superoxide anion	Consumed only	Cytosol	O2St	gap removed; added rxn for diffusion of o2s	ND
phyQ	Phylloquinone	Produced only	Cytosol	PHYQt	leave gap; knowledge gap	IT
ppa	Propionate (n-C3:0)	Consumed only	Cytosol	PPAt	gap removed; added rxn for extracellular -> cytosolic transport based on ref in thuy's mito model	ND
rbt	Ribitol	Consumed only	Cytosol	RBTt	gap is due to extracellular transport reaction (not needed now, but ok to leave in)	ND
spc_hs	sphingosylphosphorylcholine (homo sapiens)	Produced only	Cytosol	SPC_HSt	filled with SMPD4 and SPC_HSt - note that each one individually could have resolved the gap, however the evidence for both reactions was approximately the same	NJ
txa2	Thromboxane A2	Consumed only	Cytosol	TXA2te	removed gap, replaced TXA2te	NJ
whtststerone	w hydroxy testosterone	Consumed only	Cytosol	WHTSTSTERONEte	WHTSTSTERONEte - unkown transporter and metabolism	NJ
xolest2_hs	cholesterol ester (from FULLR2)	Produced only	Cytosol	XOLEST2te	xolest2_hs produced extracellularly, currently no intracellular reaction in model w/ xol from R2	NJ
gncore1	GlcNAc-alpha-1,4-Core 1	Produced only	Golgi Apparatus	A4GNT1g	gap ok; this is a core structure can undergo tissue-specific, developmentally regulated, or protein-specific modifications (which are not included in this model)	ND
gncore2	GlcNAc-alpha-1,4-Core 2	Produced only	Golgi Apparatus	A4GNT2g	gap ok; this is a core structure can undergo tissue-specific, developmentally regulated, or protein-specific modifications (which are not included in this model)	ND
chsterol	Cholesterol	Consumed only	Golgi Apparatus	CHSTEROLtg	By IT shows transport between golgi and plasma membrane	NJ
core5	Core 5	Produced only	Golgi Apparatus	CORE5GTg	gap ok; this is a core structure can undergo tissue-specific, developmentally regulated, or protein-specific modifications (which are not included in this model)	ND
core7	Core 7	Produced only	Golgi Apparatus	CORE7GTg	gap ok; this is a core structure can undergo tissue-specific, developmentally regulated, or protein-specific modifications (which are not included in this model)	ND
core8	Core 8	Produced only	Golgi Apparatus	CORE8GTg	gap ok; this is a core structure can undergo tissue-specific, developmentally regulated, or protein-specific modifications (which are not included in this model)	ND
glc1man	glucose-1,3-mannose oligosaccharide	Produced only	Golgi Apparatus	ENMAN1g	gap OK; as far as I understand, these are markers for mannosidase activity in Golgi so presumably remain there	ND
glc2man	(2)[glucose-1,3]-mannose oligosaccharide	Produced only	Golgi Apparatus	ENMAN2g	gap OK; as far as I understand, these are markers for mannosidase activity in Golgi so presumably remain there	ND
glc3man	glucose-1,2-(2)[glucose-1,3]-mannose oligosaccharide	Produced only	Golgi Apparatus	ENMAN3g	gap OK; as far as I understand, these are markers for mannosidase activity in Golgi so presumably remain there	ND
glc1man	glucose-1,3-mannose oligosaccharide	Produced only	Golgi Apparatus	ENMAN4g	gap OK; as far as I understand, these are markers for mannosidase activity in Golgi so presumably remain there	ND
glc1man	glucose-1,3-mannose oligosaccharide	Produced only	Golgi Apparatus	ENMAN5g	gap OK; as far as I understand, these are markers for mannosidase activity in Golgi so presumably remain there	ND
glc1man	glucose-1,3-mannose oligosaccharide	Produced only	Golgi Apparatus	ENMAN6g	gap OK; as far as I understand, these are markers for mannosidase activity in Golgi so presumably remain there	ND
Ser/Thr	protein-linked serine or threonine residue (O-glycosylation site)	Consumed only	Golgi Apparatus	GALNTg	gap ok; represents peptide binding site for O-glycans	ND
galside_hs	galactocerebroside (homo sapiens)	Consumed only	Cytosol	GALSIDEtg	gap resolved added GALSIDEtl	NJ
coa	Coenzyme A	Produced only	Golgi Apparatus	GAO1g	CHAT is complete (in cytosol)	NJ
coa	Coenzyme A	Produced only	Golgi Apparatus	GAO2g	CHAT is complete (in cytosol)	NJ
k	potassium	Produced only	Golgi Apparatus	Kt3g	gap is due to transporter rxn in Golgi (not needed now, but ok to leave in)	ND

Metabolite Abbreviation	Metabolite Name	Gap Type	Compartment	Reaction Abbreviation	Notes	Reviewer
n5m2masn	((N-acetyl-D-glucosaminyl)5-(alpha-D-mannosyl)2-beta-D-mannosyl-diacetylchitobiosyl)-L-asparagine (protein)	Produced only	Golgi Apparatus	M16N4Tg	gap OK; leave as dead-end of N-glycan synthesis since its degradation is not included in model	ND
f1a	F1alpha	Produced only	Golgi Apparatus	N4Tg	gap ok; this is a core structure can undergo tissue-specific, developmentally regulated, or protein-specific modifications (which are not included in this model)	ND
na1	Sodium	Produced only	Golgi Apparatus	NAt3_1g	gap is due to transport reaction in Golgi (not needed now, but ok to leave in)	ND
camp	cAMP	Consumed only	Golgi Apparatus	PDE1g	exceeds model; leave gap	IT
amp	AMP	Produced only	Golgi Apparatus	PDE1g	exceeds model; leave gap since cAMP is gap too	IT
35cgmp	3',5'-Cyclic GMP	Consumed only	Golgi Apparatus	PDE4g	exceeds model; leave gap	IT
pe_hs	phosphatidylethanolamine (homo sapiens)	Produced only	Golgi Apparatus	PE_HStg	pe_hs not used in any Golgi rxns right now	NJ
ps_hs	phosphatidylserine (homo sapiens)	Produced only	Golgi Apparatus	PS_HStg	ps_hs not used in any Golgi rxns right now	NJ
udpg	UDPglucose	Produced only	Golgi Apparatus	UDPGLCtg	gap is due to transporter rxn in Golgi (not needed now, but ok to leave in)	ND
3amp	3'-AMP	Consumed only	Lysosome	3NTD7l	nucleotide monophosphates come from DNA and RNA degradation in lysosome (by acid exonucleoase and acid ribonuclease). Will be dead-end in model as well as their efflux transport systems.	IT
pi	Phosphate	Produced only	Lysosome	3NTD7l	DNA and RNA degradation takes place in the Lysosome. The associated reactions are dead-ends in the model since we do not model DNA, RNA. Thus, pi coming from these dead-end reaction can easily stay a gap for the moment since it will not effect the model capacities but a pi-transport system from/to Lysosome is not known to me.	IT
4abut	4-Aminobutanoate	Consumed only	Lysosome	ABUTt2rL	knowledge-base gap	SAB
acgbgbside_hs	beta GalNAc globoside (homo sapiens)	Produced only	Lysosome	ACGBGBSIDEtl	gap removed by single reaction addition: NAGAIby added in analogy to NAGAIy (no real evidence that this occurs in vivo)	NJ
ade	Adenine	Consumed only	Lysosome	ADEtl	leave gap; knowledge gap: at least i have no idea of the function of adenine in lysosome but uptake was studied by PMID: 2925670	IT
ala-L	L-Alanine	Consumed only	Lysosome	ALAt2rL	model-scope gap	SAB
chsterol	Cholesterol	Consumed only	Lysosome	CHSTEROLt1	Assumed flip-flop mechanism - if not used in lysosome currently it's okay	NJ
ala-D	D-Alanine	Consumed only	Lysosome	DALAt2rL	knowledge-base gap: how does alanine get into the lysosome--good evidence for inclusion regardless of gap	SAB
fald	Formaldehyde	Produced only	Lysosome	FALDtly	gap removed; added transporter for lysosomal transport	ND
galside_hs	galactocerebroside (homo sapiens)	Consumed only	Cytosol	GALSIDEtl	gap resolved added GALSIDEtl	NJ
gly	Glycine	Consumed only	Lysosome	GLYt2rL	knowledge-base gap: how does glycine get into the lysosome--good evidence for inclusion regardless of gap	SAB
h2o2	Hydrogen peroxide	Consumed only	Lysosome	H2O2tly	gap removed; found physiological evidence that can diffuse across compartments	ND
hxan	Hypoxanthine	Consumed only	Lysosome	HXANtl	Gene associated--IT's addition	SAB
idour	L-Iduronate	Consumed only	Cytosol	IDOURtly	knowledge gap; makes sense that idour is transported to cytosol (to maintain osmotic balance in lysosome) but I can't find any specific rxn which consume it there	ND
ins	Inosine	Consumed only	Lysosome	INStl	Gene associated--IT's addition	SAB
pi	Phosphate	Produced only	Lysosome	LAPCOAl	DNA and RNA degradation takes place in the Lysosome. The associated reactions are dead-ends in the model since we do not model DNA, RNA. Thus, pi coming from these dead-end reaction can easily stay a gap for the moment since it will not effect the model capacities but a pi-transport system from/to Lysosome is not known to me.	IT
lcts	Lactose	Consumed only	Cytosol	LCTStl	gap removed; have decided to remove this reaction since it probably doesn't exist in the cytosol -- I don't want to associate it with the lysosomal complex until it has been experimentally verified	ND
meoh	Methanol	Consumed only	Lysosome	MEOHtly	gap removed; added transporter for lysosome transport	ND
malttr	Maltotriose	Consumed only	Lysosome	MLTG1ly	leave gap; this rxn is valid in vivo, malttr usually arises from glycogen deg, but does not appear in our network for modeling reasons (only made representative structure for glycogen and malttr doesn't happen to be one of its degradation products)	ND
acgbgbside_hs	beta GalNAc globoside (homo sapiens)	Produced only	Lysosome	NAGAIby	gap removed by single reaction addition: NAGAIby added in analogy to NAGAIy (no real evidence that this occurs in vivo)	NJ
ump	UMP	Consumed only	Lysosome	NTD2l	nucleotide monophosphates come from DNA and RNA degradation in lysosome (by acid exonucleoase and acid ribonuclease). Will be dead-end in model as well as their efflux transport systems.	IT
pi	Phosphate	Produced only	Lysosome	NTD2l	DNA and RNA degradation takes place in the Lysosome. The associated reactions are dead-ends in the model since we do not model DNA, RNA. Thus, pi coming from these dead-end reaction can easily stay a gap for the moment since it will not effect the model capacities but a pi-transport system from/to Lysosome is not known to me.	IT

Metabolite Abbreviation	Metabolite Name	Gap Type	Compartment	Reaction Abbreviation	Notes	Reviewer
dcmp	dCMP	Consumed only	Lysosome	NTD3l	nucleotide monophosphates come from DNA and RNA degradation in lysosome (by acid exonucleoase and acid ribonuclease). Will be dead-end in model as well as their efflux transport systems.	IT
dcyt	Deoxycytidine	Produced only	Lysosome	NTD3l	nucleotide monophosphates come from DNA and RNA degradation in lysosome (by acid exonucleoase and acid ribonuclease). Will be dead-end in model as well as their efflux transport systems.	IT
pi	Phosphate	Produced only	Lysosome	NTD3l	DNA and RNA degradation takes place in the Lysosome. The associated reactions are dead-ends in the model since we do not model DNA, RNA. Thus, pi coming from these dead-end reaction can easily stay a gap for the moment since it will not effect the model capacities but a pi-transport system from/to Lysosome is not known to me.	IT
cmp	CMP	Consumed only	Lysosome	NTD4l	nucleotide monophosphates come from DNA and RNA degradation in lysosome (by acid exonucleoase and acid ribonuclease). Will be dead-end in model as well as their efflux transport systems.	IT
pi	Phosphate	Produced only	Lysosome	NTD4l	DNA and RNA degradation takes place in the Lysosome. The associated reactions are dead-ends in the model since we do not model DNA, RNA. Thus, pi coming from these dead-end reaction can easily stay a gap for the moment since it will not effect the model capacities but a pi-transport system from/to Lysosome is not known to me.	IT
dtmp	dTMP	Consumed only	Lysosome	NTD5l	nucleotide monophosphates come from DNA and RNA degradation in lysosome (by acid exonucleoase and acid ribonuclease). Will be dead-end in model as well as their efflux transport systems.	IT
pi	Phosphate	Produced only	Lysosome	NTD5l	DNA and RNA degradation takes place in the Lysosome. The associated reactions are dead-ends in the model since we do not model DNA, RNA. Thus, pi coming from these dead-end reaction can easily stay a gap for the moment since it will not effect the model capacities but a pi-transport system from/to Lysosome is not known to me.	IT
damp	dAMP	Consumed only	Lysosome	NTD6l	nucleotide monophosphates come from DNA and RNA degradation in lysosome (by acid exonucleoase and acid ribonuclease). Will be dead-end in model as well as their efflux transport systems.	IT
dad-2	Deoxyadenosine	Produced only	Lysosome	NTD6l	nucleotide monophosphates come from DNA and RNA degradation in lysosome (by acid exonucleoase and acid ribonuclease). Will be dead-end in model as well as their efflux transport systems.	IT
pi	Phosphate	Produced only	Lysosome	NTD6l	DNA and RNA degradation takes place in the Lysosome. The associated reactions are dead-ends in the model since we do not model DNA, RNA. Thus, pi coming from these dead-end reaction can easily stay a gap for the moment since it will not effect the model capacities but a pi-transport system from/to Lysosome is not known to me.	IT
amp	AMP	Consumed only	Lysosome	NTD7l	nucleotide monophosphates come from DNA and RNA degradation in lysosome (by acid exonucleoase and acid ribonuclease). Will be dead-end in model as well as their efflux transport systems.	IT
pi	Phosphate	Produced only	Lysosome	NTD7l	DNA and RNA degradation takes place in the Lysosome. The associated reactions are dead-ends in the model since we do not model DNA, RNA. Thus, pi coming from these dead-end reaction can easily stay a gap for the moment since it will not effect the model capacities but a pi-transport system from/to Lysosome is not known to me.	IT
dgmp	dGMP	Consumed only	Lysosome	NTD8l	nucleotide monophosphates come from DNA and RNA degradation in lysosome (by acid exonucleoase and acid ribonuclease). Will be dead-end in model as well as their efflux transport systems.	IT
dgsn	Deoxyguanosine	Produced only	Lysosome	NTD8l	nucleotide monophosphates come from DNA and RNA degradation in lysosome (by acid exonucleoase and acid ribonuclease). Will be dead-end in model as well as their efflux transport systems.	IT
pi	Phosphate	Produced only	Lysosome	NTD8l	DNA and RNA degradation takes place in the Lysosome. The associated reactions are dead-ends in the model since we do not model DNA, RNA. Thus, pi coming from these dead-end reaction can easily stay a gap for the moment since it will not effect the model capacities but a pi-transport system from/to Lysosome is not known to me.	IT
gmp	GMP	Consumed only	Lysosome	NTD9l	nucleotide monophosphates come from DNA and RNA degradation in lysosome (by acid exonucleoase and acid ribonuclease). Will be dead-end in model as well as their efflux transport systems.	IT
pi	Phosphate	Produced only	Lysosome	NTD9l	DNA and RNA degradation takes place in the Lysosome. The associated reactions are dead-ends in the model since we do not model DNA, RNA. Thus, pi coming from these dead-end reaction can easily stay a gap for the moment since it will not effect the model capacities but a pi-transport system from/to Lysosome is not known to me.	IT
h2o2	Hydrogen peroxide	Consumed only	Lysosome	PRDXl	gap removed; found physiological evidence that can diffuse across compartments	ND
meoh	Methanol	Consumed only	Lysosome	PRDXl	gap removed; added transporter for lysosome transport	ND
fald	Formaldehyde	Produced only	Lysosome	PRDXl	gap removed; added transporter for lysosomal transport	ND

Metabolite Abbreviation	Metabolite Name	Gap Type	Compartment	Reaction Abbreviation	Notes	Reviewer
pro-D	D-Proline	Consumed only	Lysosome	PRODt2rL	knowledge-base gap: good evidence for inclusion regardless of gap	SAB
pro-L	L-Proline	Consumed only	Lysosome	PROt2rL	knowledge-base gap: good evidence for inclusion regardless of gap	SAB
1a2425thvitd2	1-alpha,24R,25-Trihydroxyvitamin D2	Produced only	Mitochondria	1a,24,25VITD2Hm	resolved gap; included ER import	IT
1a2425thvitd3	1-alpha,24R,25-Trihydroxyvitamin D3	Produced only	Mitochondria	1a,24,25VITD3Hm	resolved gap; included ER and cytosolic export	IT
1a2425thvitd2	1-alpha,24R,25-Trihydroxyvitamin D2	Produced only	Mitochondria	1a,25VITD2Hm	resolved gap; included ER import	IT
1a2425thvitd3	1-alpha,24R,25-Trihydroxyvitamin D3	Produced only	Mitochondria	1a,25VITD3Hm	resolved gap; included ER and cytosolic export	IT
3hbcoa-R	(R)-3-Hydroxybutanoyl-CoA	Produced only	Mitochondria	3HBCDm	Reactions not currently used since lumped FA ox rxns used, in future updates if FA ox is broken up they will be used	NJ
5hoxindact	5-Hydroxyindoleacetaldehyde	Consumed only	Mitochondria	5HOXINDACTOXm	knoweldge-base gap: unknown if/how molecules are transported	SAB
5hoxindoa	5-Hydroxyindoleacetate	Produced only	Mitochondria	5HOXINDACTOXm	knoweldge-base gap: unknown if/how molecules are transported	SAB
acglu	N-Acetyl-L-glutamate	Produced only	Mitochondria	ACGSm	knowledge-base gap	SAB
adprib	ADPribose	Consumed only	Mitochondria	ADPRDPm	leave gap; exceeds model	IT
r5p	alpha-D-Ribose 5-phosphate	Produced only	Mitochondria	ADPRDPm	leave gap; r5p is normally metabolized by pentose-phosphate pathway in cytosol. Since adprib, the substrate of the reaction, is also a gap, I will not include a mitochondrial transport reaction just for model purpose	IT
ptrc	Putrescine	Produced only	Mitochondria	AGMTm	Localization data for reactions causes this gap--OK	SAB
acg5p	N-Acetyl-L-glutamyl 5-phosphate	Consumed only	Mitochondria	AGPRim	knowledge-base gap: also reaction isn't so certain	SAB
acg5sa	N-Acetyl-L-glutamate 5-semialdehyde	Produced only	Mitochondria	AGPRim	knowledge-base gap: also reaction isn't so certain	SAB
id3acald	Indole-3-acetaldehyde	Consumed only	Mitochondria	ALDD20xm	model-scope gap	SAB
ind3ac	Indole-3-acetate	Produced only	Mitochondria	ALDD20xm	model-scope gap	SAB
bamppald	beta-Aminopropion aldehyde	Consumed only	Mitochondria	BAMPPALDOXm	knowledge-base gap: not known how/if metabolites get into and out o mitochondria	SAB
bhb	(R)-3-Hydroxybutanoate	Consumed only	Cytosol	BHBtm	gap removed; added extracellular transport rxn	ND
c2m26dcoa	cis-2-Methyl-5-isopropylhexa-2,5-dienoyl-CoA	Consumed only	Mitochondria	C2M26DCOAHLm	model-scope gap: unimportant	SAB
cbl2	Cob(II)alamin	Produced only	Mitochondria	CBL2tm	leave for the moment --> unfinished PW	IT
cbl1	Cob(I)alamin	Consumed only	Mitochondria	CBLATm	leave for the moment --> unfinished PW	IT
adocbl	Adenosylcobalamin	Produced only	Mitochondria	CBLATm	leave for the moment --> unfinished PW	IT
cca_d3	Calcitroic acid (D3)	Consumed only	Mitochondria	CCA_D3tm	knowledge gap; reactions as well as enzymes for vit D degradation are unknown	IT
chsterol	Cholesterol	Consumed only	Lysosome	CHSTEROLt1	Assumed flip-flop mechanism - if not used in lysosome currently it's okay	NJ
clpndcoa	clupanodonyl CoA	Produced only	Mitochondria	CLPNDCPT2	was not removed - technically/physiologically the reaction CAN occur, however long chain fatty acids (>C22) won't be oxidized in the mitochondria so it is unlikely to be used	NJ
pcrn	propionyl-carnitine	Produced only	Mitochondria	CSNAT2m	CSNAT3m removed and replaced with CSNAT2m, CSNAT3x made reversible	NJ
cys-L	L-Cysteine	Consumed only	Mitochondria	CYSTAm	knowledge-based gap	MM
mercppyr	Mercaptopyruvate	Produced only	Mitochondria	CYSTAm	knowledge-based gap	MM
3aib-D	D-3-Amino-isobutanoate	Consumed only	Mitochondria	D3AIBTm	gap eliminated; MM added mitochondrial transport reaction (3AIBtm)	IT
dd2coa	trans-Dodec-2-enoyl-CoA	Consumed only	Mitochondria	DCIm	Reactions not currently used since lumped FA ox rxns used, in future updates if FA ox is broken up they will be used	NJ
dd3coa	3-dodecenoyl CoA	Produced only	Mitochondria	DCIm	Reactions not currently used since lumped FA ox rxns used, in future updates if FA ox is broken up they will be used	NJ
dcyt	Deoxycytidine	Consumed only	Mitochondria	DCK1m	leave gap for the moment; i discovered the reaction (DCK1m) during the gap filling process but i could not find any other evidence how dcyt comes into the mitochondria. Dcmp will certainly originate from mtDNA. The reaction is right now reversible but i think that the most probable direction is towards the dcmp production which leaves the question where dcyt is coming from.	IT
dcmp	dCMP	Produced only	Mitochondria	DCK1m	leave gap for the moment; i discovered the reaction (DCK1m) during the gap filling process but i could not find any other evidence how dcyt comes into the mitochondria. Dcmp will certainly originate from mtDNA. The reaction is right now reversible but i think that the most probable direction is towards the dcmp production which leaves the question where dcyt is coming from.	IT
tdcoa	Tetradecanoyl-CoA (n-C14:0CoA)	Produced only	Mitochondria	FAOXC140	FAOXC140 added	NJ
glyclt	Glycolate	Produced only	Mitochondria	GCALDDm	leave gap; can't find any refs as to what happens to mitochondrial glyc -- could be transported to cytosol, but no evidence for this nor need for its transport in model	ND
ser-L	L-Serine	Consumed only	Mitochondria	GHMT2rm	knowledge-based gap	MM
3htmelys	3-Hydroxy-N6,N6,N6-trimethyl-L-lysine	Consumed only	Mitochondria	GHMT3m	knowledge-based gap	MM

Metabolite Abbreviation	Metabolite Name	Gap Type	Compartment	Reaction Abbreviation	Notes	Reviewer
4tmeabut	4-Trimethylammoniobutanal	Produced only	Mitochondria	GHMT3m	knowledge-based gap	MM
glac	D-glucurono-6,3-lactone	Consumed only	Mitochondria	GLACOm	leave gap; this reaction was added based on only modeling evidence	ND
glcr	D-Glucarate	Produced only	Mitochondria	GLACOm	ok; glucaric acid seems to be a dead end metabolite [Marsh, Carb Res 1986]	ND
glyclt	Glycolate	Produced only	Mitochondria	GLYCLTDym	leave gap; can't find any refs as to what happens to mitochondrial glyc -- could be transported to cytosol, but no evidence for this nor need for its transport in model	ND
lgt-S	(R)-S-Lactoylglutathione	Consumed only	Mitochondria	GLYOXm	gap ok; function of the mitochondrial pool of glyoxalase II activity is unknown	ND
alpa_hs	lysophosphatidic acid (homo sapiens)	Produced only	Mitochondria	GPAMm_hs	knowledge gap, pathway complete in cytosol - see PMID: 10514455, suggests that pa_hs crosses mit membrane (rat)	NJ
h2co3	carbonic acid	Produced only	Mitochondria	H2CO3D2m	genes and good evidence, passed to NCD	SAB
h2co3	carbonic acid	Produced only	Mitochondria	H2CO3Dm	genes and good evidence, passed to NCD	SAB
hexccoa	Hexacosanoyl-CoA (n-C26:0CoA)	Produced only	Mitochondria	HEXCCPT2	was not removed - technically/physiologically the reaction CAN occur, however long chain fatty acids (>C22) won't be oxidized in the mitochondria so it is unlikely to be used	NJ
4hpro-LT	trans-4-Hydroxy-L-proline	Consumed only	Mitochondria	HPROxm	model-scope gap: no collagen in model currently	SAB
hpyr	Hydroxypyruvate	Consumed only	Mitochondria	HPYRDCm	true knowledge gap; there are very few reports describing the properties of this enzyme, none in human tissues	ND
im4act	Imidazole-4-acetaldehyde	Consumed only	Mitochondria	IMACTD_m	knowledge-base gap: not known how this gets to mitochondria	SAB
im4ac	Imidazole-4-acetate	Produced only	Mitochondria	IMACTD_m	model-scope gap: potential end-product	SAB
imp	IMP	Produced only	Mitochondria	INSKm	what the hell is happening with this??? No evidence for biosynthetic pathway of atp/gtp from imp in mito	IT
lald-D	D-Lactaldehyde	Consumed only	Mitochondria	LCADi_Dm	knowledge gap; this step is not wel characterized in humans	ND
lald-L	L-Lactaldehyde	Consumed only	Mitochondria	LCADim	knowledge gap; this step is not wel characterized in humans	ND
Lcyst	L-Cysteate	Consumed only	Mitochondria	LCYSTATm	knowledge-based gap	MM
lgnccoa	lignocericyl coenzyme A	Produced only	Mitochondria	LGNCCPT2	was not removed - technically/physiologically the reaction CAN occur, however long chain fatty acids (>C22) won't be oxidized in the mitochondria so it is unlikely to be used	NJ
ACP	acyl carrier protein	Consumed only	Mitochondria	MCOATAm	FA synthesis is lumped, so activation w/ ACP will not be utilized at this point, this may be useful in a future version of the reconstruction if FAS is 'unlumped'	NJ
malACP	Malonyl-[acyl-carrier protein]	Produced only	Mitochondria	MCOATAm	FA synthesis is lumped, so activation w/ ACP will not be utilized at this point, this may be useful in a future version of the reconstruction if FAS is 'unlumped'	NJ
n4abutn	N4-Acetylaminobutanal	Consumed only	Mitochondria	NABTNOm	knowledge-base gap: not entirely clear how these metabolites are metabolized	SAB
4aabutn	4-Acetamidobutanoate	Produced only	Mitochondria	NABTNOm	knowledge-base gap: not entirely clear how these metabolites are metabolized	SAB
didp	dIDP	Consumed only	Mitochondria	NDPK10m	leave gap; knowledge gap	IT
ditp	dITP	Produced only	Mitochondria	NDPK10m	leave gap; knowledge gap	IT
utp	UTP	Produced only	Mitochondria	NDPK2m	gap eliminated; added UMPKm for modeling purpose: although no activity of such an enzyme has been shown for mitochondria up to dat the UMP kinase function has to be present in order to "restaure" UTP from UMP for/ from mRNA synthesis/degradation. PMID: 11912132 showed that cytosolic CMP-UMP kinase has no mitochondrial activity	IT
idp	IDP	Consumed only	Mitochondria	NDPK9m	leave gap; knowledge gap	IT
itp	ITP	Produced only	Mitochondria	NDPK9m	leave gap; knowledge gap	IT
nmn	NMN	Consumed only	Mitochondria	NMNATm	leave gap; i don't know how to connect rxn in mito with cytosol	IT
nicrnt	Nicotinate D-ribonucleotide	Consumed only	Mitochondria	NNATm	leave gap; i don't know how to connect rxn in mito with cytosol	IT
dnad	Deamino-NAD+	Produced only	Mitochondria	NNATm	leave gap; i don't know how to connect rxn in mito with cytosol	IT
nrvnccoa	nervonyl coenzyme A	Produced only	Mitochondria	NRVNCCPT2	was not removed - technically/physiologically the reaction CAN occur, however long chain fatty acids (>C22) won't be oxidized in the mitochondria so it is unlikely to be used	NJ
o2s	Superoxide anion	Consumed only	Cytosol	O2Stm	gap removed; added rxn for diffusion of o2s	ND
4mptnl	4-Methylpentanal	Produced only	Mitochondria	P45011A1m	metabolized to isocaproic acid and isocapryl alcohol - see PMID: 8645003	NJ
20ahchsterol	20alpha-hydroxy cholesterol	Produced only	Mitochondria	P450SCC1m	knowledge gap, model scope gap - hydroxylated cholesterol metabolism in the mitochondria - no significant literature found	NJ
pcrn	propionyl-carnitine	Produced only	Mitochondria	PCRNtm	CSNAT3m removed and replaced with CSNAT2m, CSNAT3x made reversible	NJ
phe-L	L-Phenylalanine	Consumed only	Mitochondria	PHETA1m	knowledge-base gap: leave in case transporters are found in the future	SAB
phpyr	Phenylpyruvate	Produced only	Mitochondria	PHETA1m	knowledge-base gap: leave in case transporters are found in the future	SAB
pnto-R	(R)-Pantothenate	Consumed only	Mitochondria	PNTKm	leave gap for now: Hoertnagel et al, 2003, Human Mol. genetics, 12(3), 321-327: They also proposed that a complete intramitochondrial pathway for de novo synthesis of CoA exists, but could not find further evidence for this	IT

Metabolite Abbreviation	Metabolite Name	Gap Type	Compartment	Reaction Abbreviation	Notes	Reviewer
4ppan	D-4'-Phosphopantothenate	Produced only	Mitochondria	PNTKm	leave gap for now: Hoertnagel et al, 2003, Human Mol. genetics, 12(3), 321-327: They also proposed that a complete intramitochondrial pathway for de novo synthesis of CoA exists, but could not find further evidence for this	IT
ppa	Propionate (n-C3:0)	Consumed only	Cytosol	PPAtm	gap removed; added rxn for extracellular -> cytosolic transport based on ref in thuy's mito model	ND
3hpcoa	3-Hydroxypropionyl-CoA	Produced only	Mitochondria	PRPNCOAHYDm	knowledge-base gap: good evidence for inclusion regardless of gap	SAB
pyam5p	Pyridoxamine 5'-phosphate	Produced only	Mitochondria	PYAM5Ptm	leave gap; excedds model	IT
pydx5p	Pyridoxal 5'-phosphate	Produced only	Mitochondria	PYDX5Ptm	leave gap; excedds model	IT
pylald	Perillyl aldehyde	Consumed only	Mitochondria	PYLALDOXm	knowledge-base gap: unknown where this metabolite goes in humans; low priority subsystem also	SAB
peracd	Perillic acid	Produced only	Mitochondria	PYLALDOXm	knowledge-base gap: unknown where this metabolite goes in humans; low priority subsystem also	SAB
sl-L	L-sulfolactate	Consumed only	Mitochondria	SLDxm	knowledge-based gap	MM
t2m26dcoa	trans-2-Methyl-5-isopropylhexa-2,5-dienoyl-CoA	Consumed only	Mitochondria	T2M26DCOAHLm	knowledge-base gap	SAB
tetpent3coa	tetracosapentaenoyl coenzyme A, n-3	Produced only	Mitochondria	TETPENT3CPT2	was not removed - technically/physiologically the reaction CAN occur, however long chain fatty acids (>C22) won't be oxidized in the mitochondria so it is unlikely to be used	NJ
tetpent6coa	tetracosapentaenoyl coenzyme A, n-6	Produced only	Mitochondria	TETPENT6CPT2	was not removed - technically/physiologically the reaction CAN occur, however long chain fatty acids (>C22) won't be oxidized in the mitochondria so it is unlikely to be used	NJ
tettet6coa	tetracosatetraenoyl coenzyme A	Produced only	Mitochondria	TETTET6CPT2	was not removed - technically/physiologically the reaction CAN occur, however long chain fatty acids (>C22) won't be oxidized in the mitochondria so it is unlikely to be used	NJ
thm	Thiamin	Produced only	Mitochondria	THMt2m	leave gap; knowledge based: It is thought that this SLC19A2 is also reponsible for the mitochondrial transport since cells of TRMA patients (thiamine-responive megaloblastic anemia) in this gene show no mitochondrial transport of thiamine. Role of thiamine in mitochondria is not clear (therefore will be a gap) since there is no mitochondrial thiamine diphosphokinase)	IT
trdox	Oxidized thioredoxin	Consumed only	Mitochondria	TRDRm	knowledge gap; thioredoxin is needed by ribonucleotide reductase, however, up to date only cytosolic version has been identified	IT
trdrd	Reduced thioredoxin	Produced only	Mitochondria	TRDRm	knowledge gap; thioredoxin is needed by ribonucleotide reductase, however, up to date only cytosolic version has been identified	IT
tdcoa	Tetradecanoyl-CoA (n-C14:0CoA)	Produced only	Mitochondria	TTDCPT2	FAOXC140 added	NJ
tyr-L	L-Tyrosine	Consumed only	Mitochondria	TYRTAm	knowledge-base gap: not clear how tyr-L enters mitochondria	SAB
xoldiolone	7alpha,12alpha-Dihydroxycholest-4-en-3-one	Consumed only	Mitochondria	XOLDIOLONEtm	no xoldiolone reactions in mitochondria	NJ
co2	CO2	Consumed only	Nucleus	CO2tn	gap is due to transporter rxn in nucleus (not needed now, but ok to leave in)	ND
dna	DNA	Consumed only	Nucleus	DNAMTSEn	model-scope gap: DNA not represented in model so methylation will require sinks	SAB
dna5mtc	DNA 5-methylcytosine	Produced only	Nucleus	DNAMTSEn	model-scope gap: DNA not represented in model so methylation will require sinks	SAB
dna	DNA	Consumed only	Nucleus	DNAMTn	model-scope gap: DNA not represented in model so methylation will require sinks	SAB
dna5mtc	DNA 5-methylcytosine	Produced only	Nucleus	DNAMTn	model-scope gap: DNA not represented in model so methylation will require sinks	SAB
o2s	Superoxide anion	Consumed only	Cytosol	O2Stn	gap removed; added rxn for diffusion of o2s	ND
o2s	Superoxide anion	Consumed only	Nucleus	O2Stn	gap removed; added rxn for diffusion of o2s	ND
retn	Retinoate	Produced only	Nucleus	RAtn	leave gap; excedds model	IT
thbpt	Tetrahydrobiopterin	Produced only	Nucleus	SPRn	knowledge-base gap: unknown where selmeth comes from in humans; modeling evidence only, need a source of selenomethionine	IT
ahcys	S-Adenosyl-L-homocysteine	Produced only	Endoplasmic Reticulum	AHCYStr	gap filled, added AHCYStr	NJ
dhcholoylcoa	3alpha,7alpha-Dihydroxy-5beta-cholest-24-enoyl-CoA	Produced only	Endoplasmic Reticulum	AMACR2r	leave gap for now, complete pathway in peroxisome	NJ
cholcoas	3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestanoyl-CoA(S)	Produced only	Endoplasmic Reticulum	AMACRr	leave gap for now, complete pathway in peroxisome	NJ
amet	S-Adenosyl-L-methionine	Consumed only	Endoplasmic Reticulum	AMETr	gap filled, added AMETr	NJ
bz	Benzoate	Consumed only	Cytosol	BZtr	gap filled, added BZt	NJ
nh4	Ammonium	Produced only	Endoplasmic Reticulum	CBPPer	knowledge-base gap; we don't have any rxns which consume nh4 in the ER. If need be one could potentially resolve this gap by adding ER-cytosol transport (but have not come across any evidence for that yin a preliminary search)	ND
coke	cocaine	Consumed only	Endoplasmic Reticulum	COKECBESr	11DOCRTSLtr, 11DOCRTSLtm	NJ

Metabolite Abbreviation	Metabolite Name	Gap Type	Compartment	Reaction Abbreviation	Notes	Reviewer
crtstrn	Corticosterone	Produced only	Endoplasmic Reticulum	CRTSTRNtr	CRTSTRNtr, CRTSTRNtm	NJ
crn	L-Carnitine	Consumed only	Endoplasmic Reticulum	CSNATer	Not currently used reactions, see PMID: 11257506	NJ
acrn	O-Acetylcarnitine	Produced only	Endoplasmic Reticulum	CSNATer	Not currently used reactions, see PMID: 11257506	NJ
Asn-X-Ser/Thr	protein-linked asparagine residue (N-glycosylation site)	Consumed only	Endoplasmic Reticulum	DOLASNT_Ler	gap OK; represents polypeptide which would be broken down in lysosome	ND
Asn-X-Ser/Thr	protein-linked asparagine residue (N-glycosylation site)	Consumed only	Endoplasmic Reticulum	DOLASNT_Uer	gap OK; represents polypeptide which would be broken down in lysosome	ND
estriol	estriol	Produced only	Cytosol	ESTRIOLtr	no cytosolic estriol reactions	NJ
ru5p-D	D-Ribulose 5-phosphate	Produced only	Endoplasmic Reticulum	GNDer	there has been speculation that the entire PPP occurs in the ER, but there is no direct evidence for any enzymes past this step…. Rather than inferring rest of pathway have left as a knowledge gap	ND
dem2emgacpail_prot_hs	deacylated-(phosphoethanolaminyl-dimannosyl),(phosphoethanolaminyl)-mannosyl-glucosaminyl-acylphosphatidylinositol	Produced only	Endoplasmic Reticulum	GPIDA2er	gap ok, represents additional processing of GPI anchor; this is a modeling dead-end (transport of this metabolite to plasma memebrane is beyond the scope of our network)	ND
dgpi_prot_hs	deacylated-glycophosphatidylinositol (GPI)-anchored protein	Produced only	Endoplasmic Reticulum	GPIDAer	gap ok, represents additional processing of GPI anchor; this is a modeling dead-end (transport of this metabolite to plasma memebrane is beyond the scope of our network)	ND
pre_prot	glycophosphatidylinositol (GPI)-anchored protein precursor	Consumed only	Endoplasmic Reticulum	H7'TAer	gap OK; peptide binding site for GPI anchor, its biosynthesis is outside the scope of model	ND
pre_prot	glycophosphatidylinositol (GPI)-anchored protein precursor	Consumed only	Endoplasmic Reticulum	H8TAer	gap OK; peptide binding site for GPI anchor, its biosynthesis is outside the scope of model	ND
hmgcoa	Hydroxymethylglutaryl-CoA	Consumed only	Endoplasmic Reticulum	HMGCOARr	complete reaction in peroxisomal version	NJ
mev-R	(R)-Mevalonate	Produced only	Endoplasmic Reticulum	HMGCOARr	complete reaction in peroxisomal version	NJ
pre_prot	glycophosphatidylinositol (GPI)-anchored protein precursor	Consumed only	Endoplasmic Reticulum	M4ATAer	gap OK; peptide binding site for GPI anchor, its biosynthesis is outside the scope of model	ND
m(em)3gacpail_prot_hs	mannosyl-3-(phosphoethanolaminyl-mannosyl)-glucosaminyl-acylphosphatidylinositol-Protein (M4A)	Produced only	Endoplasmic Reticulum	M4ATAer	gap OK; this is an alternative GPI structure which has recently been suggested as a substrate of human GPI transamidase	ND
pre_prot	glycophosphatidylinositol (GPI)-anchored protein precursor	Consumed only	Endoplasmic Reticulum	M4BTAer	gap OK; peptide binding site for GPI anchor, its biosynthesis is outside the scope of model	ND
mem2emgacpail_prot_hs	({[(mannosyl),(phosphoethanolaminyl)]-dimannosyl},{phosphoethanolaminyl})-mannosyl-glucosaminyl-acylphosphatidylinositol-Protein (M4B)	Produced only	Endoplasmic Reticulum	M4BTAer	gap OK; this is an alternative GPI structure which has recently been suggested as a substrate of human GPI transamidase	ND
acald	Acetaldehyde	Produced only	Endoplasmic Reticulum	P45017A2r	ACALDtr - knowledge gap, unknown mechanism	NJ
acald	Acetaldehyde	Produced only	Endoplasmic Reticulum	P45017A4r	ACALDtr - knowledge gap, unknown mechanism	NJ
whtststerone	w hydroxy testosterone	Produced only	Endoplasmic Reticulum	P4503A43r	WHTSTSTERONEte - unkown transporter and metabolism	NJ
12harachd	12 hydroxy arachidonic acid	Produced only	Endoplasmic Reticulum	P4504B1r	knowledge gap > model scope limitation, final location of many of the hydroxylated arachidonic acid products not well defined - many of these have short half-lives and are quickly metabolized	NJ
wharachd	w-hydroxyl arachidonic acid	Produced only	Endoplasmic Reticulum	P4504F121r	knowledge gap > model scope limitation, final location of many of the hydroxylated arachidonic acid products not well defined - many of these have short half-lives and are quickly metabolized	NJ
18harachd	18 hydroxy arachidonic acid	Produced only	Endoplasmic Reticulum	P4504F81r	knowledge gap > model scope limitation, final location of many of the hydroxylated arachidonic acid products not well defined - many of these have short half-lives and are quickly metabolized	NJ
leuktrB4wcooh	w-carboxy leukotriene B4	Produced only	Endoplasmic Reticulum	P450LTB4r	principally knowledge gap, partial scope limitations	NJ
pecgoncoa	Pseudoecgonyl-CoA	Produced only	Endoplasmic Reticulum	PECGONCOATr	modeling-gap: this is the end of the line in KEGG for cocaine degradation	SAB
prostgd2	Prostaglandin D2	Produced only	Endoplasmic Reticulum	PGDIr	principally a knowledge gap problem - further metabolism, etc unknown, since at the 'fringes' partial model scope gap also - see Goodman and Gilman, Murray Biochem for overall pathway	NJ

Metabolite Abbreviation	Metabolite Name	Gap Type	Compartment	Reaction Abbreviation	Notes	Reviewer
prostge2	Prostaglandin E2	Produced only	Endoplasmic Reticulum	PGESr	principally a knowledge gap problem - further metabolism, etc unknown, since at the 'fringes' partial model scope gap also - see Goodman and Gilman, Murray Biochem for overall pathway	NJ
prostgi2	Prostaglandin I2	Produced only	Endoplasmic Reticulum	PGISr	principally a knowledge gap problem - further metabolism, etc unknown, since at the 'fringes' partial model scope gap also - see Goodman and Gilman, Murray Biochem for overall pathway	NJ
pail4p_hs	1-Phosphatidyl-1D-myo-inositol 4-phosphate (Homo sapiens)	Consumed only	Endoplasmic Reticulum	PI4P3Ker	leave gap; this is just an alternative localization for enzyme in complet (functional) cytosolic pathway	ND
pail34p_hs	phosphatidylinositol-3,4-bisphosphate (Homo sapiens)	Produced only	Endoplasmic Reticulum	PI4P3Ker	leave gap; this is just an alternative localization for enzyme in complet (functional) cytosolic pathway	ND
pail5p_hs	1-Phosphatidyl-1D-myo-inositol 5-phosphate (Homo sapiens)	Consumed only	Endoplasmic Reticulum	PI5P3Ker	leave gap; this is just an alternative localization for enzyme in complet (functional) cytosolic pathway	ND
pail35p_hs	phosphatidylinositol-3,5-bisphosphate (Homo sapiens)	Produced only	Endoplasmic Reticulum	PI5P3Ker	leave gap; this is just an alternative localization for enzyme in complet (functional) cytosolic pathway	ND
pail_hs	phosphatidylinositol (homo sapiens)	Consumed only	Endoplasmic Reticulum	PIK3er	leave gap; this is just an alternative localization for enzyme in complet (functional) cytosolic pathway	ND
pail3p_hs	1-Phosphatidyl-1D-myo-inositol 3-phosphate (Homo sapiens)	Produced only	Endoplasmic Reticulum	PIK3er	leave gap; this is just an alternative localization for enzyme in complet (functional) cytosolic pathway	ND
pepslys	peptide sans lysine	Produced only	Endoplasmic Reticulum	PLYSPSer	model-scope gap; this is just a generic peptide	MM
akg	2-Oxoglutarate	Consumed only	Endoplasmic Reticulum	PROAKGOX1r	modeling gap: hydroxproline isn't currently used in the model so this reaction isn't (yet) important	SAB
pro-L	L-Proline	Consumed only	Endoplasmic Reticulum	PROAKGOX1r	modeling gap: hydroxproline isn't currently used in the model so this reaction isn't (yet) important	SAB
4hpro-LT	trans-4-Hydroxy-L-proline	Produced only	Endoplasmic Reticulum	PROAKGOX1r	modeling gap: hydroxproline isn't currently used in the model so this reaction isn't (yet) important	SAB
succ	Succinate	Produced only	Endoplasmic Reticulum	PROAKGOX1r	modeling gap: hydroxproline isn't currently used in the model so this reaction isn't (yet) important	SAB
ps_hs	phosphatidylserine (homo sapiens)	Produced only	Endoplasmic Reticulum	PS_HSter	ps_hs not used in any ER reactions currently	NJ
hxdcal	Hexadecanal	Produced only	Endoplasmic Reticulum	SGPL11r	removed due to SGPL12r	NJ
R1coa_hs	R group 1 Coenzyme A homo sapiens	Consumed only	Endoplasmic Reticulum	SOAT11r	complete reaction in cytosolic version	NJ
xolest_hs	cholesterol ester	Produced only	Endoplasmic Reticulum	SOAT11r	complete reaction in cytosolic version	NJ
R2coa_hs	R group 2 Coenzyme A homo sapiens	Consumed only	Endoplasmic Reticulum	SOAT12r	complete reaction in cytosolic version	NJ
xolest_hs	cholesterol ester	Produced only	Endoplasmic Reticulum	SOAT12r	complete reaction in cytosolic version	NJ
so4	Sulfate	Produced only	Endoplasmic Reticulum	STS1r	- knowledge gap, unknown mechanis	NJ
estrones	Estrone 3-sulfate	Consumed only	Endoplasmic Reticulum	STS2r	STS2 is completed, intracellular transport of estrones not known - knowledge gap	NJ
so4	Sulfate	Produced only	Endoplasmic Reticulum	STS2r	- knowledge gap, unknown mechanis	NJ
chsterols	cholesterol sulfate	Consumed only	Endoplasmic Reticulum	STS3r	STS3 is completed, intracellular transport of chsterols not known - knowledge gap	NJ
so4	Sulfate	Produced only	Endoplasmic Reticulum	STS3r	- knowledge gap, unknown mechanis	NJ
prgnlones	pregnenolone sulfate	Consumed only	Endoplasmic Reticulum	STS4r	STS4 is completed, intracellular transport of prgnlones not known - knowledge gap	NJ
so4	Sulfate	Produced only	Endoplasmic Reticulum	STS4r	- knowledge gap, unknown mechanis	NJ
txa2	Thromboxane A2	Consumed only	Cytosol	TXA2tr	removed gap, replaced TXA2te	NJ
udpacgal	UDP-N-acetyl-D-galactosamine	Produced only	Endoplasmic Reticulum	UGALNACter	udpacgal is not used in any ER reactions currently	NJ
andrstrnglc	androsterone glucuronide	Produced only	Endoplasmic Reticulum	UGT1A3r	ANDRSTRNGLCtr, ANDRSTRNGLCte	NJ
ahandrostan	3alpha-Hydroxy-5beta-androstan-17-one	Consumed only	Endoplasmic Reticulum	UGT1A7r	model scope and knowledge limitations	NJ
dhcholestanate	3alpha,7alpha-Dihydroxy-5beta-cholestanate	Consumed only	Endoplasmic Reticulum	VLCS2r	leave - gap in ER, complete in mit-> peroxisome	NJ
thcholstoic	3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestanoate	Consumed only	Endoplasmic Reticulum	VLCSr	leave - gap in ER, complete in mit-> peroxisome	NJ
xol7ah2	3alpha,7alpha-Dihydroxy-5beta-cholestane	Produced only	Endoplasmic Reticulum	XOL7AH2tr	no xol7ah2 reactions in ER right now	NJ
xoldiolone	7alpha,12alpha-Dihydroxycholest-4-en-3-one	Consumed only	Mitochondria	XOLDIOLONEtm	no xoldiolone reactions in mitochondria	NJ
xoltriol	3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestane	Produced only	Endoplasmic Reticulum	XOLTRIOLtr	no xoltriol reactions in ER right now	NJ

Metabolite Abbreviation	Metabolite Name	Gap Type	Compartment	Reaction Abbreviation	Notes	Reviewer
Ser-Gly/Ala-X-Gly	protein-linked serine residue (glycosaminoglycan attachment site)	Consumed only	Endoplasmic Reticulum	XYLTer	gap ok; represents peptide binding site for GAG chains	ND
3odcoa	3-Oxodecanoyl-CoA	Consumed only	Peroxisome	ACACT4p	knowledge-based gap	NJ
3oddcoa	3-Oxododecanoyl-CoA	Consumed only	Peroxisome	ACACT5p	model-scope gap: presumably will be a cellular demand	NJ
dcacoa	Decanoyl-CoA (n-C10:0CoA)	Produced only	Peroxisome	ACACT5p	peroxisomal thioesterases are known to exist, they hydrolyze acyl-Coa to their respective free FA and coa, it is believed that they may regulat FA content of perox membranes and perox prolif, at this point no info to add transporters or new reactions	NJ
3otdcoa	3-Oxotetradecanoyl-CoA	Consumed only	Peroxisome	ACACT6p	knowledge-base gap	NJ
ddcacoa	Dodecanoyl-CoA (n-C12:0CoA)	Produced only	Peroxisome	ACACT6p	peroxisomal thioesterases are known to exist, they hydrolyze acyl-Coa to their respective free FA and coa, it is believed that they may regulat FA content of perox membranes and perox prolif, at this point no info to add transporters or new reactions	NJ
3ohdcoa	3-Oxohexadecanoyl-CoA	Consumed only	Peroxisome	ACACT7p	model-scope gap	NJ
tdcoa	Tetradecanoyl-CoA (n-C14:0CoA)	Produced only	Peroxisome	ACACT7p	peroxisomal thioesterases are known to exist, they hydrolyze acyl-Coa to their respective free FA and coa, it is believed that they may regulat FA content of perox membranes and perox prolif, at this point no info to add transporters or new reactions	NJ
3ohodcoa	3-Oxooctadecanoyl-CoA	Consumed only	Peroxisome	ACACT8p	knowledge-base gap: KEGG is the only evidence for this reaction	NJ
3ohxccoa	3-Oxohexacosyl-CoA	Consumed only	Peroxisome	ACACT9p	knowledge-base gap	NJ
ttccoa	tetracosanoyl-CoA (n-C24:0CoA)	Produced only	Peroxisome	ACACT9p	peroxisomal thioesterases are known to exist, they hydrolyze acyl-Coa to their respective free FA and coa, it is believed that they may regulat FA content of perox membranes and perox prolif, at this point no info to add transporters or new reactions	NJ
alkylR1oh	hydroxy alkyl chain	Consumed only	Peroxisome	AGPSx	knowledge gap and model scope limitation - when tissue specific models are developed and specific FA of interested are identified, specific pathways (rather than general FA) can be picked and described	NJ
c2m26dcoa	cis-2-Methyl-5-isopropylhexa-2,5-dienoyl-CoA	Consumed only	Peroxisome	C2M26DCOAHLx	model-scope gap: unimportant	SAB
arg-D	D-Arginine	Consumed only	Peroxisome	DARGOp	model-scope gap: relatively unimportant at this stage	SAB
5g2oxpt	5-Guanidino-2-oxopentanoate	Produced only	Peroxisome	DARGOp	model-scope gap: relatively unimportant at this stage	SAB
oaa	Oxaloacetate	Produced only	Peroxisome	DASPO1p	knowledge-based gap	MM
Rtotalcoa	R total Coenzyme A	Consumed only	Peroxisome	DHAPAx	model-scope gap	NJ
dhap	Dihydroxyacetone phosphate	Consumed only	Peroxisome	DHAPAx	DHAPA in cytosol should be complete w/ ADHAPtx	NJ
orn-D	D-Ornithine	Consumed only	Peroxisome	DORNOp	model-scope gap: relatively unimportant at this stage	SAB
5a2opntn	5-Amino-2-oxopentanoate	Produced only	Peroxisome	DORNOp	knowledge-based gap	SAB
pro-D	D-Proline	Consumed only	Peroxisome	DPROOp	model-scope gap: relatively unimportant at this stage	SAb
1p2cbxl	1-Pyrroline-2-carboxylate	Produced only	Peroxisome	DPROOp	model-scope gap: relatively unimportant at this stage	SAB
b2coa	trans-But-2-enoyl-CoA	Produced only	Peroxisome	ECOAH1x	knowledge-base gap: localization is by enzyme similarity	SAB
icit	Isocitrate	Consumed only	Peroxisome	ICDHyp	known gap; the source of intraperoxisomal isocitrate has not been determined [Geisbrecht 1999]	ND
malcoa	Malonyl-CoA	Consumed only	Peroxisome	MCDp	peroxisomal thioesterases are known to exist, they hydrolyze acyl-Coa to their respective free FA and coa, it is believed that they may regulat FA content of perox membranes and perox prolif, at this point no info to add transporters or new reactions	NJ
mmcoa-S	(S)-Methylmalonyl-CoA	Consumed only	Peroxisome	MMCDp	knowledge-based gap	MM
o2s	Superoxide anion	Consumed only	Cytosol	O2Stx	gap removed; added rxn for diffusion of o2s	ND
o2s	Superoxide anion	Consumed only	Peroxisome	O2Stx	gap removed; added rxn for diffusion of o2s	ND
prpncoa	Propenoyl-CoA	Consumed only	Peroxisome	PRPNCOAHYDx	knowledge-base gap	SAB
3hpcoa	3-Hydroxypropionyl-CoA	Produced only	Peroxisome	PRPNCOAHYDx	knowledge-base gap	SAB
hdca	Hexadecanoate (n-C16:0)	Produced only	Peroxisome	PTE2x	peroxisomal thioesterases are known to exist, they hydrolyze acyl-Coa to their respective free FA and coa, it is believed that they may regulat FA content of perox membranes and perox prolif, at this point no info to add transporters or new reactions	NJ
phyt	phytanic acid	Produced only	Peroxisome	PTE4x	PHYTt	NJ
adrn	adrenic acid	Produced only	Peroxisome	PTE5x	peroxisomal thioesterases are known to exist, they hydrolyze acyl-Coa to their respective free FA and coa, it is believed that they may regulat FA content of perox membranes and perox prolif, at this point no info to add transporters or new reactions	NJ
fald	Formaldehyde	Produced only	Peroxisome	SARCOXp	knowledge-based gap	MM

Metabolite Abbreviation	Metabolite Name	Gap Type	Compartment	Reaction Abbreviation	Notes	Reviewer
dmnoncoa	4,8 dimethylnonanoyl-CoA	Consumed only	Cytosol	SCP22x	Will leave gap at present time, sterol carrier protein can move fatty acid derivatives (usually steroid precursors) into different compartments, details about specific substrates and mechanisms not known	NJ
t2m26dcoa	trans-2-Methyl-5-isopropylhexa-2,5-dienoyl-CoA	Consumed only	Peroxisome	T2M26DCOAHLx	knowledge-base gap	SAB

Table 10: *H. sapiens* Recon 1 network confidence scores and citations. Alphabetized list of reactions and their corresponding confidence scores, literature citations, and curator notes. Confidence scores (ranging from 0 to 3) are defined in the text.

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
24,25VITD2Hm	3	Labuda M, Lemieux N, Tihy F, Prinster C, Glorieux FH.	Human 25-hydroxyvitamin D 24-hydroxylase cytochrome P450 subunit maps to a different chromosomal location than that of pseudovitamin D-deficient rickets.	J Bone Miner Res	1993	8266831	This reaction takes place in kidney based on Vitamins, G.F.M. Ball,2004, Blackwell publishing, 1st ed (book) pg.196 1-4 ng/ml blood is produced if neither ca2+ nor pi i needed (regulated by these compounds concentration) IT
24,25VITD2Hm	3	Kusudo T, Sakaki T, Abe D, Fujishima T, Kittaka A, Takayama H, Hatakeyama S, Ohta M, Inouye K.	Metabolism of A-ring diastereomers of 1alpha,25-dihydroxyvitamin D3 by CYP24A1.	Biochem Biophys Res Commun	2004	15358094	This reaction takes place in kidney based on Vitamins, G.F.M. Ball,2004, Blackwell publishing, 1st ed (book) pg.196 1-4 ng/ml blood is produced if neither ca2+ nor pi i needed (regulated by these compounds concentration) IT
25VITD3Hm	3	St-Arnaud R, Messerlian S, Moir JM, Omdahl JL, Glorieux FH.	The 25-hydroxyvitamin D 1-alpha-hydroxylase gene maps to the pseudovitamin D-deficiency rickets (PDDR) disease locus.	J Bone Miner Res	1997	9333115	This reaction takes place in kidney based on Vitamins, G.F.M. Ball,2004, Blackwell publishing, 1st ed (book) pg.196 this form is the biological acitve hormon (25-70pg/ml blood) IT is produced if ca2+ or pi i needed (regulated by these compounds concentration)
25VITD3Hm	3	Yokomura K, Suda T, Sasaki S, Inui N, Chida K, Nakamura H.	Increased expression of the 25-hydroxyvitamin D(3)-1alpha-hydroxylase gene in alveolar macrophages of patients with lung cancer.	J Clin Endocrinol Metab	2003	14671156	This reaction takes place in kidney based on Vitamins, G.F.M. Ball,2004, Blackwell publishing, 1st ed (book) pg.196 this form is the biological acitve hormon (25-70pg/ml blood) IT is produced if ca2+ or pi i needed (regulated by these compounds concentration)
2AMACHYD	3	Gavaret JM, Cahnmann HJ, Nunez J	The fate of the "lost side chain" during thyroid hormonogenesis	J Biol Chem	1979	500639	The reference indicates this is a spontaneous reaction. It is needed to get rid of 2amac that is a byproduct of thyroid hormone synthesis. added by MM- PMID 14596599: Formation of pyruvate by SDH is a two-step reaction in which the hydroxyl group of serine is cleaved to produce aminoacrylate, and then the aminoacrylate is deaminated by nonenzymatic hydrolysis to produce pyruvate.
2AMACSULT	2	Cooper AJ	Biochemistry of sulfur-containing amino acids.		1983	6351723	-L-cysteate can be synthesized from 2-aminoacrylate in rat (PMID: 6351723) -this is a lumped rxn w/ an inferred reduction rxn that occurs in conjunction w/ the sulfotransferase step; this reduction step has to occur in order for the transformation (2amac-->Lcyst) to be valid -used NADPH as electron donor since it is a common cofactor involved in biosynthetic steps utilizing oxygen (see Neema for further explanations) MM
2HBO	3	Komoda T, Sakagishi Y, Mizushima H	Determination of isoenzyme contents of lactic dehydrogenase activity and 2-hydroxybutyric dehydrogenase activity in lactic dehydrogenase preparations	Clin Chim Acta	1976	10108	- another function of L-lactate dehydrogenase [Naghizadeh, Clin Chim Acta 1977], [Komoda, Clin Chim Acta 1976]
2HBO	3	Naghizadeh F	Oxidation of alpha-hydroxybutyrate by human serum	Clin Chim Acta	1977	21765	- another function of L-lactate dehydrogenase [Naghizadeh, Clin Chim Acta 1977], [Komoda, Clin Chim Acta 1976]
2OXOADOXm	2	Cox, RP	Errors of lysine metabolism	The Metabolic and Molecular Bases of Inherited Disease, 8th ed	2001		0
2OXOADPTm	3	Fiermonte G, Dolce V, Palmieri L, Ventura M, Runswick MJ, Palmieri F, Walker JE	Identification of the human mitochondrial oxodicarboxylate carrier. Bacterial expression, reconstitution, functional characterization, tissue distribution, and chromosomal location	J Biol Chem	2001	11083877	reference says other transport reactions done by this gene as well
34DHOXPEGOX	3	Mardh G, Dingley AL, Auld DS, Vallee BL	Human class II (pi) alcohol dehydrogenase has a redox-specific function in norepinephrine metabolism	Proc Natl Acad Sci U S A	1986	3466164	Citation in abstract indicates that ADH does this reaction.
34DHOXPEGt	2	Kurz T, Richardt G, Hagl S, Seyfarth M, Schomig A	Two different mechanisms of noradrenaline release during normoxia and simulated ischemia in human cardiac tissue	J Mol Cell Cardiol	1995	7473774	Citation indicates that this compound is found in the blood. Mechanism and gene unknown.
34DHPLACOX(NADP)	3	Ambroziak W, Pietruszko R	Human aldehyde dehydrogenase. Activity with aldehyde metabolites of monoamines, diamines, and polyamines	J Biol Chem	1991	2071588	First citation has catalytic constants. Only Aldh3a1 is known to use NADP, but the other two have not yet been determined.
34DHPLACOX(NADP)	3	Keung WM	Biogenic aldehyde(s) derived from the action of monoamine oxidase may mediate the antidipsotropic effect of daidzin	Chem Biol Interact	2001	11306106	First citation has catalytic constants. Only Aldh3a1 is known to use NADP, but the other two have not yet been determined.
34DHXMANDACOX(NADP)	3	Kawamura M, Eisenhofer G, Kopin IJ, Kador PF, Lee YS, Tsai JY, Fujisawa S, Lizak MJ, Sinz A, Sato S	Aldose reductase, a key enzyme in the oxidative deamination of norepinephrine in rats	Biochem Pharmacol	1999	10424772	First citation indicates that aldh1a3 does not use NADP. Aldh3b1, 3b2 are yet to be determined according to citation and left with both forms of the reaction. Second citation is based on evidence in rats. This reaction is left reversible because the loop was eliminated by making the NAD dependent reaction irreversible.

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
3DPHBH1	2	Szkopinska A.	Ubiquinone. Biosynthesis of quinone ring and its isoprenoid side chain. Intracellular localization.	Acta Biochim Pol	2000	11051212	IT the enzyme responsible for this reaction has not been identified in any organism. Szekopinspka (2000) describes reaction as hydroxylation, Stryer (Biochemistry) notes that NADPH is a required secondary metabolite for the hydroxylation reaction of sterols. Based on these information the reaction was created (plus for NADH since we cannot exclude the action of NADH instead of NADPH)
3HAO	3	Malherbe P, Kohler C, Da Prada M, Lang G, Kiefer V, Schwarcz R, Lahm HW, Cesura AM	Molecular cloning and functional expression of human 3-hydroxyanthranilic-acid dioxygenase	J Biol Chem	1994	7514594	Reaction and gene detailed in citation.
3HKYNAKGAT	2	BONNER DM, JAKOBY WB	Kynurenine transaminase from neurospora	J Biol Chem	1956	13357462	The citation states that the same enzyme that takes Lkynr as a substrate in neurospora also takes this as a substrate. Physiological data was chosen for this reaction, but that characterization may not be entirely accurate.
3HPCOAHYD	3	Hawes JW, Jaskiewicz J, Shimomura Y, Huang B, Bunting J, Harper ET, Harris RA.	Primary structure and tissue-specific expression of human beta-hydroxyisobutyryl-coenzyme A hydrolase.	J Biol Chem	1996	8824301	Citation has details. It is unclear why it is included in this pathway.
3MLDAt	2	Johansson AC, Lonnqvist B, Granerus G	The relationship between body size and the urinary excretion of the main histamine metabolite tele-methylimidazoleacetic acid in man	Inflamm Res	2001	11411609	SAB Added because this compound is known to be in the urine. Mechanism and gene unknown.
3MOPt2im	3	Hutson SM, Hall TR.	Identification of the mitochondrial branched chain aminotransferase as a branched chain alpha-keto acid transport protein.		1993	8428987	PMID 8428987: transport of branched chain alpha-keto acid via proton symport shown in rat mitochondria; possibly a bifunctional activity of mitochondrial branched chain aminotransferase MM
3MOXTYROX	3	Jonsson EG, Norton N, Gustavsson JP, Oreland L, Owen MJ, Sedvall GC	A promoter polymorphism in the monoamine oxidase A gene and its relationships to monoamine metabolite concentrations in CSF of healthy volunteers	J Psychiatr Res	2000	10867119	MAOA seems to participate a bit more than MAOB in this reaction
3NTD7l	3	R.L. Pisoni	Lysosomal Nucleic Acid and Phosphate Metabolism and Related Metabolic Reactions, Chapter 9		1996		nucleotide monophosphates come from DNA and RNA degradation in lysosome (by acid exonucleoase and acid ribonuclease). Will be dead-end in model as well as their efflux transport systems. IT Their is also a acid nucleotidase which carries out these reactions but i could not find the gene for this lysososmal enzyme
4ABUTtm	2	Medina-Kauwe LK, Tobin AJ, De Meirleir L, Jaeken J, Jakobs C, Nyhan WL, Gibson KM.	4-Aminobutyrate aminotransferase (GABA-transaminase) deficiency.		1999	10407778	- needed in the degradation of 4abut (GABA) in the mitochondria -allows 4abut (which resides/is synthesized in cytosol) degradation to succ, which occurs in the mitochondria; transport mechanism not found/specified for humans so this rxn is used for the time being, although there is a possible 4abut/glu L antiport mechanism based on evidence in rat mitochondria (PMID:10407778) MM
4HBZCOAFm	2	Meganathan R.	Ubiquinone biosynthesis in microorganisms.	FEMS Microbiol Lett	2001	11583838	IT I assumed that reaction takes place in mito as whole ubiquinone biosynthesis.- first reaction from tyr to 34hpp has also been assigned to the mito Booth et al proposed this mechanism from tyrosine to 4hbz. Loescher + Heide found this mechanism in higher plant cells and these results make it highly probable that this mechanism also occurs in mammalian cells.
4HBZCOAFm	2	Loscher R, Heide L.	Biosynthesis of p-Hydroxybenzoate from p-Coumarate and p-Coumaroyl-Coenzyme A in Cell-Free Extracts of Lithospermum erythrorhizon Cell Cultures.	Plant Physiol	1994	12232327	IT I assumed that reaction takes place in mito as whole ubiquinone biosynthesis.- first reaction from tyr to 34hpp has also been assigned to the mito Booth et al proposed this mechanism from tyrosine to 4hbz. Loescher + Heide found this mechanism in higher plant cells and these results make it highly probable that this mechanism also occurs in mammalian cells.
4HBZCOAFm	2	Booth, A. N., Masri, M. S., Robbins, D. J., Emerson, O. H., Jones, F. T. & DeEds, F.	Urinary Phenolic Acid Metabolites of Tyrosine	J Biol Chem	1960		IT I assumed that reaction takes place in mito as whole ubiquinone biosynthesis.- first reaction from tyr to 34hpp has also been assigned to the mito Booth et al proposed this mechanism from tyrosine to 4hbz. Loescher + Heide found this mechanism in higher plant cells and these results make it highly probable that this mechanism also occurs in mammalian cells.

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
4HGLSDm	1	Knight J, Holmes RP	Mitochondrial hydroxyproline metabolism: implications for primary hyperoxaluria	Am J Nephrol	2005	15849464	included based on KEGG indicating that the enzyme does this substrate too, but could not track evidence back to anything certain enzyme may use other substrates as well (other 1-pyrrolines) this reaction is written wrong in KEGG (NAD and NADH on wrong side of eqn) - isolated mouse liver mitochondria produced glyoxylate from hydroxyproline [Knight 2005]
4HOXPACDOX(NADP)	2	Shimamura M, Kamada S, Hayashi T, Naruse H, Iida Y.	Sensitive determination of tyrosine metabolites, p-hydroxyphenylacetic acid, 4-hydroxy-3-methoxyphenyl-acetic acid and 4-hydroxy-3-methoxymandelic acid, by gas chromatography-negative-ion chemical-ionization mass spectrometry.	J Chromatogr	1986	3753983	Physiological data based on citation. This metabolite comes from tyrosine.
5HLTDL	3	Sumi-Ichinose C, Ichinose H, Takahashi E, Hori T, Nagatsu T	Molecular cloning of genomic DNA and chromosomal assignment of the gene for human aromatic L-amino acid decarboxylase, the enzyme for catecholamine and serotonin biosynthesis	Biochemistry	1992	1540578	Gene and enzyme characterized.
5HOXINOXDA	3	Geha RM, Rebrin I, Chen K, Shih JC	Substrate and inhibitor specificities for human monoamine oxidase A and B are influenced by a single amino acid	J Biol Chem	2001	11134050	Fourth citation gives some information about substrate specificities for each enzyme.
5HTRPVESSEC	3	Eiden LE, Schafer MK, Weihe E, Schutz B	The vesicular amine transporter family (SLC18): amine/proton antiporters required for vesicular accumulation and regulated exocytotic secretion of monoamines and acetylcholine	Pflugers Arch	2004	12827358	From PMID 12827358: VATs accumulate singly positively-charged amines into the relatively proton-impermeable acidic secretory vesicles at the expense of proton antiport through the transporter protein (protons are first accumulated in secretory vesicles via a vacuolar ATPase not physically associated with the transporter) with a two proton:one amine stoichiometry, and to a final substrate concentration of up to 500 mM, exceeding that found in the cytosol by 100-fold (ACh) to 10,000-fold (biogenic amines)[29]. From PMID 15383652: In addition to this intrinsic dependency on the transmembrane electrochemical gradient, the transport rate can also be modulated by alterations in the rate of ATP hydrolysis and its coupling to H+ translocation. A recent detailed analysis of current-voltage relationships in the absence and presence of several ions, ATP or ADP and imposing different pH gradients, described different coupling ratios for vacuolar H+-ATPases from yeast. In the presence of large pH gradients (4 pH units), the approximate ratio was 2 H+/ATP and increased to more than 3 H: 1 ATP averaged to arrive at 3 substrate: 2 ATP transport vesicle not accounted for--this is a net transport reaction
A_MANASEly	0	Liao YF, Lal A, Moremen KW.	Cloning, expression, purification, and characterization of the human broad specificity lysosomal acid alpha-mannosidase	J Biol Chem	1996	8910458	MAN2B1 encodes an enzyme that hydrolyzes terminal, non-reducing alpha-D-mannose residues in alpha-D-mannosides. Its activity is necessary for the catabolism of N-linked carbohydrates released during glycoprotein turnover and it is member of family 38 of glycosyl hydrolases. Defects in this gene have been shown to be the cause of lysosomal alpha-mannosidosis (AM), a lysosomal storage disease characterized by the accumulation of unbranched oligosaccharide chains. [RefSeq] Man2b1p ubiquitously expressed [Liao et al, J Biol Chem 1996]
A4GALTg	3	Steffensen R, Carlier K, Wiels J, Levery SB, Stroud M, Cedergren B, Nilsson Sojka B, Bennett EP, Jersild C, Clausen H.	Cloning and expression of the histo-blood group Pk UDP-galactose: Ga1beta-4G1cbeta1-cer alpha1, 4-galactosyltransferase. Molecular genetic basis of the p phenotype.	J Biol Chem	2000	10747952	Golgi - lumen side - see ref Kolter and Sanhoff; also noted in uniprot also cytoplasmic domain - see ref Kojima strongly expressed in heart, kidney, spleen, and placenta and weakly in colon, small intestine, and brain NJ
A4GALTg	3	Kojima Y, Fukumoto S, Furukawa K, Okajima T, Wiels J, Yokoyama K, Suzuki Y, Urano T, Ohta M, Furukawa K.	Molecular cloning of globotriaosylceramide/CD77 synthase, a glycosyltransferase that initiates the synthesis of globo series glycosphingolipids.	J Biol Chem	2000	10748143	Golgi - lumen side - see ref Kolter and Sanhoff; also noted in uniprot also cytoplasmic domain - see ref Kojima strongly expressed in heart, kidney, spleen, and placenta and weakly in colon, small intestine, and brain NJ
A4GNT2g	0	Nakayama J, Yeh JC, Misra AK, Ito S, Katsuyama T, Fukuda M.	Expression cloning of a human alpha1, 4-N-acetylglucosaminyltransferase that forms GlcNAcalpha1-->4Galbeta-->R, a glycan specifically expressed in the gastric gland mucous cell-type mucin	Proc Natl Acad Sci U S A	1999	10430883	A4gnt attaches GlcNAc to Core 2 glycans, also acts less efficiently on Core 1 glycans; characteristic for gastric glan mucous cell-type mucins; found primarily in the stomach and pancreas [Nakayama et al, PNAS 1999]
AACTOOR	3	Deng Y, Yu PH.	Assessment of the deamination of aminoacetone, an endogenous substrate for semicarbazide-sensitive amine oxidase.		1999	10328770	this rxn is catalyzed only by SSAO (AOC3) (see PMID: 10328770) MM
AACTOOR	3	Dalfo E, Hernandez M, Lizcano JM, Tipton KF, Unzeta M.	Activation of human lung semicarbazide sensitive amine oxidase by a low molecular weight component present in human plasma.		2003	12878330	this rxn is catalyzed only by SSAO (AOC3) (see PMID: 10328770) MM
AATAi	3	Goh,D.L.M., Patel,A., Thomas,G.H., Salomons,G.S., Schor,D.S.M., Jakobs,C., Geraghty,M.T.,	Characterization of the human gene encoding alpha-aminoadipate aminotransferase (AADAT).		2002	12126930	cytosolic according to Reactome also needs to be cytosolic since 2-oxoadipate is produced in cytosol and subsequently transported to mitochondria (PMID: 11083877)

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
ABO1g	3	Yamamoto F.-I., Hakomori S.-I.;	Sugar-nucleotide donor specificity of histo-blood group A and B transferases is based on amino acid substitutions	J Biol Chem	1990	2121736	localization: golgi - Type II membrane protein. Membrane-bound form in trans cisternae of Golgi. Soluble form in body fluids. biochemistry and review of blood group Ag synthesis: PMID: 11421346. structure: PMID: 12198488 characterization: PMID 2121736 This protein is the basis of the ABO blood group system. The histo-blood group ABO involves three carbohydrate antigens: A, B, and H. A, B, and AB individuals express a glycosyltransferase activity that converts the H antigen to the A antigen (by addition of UDP-GalNac) or to the B antigen (by addition of UDP-Gal), whereas O individuals lack such activity. NJ
ABO1g	3	Lloyd KO.	The chemistry and immunochemistry of blood group A, B, H, and Lewis antigens: past, present and future.	Glycoconj J	2000	11421346	localization: golgi - Type II membrane protein. Membrane-bound form in trans cisternae of Golgi. Soluble form in body fluids. biochemistry and review of blood group Ag synthesis: PMID: 11421346. structure: PMID: 12198488 characterization: PMID 2121736 This protein is the basis of the ABO blood group system. The histo-blood group ABO involves three carbohydrate antigens: A, B, and H. A, B, and AB individuals express a glycosyltransferase activity that converts the H antigen to the A antigen (by addition of UDP-GalNac) or to the B antigen (by addition of UDP-Gal), whereas O individuals lack such activity. NJ
ABO1g	3	Patenaude S.I., Seto N.O.L., Borisova S.N., Szpacenko A., Marcus S.L., Palcic M.M., Evans S.V.;	The structural basis for specificity in human ABO(H) blood group biosynthesis	Nat Struct Biol	2002	12198488	localization: golgi - Type II membrane protein. Membrane-bound form in trans cisternae of Golgi. Soluble form in body fluids. biochemistry and review of blood group Ag synthesis: PMID: 11421346. structure: PMID: 12198488 characterization: PMID 2121736 This protein is the basis of the ABO blood group system. The histo-blood group ABO involves three carbohydrate antigens: A, B, and H. A, B, and AB individuals express a glycosyltransferase activity that converts the H antigen to the A antigen (by addition of UDP-GalNac) or to the B antigen (by addition of UDP-Gal), whereas O individuals lack such activity. NJ
ABTArm	3	Osei,Y.D. , Churchich,J.E.	Screening and sequence determination of a cDNA encoding the human brain 4-aminobutyrate aminotransferase.		1995	7721088	Entrez Gene - 4-aminobutyrate aminotransferase (ABAT) is responsible for catabolism of gamma-aminobutyric acid (GABA), an important, mostly inhibitory neurotransmitter in the central nervous system, into succinic semialdehyde. The active enzyme is a homodimer of 50-kD subunits complexed to pyridoxal-5-phosphate. The protein sequence is over 95% similar to the pig protein. GABA is estimated to be present in nearly one-third of human synapses. ABAT in liver and brain is controlled by 2 codominant alleles with a frequency in a Caucasian population of 0.56 and 0.44. The ABAT deficiency phenotype includes psychomotor retardation, hypotonia, hyperreflexia, lethargy, refractory seizures, and EEG abnormalities. Two alternatively spliced transcript variants encoding the same protein isoform have been found for this gene. MM
ABTD	2	Touster O, Shaw DR	Biochemistry of the acyclic polyols	Physiol Rev	1962	13922173	- authors infer L-arabitol dehydrogenase exists in humans based on observations of patient with presumed deficiency (L-arabinose in diet led to high excretion of L-arabitol and arabinoic acid (-lactone)) [Onkenhout, Mol Genet Metab 2002] - accumulated L-xylulose in pentosuric individuals probably is reduced in part to L-arabitol by the relatively nonspecific DPN-linked polyol dehydrogenase; urinary L-arabitol is in fact labeled when a pentosuric is given D-glucuronolactone-C13 (see refs in [Touster 1962]) - utilization of D-arabitol-C14 and L-arabitol-C14 in rat has been studied; D-isomer led to extremely low labeling of liver glycogen, but the L-isomer caused appreciable incorporation of the isotope (see refs in [Touster 1962])

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ABUTD	3	Lin SW, Chen JC, Hsu LC, Hsieh CL, Yoshida A.	Human gamma-aminobutyraldehyde dehydrogenase (ALDH9): cDNA sequence, genomic organization, polymorphism, chromosomal localization, and tissue expression.		1996	8786138	gene and reaction characterized
ACACT1	3	Olivier LM, Krisans SK	Peroxisomal protein targeting and identification of peroxisomal targeting signals in cholesterol biosynthetic enzymes	Biochimica et Biophysica Acta	2000		ACAT1 - mitochondrial: involved in beta ox ACAT2 - cytoplasmic - involved in HMG-CoA synthesis for subsequent xol biosynthesis also peroxisomal and mitochondrial subtypes - see liter refs uniprot + lit NJ
ACACt2m	3	Halestrap AP.	Pyruvate and ketone-body transport across the mitochondrial membrane. Exchange properties, pH-dependence and mechanism of the carrier.	Biochem J	1978	28726	- Added by RS/TV - No genes found. "acac can also travel by diffusion" Halestrap AP Biochem J. 1978 Jun 15;172(3):377-87. Pyruvate and ketone-body transport across the mitochondrial membrane. Exchange properties, pH-dependence and mechanism of the carrier - Possible mechanism for acetoacetate transport via proton symport. Pande SV, Parvin R J Biol Chem. 1978 Mar 10;253(5):1565-73. Pyruvate and acetoacetate transport in mitochondria. A reappraisal
ACACt2m	3	Pande SV, Parvin R.	Pyruvate and acetoacetate transport in mitochondria. A reappraisal.	J Biol Chem	1975	627555	- Added by RS/TV - No genes found. "acac can also travel by diffusion" Halestrap AP Biochem J. 1978 Jun 15;172(3):377-87. Pyruvate and ketone-body transport across the mitochondrial membrane. Exchange properties, pH-dependence and mechanism of the carrier - Possible mechanism for acetoacetate transport via proton symport. Pande SV, Parvin R J Biol Chem. 1978 Mar 10;253(5):1565-73. Pyruvate and acetoacetate transport in mitochondria. A reappraisal
ACACT8p	3	Bout A, Franse MM, Collins J, Blonden L, Tager JM, Benne R.	Characterization of the gene encoding human peroxisomal 3-oxoacyl-CoA thiolase (ACAA). No large DNA rearrangement in a thiolase-deficient patient.	Biochim Biophys Acta	1991	1679347	Acetyl-Coenzyme A acyltransferase (ACAA1) is an enzyme operative in the beta-oxidation system of the peroxisomes. Deficiency of this enzyme leads to pseudo-Zellweger syndrome. NJ
ACALDtm	2	Lieber CS	Ethanol metabolism, cirrhosis and alcoholism	Clin Chim Acta	1997	9028626	- in hepatocytes, acetaldehyde is transported from cytosol to mitochondria for oxidation to acetate (see [Lieber 1997])
ACCOACm	3	Abu-Elheiga L, Brinkley WR, Zhong L, Chirala SS, Woldegiorgis G, Wakil SJ.	The subcellular localization of acetyl-CoA carboxylase 2.	Proc Natl Acad Sci U S A	2000	10677481	- Added by RS/TV NOTE: This reaction was under the accoa subsystem in Thuy's model; however, since all the reactions in this subsystem are scattered throughout various pathways in this model, I haven't assigned a subsystem. - ACC catalyzes the carboxylation of acetyl-CoA to form malonyl-CoA. - There are two isozymes enocded by separate genes: 1) Acaca (ACC1) are highly expressed in lipogenic tissues, such as liver and adipose. 7 transcriptional variants have been found for this protein. 2) Acacb(ACC2) is also expressed in the liver, but is the predominant form of carboxylase in heart and skeletal muscle. Both isozymes are shown to occur in the mitochondria. All this according to Abu-Elheiga L, Brinkley WR, Zhong L, Chirala SS, Woldegiorgis G, Wakil SJ.Proc Natl Acad Sci U S A. 2000 Feb 15;97(4):1444-9.
ACCOAgt	3	Hirabayashi Y, Kanamori A, Nomura KH, Nomura K.	The acetyl-CoA transporter family SLC33.	Pflugers Arch	2004	12739170	AcCoa transport into Golgi/ER where o-acetylation can occur. Varying evidence for cytoplasmic vs Golgi localization of rxn. Hirabayashi paper describing cloning (PMID: 9096318) supports cytoplasmic localization, but Hirabayashi paper reviewing SLC33A1 (PMID: 12739170) describes rxn occuring in Golgi lumen. Uniprot: The encoded protein is required for the formation of O acetylated (Ac) gangliosides. It is predicted to contain 6 to 10 transmembrane domains, and a leucine zipper motif in transmembrane domain III. Studies indicate that the protein is localized to the cytoplasm. NJ

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ACGALtly	2	Jonas AJ, Speller RJ, Conrad PB, Dubinsky WP	Transport of N-acetyl-D-glucosamine and N-acetyl-D galactosamine by rat liver lysosomes	J Biol Chem	1989	2784441	-N-acetyl-glucosamine and N-acetyl-galactosamine are transported out of rat liver lysosome via carrier-mediated transport; biochemical characterization described in [Jonas 1989] - transport was not dependent upon NaCl, KCl, MgCl2, or ATP/MgCl2 and was unaffected by 5 mM dithiothreitol or variation of buffer pH between 6.0 and 8.0 [Jonas 1989] - studies with cultured human fibroblasts have shown that free N-acetyl-glucosamine and N-acetyl-galactosamine are released from lysosomes and recycled by the cell [Rome 1986]
ACGALtly	2	Rome LH, Hill DF	Lysosomal degradation of glycoproteins and glycosaminoglycans. Efflux and recycling of sulphate and N-acetylhexosamines	Biochem J	1986	3753439	-N-acetyl-glucosamine and N-acetyl-galactosamine are transported out of rat liver lysosome via carrier-mediated transport; biochemical characterization described in [Jonas 1989] - transport was not dependent upon NaCl, KCl, MgCl2, or ATP/MgCl2 and was unaffected by 5 mM dithiothreitol or variation of buffer pH between 6.0 and 8.0 [Jonas 1989] - studies with cultured human fibroblasts have shown that free N-acetyl-glucosamine and N-acetyl-galactosamine are released from lysosomes and recycled by the cell [Rome 1986]
ACGAM2E	3	Luchansky SJ, Yarema KJ, Takahashi S, Bertozzi CR	GlcNAc 2-epimerase can serve a catabolic role in sialic acid metabolism	J Biol Chem	2003	12499362	- reversible [Luchansky, J Biol Chem 2003]
ACGAMK	3	Hinderlich S, Berger M, Schwarzkopf M, Effertz K, Reutter W	Molecular cloning and characterization of murine and human N-acetylglucosamine kinase	Eur J Biochem	2000	10824116	- gene has been cloned and characterized [Hinderlich, Eur J Biochem 2000] - reaction shown as irreversible in Varki p. 74 - kinase can use either GlcNAc or ManNac [Varki, p. 77]
ACGAMPM	3	Mio T, Yamada-Okabe T, Arisawa M, Yamada-Okabe H	Functional cloning and mutational analysis of the human cDNA for phosphoacetylglucosamine mutase: identification of the amino acid residues essential for the catalysis	Biochim Biophys Acta	2000	11004509	- shown as reversible in Devlin p. 672, Varki p. 74, Orten p. 246 - Found in many tissues except lung. Relatively high expression in pancreas, heart, liver, and placenta, and relatively low expression in brain, skeletal muscle and kidney [UniProt]
ACGPID	3	Watanabe R, Ohishi K, Maeda Y, Nakamura N, Kinoshita T	Mammalian PIG-L and its yeast homologue Gpi12p are N-acetylglucosaminylphosphatidylinositol de-N-acetylases essential in glycosylphosphatidylinositol biosynthesis	Biochem J	1999	10085243	- catalyzes de-N-acetylation of GlcNAc-PI [RefSeq], [UniProt] - gene was identified, 77% similarity to rat homolog [Watanabe, Biochem J 1999] - protein was characterized, localization analyzed Pottekat, J Biol Chem 2004]
ACGPID	3	Pottekat A, Menon AK	Subcellular localization and targeting of N-acetylglucosaminyl phosphatidylinositol de-N-acetylase, the second enzyme in the glycosylphosphatidylinositol biosynthetic pathway	J Biol Chem	2004	14742432	- catalyzes de-N-acetylation of GlcNAc-PI [RefSeq], [UniProt] - gene was identified, 77% similarity to rat homolog [Watanabe, Biochem J 1999] - protein was characterized, localization analyzed Pottekat, J Biol Chem 2004]
ACGSm	3	Caldovic L, Morizono H, Gracia Panglao M, Gallegos R, Yu X, Shi D, Malamy MH, Allewell NM, Tuchman M	Cloning and expression of the human N-acetylglutamate synthase gene	Biochem Biophys Res Commun	2002	12459178	Gene characterized and sequence encodes functional enzyme in E. coli system. Biochemical evidence noted, but is perhaps questionable.
ACHEe	3	Shafferman A, Kronman C, Flashner Y, Leitner M, Grosfeld H, Ordentlich A, Gozes Y, Cohen S, Ariel N, Barak D, et al.	Mutagenesis of human acetylcholinesterase. Identification of residues involved in catalytic activity and in polypeptide folding.	J Biol Chem	1992		extraceullular - from phys data - no refs found for other compartments - f/u in future Acetylcholinesterase hydrolyzes the neurotransmitter, acetylcholine at neuromuscular junctions and brain cholinergic synapses, and thus terminates signal transmission. It is also found on the red blood cell membranes, where it constitutes the Yt blood group antigen. Acetylcholinesterase exists in multiple molecular forms which possess similar catalytic properties, but differ in their oligomeric assembly and mode of cell attachment to the cell surface. It is encoded by the single ACHE gene, and the structural diversity in the gene products arises from alternative mRNA splicing, and post-translational associations of catalytic and structural subunits. The major form of acetylcholinesterase found in brain, muscle and other tissues is the hydrophilic species, which forms disulfide-linked oligomers with collagenous, or lipid-containing structural subunits. The other, alternatively spliced form, expressed primarily in the erythroid tissues, differs at the C-terminal end, and contains a cleavable hydrophobic peptide with a GPI-anchor site. It associa NJ

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ACHEe	3	Soreq H, Seidman S.	Acetylcholinesterase--new roles for an old actor.	Nat Rev Neurosci	2001	11283752	extraceullular - from phys data - no refs found for other compartments - f/u in future Acetylcholinesterase hydrolyzes the neurotransmitter, acetylcholine at neuromuscular junctions and brain cholinergic synapses, and thus terminates signal transmission. It is also found on the red blood cell membranes, where it constitutes the Yt blood group antigen. Acetylcholinesterase exists in multiple molecular forms which possess similar catalytic properties, but differ in their oligomeric assembly and mode of cell attachment to the cell surface. It is encoded by the single ACHE gene, and the structural diversity in the gene products arises from alternative mRNA splicing, and post-translational associations of catalytic and structural subunits. The major form of acetylcholinesterase found in brain, muscle and other tissues is the hydrophilic species, which forms disulfide-linked oligomers with collagenous, or lipid-containing structural subunits. The other, alternatively spliced form, expressed primarily in the erythroid tissues, differs at the C-terminal end, and contains a cleavable hydrophobic peptide with a GPI-anchor site. It associa NJ
ACITL	0	Elshourbagy NA, Near JC, Kmetz PJ, Sathe GM, Southan C, Strickler JE, Gross M, Young JF, Wells TN, Groot PH.	Rat ATP citrate-lyase. Molecular cloning and sequence analysis of a full-length cDNA and mRNA abundance as a function of diet, organ, and age	J Biol Chem	1990	2295639	- responsible for cytosolic accoa production in many tissues [RefSeq] - cytoplasmic [UniProt] - Additional info added by RS/TV: Myriame Poirier1, Geneviève Vincent1, et al. Probing the link between citrate and malonyl-CoA in perfused rat hearts. Am J Physiol Heart Circ Physiol. 2002 Oct;283(4):H1379-86. High activity in liver, lower in heart Cytosolic according to Entrez Gene Database Catalytic Activity: Catalyzes the formation of acetyl-CoA and oxaloacetate from citrate and CoA with a concomitant hydrolysis of ATP to ADP and phosphate Two transcript variants according to Entrez Gene Database. Tissue Specificity: Although expressed in a wide variety of tissues, it is found to be in greater concentrations in the liver, kidney, lung, and brain. All this according to Elshourbagy NA, etc; J Biol Chem. 1990 Jan 25;265(3):1430-5; Rat ATP citrate-lyase. Molecular cloning and sequence analysis of a full-length cDNA and mRNA abundance as a function of diet, organ, and age. Awan MM, Saggerson ED.; Biochem J. 1993 Oct 1;295 (Pt 1):61-6; Malonyl-CoA metabolism in cardiac myocytes and its Pierce MW, Palmer JL, Keutmann HT, Avruch J; J Biol Chem. ATP-citrate lyase. Structure of a tryptic peptide containing the p
ACN13ACNGALGBSIDEtg	1	Sandhoff K, Klein A.	Intracellular trafficking of glycosphingolipids: role of sphingolipid activator proteins in the topology of endocytosis and lysosomal digestion.	FEBS Lett	1994	8206147	Since specific mechanism is unknown (caveoli vs vesicular vs ...) and energy dependence/requirement is not known either, evidence is left as modeling only, however intracellular trafficking and transport is known to occur for sphingolipids, additionally some forms are transferred to the outer plasma membrane, so a mechanism for EC transport is also present. See Varki glycolipids text (notably glycosphingolipids chapter - p121) and various literature reviews (PMID: 8206147). NJ
ACNAM9PL	3	Lawrence SM, Huddleston KA, Pitts LR, Nguyen N, Lee YC, Vann WF, Coleman TA, Betenbaugh MJ	Cloning and expression of the human N-acetylneuraminic acid phosphate synthase gene with 2-keto-3-deoxy-D-glycero- D-galacto-nononic acid biosynthetic ability	J Biol Chem	2000	10749855	- shown as irreversible in Devlin p. 672 & 677, Orten p.245, Varki p. 74 - NeuAcP synthase uses ManNAc6P and man6p as substrates, but exhibits much higher activity towards ManNAc6P [Lawrence, J Biol Chem 2000] - unlike the E. coli homolog, the human enzyme only uses phosphorylate substrates [Lawrence, J Biol Chem 2000] - cytosolic [Varki, p.78]
ACOAD10m	3	Andresen,B.S., Christensen,E., Corydon,T.J., Bross,P., etc.	Isolated 2-methylbutyrylglycinuria caused by short/branched-chain acyl-CoA dehydrogenase deficiency....		2000	11013134	0
ACOAD8m	3	Tiffany,K.A., Roberts,D.L., Wang,M., Paschke,R., Mohsen,A.W., Vockley,J., Kim,J.-J.P.,	Structure of human isovaleryl-CoA dehydrogenase at 2.6-A resolution: structural basis for substrate specificity. .		1997	9214289	mitochondrial, FAD used as cofactor - see references MM
ACOAD8m	3	Vockley J, Nagao M, Parimoo B, Tanaka K.	The variant human isovaleryl-CoA dehydrogenase gene responsible...		1992		mitochondrial, FAD used as cofactor - see references MM

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ACOAO7p	3	Chu R, Varanasi U, Chu S, Lin Y, Usuda N, Rao MS, Reddy JK.	Overexpression and characterization of the human peroxisomal acyl-CoA oxidase in insect cells.	J Biol Chem	1995	7876265	peroxisomal - uniprot seq + kinetic data in chu ref Defects in ACOX1 are the cause of pseudoneonatal adrenoleukodystrophy [MIM:264470]. It is a disease biochemically characterized by an accumulation of very long chain fatty acids. NJ
ACOAO7p	3	Varanasi U, Chu R, Chu S, Espinosa R, LeBeau MM, Reddy JK.	Isolation of the human peroxisomal acyl-CoA oxidase gene: organization, promoter analysis, and chromosomal localization.	Proc Natl Acad Sci	1994	8159712	peroxisomal - uniprot seq + kinetic data in chu ref Defects in ACOX1 are the cause of pseudoneonatal adrenoleukodystrophy [MIM:264470]. It is a disease biochemically characterized by an accumulation of very long chain fatty acids. NJ
ACODA	1	Jones WM, Scaloni A, Bossa F, Popowicz AM, Schneewind O, Manning JM	Genetic relationship between acylpeptide hydrolase and acylase, two hydrolytic enzymes with similar binding but different catalytic specificities	Proc Natl Acad Sci U S A	1991	2006156	based on KEGG map and broad enzyme specificity
ACOX2x	3	Baumgart E, Vanhooren JCT, Fransen M, Marynen P, Puype M, Vandekerckhove J, Leunissen JAM, Fahimi HD, Mannaerts GP, Veldhoven PP	Molecular characterization of the human peroxisomal branched-chain acyl-CoA oxidase	Proc Natl Acad Sci	1996		peroxisome - literature The product of this gene belongs to the acyl-CoA oxidases family. It encodes the branched-chain acyl-CoA oxidase which is involved in the degradation of long branched fatty acids and bile acid intermediates in peroxisomes. Deficiency of this enzyme results in the accumulation of branched fatty acids and bile acid intermediates, and may lead to Zellweger syndrome, severe mental retardation and death in children. NJ
ACRNtm	3	Pande SV, Parvin R.	Characterization of carnitine acylcarnitine translocase system of heart mitochondria.	J Biol Chem	1976	977593	- Added by RS/TV Pande SV, Parvin R. J Biol Chem. 1976 Nov 10;251(21):6683-91 Characterization of carnitine acylcarnitine translocase system of heart mitochondria Mitochondrial according to Entrez gene database. Reaction description: Slc25a20.1-m catalyses the electroneutral exchange of cytosolic acylcarnitine for mitochondrial carnitine. Thus preferred substrates include carnitine and acylcarnitine in exchange for carnitine or acylcarnitines. Tissue localization: Slc25a20.1-m is expressed in the heart, skeletal muscle, liver, lung, kidney, brain, pancreas, and placenta. All of this according to Table 1 in Palmieri, F. The mitochondrial transporter family (SLC25): physiological and pathological implications. Pflugers Arch. 2004 Feb. (PMID: 14598172)
ACS	3	Luong A, Hannah VC, Brown MS, Goldstein JL	Molecular characterization of human acetyl-CoA synthetase, an enzyme regulated by sterol regulatory element-binding proteins	J Biol Chem	2000	10843999	55902: - catalyzes irreversible reaction between acetate and ATP to acetyl-CoA [RefSeq], [Luong, J Biol Chem 2000] - cytosolic [LocusLink], [UniProt], [Luong, J Bil Chem 2000] 65985: - annotated as 6.2.1.1 [HInv-Db] - cytosolic [Ohgami et al,Biochem Pharmacol. 2003 Mar 15;65(6):989-94]
ACS	3	Ohgami M, Takahashi N, Yamasaki M, Fukui T	Expression of acetoacetyl-CoA synthetase, a novel cytosolic ketone body-utilizing enzyme, in human brain	Biochem Pharmacol	2003	12623130	55902: - catalyzes irreversible reaction between acetate and ATP to acetyl-CoA [RefSeq], [Luong, J Biol Chem 2000] - cytosolic [LocusLink], [UniProt], [Luong, J Bil Chem 2000] 65985: - annotated as 6.2.1.1 [HInv-Db] - cytosolic [Ohgami et al,Biochem Pharmacol. 2003 Mar 15;65(6):989-94]

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ACSm	2	Scholte HR, Wit-Peeters EM, Bakker JC.	The intracellular and intramitochondrial distribution of short-chain acyl-CoA synthetases in guinea-pig heart.	Biochim Biophys Acta	1971	4326157	- catalyzes irreversible reaction between acetate and ATP to acetyl-CoA [RefSeq] - mitochondrial matrix [UniProt] - primarily a cardiac enzyme [RefSeq] - enzyme has been characterized in mouse and cow, assumed to have a similar function in humans [Fujino, J Biol Chem 2001] - Additional information by RS/TV: 1) localized in the mitochondria 2) Loosely bound to the inner side of the inner membrane 3) Found to be localized in the gut, liver, and heart. 4) In rat-liver it is found to be mainly localized on the outer membrane All this according to H. R. Scholte, E. M. Wit-Peeters and J. C. Bakker The intraçellular and intramitochondrial distribution of short-chain acyl-CoA synthetases in guinea-pig heart
ACSm	2	Fujino T, Kondo J, Ishikawa M, Morikawa K, Yamamoto TT	Acetyl-CoA synthetase 2, a mitochondrial matrix enzyme involved in the oxidation of acetate	J Biol Chem	2001	11150295	- catalyzes irreversible reaction between acetate and ATP to acetyl-CoA [RefSeq] - mitochondrial matrix [UniProt] - primarily a cardiac enzyme [RefSeq] - enzyme has been characterized in mouse and cow, assumed to have a similar function in humans [Fujino, J Biol Chem 2001] - Additional information by RS/TV: 1) localized in the mitochondria 2) Loosely bound to the inner side of the inner membrane 3) Found to be localized in the gut, liver, and heart. 4) In rat-liver it is found to be mainly localized on the outer membrane All this according to H. R. Scholte, E. M. Wit-Peeters and J. C. Bakker The intraçellular and intramitochondrial distribution of short-chain acyl-CoA synthetases in guinea-pig heart
ACSRTNMT	3	Donohue SJ, Roseboom PH, Illnerova H, Weller JL, Klein DC	Human hydroxyindole-O-methyltransferase: presence of LINE-1 fragment in a cDNA clone and pineal mRNA	DNA Cell Biol	1993	8397829	Catalyzes the last step in melatonin synthesis.
ACt2m	2	Casal M, Paiva S, Andrade RP, Gancedo C, Leao C.	The lactate-proton symport of Saccharomyces cerevisiae is encoded by JEN1.	J Bacteriol	1999	10198029	- Added by RS/TV - No genes found. - However, there is strong physiological results indicating the existence of different monocarboxylate permeases in S. cerevisiae, four open reading frames (ORFs) with important similarities to mammalian monocarboxylate permeases were found in the genome of S. cerevisiae. (Casal M, Paiva S, Andrade RP, Gancedo C, Leao C.J Bacteriol. 1999 Apr;181(8):2620-3.) - [Wolfe 2005] suggest that acetate can freely diffuse across subcellular membranes since it is lipophilic
ACt2m	2	Wolfe AJ.	The acetate switch	Microbiol Mol Biol Rev	2005	15755952	- Added by RS/TV - No genes found. - However, there is strong physiological results indicating the existence of different monocarboxylate permeases in S. cerevisiae, four open reading frames (ORFs) with important similarities to mammalian monocarboxylate permeases were found in the genome of S. cerevisiae. (Casal M, Paiva S, Andrade RP, Gancedo C, Leao C.J Bacteriol. 1999 Apr;181(8):2620-3.) - [Wolfe 2005] suggest that acetate can freely diffuse across subcellular membranes since it is lipophilic
ACt2r	3	Waniewski RA, Martin DL.	Preferential utilization of acetate by astrocytes is attributable to transport.	J Neurosci	1998	9651205	- acetate generated from ethanol in hepatocytes can be excreted into the blood [Smith 2004] or be taken up by other cells such as astrocytes - acetate uptake by astrocytes has many of the properties of the proton-coupled, monocarboxylate transport process found in erythrocytes, heart, kidney, and skeletal muscle cells [Waniewski 1998]
ACt2r	3	Colleen Smith, Allan Marks, Michael Lieberman	Marks' Basic Medical Biochemistry		2004		- acetate generated from ethanol in hepatocytes can be excreted into the blood [Smith 2004] or be taken up by other cells such as astrocytes - acetate uptake by astrocytes has many of the properties of the proton-coupled, monocarboxylate transport process found in erythrocytes, heart, kidney, and skeletal muscle cells [Waniewski 1998]
ADA	3	Iwaki-Egawa S, Watanabe Y.	Characterization and purification of adenosine deaminase 1 from human and chicken liver.	Comp Biochem Physiol B Biochem Mol Biol	2002	12381379	some paper mentioned a ADA2, however, I could not find a gene for it --> keep in mind IT
ADA	3	Gonzalez-Gronow M, Hershfield MS, Arredondo-Vega FX, Pizzo SV.	Cell surface adenosine deaminase binds and stimulates plasminogen activation on 1-LN human prostate cancer cells.	J Biol Chem	2004	15016824	some paper mentioned a ADA2, however, I could not find a gene for it --> keep in mind IT

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ADK1	3	Zuffardi O, Caiulo A, Maraschio P, Tupler R, Bianchi E, Amisano P, Beluffi G, Moratti R, Liguri G.	Regional assignment of the loci for adenylate kinase to 9q32 and for alpha 1-acid glycoprotein to 9q31-q32. A locus for Goltz syndrome in region 9q32-qter?	Hum Genet	1989	2541064	IT
ADK1	3	Matsuura S, Igarashi M, Tanizawa Y, Yamada M, Kishi F, Kajii T, Fujii H, Miwa S, Sakurai M, Nakazawa A.	Human adenylate kinase deficiency associated with hemolytic anemia. A single base substitution affecting solubility and catalytic activity of the cytosolic adenylate kinase.	J Biol Chem	1989	2542324	IT
ADK1	3	Miwa S, Fujii H, Tani K, Takahashi K, Takizawa T, Igarashi T.	Red cell adenylate kinase deficiency associated with hereditary nonspherocytic hemolytic anemia: clinical and biochemical studies.	Am J Hematol	1983	6305188	IT
ADK1	3	Van Rompay AR, Johansson M, Karlsson A.	Identification of a novel human adenylate kinase. cDNA cloning, expression analysis, chromosome localization and characterization of the recombinant protein.	Eur J Biochem	1999	10215863	IT
ADK1m	3	Bruns GA, Regina VM.	Adenylate kinase 2, a mitochondrial enzyme.	Biochem Genet	1977	195572	IT 204:mRNAs:strongly expressed in liver, heart, skeletal muscle and pancreas, and moderately in kidney, placenta and brain, and weakly in lung AK2 protein was present in large amounts in liver, heart, kidney, and in a small amount in lung, and undetectable in brain and skeletal muscle
ADK1m	3	Lee Y, Kim JW, Lee IA, Kang HB, Choe YK, Lee HG, Lim JS, Kim HJ, Park C, Choe IS.	Cloning and characterization of cDNA for human adenylate kinase 2A.	Biochem Mol Biol Int	1996	8843353	IT 204:mRNAs:strongly expressed in liver, heart, skeletal muscle and pancreas, and moderately in kidney, placenta and brain, and weakly in lung AK2 protein was present in large amounts in liver, heart, kidney, and in a small amount in lung, and undetectable in brain and skeletal muscle
ADK1m	3	Noma T, Fujisawa K, Yamashiro Y, Shinohara M, Nakazawa A, Gondo T, Ishihara T, Yoshinobu K.	Structure and expression of human mitochondrial adenylate kinase targeted to the mitochondrial matrix	Biochem J	2001	11485571	IT 204:mRNAs:strongly expressed in liver, heart, skeletal muscle and pancreas, and moderately in kidney, placenta and brain, and weakly in lung AK2 protein was present in large amounts in liver, heart, kidney, and in a small amount in lung, and undetectable in brain and skeletal muscle
ADK3	3	Noma T, Song S, Yoon YS, Tanaka S, Nakazawa A.	cDNA cloning and tissue-specific expression of the gene encoding human adenylate kinase isozyme 2.	Biochim Biophys Acta	1998	9434148	IT
ADMDC	3	Pajunen A, Crozat A, Janne OA, Ihalainen R, Laitinen PH, Stanley B, Madhubala R, Pegg AE	Structure and regulation of mammalian S-adenosylmethionine decarboxylase	J Biol Chem	1988	2460457	Enzyme and reaction characterized
ADNCYC	3	Stengel D, Parma J, Gannage MH, Roeckel N, Mattei MG, Barouki R, Hanoune J.	Different chromosomal localization of two adenylyl cyclase genes expressed in human brain.	Hum Genet	1992	1427768	membrane protein but Ding et al. 2005 report 2 cytoplasmatic domain of ADNCYC protein (in their introduction) IT 107(1): brain 108(2): brain (also olfactory cilia - locuslink) 109(3): paletes, thyroid, germ cells (also olfactory cilia - locuslink) 196883(4): thyroid (also olfactory cilia - locuslink) 111(5): colon, heart, liver, lung (mRNA 60 more abundant in heart than 112) Raimundo et al. 1999 112(6): colon, heart, liver, lung and MNL - Raimundo et al. 1999 113(7): paletes 114(8):brain, May be involved in learning, in memory and in drug dependence.(Genecards) 115(9): brain, neuronal signaling all bind 2 Mg2+ per subunit some isoforms are sensitive to calmodulin/calcium other ones are not 55811(SAC): soluble ADNCYC - is regulated by bicarbonate instead of protein G; broadly present in human tissue, also germ cells
ADNCYC	3	Hellevuo K, Berry R, Sikela JM, Tabakoff B.	Localization of the gene for a novel human adenylyl cyclase (ADCY7) to chromosome 16.	Hum Genet	1995	7860067	membrane protein but Ding et al. 2005 report 2 cytoplasmatic domain of ADNCYC protein (in their introduction) IT 107(1): brain 108(2): brain (also olfactory cilia - locuslink) 109(3): paletes, thyroid, germ cells (also olfactory cilia - locuslink) 196883(4): thyroid (also olfactory cilia - locuslink) 111(5): colon, heart, liver, lung (mRNA 60 more abundant in heart than 112) Raimundo et al. 1999 112(6): colon, heart, liver, lung and MNL - Raimundo et al. 1999 113(7): paletes 114(8):brain, May be involved in learning, in memory and in drug dependence.(Genecards) 115(9): brain, neuronal signaling all bind 2 Mg2+ per subunit some isoforms are sensitive to calmodulin/calcium other ones are not 55811(SAC): soluble ADNCYC - is regulated by bicarbonate instead of protein G; broadly present in human tissue, also germ cells

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ADNCYC	3	Gaudin C, Homcy CJ, Ishikawa Y.	Mammalian adenylyl cyclase family members are randomly located on different chromosomes.	Hum Genet	1994	7959689	membrane protein but Ding et al. 2005 report 2 cytoplasmatic domain of ADNCYC protein (in their introduction) IT 107(1): brain 108(2): brain (also olfactory cilia - locuslink) 109(3): paletes, thyroid, germ cells (also olfactory cilia - locuslink) 196883(4): thyroid (also olfactory cilia - locuslink) 111(5): colon, heart, liver, lung (mRNA 60 more abundant in heart than 112) Raimundo et al. 1999 112(6): colon, heart, liver, lung and MNL - Raimundo et al. 1999 113(7): paletes 114(8):brain, May be involved in learning, in memory and in drug dependence.(Genecards) 115(9): brain, neuronal signaling all bind 2 Mg2+ per subunit some isoforms are sensitive to calmodulin/calcium other ones are not 55811(SAC): soluble ADNCYC - is regulated by bicarbonate instead of protein G; broadly present in human tissue, also germ cells
ADNCYC	3	Defer N, Marinx O, Stengel D, Danisova A, Iourgenko V, Matsuoka I, Caput D, Hanoune J.	Molecular cloning of the human type VIII adenylyl cyclase.	FEBS Lett	1994	8076676	membrane protein but Ding et al. 2005 report 2 cytoplasmatic domain of ADNCYC protein (in their introduction) IT 107(1): brain 108(2): brain (also olfactory cilia - locuslink) 109(3): paletes, thyroid, germ cells (also olfactory cilia - locuslink) 196883(4): thyroid (also olfactory cilia - locuslink) 111(5): colon, heart, liver, lung (mRNA 60 more abundant in heart than 112) Raimundo et al. 1999 112(6): colon, heart, liver, lung and MNL - Raimundo et al. 1999 113(7): paletes 114(8):brain, May be involved in learning, in memory and in drug dependence.(Genecards) 115(9): brain, neuronal signaling all bind 2 Mg2+ per subunit some isoforms are sensitive to calmodulin/calcium other ones are not 55811(SAC): soluble ADNCYC - is regulated by bicarbonate instead of protein G; broadly present in human tissue, also germ cells
ADNCYC	3	Raimundo S, Giray J, Volff JN, Schwab M, Altenbuchner J, Ratge D, Wisser H.	Cloning and sequence of partial cDNAs encoding the human type V and VI adenylyl cyclases and subsequent RNA-quantification in various tissues.	Clin Chim Acta	1999	10481931	membrane protein but Ding et al. 2005 report 2 cytoplasmatic domain of ADNCYC protein (in their introduction) IT 107(1): brain 108(2): brain (also olfactory cilia - locuslink) 109(3): paletes, thyroid, germ cells (also olfactory cilia - locuslink) 196883(4): thyroid (also olfactory cilia - locuslink) 111(5): colon, heart, liver, lung (mRNA 60 more abundant in heart than 112) Raimundo et al. 1999 112(6): colon, heart, liver, lung and MNL - Raimundo et al. 1999 113(7): paletes 114(8):brain, May be involved in learning, in memory and in drug dependence.(Genecards) 115(9): brain, neuronal signaling all bind 2 Mg2+ per subunit some isoforms are sensitive to calmodulin/calcium other ones are not 55811(SAC): soluble ADNCYC - is regulated by bicarbonate instead of protein G; broadly present in human tissue, also germ cells
ADNCYC	3	Patrizio M, Colucci M, Levi G.	Human immunodeficiency virus type 1 Tat protein decreases cyclic AMP synthesis in rat microglia cultures.	J Neurochem	2001	11299302	membrane protein but Ding et al. 2005 report 2 cytoplasmatic domain of ADNCYC protein (in their introduction) IT 107(1): brain 108(2): brain (also olfactory cilia - locuslink) 109(3): paletes, thyroid, germ cells (also olfactory cilia - locuslink) 196883(4): thyroid (also olfactory cilia - locuslink) 111(5): colon, heart, liver, lung (mRNA 60 more abundant in heart than 112) Raimundo et al. 1999 112(6): colon, heart, liver, lung and MNL - Raimundo et al. 1999 113(7): paletes 114(8):brain, May be involved in learning, in memory and in drug dependence.(Genecards) 115(9): brain, neuronal signaling all bind 2 Mg2+ per subunit some isoforms are sensitive to calmodulin/calcium other ones are not 55811(SAC): soluble ADNCYC - is regulated by bicarbonate instead of protein G; broadly present in human tissue, also germ cells

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ADNCYC	3	Jaiswal BS, Conti M.	Identification and functional analysis of splice variants of the germ cell soluble adenylyl cyclase.	J Biol Chem	2001	11423534	membrane protein but Ding et al. 2005 report 2 cytoplasmatic domain of ADNCYC protein (in their introduction) IT 107(1): brain 108(2): brain (also olfactory cilia - locuslink) 109(3): paletes, thyroid, germ cells (also olfactory cilia - locuslink) 196883(4): thyroid (also olfactory cilia - locuslink) 111(5): colon, heart, liver, lung (mRNA 60 more abundant in heart than 112) Raimundo et al. 1999 112(6): colon, heart, liver, lung and MNL - Raimundo et al. 1999 113(7): paletes 114(8):brain, May be involved in learning, in memory and in drug dependence.(Genecards) 115(9): brain, neuronal signaling all bind 2 Mg2+ per subunit some isoforms are sensitive to calmodulin/calcium other ones are not 55811(SAC): soluble ADNCYC - is regulated by bicarbonate instead of protein G; broadly present in human tissue, also germ cells
ADNCYC	3	Toyota T, Hattori E, Meerabux J, Yamada K, Saito K, Shibuya H, Nankai M, Yoshikawa T.	Molecular analysis, mutation screening, and association study of adenylate cyclase type 9 gene (ADCY9) in mood disorders.	Am J Med Genet	2002	11840511	membrane protein but Ding et al. 2005 report 2 cytoplasmatic domain of ADNCYC protein (in their introduction) IT 107(1): brain 108(2): brain (also olfactory cilia - locuslink) 109(3): paletes, thyroid, germ cells (also olfactory cilia - locuslink) 196883(4): thyroid (also olfactory cilia - locuslink) 111(5): colon, heart, liver, lung (mRNA 60 more abundant in heart than 112) Raimundo et al. 1999 112(6): colon, heart, liver, lung and MNL - Raimundo et al. 1999 113(7): paletes 114(8):brain, May be involved in learning, in memory and in drug dependence.(Genecards) 115(9): brain, neuronal signaling all bind 2 Mg2+ per subunit some isoforms are sensitive to calmodulin/calcium other ones are not 55811(SAC): soluble ADNCYC - is regulated by bicarbonate instead of protein G; broadly present in human tissue, also germ cells
ADNCYC	3	Ludwig MG, Seuwen K.	Characterization of the human adenylyl cyclase gene family: cDNA, gene structure, and tissue distribution of the nine isoforms.	J Recept Signal Transduct Res	2002	12503609	membrane protein but Ding et al. 2005 report 2 cytoplasmatic domain of ADNCYC protein (in their introduction) IT 107(1): brain 108(2): brain (also olfactory cilia - locuslink) 109(3): paletes, thyroid, germ cells (also olfactory cilia - locuslink) 196883(4): thyroid (also olfactory cilia - locuslink) 111(5): colon, heart, liver, lung (mRNA 60 more abundant in heart than 112) Raimundo et al. 1999 112(6): colon, heart, liver, lung and MNL - Raimundo et al. 1999 113(7): paletes 114(8):brain, May be involved in learning, in memory and in drug dependence.(Genecards) 115(9): brain, neuronal signaling all bind 2 Mg2+ per subunit some isoforms are sensitive to calmodulin/calcium other ones are not 55811(SAC): soluble ADNCYC - is regulated by bicarbonate instead of protein G; broadly present in human tissue, also germ cells
ADNCYC	3	Litvin TN, Kamenetsky M, Zarifyan A, Buck J, Levin LR.	Kinetic properties of "soluble" adenylyl cyclase. Synergism between calcium and bicarbonate.	J Biol Chem	2003	12609998	membrane protein but Ding et al. 2005 report 2 cytoplasmatic domain of ADNCYC protein (in their introduction) IT 107(1): brain 108(2): brain (also olfactory cilia - locuslink) 109(3): paletes, thyroid, germ cells (also olfactory cilia - locuslink) 196883(4): thyroid (also olfactory cilia - locuslink) 111(5): colon, heart, liver, lung (mRNA 60 more abundant in heart than 112) Raimundo et al. 1999 112(6): colon, heart, liver, lung and MNL - Raimundo et al. 1999 113(7): paletes 114(8):brain, May be involved in learning, in memory and in drug dependence.(Genecards) 115(9): brain, neuronal signaling all bind 2 Mg2+ per subunit some isoforms are sensitive to calmodulin/calcium other ones are not 55811(SAC): soluble ADNCYC - is regulated by bicarbonate instead of protein G; broadly present in human tissue, also germ cells

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ADNCYC	3	Katsel PL, Tagliente TM, Schwarz TE, Craddock-Royal BD, Patel ND, Maayani S.	Molecular and biochemical evidence for the presence of type III adenylyl cyclase in human platelets.	Platelets	2003	12623444	membrane protein but Ding et al. 2005 report 2 cytoplasmatic domain of ADNCYC protein (in their introduction) IT 107(1): brain 108(2): brain (also olfactory cilia - locuslink) 109(3): paletes, thyroid, germ cells (also olfactory cilia - locuslink) 196883(4): thyroid (also olfactory cilia - locuslink) 111(5): colon, heart, liver, lung (mRNA 60 more abundant in heart than 112) Raimundo et al. 1999 112(6): colon, heart, liver, lung and MNL - Raimundo et al. 1999 113(7): paletes 114(8):brain, May be involved in learning, in memory and in drug dependence.(Genecards) 115(9): brain, neuronal signaling all bind 2 Mg2+ per subunit some isoforms are sensitive to calmodulin/calcium other ones are not 55811(SAC): soluble ADNCYC - is regulated by bicarbonate instead of protein G; broadly present in human tissue, also germ cells
ADNCYC	3	Cumbay MG, Watts VJ.	Novel regulatory properties of human type 9 adenylate cyclase.	J Pharmacol Exp Ther	2004	14996950	membrane protein but Ding et al. 2005 report 2 cytoplasmatic domain of ADNCYC protein (in their introduction) IT 107(1): brain 108(2): brain (also olfactory cilia - locuslink) 109(3): paletes, thyroid, germ cells (also olfactory cilia - locuslink) 196883(4): thyroid (also olfactory cilia - locuslink) 111(5): colon, heart, liver, lung (mRNA 60 more abundant in heart than 112) Raimundo et al. 1999 112(6): colon, heart, liver, lung and MNL - Raimundo et al. 1999 113(7): paletes 114(8):brain, May be involved in learning, in memory and in drug dependence.(Genecards) 115(9): brain, neuronal signaling all bind 2 Mg2+ per subunit some isoforms are sensitive to calmodulin/calcium other ones are not 55811(SAC): soluble ADNCYC - is regulated by bicarbonate instead of protein G; broadly present in human tissue, also germ cells
ADNCYC	3	Ding Q, Gros R, Chorazyczewski J, Ferguson SS, Feldman RD.	Isoform-specific regulation of adenylyl cyclase function by disruption of membrane trafficking.	Mol Pharmacol	2005	15547246	membrane protein but Ding et al. 2005 report 2 cytoplasmatic domain of ADNCYC protein (in their introduction) IT 107(1): brain 108(2): brain (also olfactory cilia - locuslink) 109(3): paletes, thyroid, germ cells (also olfactory cilia - locuslink) 196883(4): thyroid (also olfactory cilia - locuslink) 111(5): colon, heart, liver, lung (mRNA 60 more abundant in heart than 112) Raimundo et al. 1999 112(6): colon, heart, liver, lung and MNL - Raimundo et al. 1999 113(7): paletes 114(8):brain, May be involved in learning, in memory and in drug dependence.(Genecards) 115(9): brain, neuronal signaling all bind 2 Mg2+ per subunit some isoforms are sensitive to calmodulin/calcium other ones are not 55811(SAC): soluble ADNCYC - is regulated by bicarbonate instead of protein G; broadly present in human tissue, also germ cells
ADNK1	3	McNally T, Helfrich RJ, Cowart M, Dorwin SA, Meuth JL, Idler KB, Klute KA, Simmer RL, Kowaluk EA, Halbert DN.	Cloning and expression of the adenosine kinase gene from rat and human tissues.	Biochem Biophys Res Commun	1997	9070863	monomer needs Mg2+ IT
ADPRDP	3	Gasmi L, Cartwright JL, McLennan AG.	Cloning, expression and characterization of YSA1H, a human adenosine 5'-diphosphosugar pyrophosphatase possessing a MutT motif.	Biochem J	1999	10567213	no information for compartiment. Activity is relatively the same for Mannose, Glucose and ribose. Enzyme cannot act on ribo - or deoxyribonucleoside-tri-phosphates. Needs Mg2+. Is widely expressed, but most abundant in liver (Genecards) ADPglucose is an important precursor bacterial glycogen and plant starch synthesis, whereas ADP-mannose has no known physiological function, although the commercially available synthetic compound can replace ADP-heptoses in bacterial outer-membrane lipopolysaccharide synthesis in vitro . ADP-ribose might therefore also be the most important substrate for human in vivo (from discussion of Gasmi et al, 1999) IT

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ADPRDP	3	Yang H, Slupska MM, Wei YF, Tai JH, Luther WM, Xia YR, Shih DM, Chiang JH, Baikalov C, Fitz-Gibbon S, Phan IT, Conrad A, Miller JH.	Cloning and characterization of a new member of the Nudix hydrolases from human and mouse.	J Biol Chem	2000	10722730	no information for compartiment. Activity is relatively the same for Mannose, Glucose and ribose. Enzyme cannot act on ribo - or deoxyribonucleoside-tri-phosphates. Needs Mg2+. Is widely expressed, but most abundant in liver (Genecards) ADPglucose is an important precursor bacterial glycogen and plant starch synthesis, whereas ADP-mannose has no known physiological function, although the commercially available synthetic compound can replace ADP-heptoses in bacterial outer-membrane lipopolysaccharide synthesis in vitro . ADP-ribose might therefore also be the most important substrate for human in vivo (from discussion of Gasmi et al, 1999) IT
ADPRDP	3	Ishibashi T, Hayakawa H, Sekiguchi M.	A novel mechanism for preventing mutations caused by oxidation of guanine nucleotides.	EMBO Rep	2003	12717453	no information for compartiment. Activity is relatively the same for Mannose, Glucose and ribose. Enzyme cannot act on ribo - or deoxyribonucleoside-tri-phosphates. Needs Mg2+. Is widely expressed, but most abundant in liver (Genecards) ADPglucose is an important precursor bacterial glycogen and plant starch synthesis, whereas ADP-mannose has no known physiological function, although the commercially available synthetic compound can replace ADP-heptoses in bacterial outer-membrane lipopolysaccharide synthesis in vitro . ADP-ribose might therefore also be the most important substrate for human in vivo (from discussion of Gasmi et al, 1999) IT
ADPRDPm	3	Perraud AL, Shen B, Dunn CA, Rippe K, Smith MK, Bessman MJ, Stoddard BL, Scharenberg AM.	NUDT9, a member of the Nudix hydrolase family, is an evolutionarily conserved mitochondrial ADP-ribose pyrophosphatase.	J Biol Chem	2003	12427752	IT location in mito based on signal-sequence
ADPRDPm	3	Shen BW, Perraud AL, Scharenberg A, Stoddard BL.	The crystal structure and mutational analysis of human NUDT9.	J Mol Biol	2003	12948489	IT location in mito based on signal-sequence
ADPRDPm	3	Kuhn FJ, Luckhoff A.	Sites of the NUDT9-H domain critical for ADP-ribose activation of the cation channel TRPM2.	J Biol Chem	2005	15347676	IT location in mito based on signal-sequence
ADPT	3	Crespillo J, Llorente P, Argomaniz L, Montero C.	APRT from erythrocytes of HGPRT deficient patients: kinetic, regulatory and thermostability properties.	Mol Cell Biochem	2003	14674717	no infos for compartiment IT purine salvage
ADPT	3	Silva M, Silva CH, Iulek J, Thiemann OH.	Three-dimensional structure of human adenine phosphoribosyltransferase and its relation to DHA-urolithiasis.	Biochemistry	2004	15196008	no infos for compartiment IT purine salvage
ADSL1	3	Stone RL, Aimi J, Barshop BA, Jaeken J, Van den Berghe G, Zalkin H, Dixon JE.	A mutation in adenylosuccinate lyase associated with mental retardation and autistic features.	Nat Genet	1992	1302001	IT no info for compartiment
ADSL1	3	Barton JW, Hart IM, Patterson D.	Mapping of a locus correcting lack of phosphoribosylaminoimidazole carboxylase activity in Chinese hamster ovary cell Ade-D mutants to human chromosome 4.	Genomics	1991	2004782	IT no info for compartiment
AG13T4g	3	Sasaki K, Kurata-Miura K, Ujita M, Angata K, Nakagawa S, Sekine S, Nishi T, Fukuda M	Expression cloning of cDNA encoding a human beta-1,3-N-acetylglucosaminyltransferase that is essential for poly-N-acetyllactosamine synthesis	Proc Natl Acad Sci U S A	1997	9405606	- N-glycans: most efficiently synthesized by beta4Gal-TI and iGnT; iGnT acts less efficiently on acceptors w/ large number of repeats, beta4Gal-TI exhibits no significant change - O-glycans: extension of core 4 branches synthesized most efficiently by iGnT and beta4Gal-TI; core 2 branch synthesis requires iGnT and beta4Gal-TIV - extension of core 4 branches less efficient than N-glycans, core 2 from [Shiraishi, J Biol Chem 2001]: - 10331, 10678, 79369 identified and characterized - 10331, 10678, 79369 involved in the initiation and elongation of poly-N-acetyllactosamine synthesis - sequence of biosynthetic pathway reviewed in [Funderburgh, IUBMB Life2002] 10331: - Golgi [UniProt] - expressed in colon, jejunum, stomach, esophagus, placenta, and trachea [Shiraishi, J Biol Chem 2001] 10678: - Golgi [UniProt] - ubiquitously expressed [Shiraishi, J Biol Chem 2001] 79369: - Golgi [UniProt] - expressed in brain [Shiraishi, J Biol Chem 2001] 93010: - mouse gene was identified and characterized; human ortholog identified by BLAST, human and mouse genes have 87% ident 11041: - essential for NAcLac chain biosynthesis [RefSeq] - Golgi [UniProt] - gene was isolated and expressed [Sasaki, PNAS 1997]

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AG13T4g	3	Ujita M, Misra AK, McAuliffe J, Hindsgaul O, Fukuda M	Poly-N-acetyllactosamine extension in N-glycans and core 2- and core 4-branched O-glycans is differentially controlled by i-extension enzyme and different members of the beta 1,4-galactosyltransferase gene family	J Biol Chem	2000	10747980	- N-glycans: most efficiently synthesized by beta4Gal-TI and iGnT; iGnT acts less efficiently on acceptors w/ large number of repeats, beta4Gal-TI exhibits no significant change - O-glycans: extension of core 4 branches synthesized most efficiently by iGnT and beta4Gal-TI; core 2 branch synthesis requires iGnT and beta4Gal-TIV - extension of core 4 branches less efficient than N-glycans, core 2 from [Shiraishi, J Biol Chem 2001]: - 10331, 10678, 79369 identified and characterized - 10331, 10678, 79369 involved in the initiation and elongation of poly-N-acetyllactosamine synthesis - sequence of biosynthetic pathway reviewed in [Funderburgh, IUBMB Life2002] 10331: - Golgi [UniProt] - expressed in colon, jejunum, stomach, esophagus, placenta, and trachea [Shiraishi, J Biol Chem 2001] 10678: - Golgi [UniProt] - ubiquitously expressed [Shiraishi, J Biol Chem 2001] 79369: - Golgi [UniProt] - expressed in brain [Shiraishi, J Biol Chem 2001] 93010: - mouse gene was identified and characterized; human ortholog identified by BLAST, human and mouse genes have 87% ident 11041: - essential for NAcLac chain biosynthesis [RefSeq] - Golgi [UniProt] - gene was isolated and expressed [Sasaki, PNAS 1997]
AG13T4g	3	Shiraishi N, Natsume A, Togayachi A, Endo T, Akashima T, Yamada Y, Imai N, Nakagawa S, Koizumi S, Sekine S, Narimatsu H, Sasaki K	Identification and characterization of three novel beta 1,3-N-acetylglucosaminyltransferases structurally related to the beta 1,3-galactosyltransferase family	J Biol Chem	2001	11042166	- N-glycans: most efficiently synthesized by beta4Gal-TI and iGnT; iGnT acts less efficiently on acceptors w/ large number of repeats, beta4Gal-TI exhibits no significant change - O-glycans: extension of core 4 branches synthesized most efficiently by iGnT and beta4Gal-TI; core 2 branch synthesis requires iGnT and beta4Gal-TIV - extension of core 4 branches less efficient than N-glycans, core 2 from [Shiraishi, J Biol Chem 2001]: - 10331, 10678, 79369 identified and characterized - 10331, 10678, 79369 involved in the initiation and elongation of poly-N-acetyllactosamine synthesis - sequence of biosynthetic pathway reviewed in [Funderburgh, IUBMB Life2002] 10331: - Golgi [UniProt] - expressed in colon, jejunum, stomach, esophagus, placenta, and trachea [Shiraishi, J Biol Chem 2001] 10678: - Golgi [UniProt] - ubiquitously expressed [Shiraishi, J Biol Chem 2001] 79369: - Golgi [UniProt] - expressed in brain [Shiraishi, J Biol Chem 2001] 93010: - mouse gene was identified and characterized; human ortholog identified by BLAST, human and mouse genes have 87% ident 11041: - essential for NAcLac chain biosynthesis [RefSeq] - Golgi [UniProt] - gene was isolated and expressed [Sasaki, PNAS 1997]

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
AG13T4g	3	Kataoka K, Huh NH	A novel beta1,3-N-acetylglucosaminyltransferase involved in invasion of cancer cells as assayed in vitro	Biochem Biophys Res Commun	2002	12061784	- N-glycans: most efficiently synthesized by beta4Gal-TI and iGnT; iGnT acts less efficiently on acceptors w/ large number of repeats, beta4Gal-TI exhibits no significant change - O-glycans: extension of core 4 branches synthesized most efficiently by iGnT and beta4Gal-TI; core 2 branch synthesis requires iGnT and beta4Gal-TIV - extension of core 4 branches less efficient than N-glycans, core 2 from [Shiraishi, J Biol Chem 2001]: - 10331, 10678, 79369 identified and characterized - 10331, 10678, 79369 involved in the initiation and elongation of poly-N-acetyllactosamine synthesis - sequence of biosynthetic pathway reviewed in [Funderburgh, IUBMB Life2002] 10331: - Golgi [UniProt] - expressed in colon, jejunum, stomach, esophagus, placenta, and trachea [Shiraishi, J Biol Chem 2001] 10678: - Golgi [UniProt] - ubiquitously expressed [Shiraishi, J Biol Chem 2001] 79369: - Golgi [UniProt] - expressed in brain [Shiraishi, J Biol Chem 2001] 93010: - mouse gene was identified and characterized; human ortholog identified by BLAST, human and mouse genes have 87% ident 11041: - essential for NAcLac chain biosynthesis [RefSeq] - Golgi [UniProt] - gene was isolated and expressed [Sasaki, PNAS 1997]
AG13T4g	3	Zheng H, Li Y, Ji C, Li J, Zhang J, Yin G, Xu J, Ye X, Wu M, Zou X, Gu S, Xie Y, Mao Y	Characterization of a cDNA encoding a protein with limited similarity to beta1, 3-N-acetylglucosaminyltransferase	Mol Biol Rep	2004	15560372	- N-glycans: most efficiently synthesized by beta4Gal-TI and iGnT; iGnT acts less efficiently on acceptors w/ large number of repeats, beta4Gal-TI exhibits no significant change - O-glycans: extension of core 4 branches synthesized most efficiently by iGnT and beta4Gal-TI; core 2 branch synthesis requires iGnT and beta4Gal-TIV - extension of core 4 branches less efficient than N-glycans, core 2 from [Shiraishi, J Biol Chem 2001]: - 10331, 10678, 79369 identified and characterized - 10331, 10678, 79369 involved in the initiation and elongation of poly-N-acetyllactosamine synthesis - sequence of biosynthetic pathway reviewed in [Funderburgh, IUBMB Life2002] 10331: - Golgi [UniProt] - expressed in colon, jejunum, stomach, esophagus, placenta, and trachea [Shiraishi, J Biol Chem 2001] 10678: - Golgi [UniProt] - ubiquitously expressed [Shiraishi, J Biol Chem 2001] 79369: - Golgi [UniProt] - expressed in brain [Shiraishi, J Biol Chem 2001] 93010: - mouse gene was identified and characterized; human ortholog identified by BLAST, human and mouse genes have 87% ident 11041: - essential for NAcLac chain biosynthesis [RefSeq] - Golgi [UniProt] - gene was isolated and expressed [Sasaki, PNAS 1997]

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AG13T4g	3	Ishida H, Togayachi A, Sakai T, Iwai T, Hiruma T, Sato T, Okubo R, Inaba N, Kudo T, Gotoh M, Shoda J, Tanaka N, Narimatsu H	A novel beta1,3-N-acetylglucosaminyltransferase (beta3Gn-T8), which synthesizes poly-N-acetyllactosamine, is dramatically upregulated in colon cancer	FEBS Lett	2005	15620693	- N-glycans: most efficiently synthesized by beta4Gal-TI and iGnT; iGnT acts less efficiently on acceptors w/ large number of repeats, beta4Gal-TI exhibits no significant change - O-glycans: extension of core 4 branches synthesized most efficiently by iGnT and beta4Gal-TI; core 2 branch synthesis requires iGnT and beta4Gal-TIV - extension of core 4 branches less efficient than N-glycans, core 2 from [Shiraishi, J Biol Chem 2001]: - 10331, 10678, 79369 identified and characterized - 10331, 10678, 79369 involved in the initiation and elongation of poly-N-acetyllactosamine synthesis - sequence of biosynthetic pathway reviewed in [Funderburgh, IUBMB Life2002] 10331: - Golgi [UniProt] - expressed in colon, jejunum, stomach, esophagus, placenta, and trachea [Shiraishi, J Biol Chem 2001] 10678: - Golgi [UniProt] - ubiquitously expressed [Shiraishi, J Biol Chem 2001] 79369: - Golgi [UniProt] - expressed in brain [Shiraishi, J Biol Chem 2001] 93010: - mouse gene was identified and characterized; human ortholog identified by BLAST, human and mouse genes have 87% ident 11041: - essential for NAcLac chain biosynthesis [RefSeq] - Golgi [UniProt] - gene was isolated and expressed [Sasaki, PNAS 1997]
AGLPR	0	Brites P, Waterham HR, Wander RJA	Functions and biosynthesis of plasmalogens in health and disease	Biochimica et Biophysica Acta	2004		cytosolic - integral membrane protein on outer membrane of peroxisomes and ER - uniport and refs. Gene for this reaction has not yet been identified, however it is known to exist. Additionally, the transmembrane reaction takes in substrate from peroxisome/ER and produces product on cytosolic side of organelle - AGPex added to accomadate this. NJ
AGLPT	0	Nagan N, Zoeller RA	Plasmalogens: biosynthesis and functions	Progress in Lipid Research	2001		cytosol - see refs no GPR - documented biochemical activity, but no ORF associated w/ it at this time NJ
AGMTm	3	Mistry SK, Burwell TJ, Chambers RM, Rudolph-Owen L, Spaltmann F, Cook WJ, Morris SM Jr.	Cloning of human agmatinase. An alternate path for polyamine synthesis induced in liver by hepatitis B virus.	Am J Physiol Gastrointest Liver Physiol	2002	11804860	cellular location not specified in papers 4th citation indicates bidirectionality of pathway
AGMTm	3	Iyer RK, Kim HK, Tsoa RW, Grody WW, Cederbaum SD.	Cloning and characterization of human agmatinase.	Mol Genet Metab	2002	11914032	cellular location not specified in papers 4th citation indicates bidirectionality of pathway
AGMTm	3	Morris SM Jr.	Vertebrate agmatinases: what role do they play in agmatine catabolism?	Ann N Y Acad Sci	2003	15028567	cellular location not specified in papers 4th citation indicates bidirectionality of pathway
AGMTm	3	Morris SM Jr	Enzymes of arginine metabolism	J Nutr	2004	15465778	cellular location not specified in papers 4th citation indicates bidirectionality of pathway
AGPSx	3	deVet ECJM, vandenBosch H	Alkyl-dihydroxyacetonephosphate synthase	Cell Biochemsitry and Biophysics	2000		peroxisomal inner membrane - uniprot + refs NJ
AGPSx	3	Hajra AK	Glycerolipid biosynthesis in peroxisomes	Prog Lipid Res	1995		peroxisomal inner membrane - uniprot + refs NJ
AGTix	3	Purdue PE, Takada Y, Danpure CJ.	Identification of mutations associated with peroxisome-to-mitochondrion mistargeting of alanine/glyoxylate aminotransferase in primary hyperoxaluria type 1.		1990	1703535	Entrez Gene - The human AGXT protein product is normally localized in the peroxisomes of liver where it is involved in glyoxylate detoxification. Defects in the AGXT gene, some of which alter subcellular targetting, are the cause of Oxalosis I. MM - primarily found in the peroxisome; has a high affinity for glyoxylate; removes >99% of glyoxylate, permitting only a small fraction to be oxidize to oxalate [Poore 1998]
AHC	3	Coulter-Karis DE, Hershfield MS.	Sequence of full length cDNA for human S-adenosylhomocysteine hydrolase.		1989	2596825	Entrez Gene: S-adenosylhomocysteine hydrolase catalyzes the reversible hydrolysis of S-adenosylhomocysteine (AdoHcy) to adenosine (Ado) and L-homocysteine (Hcy). Thus, it regulates the intracellular S-adenosylhomocysteine (SAH) concentration thought to be important for transmethylation reactions. Deficiency in this protein is one of the different causes of hypermethioninemia. S-adenosylhomocysteine hydrolase belongs to the adenosylhomocysteinase family.

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AHC	3	Yang X, Hu Y, Yin DH, Turner MA, Wang M, Borchardt RT, Howell PL, Kuczera K, Schowen RL.	Catalytic strategy of S-adenosyl-L-homocysteine hydrolase: transition-state stabilization and the avoidance of abortive reactions.		2003	12590576	Entrez Gene: S-adenosylhomocysteine hydrolase catalyzes the reversible hydrolysis of S-adenosylhomocysteine (AdoHcy) to adenosine (Ado) and L-homocysteine (Hcy). Thus, it regulates the intracellular S-adenosylhomocysteine (SAH) concentration thought to be important for transmethylation reactions. Deficiency in this protein is one of the different causes of hypermethioninemia. S-adenosylhomocysteine hydrolase belongs to the adenosylhomocysteinase family.
AHEXASE2ly	3	Liu B, Ahmad W, Aronson NN Jr	Structure of the human gene for lysosomal di-N-acetylchitobiase	Glycobiology	1999	10336991	3073, 3074: -The subunits encoded by the genes HEXA and HEXB are synthesized as precursor proteins; processing and subunit assembly in the endoplasmatic reticulum yields three isoforms; beta-hexosaminidase A (alpha, beta), beta-hexosaminidase B (beta, beta) and beta-hexosaminidase S (alpha, alpha). The proteins are targeted to the lysosomes, where final processing produces the mature enzymes. [Maier et al, J Mol Biol. 328(3):669-81 (2003)] - lysosomal [Liu, Glycobiology 1999] - occurs in degradation of Asn-linked glycoproteins [Liu, Glycobiology 1999] - the active site of the beta -subunit hydrolyzes uncharged substrates, whereas the alpha -subunit, in addition, cleaves negatively charged substrate [Hepbildikler 2002] - Hexb -/- mice (expressing only HexS) showed no increased accumulation of glycosaminoglycans, indicating that Hex S involved in their catabolism [Hepbildikler 2002]
AHEXASE2ly	3	Hepbildikler ST, Sandhoff R, Kolzer M, Proia RL, Sandhoff K	Physiological substrates for human lysosomal beta -hexosaminidase S.	J Biol Chem	2002	11707436	3073, 3074: -The subunits encoded by the genes HEXA and HEXB are synthesized as precursor proteins; processing and subunit assembly in the endoplasmatic reticulum yields three isoforms; beta-hexosaminidase A (alpha, beta), beta-hexosaminidase B (beta, beta) and beta-hexosaminidase S (alpha, alpha). The proteins are targeted to the lysosomes, where final processing produces the mature enzymes. [Maier et al, J Mol Biol. 328(3):669-81 (2003)] - lysosomal [Liu, Glycobiology 1999] - occurs in degradation of Asn-linked glycoproteins [Liu, Glycobiology 1999] - the active site of the beta -subunit hydrolyzes uncharged substrates, whereas the alpha -subunit, in addition, cleaves negatively charged substrate [Hepbildikler 2002] - Hexb -/- mice (expressing only HexS) showed no increased accumulation of glycosaminoglycans, indicating that Hex S involved in their catabolism [Hepbildikler 2002]
AHEXASE2ly	3	Maier T, Strater N, Schuette CG, Klingenstein R, Sandhoff K, Saenger W.	The X-ray crystal structure of human beta-hexosaminidase B provides new insights into Sandhoff disease	J Mol Biol	2003	12706724	3073, 3074: -The subunits encoded by the genes HEXA and HEXB are synthesized as precursor proteins; processing and subunit assembly in the endoplasmatic reticulum yields three isoforms; beta-hexosaminidase A (alpha, beta), beta-hexosaminidase B (beta, beta) and beta-hexosaminidase S (alpha, alpha). The proteins are targeted to the lysosomes, where final processing produces the mature enzymes. [Maier et al, J Mol Biol. 328(3):669-81 (2003)] - lysosomal [Liu, Glycobiology 1999] - occurs in degradation of Asn-linked glycoproteins [Liu, Glycobiology 1999] - the active site of the beta -subunit hydrolyzes uncharged substrates, whereas the alpha -subunit, in addition, cleaves negatively charged substrate [Hepbildikler 2002] - Hexb -/- mice (expressing only HexS) showed no increased accumulation of glycosaminoglycans, indicating that Hex S involved in their catabolism [Hepbildikler 2002]
AICART	3	Sugita T, Aya H, Ueno M, Ishizuka T, Kawashima K.	Characterization of molecularly cloned human 5-aminoimidazole-4-carboxamide ribonucleotide transformylase.	J Biochem (Tokyo)	1997	9378707	no infos for compartiment IT
AICART	3	Bulock KG, Beardsley GP, Anderson KS.	The kinetic mechanism of the human bifunctional enzyme ATIC (5-amino-4-imidazolecarboxamide ribonucleotide transformylase/inosine 5'-monophosphate cyclohydrolase). A surprising lack of substrate channeling.	J Biol Chem	2002	11948179	no infos for compartiment IT
AICART	3	Cheong CG, Wolan DW, Greasley SE, Horton PA, Beardsley GP, Wilson IA.	Crystal structures of human bifunctional enzyme aminoimidazole-4-carboxamide ribonucleotide transformylase/IMP cyclohydrolase in complex with potent sulfonyl-containing antifolates.	J Biol Chem	2004	14966129	no infos for compartiment IT
AIRCr	3	Minet M, Lacroute F.	Cloning and sequencing of a human cDNA coding for a multifunctional polypeptide of the purine pathway by complementation of the ade2-101 mutant in Saccharomyces cerevisiae.	Curr Genet	1990	2253271	IT (no info for compartiment)

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AIRCr	3	Brayton KA, Chen Z, Zhou G, Nagy PL, Gavalas A, Trent JM, Deaven LL, Dixon JE, Zalkin H.	Two genes for de novo purine nucleotide synthesis on human chromosome 4 are closely linked and divergently transcribed.	J Biol Chem	1994	8106516	IT (no info for compartiment)
AKR1C1	3	Stolz A, Hammond L, Lou H, Takikawa H, Ronk M, Shively JE.	cDNA cloning and expression of the human hepatic bile acid-binding protein. A member of the monomeric reductase gene family.	J Biol Chem	1993	8486699	localization: cytosol (uniprot) specificity: Expressed in all tissues tested including liver, prostate, testis, adrenal gland, brain, uterus, mammary gland and keratinocytes. Highest levels found in liver, mammary gland and brain. This gene encodes a member of the aldo/keto reductase superfamily, which consists of more than 40 known enzymes and proteins. These enzymes catalyze the conversion of aldehydes and ketones to their corresponding alcohols by utilizing NADH and/or NADPH as cofactors. The enzymes display overlapping but distinct substrate specificity. This enzyme catalyzes the reaction of progesterone to the inactive form 20-alpha-hydroxy-progesterone. This gene shares high sequence identity with three other gene members and is clustered with those three genes at chromosome 10p15-p14. May assist in the rapid intracellular transport of bile acids from the sinusoidal to the canalicular pole of the cell. Have a role in monitoring the intrahepatic bile acid concentration. NJ
ALASm	2	Bishop DF.	Two different genes encode delta-aminolevulinate synthase in humans: nucleotide sequences of cDNAs for the housekeeping and erythroid genes.		1990	2263504	TV/RS
ALAt2r	2	Sagne C, Agulhon C, Ravassard P, Darmon M, Hamon M, El Mestikawy S, Gasnier B, Giros B	Identification and characterization of a lysosomal transporter for small neutral amino acids	Proc Natl Acad Sci U S A	2001	11390972	The transporter here is thought to principally transport small neutral amino acids and related metabolites from the lysosome to the cytosol. Overexpression experiments have clearly shown that transport from the extracellular media into the cell cytoplasm occurs, but is is not clear if this is an experimental artifact. The evidence is thus physiological for extracellular transport and biochemical for lysosomal transport.
ALAt2r	2	Boll M, Foltz M, Rubio-Aliaga I, Kottra G, Daniel H	Functional characterization of two novel mammalian electrogenic proton-dependent amino acid cotransporters	J Biol Chem	2002	11959859	The transporter here is thought to principally transport small neutral amino acids and related metabolites from the lysosome to the cytosol. Overexpression experiments have clearly shown that transport from the extracellular media into the cell cytoplasm occurs, but is is not clear if this is an experimental artifact. The evidence is thus physiological for extracellular transport and biochemical for lysosomal transport.
ALAt4	3	Albritton LM, Bowcock AM, Eddy RL, Morton CC, Tseng L, Farrer LA, Cavalli-Sforza LL, Shows TB, Cunningham JM	The human cationic amino acid transporter (ATRC1): physical and genetic mapping to 13q12-q14	Genomics	1992	1348489	SLC38A4 is found predominantly in liver and transports both cationic and neutral amino acids. The transport of cationic amino acids by SLC38A4 is Na(+) and pH independent, while the transport of neutral amino acids is Na(+) and pH dependent (Hatanaka et al., 2001).[supplied by OMIM] When expressed in mammalian cells, hATA2 mediates Na+-dependent transport of alpha-(methylamino)isobutyric acid, a specific model substrate for system A. The transporter is specific for neutral amino acids. It is pH-sensitive and Li+-intolerant. The Na+:amino acid stoichiometry is 1:1. (PMID 10930503) Slc38a1: PMID 10891391 ATA2 mRNA is present in all tissues tested including the liver, kidney, colon, and small intestine as has been reported recently from our laboratory The transport of [14C]MeAIB is inhibited most markedly by alanine, serine, methionine, asparagine and glutamine. Moderate inhibition is observed with glycine, proline, threonine, leucine, and phenylalanine 1:1 Na: aa, no H transport reported SLC7A1 (and presumably 2,3): its role in normal cell metabolism is transport of the cationic amino acids, arginine, ly

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ALAt4	3	Furesz TC, Moe AJ, Smith CH	Lysine uptake by human placental microvillous membrane: comparison of system y+ with basal membrane	Am J Physiol	1995	7534987	SLC38A4 is found predominantly in liver and transports both cationic and neutral amino acids. The transport of cationic amino acids by SLC38A4 is Na(+) and pH independent, while the transport of neutral amino acids is Na(+) and pH dependent (Hatanaka et al., 2001).[supplied by OMIM] When expressed in mammalian cells, hATA2 mediates Na+-dependent transport of alpha-(methylamino)isobutyric acid, a specific model substrate for system A. The transporter is specific for neutral amino acids. It is pH-sensitive and Li+-intolerant. The Na+:amino acid stoichiometry is 1:1. (PMID 10930503) Slc38a1: PMID 10891391 ATA2 mRNA is present in all tissues tested including the liver, kidney, colon, and small intestine as has been reported recently from our laboratory The transport of [14C]MeAIB is inhibited most markedly by alanine, serine, methionine, asparagine and glutamine. Moderate inhibition is observed with glycine, proline, threonine, leucine, and phenylalanine 1:1 Na: aa, no H transport reported SLC7A1 (and presumably 2,3): its role in normal cell metabolism is transport of the cationic amino acids, arginine, ly
ALAt4	3	Hoshide R, Ikeda Y, Karashima S, Matsuura T, Komaki S, Kishino T, Niikawa N, Endo F, Matsuda I	Molecular cloning, tissue distribution, and chromosomal localization of human cationic amino acid transporter 2 (HCAT2)	Genomics	1996	8954799	SLC38A4 is found predominantly in liver and transports both cationic and neutral amino acids. The transport of cationic amino acids by SLC38A4 is Na(+) and pH independent, while the transport of neutral amino acids is Na(+) and pH dependent (Hatanaka et al., 2001).[supplied by OMIM] When expressed in mammalian cells, hATA2 mediates Na+-dependent transport of alpha-(methylamino)isobutyric acid, a specific model substrate for system A. The transporter is specific for neutral amino acids. It is pH-sensitive and Li+-intolerant. The Na+:amino acid stoichiometry is 1:1. (PMID 10930503) Slc38a1: PMID 10891391 ATA2 mRNA is present in all tissues tested including the liver, kidney, colon, and small intestine as has been reported recently from our laboratory The transport of [14C]MeAIB is inhibited most markedly by alanine, serine, methionine, asparagine and glutamine. Moderate inhibition is observed with glycine, proline, threonine, leucine, and phenylalanine 1:1 Na: aa, no H transport reported SLC7A1 (and presumably 2,3): its role in normal cell metabolism is transport of the cationic amino acids, arginine, ly
ALAt4	3	Sugawara M, Nakanishi T, Fei YJ, Huang W, Ganapathy ME, Leibach FH, Ganapathy V	Cloning of an amino acid transporter with functional characteristics and tissue expression pattern identical to that of system A	J Biol Chem	2000	10747860	SLC38A4 is found predominantly in liver and transports both cationic and neutral amino acids. The transport of cationic amino acids by SLC38A4 is Na(+) and pH independent, while the transport of neutral amino acids is Na(+) and pH dependent (Hatanaka et al., 2001).[supplied by OMIM] When expressed in mammalian cells, hATA2 mediates Na+-dependent transport of alpha-(methylamino)isobutyric acid, a specific model substrate for system A. The transporter is specific for neutral amino acids. It is pH-sensitive and Li+-intolerant. The Na+:amino acid stoichiometry is 1:1. (PMID 10930503) Slc38a1: PMID 10891391 ATA2 mRNA is present in all tissues tested including the liver, kidney, colon, and small intestine as has been reported recently from our laboratory The transport of [14C]MeAIB is inhibited most markedly by alanine, serine, methionine, asparagine and glutamine. Moderate inhibition is observed with glycine, proline, threonine, leucine, and phenylalanine 1:1 Na: aa, no H transport reported SLC7A1 (and presumably 2,3): its role in normal cell metabolism is transport of the cationic amino acids, arginine, ly

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ALAt4	3	Wang H, Huang W, Sugawara M, Devoe LD, Leibach FH, Prasad PD, Ganapathy V	Cloning and functional expression of ATA1, a subtype of amino acid transporter A, from human placenta	Biochem Biophys Res Commun	2000	10891391	SLC38A4 is found predominantly in liver and transports both cationic and neutral amino acids. The transport of cationic amino acids by SLC38A4 is Na(+) and pH independent, while the transport of neutral amino acids is Na(+) and pH dependent (Hatanaka et al., 2001).[supplied by OMIM] When expressed in mammalian cells, hATA2 mediates Na+-dependent transport of alpha-(methylamino)isobutyric acid, a specific model substrate for system A. The transporter is specific for neutral amino acids. It is pH-sensitive and Li+-intolerant. The Na+:amino acid stoichiometry is 1:1. (PMID 10930503) Slc38a1: PMID 10891391 ATA2 mRNA is present in all tissues tested including the liver, kidney, colon, and small intestine as has been reported recently from our laboratory The transport of [14C]MeAIB is inhibited most markedly by alanine, serine, methionine, asparagine and glutamine. Moderate inhibition is observed with glycine, proline, threonine, leucine, and phenylalanine 1:1 Na: aa, no H transport reported SLC7A1 (and presumably 2,3): its role in normal cell metabolism is transport of the cationic amino acids, arginine, ly
ALAt4	3	Hatanaka T, Huang W, Wang H, Sugawara M, Prasad PD, Leibach FH, Ganapathy V	Primary structure, functional characteristics and tissue expression pattern of human ATA2, a subtype of amino acid transport system A	Biochim Biophys Acta	2000	10930503	SLC38A4 is found predominantly in liver and transports both cationic and neutral amino acids. The transport of cationic amino acids by SLC38A4 is Na(+) and pH independent, while the transport of neutral amino acids is Na(+) and pH dependent (Hatanaka et al., 2001).[supplied by OMIM] When expressed in mammalian cells, hATA2 mediates Na+-dependent transport of alpha-(methylamino)isobutyric acid, a specific model substrate for system A. The transporter is specific for neutral amino acids. It is pH-sensitive and Li+-intolerant. The Na+:amino acid stoichiometry is 1:1. (PMID 10930503) Slc38a1: PMID 10891391 ATA2 mRNA is present in all tissues tested including the liver, kidney, colon, and small intestine as has been reported recently from our laboratory The transport of [14C]MeAIB is inhibited most markedly by alanine, serine, methionine, asparagine and glutamine. Moderate inhibition is observed with glycine, proline, threonine, leucine, and phenylalanine 1:1 Na: aa, no H transport reported SLC7A1 (and presumably 2,3): its role in normal cell metabolism is transport of the cationic amino acids, arginine, ly
ALAt4	3	Gu S, Roderick HL, Camacho P, Jiang JX	Characterization of an N-system amino acid transporter expressed in retina and its involvement in glutamine transport	J Biol Chem	2001	11325958	SLC38A4 is found predominantly in liver and transports both cationic and neutral amino acids. The transport of cationic amino acids by SLC38A4 is Na(+) and pH independent, while the transport of neutral amino acids is Na(+) and pH dependent (Hatanaka et al., 2001).[supplied by OMIM] When expressed in mammalian cells, hATA2 mediates Na+-dependent transport of alpha-(methylamino)isobutyric acid, a specific model substrate for system A. The transporter is specific for neutral amino acids. It is pH-sensitive and Li+-intolerant. The Na+:amino acid stoichiometry is 1:1. (PMID 10930503) Slc38a1: PMID 10891391 ATA2 mRNA is present in all tissues tested including the liver, kidney, colon, and small intestine as has been reported recently from our laboratory The transport of [14C]MeAIB is inhibited most markedly by alanine, serine, methionine, asparagine and glutamine. Moderate inhibition is observed with glycine, proline, threonine, leucine, and phenylalanine 1:1 Na: aa, no H transport reported SLC7A1 (and presumably 2,3): its role in normal cell metabolism is transport of the cationic amino acids, arginine, ly

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ALAt4	3	Hatanaka T, Huang W, Ling R, Prasad PD, Sugawara M, Leibach FH, Ganapathy V	Evidence for the transport of neutral as well as cationic amino acids by ATA3, a novel and liver-specific subtype of amino acid transport system A	Biochim Biophys Acta	2001	11342143	SLC38A4 is found predominantly in liver and transports both cationic and neutral amino acids. The transport of cationic amino acids by SLC38A4 is Na(+) and pH independent, while the transport of neutral amino acids is Na(+) and pH dependent (Hatanaka et al., 2001).[supplied by OMIM] When expressed in mammalian cells, hATA2 mediates Na+-dependent transport of alpha-(methylamino)isobutyric acid, a specific model substrate for system A. The transporter is specific for neutral amino acids. It is pH-sensitive and Li+-intolerant. The Na+:amino acid stoichiometry is 1:1. (PMID 10930503) Slc38a1: PMID 10891391 ATA2 mRNA is present in all tissues tested including the liver, kidney, colon, and small intestine as has been reported recently from our laboratory The transport of [14C]MeAIB is inhibited most markedly by alanine, serine, methionine, asparagine and glutamine. Moderate inhibition is observed with glycine, proline, threonine, leucine, and phenylalanine 1:1 Na: aa, no H transport reported SLC7A1 (and presumably 2,3): its role in normal cell metabolism is transport of the cationic amino acids, arginine, ly
ALAt4	3	Gu S, Adan-Rice D, Leach RJ, Jiang JX	A novel human amino acid transporter, hNAT3: cDNA cloning, chromosomal mapping, genomic structure, expression, and functional characterization	Genomics	2001	11414754	SLC38A4 is found predominantly in liver and transports both cationic and neutral amino acids. The transport of cationic amino acids by SLC38A4 is Na(+) and pH independent, while the transport of neutral amino acids is Na(+) and pH dependent (Hatanaka et al., 2001).[supplied by OMIM] When expressed in mammalian cells, hATA2 mediates Na+-dependent transport of alpha-(methylamino)isobutyric acid, a specific model substrate for system A. The transporter is specific for neutral amino acids. It is pH-sensitive and Li+-intolerant. The Na+:amino acid stoichiometry is 1:1. (PMID 10930503) Slc38a1: PMID 10891391 ATA2 mRNA is present in all tissues tested including the liver, kidney, colon, and small intestine as has been reported recently from our laboratory The transport of [14C]MeAIB is inhibited most markedly by alanine, serine, methionine, asparagine and glutamine. Moderate inhibition is observed with glycine, proline, threonine, leucine, and phenylalanine 1:1 Na: aa, no H transport reported SLC7A1 (and presumably 2,3): its role in normal cell metabolism is transport of the cationic amino acids, arginine, ly
ALAt4	3	Vekony N, Wolf S, Boissel JP, Gnauert K, Closs EI	Human cationic amino acid transporter hCAT-3 is preferentially expressed in peripheral tissues	Biochemistry	2001	11591158	SLC38A4 is found predominantly in liver and transports both cationic and neutral amino acids. The transport of cationic amino acids by SLC38A4 is Na(+) and pH independent, while the transport of neutral amino acids is Na(+) and pH dependent (Hatanaka et al., 2001).[supplied by OMIM] When expressed in mammalian cells, hATA2 mediates Na+-dependent transport of alpha-(methylamino)isobutyric acid, a specific model substrate for system A. The transporter is specific for neutral amino acids. It is pH-sensitive and Li+-intolerant. The Na+:amino acid stoichiometry is 1:1. (PMID 10930503) Slc38a1: PMID 10891391 ATA2 mRNA is present in all tissues tested including the liver, kidney, colon, and small intestine as has been reported recently from our laboratory The transport of [14C]MeAIB is inhibited most markedly by alanine, serine, methionine, asparagine and glutamine. Moderate inhibition is observed with glycine, proline, threonine, leucine, and phenylalanine 1:1 Na: aa, no H transport reported SLC7A1 (and presumably 2,3): its role in normal cell metabolism is transport of the cationic amino acids, arginine, ly

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ALAt4	3	Cariappa R, Heath-Monnig E, Furesz TC, Kamath SG, Smith CH	Stable polarized expression of hCAT-1 in an epithelial cell line	J Membr Biol	2002	11891586	SLC38A4 is found predominantly in liver and transports both cationic and neutral amino acids. The transport of cationic amino acids by SLC38A4 is Na(+) and pH independent, while the transport of neutral amino acids is Na(+) and pH dependent (Hatanaka et al., 2001).[supplied by OMIM] When expressed in mammalian cells, hATA2 mediates Na+-dependent transport of alpha-(methylamino)isobutyric acid, a specific model substrate for system A. The transporter is specific for neutral amino acids. It is pH-sensitive and Li+-intolerant. The Na+:amino acid stoichiometry is 1:1. (PMID 10930503) Slc38a1: PMID 10891391 ATA2 mRNA is present in all tissues tested including the liver, kidney, colon, and small intestine as has been reported recently from our laboratory The transport of [14C]MeAIB is inhibited most markedly by alanine, serine, methionine, asparagine and glutamine. Moderate inhibition is observed with glycine, proline, threonine, leucine, and phenylalanine 1:1 Na: aa, no H transport reported SLC7A1 (and presumably 2,3): its role in normal cell metabolism is transport of the cationic amino acids, arginine, ly
ALAt4	3	Wolf S, Janzen A, Vekony N, Martine U, Strand D, Closs EI	Expression of solute carrier 7A4 (SLC7A4) in the plasma membrane is not sufficient to mediate amino acid transport activity	Biochem J	2002	12049641	SLC38A4 is found predominantly in liver and transports both cationic and neutral amino acids. The transport of cationic amino acids by SLC38A4 is Na(+) and pH independent, while the transport of neutral amino acids is Na(+) and pH dependent (Hatanaka et al., 2001).[supplied by OMIM] When expressed in mammalian cells, hATA2 mediates Na+-dependent transport of alpha-(methylamino)isobutyric acid, a specific model substrate for system A. The transporter is specific for neutral amino acids. It is pH-sensitive and Li+-intolerant. The Na+:amino acid stoichiometry is 1:1. (PMID 10930503) Slc38a1: PMID 10891391 ATA2 mRNA is present in all tissues tested including the liver, kidney, colon, and small intestine as has been reported recently from our laboratory The transport of [14C]MeAIB is inhibited most markedly by alanine, serine, methionine, asparagine and glutamine. Moderate inhibition is observed with glycine, proline, threonine, leucine, and phenylalanine 1:1 Na: aa, no H transport reported SLC7A1 (and presumably 2,3): its role in normal cell metabolism is transport of the cationic amino acids, arginine, ly
ALAt4	3	Verrey F, Closs EI, Wagner CA, Palacin M, Endou H, Kanai Y	CATs and HATs: the SLC7 family of amino acid transporters	Pflugers Arch	2004	14770310	SLC38A4 is found predominantly in liver and transports both cationic and neutral amino acids. The transport of cationic amino acids by SLC38A4 is Na(+) and pH independent, while the transport of neutral amino acids is Na(+) and pH dependent (Hatanaka et al., 2001).[supplied by OMIM] When expressed in mammalian cells, hATA2 mediates Na+-dependent transport of alpha-(methylamino)isobutyric acid, a specific model substrate for system A. The transporter is specific for neutral amino acids. It is pH-sensitive and Li+-intolerant. The Na+:amino acid stoichiometry is 1:1. (PMID 10930503) Slc38a1: PMID 10891391 ATA2 mRNA is present in all tissues tested including the liver, kidney, colon, and small intestine as has been reported recently from our laboratory The transport of [14C]MeAIB is inhibited most markedly by alanine, serine, methionine, asparagine and glutamine. Moderate inhibition is observed with glycine, proline, threonine, leucine, and phenylalanine 1:1 Na: aa, no H transport reported SLC7A1 (and presumably 2,3): its role in normal cell metabolism is transport of the cationic amino acids, arginine, ly

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ALATA_L	3	Yang RZ, Blaileanu G, Hansen BC, Shuldiner AR, Gong DW.	cDNA cloning, genomic structure, chromosomal mapping, and functional expression of a novel human alanine aminotransferase.	Genomics	2002	11863375	- Some info added by RS/TV - alanine aminotransferase catalyzes the reversible transamination between alanine and 2-oxoglutarate to form pyruvate and glutamate. - two isozymes are known to occur GPT and GPT2 - GPT2 is highly expressed in muscle, fat, and kidney. - GPT mainly expressed in kidney, liver, and heart. All this according to Yang RZ, Blaileanu G, Hansen BC, Shuldiner AR, Gong DW. Genomics. 2002 Mar;79(3):445-50.
ALCD1	3	Dawidek-Pietryka K, Szczepaniak S, Dudka J, Mazur M	In vitro studies of human alcohol dehydrogenase inhibition in the process of methanol and ethylene glycol oxidation	Arch Toxicol	1998	9806434	- Methanol is oxidized by alcohol dehydrogenase in the presence of NAD to formaldehyde [Abramson 2000] -Ethanol is preferentially metabolized by alcohol dehydrogenase and therefore can be effective in treatment of methanol poisoning [Dawidek-Pietryka 1998] - alcohol dehydrogenase is a predominant enzyme for methanol and ethylene glycol ox- idation (see [Ziegler 1988] ref in [Dawidek-Pietryka 1998] - ethanol metabolism by alcohol dehydrogenases occurs in the cytosol [Salway] - Class I isozymes are homo- and heterodimers (aa, bb, cc, ab, ac, bc) [Ramchandani et al, Pathol Biol 2001] Also from Ramchandani paper: - 124 (formerly ADH1 alpha subunit, now ADH1A) has low ethanol catalytic efficiency - 125 (formerly ADH2 beta subunit, now ADH1B) has high ethanol catalytic efficiency -126 (formerly ADH3 gamma subunit, now ADH1C) has high ethanol catalytic efficiency -127 (formerly ADH4 pi subunit, now ADH2) has low ethanol catalytic efficiency and is only expressed in the liver -128 (formerly ADH chi subunit, now ADH3) has very low ethanol catalytic efficiency and is ubiquitously expressed -131 (formerly ADH7 sigma subunit, now ADH4) has high etha - 130 (formerly ADH6, now ADH) ethanol catalytic activity no 137872: -only expressed in the liver [Deng et al, DNA Seq 2002]
ALCD1	3	Abramson S, Singh AK.	Treatment of the alcohol intoxications: ethylene glycol, methanol and isopropanol.	Curr Opin Nephrol Hypertens	2000	11128434	- Methanol is oxidized by alcohol dehydrogenase in the presence of NAD to formaldehyde [Abramson 2000] -Ethanol is preferentially metabolized by alcohol dehydrogenase and therefore can be effective in treatment of methanol poisoning [Dawidek-Pietryka 1998] - alcohol dehydrogenase is a predominant enzyme for methanol and ethylene glycol ox- idation (see [Ziegler 1988] ref in [Dawidek-Pietryka 1998] - ethanol metabolism by alcohol dehydrogenases occurs in the cytosol [Salway] - Class I isozymes are homo- and heterodimers (aa, bb, cc, ab, ac, bc) [Ramchandani et al, Pathol Biol 2001] Also from Ramchandani paper: - 124 (formerly ADH1 alpha subunit, now ADH1A) has low ethanol catalytic efficiency - 125 (formerly ADH2 beta subunit, now ADH1B) has high ethanol catalytic efficiency -126 (formerly ADH3 gamma subunit, now ADH1C) has high ethanol catalytic efficiency -127 (formerly ADH4 pi subunit, now ADH2) has low ethanol catalytic efficiency and is only expressed in the liver -128 (formerly ADH chi subunit, now ADH3) has very low ethanol catalytic efficiency and is ubiquitously expressed -131 (formerly ADH7 sigma subunit, now ADH4) has high etha - 130 (formerly ADH6, now ADH) ethanol catalytic activity no 137872: -only expressed in the liver [Deng et al, DNA Seq 2002]

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ALCD1	3	Ramchandani VA, Bosron WF, Li TK	Research advances in ethanol metabolism	Pathol Biol (Paris)	2001	11762128	- Methanol is oxidized by alcohol dehydrogenase in the presence of NAD to formaldehyde [Abramson 2000] -Ethanol is preferentially metabolized by alcohol dehydrogenase and therefore can be effective in treatment of methanol poisoning [Dawidek-Pietryka 1998] - alcohol dehydrogenase is a predominant enzyme for methanol and ethylene glycol ox- idation (see [Ziegler 1988] ref in [Dawidek-Pietryka 1998] - ethanol metabolism by alcohol dehydrogenases occurs in the cytosol [Salway] - Class I isozymes are homo- and heterodimers (aa, bb, cc, ab, ac, bc) [Ramchandani et al, Pathol Biol 2001] Also from Ramchandani paper: - 124 (formerly ADH1 alpha subunit, now ADH1A) has low ethanol catalytic efficiency - 125 (formerly ADH2 beta subunit, now ADH1B) has high ethanol catalytic efficiency -126 (formerly ADH3 gamma subunit, now ADH1C) has high ethanol catalytic efficiency -127 (formerly ADH4 pi subunit, now ADH2) has low ethanol catalytic efficiency and is only expressed in the liver -128 (formerly ADH chi subunit, now ADH3) has very low ethanol catalytic efficiency and is ubiquitously expressed -131 (formerly ADH7 sigma subunit, now ADH4) has high etha - 130 (formerly ADH6, now ADH) ethanol catalytic activity no 137872: -only expressed in the liver [Deng et al, DNA Seq 2002]
ALCD1	3	Deng Y, Wang Z, Gu S, Ji C, Ying K, Xie Y, Mao Y	Cloning and characterization of a novel human alcohol dehydrogenase gene (ADHFe1)	DNA Seq	2002	12592711	- Methanol is oxidized by alcohol dehydrogenase in the presence of NAD to formaldehyde [Abramson 2000] -Ethanol is preferentially metabolized by alcohol dehydrogenase and therefore can be effective in treatment of methanol poisoning [Dawidek-Pietryka 1998] - alcohol dehydrogenase is a predominant enzyme for methanol and ethylene glycol ox- idation (see [Ziegler 1988] ref in [Dawidek-Pietryka 1998] - ethanol metabolism by alcohol dehydrogenases occurs in the cytosol [Salway] - Class I isozymes are homo- and heterodimers (aa, bb, cc, ab, ac, bc) [Ramchandani et al, Pathol Biol 2001] Also from Ramchandani paper: - 124 (formerly ADH1 alpha subunit, now ADH1A) has low ethanol catalytic efficiency - 125 (formerly ADH2 beta subunit, now ADH1B) has high ethanol catalytic efficiency -126 (formerly ADH3 gamma subunit, now ADH1C) has high ethanol catalytic efficiency -127 (formerly ADH4 pi subunit, now ADH2) has low ethanol catalytic efficiency and is only expressed in the liver -128 (formerly ADH chi subunit, now ADH3) has very low ethanol catalytic efficiency and is ubiquitously expressed -131 (formerly ADH7 sigma subunit, now ADH4) has high etha - 130 (formerly ADH6, now ADH) ethanol catalytic activity no 137872: -only expressed in the liver [Deng et al, DNA Seq 2002]
ALDD21	2	De Laurenzi V, Rogers GR, Hamrock DJ, Marekov LN, Steinert PM, Compton JG, Markova N, Rizzo WB.	Sjogren-Larsson syndrome is caused by mutations in the fatty aldehyde dehydrogenase gene.	Nat Genet	1996	8528251	Role in fatty acid metabolism - see PMID 11591435. Aldehyde dehydrogenase isozymes are thought to play a major role in the detoxification of aldehydes generated by alcohol metabolism and lipid peroxidation. This gene product catalyzes the oxidation of long-chain aliphatic aldehydes to fatty acid. Mutations in the gene cause Sjogren-Larsson syndrome. NJ
ALDD21	2	Verhoeven NM, Jakobs C.	Human metabolism of phytanic acid and pristanic acid.	Prog Lipid Res	2001	11591435	Role in fatty acid metabolism - see PMID 11591435. Aldehyde dehydrogenase isozymes are thought to play a major role in the detoxification of aldehydes generated by alcohol metabolism and lipid peroxidation. This gene product catalyzes the oxidation of long-chain aliphatic aldehydes to fatty acid. Mutations in the gene cause Sjogren-Larsson syndrome. NJ

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ALDD2x	0	Sladek NE	Human aldehyde dehydrogenases: potential pathological, pharmacological, and toxicological impact	J Biochem Mol Toxicol	2003	12616643	-cytosolic [Sladek, J Biocehm Molecular Toxicology, 2003], [RefSeq] - acetaldehdyde is known substrate; NAD is cofactor [Sladek, J Biocehm Molecular Toxicology, 2003] 8854: -cytosolic [Sladek, J Biocehm Molecular Toxicology, 2003] - doesn't metabolize acetaldehyde very efficiently; NAD, NADP are cofactors [Sladek, J Biocehm Molecular Toxicology, 2003] 220: -cytosolic [Sladek, J Biocehm Molecular Toxicology, 2003], [UniProt] - NAD is cofactor [Sladek, J Biocehm Molecular Toxicology, 2003] 217, 219: - mitochondrial [Sladek, J Biocehm Molecular Toxicology, 2003], [UniProt] - acetaldehyde is preferred substrate, NAD is cofactor [Sladek, J Biocehm Molecular Toxicology, 2003] 218: -cytosolic [Sladek, J Biocehm Molecular Toxicology, 2003] - NAD, NADP are cofactors [Sladek, J Biocehm Molecular Toxicology, 2003] 224: - integral to ER membrane (GO) - cytoplasmic surface of ER mem [UniProt] - NAD, NADP are cofactors [Sladek, J Biocehm Molecular Toxicology, 2003] 221: - inferred to be associated with ER; assume its localization is similar to 224
ALKP	3	Knoll BJ, Rothblum KN, Longley M.	Nucleotide sequence of the human placental alkaline phosphatase gene. Evolution of the 5' flanking region by deletion/substitution.	J Biol Chem	1988	3042787	cytosolic - uniprot may have activity of fatty acid phosphate esters (?) There are at least four distinct but related alkaline phosphatases: intestinal, placental, placental-like, and liver/bone/kidney (tissue non-specific). The first three are located together on chromosome 2 while the tissue non-specific form is located on chromosome 1. The product of this gene is a membrane bound glycosylated enzyme that is not expressed in any particular tissue and is, therefore, referred to as the tissue-nonspecific form of the enzyme. The exact physiological function of the alkaline phosphatases is not known. A proposed function of this form of the enzyme is matrix mineralization, however, mice that lack a functional form of this enzyme show normal skeletal development. This enzyme has been linked directly to a disorder known as hypophosphatasia, a disorder that is characterized by hypercalcemia and includes skeletal defects. The character of this disorder can vary, however, depending on the specific mutation since this determines age of onset and severity of symptoms. The coding sequence for this form of alkaline phosphatase is un NJ
ALOX12	3	Izumi T, Hoshiko S, Radmark O, Samuelsson B.	Cloning of the cDNA for human 12-lipoxygenase.	Proc Natl Acad Sci	1990	2217179	cytoplasmic - uniprot + refs Leukotrienes biosynthesis gene identification - Izumi and Funk refs NJ
ALOX12	3	Funk CD, Furci L, FitzGerald GA.	Molecular cloning, primary structure, and expression of the human platelet/erythroleukemia cell 12-lipoxygenase.	Proc Natl Acad Sci	1990	2377602	cytoplasmic - uniprot + refs Leukotrienes biosynthesis gene identification - Izumi and Funk refs NJ
ALOX12R	3	Boeglin WE, Kim RB, Brash AR.	A 12R-lipoxygenase in human skin: mechanistic evidence, molecular cloning, and expression.	Proc Natl Acad Sci	1998	9618483	cyt - uniprot Expressed in B-cells, hair follicles, foreskin keratinocytes and adult skin. Also expressed in psoriatic tissue. Converts arachidonic acid to 12R- hydroperoxyeicosatetraenoic acid (12R-HPETE). NJ
ALOX15	3	Tang S, Bhatia B, Maldonado CJ, Yang P, Newman RA, Liu J, Chandra D, Traag J, KIein RD, Fischer SM, Chopra D, Shen J, Zhau HE, Chung LW, Tang DG.	Evidence that arachidonate 15-lipoxygenase 2 is a negative cell cycle regulator in normal prostate epithelial cells.	J Biol Chem	2002	11839751	cytoplasmic - uniprot + refs Leukotrienes biosynthesis gene identification - Tang ref NJ
ALOX5	3	Matsumoto T, Funk CD, Radmark O, Hoog JO, Jornvall H, Samuelsson B.	Molecular cloning and amino acid sequence of human 5-lipoxygenase.	Proc Natl Acad Sci	1988	2829172	cytoplasmic - uniprot + refs Leukotrienes biosynthesis seq see Matsuomoto ref NJ

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ALOX52	3	Leff AR.	Regulation of leukotrienes in the management of asthma: biology and clinical therapy.	Annu Rev Med	2001	11160764	cytosoloic by default (no detailed info) cofactors + usage still not clear unknown mechanism - biochemistry supported by PMID: 2829172, 11160764 NJ
AMACRp	3	VanVeldhoven PP, Croes K, Casteels M, Mannaerts GP	2-methylacyl racemase: a couple assay based on the use of pristanoyl-CoA oxidase/peroxidase and reinvestigation of its subcellular distribution in rat and human liver	Biochimica et Biophysica Acta	1997		Uniprot states evidence for mit, perox, and cytoplasmic, most lit refs only seemed to focus on perox and mit. This enzyme may have issues similar to other enzymes w/ ER outer membrane bound enzymes. Need to follow lit for future articles. Only in LocusLink db at present NJ
AMANK	3	Seppala R, Lehto VP, Gahl WA	Mutations in the human UDP-N-acetylglucosamine 2 epimerase gene define the disease sialuria and the allosteric site of the enzyme	Am J Hum Genet	1999	10330343	- shown as irreversible Devlin p. 672, Varki p. 74 10020: - cytoplasmic [UniProt], [Varki, p. 78] - Highest expression in liver and placenta. Also found in heart, brain, lung, kidney, skeletal muscle and pancreas. [UniProt] 55577: - GlcNAc kinase (10020) was shown to catalyze ManNAc kinase reaction when ManNAc gene was knocked out [Hinderlich, Biol Chem 2001] - ManNAc6P can be formed from ManNAc by kinase that can use either ManNAc or GlcNAc [Varki, p.77]
AMANK	3	Lucka L, Krause M, Danker K, Reutter W, Horstkorte R	Primary structure and expression analysis of human UDP-N-acetyl-glucosamine-2-epimerase/N-acetylmannosamine kinase, the bifunctional enzyme in neuraminic acid biosynthesis	FEBS Lett	1999	10431835	- shown as irreversible Devlin p. 672, Varki p. 74 10020: - cytoplasmic [UniProt], [Varki, p. 78] - Highest expression in liver and placenta. Also found in heart, brain, lung, kidney, skeletal muscle and pancreas. [UniProt] 55577: - GlcNAc kinase (10020) was shown to catalyze ManNAc kinase reaction when ManNAc gene was knocked out [Hinderlich, Biol Chem 2001] - ManNAc6P can be formed from ManNAc by kinase that can use either ManNAc or GlcNAc [Varki, p.77]
AMANK	3	Hinderlich S, Berger M, Keppler OT, Pawlita M, Reutter W	Biosynthesis of N-acetylneuraminic acid in cells lacking UDP-N-acetylglucosamine 2-epimerase/N-acetylmannosamine kinase	Biol Chem	2001	11308027	- shown as irreversible Devlin p. 672, Varki p. 74 10020: - cytoplasmic [UniProt], [Varki, p. 78] - Highest expression in liver and placenta. Also found in heart, brain, lung, kidney, skeletal muscle and pancreas. [UniProt] 55577: - GlcNAc kinase (10020) was shown to catalyze ManNAc kinase reaction when ManNAc gene was knocked out [Hinderlich, Biol Chem 2001] - ManNAc6P can be formed from ManNAc by kinase that can use either ManNAc or GlcNAc [Varki, p.77]
AMETt2m	3	Agrimi G, Di Noia MA, Marobbio CM, Fiermonte G, Lasorsa FM, Palmieri F	Identification of the human mitochondrial S-adenosylmethionine transporter: bacterial expression, reconstitution, functional characterization and tissue distribution	Biochem J	2004	14674884	- Added by KS, PV - Mitochondrial according to Agrimi G, et al. Biochem J. 2004 Apr 1;379(Pt 1):183-90. - SAM (S-adenosylmethionine) is the methyl group donor for almost all biological methylation reactions. In mitochondria, it is required for the methylation of DNA, RNA and proteins and as an intermediate in the biosynthesis of lipoic acid, and ubiquinone - As SAM is produced in the cytosol and is required inmitochondria, the primary function of SAMC is to catalyse the uptake of SAM into mitochondria. However, since SAMC functions almost exclusively by a counter-exchange mechanism, the carrier-mediated uptake of SAM requires the efflux of a counter-substrate. On the basis of transport measurements, SAHC produced from SAM in the methylation reactions and hydrolysed exclusively in the cytosol may serve as the counter-substrate of SAMC for SAM. Therefore the physiological role of the human SAMC is most probably to catalyse the uptake of SAM into the mitochondrial matrix in exchange for internal SAHC. - Very similar to yeast orthologue, except for need of a countertransport mechanism. - Expressed in all tissues. All this according to Agrimi G, et al. Biochem J. 2004 Apr 1;37
AMPDA	3	Mahnke-Zizelman DK, Sabina RL.	Cloning of human AMP deaminase isoform E cDNAs. Evidence for a third AMPD gene exhibiting alternatively spliced 5'-exons.	J Biol Chem	1992	1400401	IT 270: skeletal muscle, homotetramer 271: liver specific, homotetramer 272: erythrocytes specific

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AMPDA	3	Sabina RL, Morisaki T, Clarke P, Eddy R, Shows TB, Morton CC, Holmes EW.	Characterization of the human and rat myoadenylate deaminase genes.	J Biol Chem	1990	2345176	IT 270: skeletal muscle, homotetramer 271: liver specific, homotetramer 272: erythrocytes specific
AOBUTDsm	2	Edgar AJ.	Molecular cloning and tissue distribution of mammalian L-threonine 3-dehydrogenases.		2002	12097150	according to KEGG and MetaCyc spontaneous reaction PMID 12097150: the highly reactive intermediate, 2-amino-3-ketobutyrate, rapidly undergoes decarboxylation to form aminoacetone and CO2 MM
AP4AH1	3	Hankin S, Matthew N, Thorne H, McLennan AG.	Diadenosine 5',5'''-P1,P4-tetraphosphate hydrolase is present in human erythrocytes, leukocytes and platelets.	Int J Biochem Cell Biol	1995	7767787	IT -present in erys, leukocytes, plateles (Hankin, 1995) - requires divalemt ions (GeneCards) - compounds such as ap3a, ap4a, ap5a, ap6a have been shown to be present in and secreted from certain neurosecretory granules and the desnse granules of blood platelets. these compounds have neurotransmitter and vasomotor activity, affect platelet aggregation and may be novel regulators of blood pressure with properties distinct from ATP. In addition, virtually all cells contain submicromolar to micromolar cytosolic levels of ap3a and ap4a with the latter compound having been implicated in a number of intracellular events, including DNA replication and cellular response to metabolic stress (introduction from Hankin et al., 1995) - they are synthesized by aminoacyl tRNA-transferase (rxns not included)
AP4AH1	3	McLennan AG, Flannery AV, Morten JE, Ridanpaa M.	Chromosomal localization of the human diadenosine 5',5'''-P1,P4-tetraphosphate pyrophosphohydrolase (Ap4A hydrolase) gene (APAH1) to 9p13.	Genomics	1998	9479504	IT -present in erys, leukocytes, plateles (Hankin, 1995) - requires divalemt ions (GeneCards) - compounds such as ap3a, ap4a, ap5a, ap6a have been shown to be present in and secreted from certain neurosecretory granules and the desnse granules of blood platelets. these compounds have neurotransmitter and vasomotor activity, affect platelet aggregation and may be novel regulators of blood pressure with properties distinct from ATP. In addition, virtually all cells contain submicromolar to micromolar cytosolic levels of ap3a and ap4a with the latter compound having been implicated in a number of intracellular events, including DNA replication and cellular response to metabolic stress (introduction from Hankin et al., 1995) - they are synthesized by aminoacyl tRNA-transferase (rxns not included)
APAT2rm	1	Ohyama T, Matsuda K, Tachibana H, Fujimoto Sakata S, Mori M, Horiuchi M, Tamaki N	Purification and expression of a processing protease on beta-alanine-oxoglutarate aminotransferase from rat liver mitochondria	FEBS Lett	2004	15304357	This reaction is based on rat data as noted in the citation, so modeling data only.
ARAB-Lt	2	Lobley RW, Burrows PC, Warwick R, Dawson DJ, Holmes R	Simultaneous assessment of intestinal permeability and lactose tolerance with orally administered raffinose, lactose and L-arabinose	Clin Sci (Lond)	1990	2167807	- physiologial evidence that L-arabinose is taken up by intestine and excreted into bloodstream/urine; don't have any info on specific transport mechanism - it is generally accepted that no L-arabinose digestion occurs in humans; however, a patient with a presumed arabitol dehydrogenase deficiency has been identified [Onkenhout, Mol Genet Metab 2002] - oral arabinose loading has once been performed in man to asses intestinal permeability; median 5 h urinary excretion was 17.5% of the ingested amount indicating quite efficient absorption [Lobley 1990] - d-arabinose and d-ribose could cross cell membrane of cultured human fibroblasts [Huck 2004]
ARABR	3	Praml C, Savelyeva L, Perri P, Schwab M.	Cloning of the human aflatoxin B1-aldehyde reductase gene at 1p35-1p36.1 in a region frequently altered in human tumor cells.	Cancer Res	1998	9823300	pentoses in human fibroblasts; these reactions are most likely catalyzed by a pentose reductase [Huck, Mol Genet Metab 2004] - inferred from observations of patient with presumed deficiency (L-arabinose in diet led to high excretion of L-arabitol and arabinoic acid (-lactone)) [Onkenhout, Mol Genet Metab 2002] 8574: - gene has been cloned, 78% identical with the Rattus norvegicus aflatoxin B1 aldehyde reductase (Afar) [Praml 1998] -rat homolog appears to be Golgi-associated [Kelly 2002] based on N-terminal sequence and immunohistochemistry, however I believe these results more strongly support localization in the outer Golgi membrane (cytosolic in our model) - human AKR7A2 also has Golgi signal sequence and [GO, UniProt] list as Golgi by similarity; however, I've assumed protein is cytosolic due to lack of specific info on location of functional domain and the fact that the only (weak) evidence thus far has come from the rat homolog - NADH or NADPH [UniProt]; specificity is based on mouse homology AFAR2 [Kelly 2002]

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ARABR	3	Kelly VP, Sherratt PJ, Crouch DH, Hayes JD	Novel homodimeric and heterodimeric rat gamma-hydroxybutyrate synthases that associate with the Golgi apparatus define a distinct subclass of aldo-keto reductase 7 family proteins.	Biochem J	2002	12071861	pentoses in human fibroblasts; these reactions are most likely catalyzed by a pentose reductase [Huck, Mol Genet Metab 2004] - inferred from observations of patient with presumed deficiency (L-arabinose in diet led to high excretion of L-arabitol and arabinoic acid (-lactone)) [Onkenhout, Mol Genet Metab 2002] 8574: - gene has been cloned, 78% identical with the Rattus norvegicus aflatoxin B1 aldehyde reductase (Afar) [Praml 1998] -rat homolog appears to be Golgi-associated [Kelly 2002] based on N-terminal sequence and immunohistochemistry, however I believe these results more strongly support localization in the outer Golgi membrane (cytosolic in our model) - human AKR7A2 also has Golgi signal sequence and [GO, UniProt] list as Golgi by similarity; however, I've assumed protein is cytosolic due to lack of specific info on location of functional domain and the fact that the only (weak) evidence thus far has come from the rat homolog - NADH or NADPH [UniProt]; specificity is based on mouse homology AFAR2 [Kelly 2002]
ARABR	3	Onkenhout W, Groener JE, Verhoeven NM, Yin C, Laan LA	L-Arabinosuria: a new defect in human pentose metabolism	Mol Genet Metab	2002	12359133	pentoses in human fibroblasts; these reactions are most likely catalyzed by a pentose reductase [Huck, Mol Genet Metab 2004] - inferred from observations of patient with presumed deficiency (L-arabinose in diet led to high excretion of L-arabitol and arabinoic acid (-lactone)) [Onkenhout, Mol Genet Metab 2002] 8574: - gene has been cloned, 78% identical with the Rattus norvegicus aflatoxin B1 aldehyde reductase (Afar) [Praml 1998] -rat homolog appears to be Golgi-associated [Kelly 2002] based on N-terminal sequence and immunohistochemistry, however I believe these results more strongly support localization in the outer Golgi membrane (cytosolic in our model) - human AKR7A2 also has Golgi signal sequence and [GO, UniProt] list as Golgi by similarity; however, I've assumed protein is cytosolic due to lack of specific info on location of functional domain and the fact that the only (weak) evidence thus far has come from the rat homolog - NADH or NADPH [UniProt]; specificity is based on mouse homology AFAR2 [Kelly 2002]
ARGDCm	3	Grillo MA, Colombatto S	Metabolism and function in animal tissues of agmatine, a biogenic amine formed from arginine	Amino Acids	2004	14752610	the enzyme that catalyzes this reaction does not decarboxylate ornthine
ARGNm	3	Gotoh T, Araki M, Mori M	Chromosomal localization of the human arginase II gene and tissue distribution of its mRNA	Biochem Biophys Res Commun	1997	9144563	The physiological function of this enzyme is apparantly poorly understood, but the biochemical characterization seems legitimate.
ARGSL	3	O'Brien WE, McInnes R, Kalumuck K, Adcock M.	Cloning and sequence analysis of cDNA for human argininosuccinate lyase.	Proc Natl Acad Sci U S A	1986	3463959	- reversible according to Sampaleanu et al., 2001 - Additional information by RS/TV: - Argininosuccinate lyase catalyzes the conversion of of argininosuccinic acid into fumaric acid and arginine. The enzyme's primary physiological role is in the liver, where it functions in the urea cycle for the disposal of ingested nitrogen. (O'Brien WE, McInnes R, Kalumuck K, Adcock M. Proc Natl Acad Sci U S A. 1986 Oct;83(19):7211-5.)
ARGSL	3	Sampaleanu LM, Vallee F, Thompson GD, Howell PL.	Three-dimensional structure of the argininosuccinate lyase frequently complementing allele Q286R.		2001	11747432	- reversible according to Sampaleanu et al., 2001 - Additional information by RS/TV: - Argininosuccinate lyase catalyzes the conversion of of argininosuccinic acid into fumaric acid and arginine. The enzyme's primary physiological role is in the liver, where it functions in the urea cycle for the disposal of ingested nitrogen. (O'Brien WE, McInnes R, Kalumuck K, Adcock M. Proc Natl Acad Sci U S A. 1986 Oct;83(19):7211-5.)
ARGSL	3	Kleijer WJ et al.	Clinical, enzymatic, and molecular genetic characterization of a biochemical variant type of argininosuccinic aciduria: prenatal and postnatal diagnosis in five unrelated families.		2002	12408190	- reversible according to Sampaleanu et al., 2001 - Additional information by RS/TV: - Argininosuccinate lyase catalyzes the conversion of of argininosuccinic acid into fumaric acid and arginine. The enzyme's primary physiological role is in the liver, where it functions in the urea cycle for the disposal of ingested nitrogen. (O'Brien WE, McInnes R, Kalumuck K, Adcock M. Proc Natl Acad Sci U S A. 1986 Oct;83(19):7211-5.)
ARGSS	3	Metzler, David E	Biochemistry : the chemical reactions of living cells 2 ed vol 2		2001		- Reviewed by RS/TV

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ARGt4	2	Van Winkle LJ	Amino acid transport regulation and early embryo development	Biol Reprod	2001	11133652	From PMID 12719981: Multiple Na+-independent and Na+-dependent transport systems for amino acids have been identified by physiological and pharmacological approaches. One of these is system B0+, so named because it transports a broad array of neutral and cationic amino acids in a Na+-dependent manner, that is present in blastocysts, oocytes, intestine, pituitary, and lung [80]. Interestingly, the protein responsible for transport in this system is encoded by a member of the SLC6A gene family [69], members of which typically show more narrow substrate specificity. hATB0+ is a 645-amino acid protein, most similar to glycine and proline transporters, that is found in many non-neural tissues and which demonstrates high affinity uptake of hydrophobic amino acids. Transport is inhibited pharmacologically by 2-aminobicyclo-(2,2,1)-heptane-2-carboxylic acid (BCH). hATB0+ is highly expressed in the pituitary, where it may play a role in amino acid-induced secretion, and on the apical membrane of airway epithelia, where it may contribute to lung defense by clearing accumulated protein [70]
ARGt4	2	Chen NH, Reith ME, Quick MW	Synaptic uptake and beyond: the sodium- and chloride-dependent neurotransmitter transporter family SLC6	Pflugers Arch	2004	12719981	From PMID 12719981: Multiple Na+-independent and Na+-dependent transport systems for amino acids have been identified by physiological and pharmacological approaches. One of these is system B0+, so named because it transports a broad array of neutral and cationic amino acids in a Na+-dependent manner, that is present in blastocysts, oocytes, intestine, pituitary, and lung [80]. Interestingly, the protein responsible for transport in this system is encoded by a member of the SLC6A gene family [69], members of which typically show more narrow substrate specificity. hATB0+ is a 645-amino acid protein, most similar to glycine and proline transporters, that is found in many non-neural tissues and which demonstrates high affinity uptake of hydrophobic amino acids. Transport is inhibited pharmacologically by 2-aminobicyclo-(2,2,1)-heptane-2-carboxylic acid (BCH). hATB0+ is highly expressed in the pituitary, where it may play a role in amino acid-induced secretion, and on the apical membrane of airway epithelia, where it may contribute to lung defense by clearing accumulated protein [70]
ARSA	3	Stein C, Gieselmann V, Kreysing J, Schmidt B, Pohlmann R, Waheed A, Meyer HE, O'Brien JS, von Figura K.	Cloning and expression of human arylsulfatase A.	J Biol Chem	1989	2562955	lysosomal - uniprot + stein ref The protein encoded by this gene hydrolyzes cerebroside sulfate to cerebroside and sulfate. Defects in this gene lead to metachromatic leucodystrophy (MLD), a progressive demyelination disease which results in a variety of neurological symptoms and ultimately death. NJ
ASAH1	3	Koch J, Gartner S, Li CM, Quintern LE, Bernardo K, Levran O, Schnabel D, Desnick RJ, Schuchman EH, Sandhoff K.	Molecular cloning and characterization of a full-length complementary DNA encoding human acid ceramidase. Identification Of the first molecular lesion causing Farber disease.	J Biol Chem	1996	8955159	lysosomal - uniprot + Koch ref This gene encodes a heterodimeric protein consisting of a nonglycosylated alpha subunit and a glycosylated beta subunit that is cleaved to the mature enzyme posttranslationally. The encoded protein catalyzes the synthesis and degradation of ceramide into sphingosine and fatty acid. Mutations in this gene have been associated with a lysosomal storage disorder known as Farber disease. Two transcript variants encoding distinct isoforms have been identified for this gene. NJ
ASCBt	2	Bianchi J, Rose RC	Dehydroascorbic acid and cell membranes: possible disruptive effects	Toxicology	1986	3715892	- see [Wilson 2005], [Balll 2004] for a comprehensive review of ascorbate transport - ascorbate leaves enterocytes by soidum-independent facilitated diffusion at the basolateral membrane [Bianchi 1986] - existence of ascorbate homeoexchange system has not been demonstrated conclusively and the molecular identities of the membrane proteins responsible for homeoexchange have not been identified [Wilson 2005]

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ASCBt4	3	Rajan DP, Huang W, Dutta B, Devoe LD, Leibach FH, Ganapathy V, Prasad PD	Human placental sodium-dependent vitamin C transporter (SVCT2): molecular cloning and transport function	Biochem Biophys Res Commun	1999	10471399	- see [Wilson 2004], [Ball 2004] for a comprehensive review of ascorbate transport 9962: - cloned [Daruwala 1999], [Wang, Biochim Biophys Acta 1999], [Wang, Biochem Biophys Res Commun. 2000] - ascorbate & Na+ cotransport; does not transport dehydroascorbate [Daruwala 1999] - kidney, liver, small intestine, thymus and prostate [Wang, Biochim Biophys Acta 1999], also colon, ovary [Wang, Biochem Biophys Res Commun. 2000] - Na(+):ascorbate stoichiometry of 2:1 [Wang, Biochim Biophys Acta 1999]; electrogenic [Wang, Biochem Biophys Res Commun. 2000] 9963: - cloned [Daruwala 1999], [Wang, Biochem Biophys Res Commun. 2000] - ovary, spleen, testis, placenta, brain, prostate, WBC [Wang, Biochem Biophys Res Commun. 2000]; heart, brain, placenta [Rajan 1999] - ascorbate & Na+ cotransport; does not transport dehydroascorbate [Daruwala 1999], [Rajan 1999] - Na(+):ascorbate stoichiometry of 2:1 [Rajan 1999]; electrogenic [Wang, Biochem Biophys Res Commun. 2000]
ASCBt4	3	Wang H, Dutta B, Huang W, Devoe LD, Leibach FH, Ganapathy V, Prasad PD	Human Na(+)-dependent vitamin C transporter 1 (hSVCT1): primary structure, functional characteristics and evidence for a non-functional splice variant.	Biochim Biophys Acta	1999	10556483	- see [Wilson 2004], [Ball 2004] for a comprehensive review of ascorbate transport 9962: - cloned [Daruwala 1999], [Wang, Biochim Biophys Acta 1999], [Wang, Biochem Biophys Res Commun. 2000] - ascorbate & Na+ cotransport; does not transport dehydroascorbate [Daruwala 1999] - kidney, liver, small intestine, thymus and prostate [Wang, Biochim Biophys Acta 1999], also colon, ovary [Wang, Biochem Biophys Res Commun. 2000] - Na(+):ascorbate stoichiometry of 2:1 [Wang, Biochim Biophys Acta 1999]; electrogenic [Wang, Biochem Biophys Res Commun. 2000] 9963: - cloned [Daruwala 1999], [Wang, Biochem Biophys Res Commun. 2000] - ovary, spleen, testis, placenta, brain, prostate, WBC [Wang, Biochem Biophys Res Commun. 2000]; heart, brain, placenta [Rajan 1999] - ascorbate & Na+ cotransport; does not transport dehydroascorbate [Daruwala 1999], [Rajan 1999] - Na(+):ascorbate stoichiometry of 2:1 [Rajan 1999]; electrogenic [Wang, Biochem Biophys Res Commun. 2000]
ASCBt4	3	Daruwala R, Song J, Koh WS, Rumsey SC, Levine M	Cloning and functional characterization of the human sodium-dependent vitamin C transporters hSVCT1 and hSVCT2	FEBS Lett	1999	10556521	- see [Wilson 2004], [Ball 2004] for a comprehensive review of ascorbate transport 9962: - cloned [Daruwala 1999], [Wang, Biochim Biophys Acta 1999], [Wang, Biochem Biophys Res Commun. 2000] - ascorbate & Na+ cotransport; does not transport dehydroascorbate [Daruwala 1999] - kidney, liver, small intestine, thymus and prostate [Wang, Biochim Biophys Acta 1999], also colon, ovary [Wang, Biochem Biophys Res Commun. 2000] - Na(+):ascorbate stoichiometry of 2:1 [Wang, Biochim Biophys Acta 1999]; electrogenic [Wang, Biochem Biophys Res Commun. 2000] 9963: - cloned [Daruwala 1999], [Wang, Biochem Biophys Res Commun. 2000] - ovary, spleen, testis, placenta, brain, prostate, WBC [Wang, Biochem Biophys Res Commun. 2000]; heart, brain, placenta [Rajan 1999] - ascorbate & Na+ cotransport; does not transport dehydroascorbate [Daruwala 1999], [Rajan 1999] - Na(+):ascorbate stoichiometry of 2:1 [Rajan 1999]; electrogenic [Wang, Biochem Biophys Res Commun. 2000]

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ASCBt4	3	Wang Y, Mackenzie B, Tsukaguchi H, Weremowicz S, Morton CC, Hediger MA	Human vitamin C (L-ascorbic acid) transporter SVCT1	Biochem Biophys Res Commun	2000	10631088	- see [Wilson 2004], [Ball 2004] for a comprehensive review of ascorbate transport 9962: - cloned [Daruwala 1999], [Wang, Biochim Biophys Acta 1999], [Wang, Biochem Biophys Res Commun. 2000] - ascorbate & Na+ cotransport; does not transport dehydroascorbate [Daruwala 1999] - kidney, liver, small intestine, thymus and prostate [Wang, Biochim Biophys Acta 1999], also colon, ovary [Wang, Biochem Biophys Res Commun. 2000] - Na(+):ascorbate stoichiometry of 2:1 [Wang, Biochim Biophys Acta 1999]; electrogenic [Wang, Biochem Biophys Res Commun. 2000] 9963: - cloned [Daruwala 1999], [Wang, Biochem Biophys Res Commun. 2000] - ovary, spleen, testis, placenta, brain, prostate, WBC [Wang, Biochem Biophys Res Commun. 2000]; heart, brain, placenta [Rajan 1999] - ascorbate & Na+ cotransport; does not transport dehydroascorbate [Daruwala 1999], [Rajan 1999] - Na(+):ascorbate stoichiometry of 2:1 [Rajan 1999]; electrogenic [Wang, Biochem Biophys Res Commun. 2000]
ASNNm	2	Bush LA, Herr JC, Wolkowicz M, Sherman NE, Shore A, Flickinger CJ.	A novel asparaginase-like protein is a sperm autoantigen in rats.		2002	11984834	-only sequence has been detected -possible mitochondrial localisation (Bush et. al, 2002)
ASNS1	3	Van Heeke G, Schuster SM.	Expression of human asparagine synthetase in Escherichia coli.		1989	2564390	- necessary in the synthesis of non-essential amino acid asparagine -irreversible since it requires ATP hydrolysis Entrez Gene - The protein encoded by this gene is involved in the synthesis of asparagine. This gene complements a mutation in the temperature-sensitive hamster mutant ts11, which blocks progression through the G1 phase of the cell cycle at nonpermissive temperature. There are three alternatively spliced transcript variants encoding the same protein described for this gene.
ASNS1	3	Andrulis IL, Chen J, Ray PN.	Isolation of human cDNAs for asparagine synthetase and expression in Jensen rat sarcoma cells.		1987	2886907	- necessary in the synthesis of non-essential amino acid asparagine -irreversible since it requires ATP hydrolysis Entrez Gene - The protein encoded by this gene is involved in the synthesis of asparagine. This gene complements a mutation in the temperature-sensitive hamster mutant ts11, which blocks progression through the G1 phase of the cell cycle at nonpermissive temperature. There are three alternatively spliced transcript variants encoding the same protein described for this gene.
ASPNATm	3	Moreno A, Ross BD, Bluml S.	Direct determination of the N-acetyl-L-aspartate synthesis rate in the human brain by (13)C MRS and [1-(13)C]glucose infusion.		2001	11279290	PMID 11279290: N-Acetyl-l-aspartate (NAA) is an important amino-acid derivative in vertebrate brain and reaches its highest concentrations in neurons and axons (Tallan 1957; Passani et al. 1990). It is principally synthesized in neurons by the energy-dependent condensation of aspartate and acetyl coenzyme A (AcCoA), catalyzed by the mitochondrial enzyme NAA synthase (l-aspartate-N-acetyltransferase; EC 2.3.1.17), and is exported to the cytosolic compartment. MM
ASPTA	3	Panteghini M.	Aspartate aminotransferase isoenzymes.	Clin Biochem	1990	2225456	- Additional info added by RS/TV: Biochem text Cytosolic according to Entrez gene database Catalytic activity of protein synthesized by this gene (GPR association) according to GeneCards "Aspartate aminotransferase exists in human tissues as two distinct isozymes, one located in the cytoplasm" according to Panteghini M., Aspartate aminotransferase isoenzymes., Clin Biochem. 1990 Aug;23(4):311-9. Review. PMID: 2225456 reaction reversible according to Ford GC, Eichele G, Jansonius JN. Three-dimensional structure of a pyridoxal-phosphate-dependent enzyme, mitochondrial aspartate aminotransferase. Proc Natl Acad Sci U S A. 1980 May;77(5):2559-63. PMID: 6930651 NOTE: This reaction was classified under the Mal-Asp shuttle subsystem in the mitochondrial model.

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ASPTA	3	Ford GC, Eichele G, Jansonius JN.	Three-dimensional structure of a pyridoxal-phosphate dependent enzyme, mitochondrial aspartate aminotransferase.	Proc Natl Acad Sci U S A	1980	6930651	- Additional info added by RS/TV: Biochem text Cytosolic according to Entrez gene database Catalytic activity of protein synthesized by this gene (GPR association) according to GeneCards "Aspartate aminotransferase exists in human tissues as two distinct isozymes, one located in the cytoplasm" according to Panteghini M., Aspartate aminotransferase isoenzymes., Clin Biochem. 1990 Aug;23(4):311-9. Review. PMID: 2225456 reaction reversible according to Ford GC, Eichele G, Jansonius JN. Three-dimensional structure of a pyridoxal-phosphate-dependent enzyme, mitochondrial aspartate aminotransferase. Proc Natl Acad Sci U S A. 1980 May;77(5):2559-63. PMID: 6930651 NOTE: This reaction was classified under the Mal-Asp shuttle subsystem in the mitochondrial model.
ATPasel	3	Forgac M.	Structure and properties of the vacuolar (H+)-ATPases	J Biol Chem	1999	10224039	Added by RS/DK - ATP is converted to ADP in the cytosol; this drives the protons from the cytosol into the lumen of the lysosome (See Figure 1 in Eskelinen, et al.) - Mechanism of lysosomal V-type ATPase is thought to be similar to F-type ATPSynthase of the mitochondrion. (See Forgac) - "The V-ATPase is composed of a peripheral V1 domain responsible for ATP hydrolysis and an integral V0 domain responsible for proton translocation" (See Forgac)
ATPasel	3	Eskelinen EL, Tanaka Y, Saftig P.	At the acidic edge: emerging functions for lysosomal membrane proteins	Trends Cell Biol	2003	12628346	Added by RS/DK - ATP is converted to ADP in the cytosol; this drives the protons from the cytosol into the lumen of the lysosome (See Figure 1 in Eskelinen, et al.) - Mechanism of lysosomal V-type ATPase is thought to be similar to F-type ATPSynthase of the mitochondrion. (See Forgac) - "The V-ATPase is composed of a peripheral V1 domain responsible for ATP hydrolysis and an integral V0 domain responsible for proton translocation" (See Forgac)
ATPH1e	3	Kaczmarek E, Koziak K, Sevigny J, Siegel JB, Anrather J, Beaudoin AR, Bach FH, Robson SC.	Identification and characterization of CD39/vascular ATP diphosphohydrolase.	J Biol Chem	1996	8955160	IT 953: expressed in placenta, lung, skeletal muscle, kidney, heart but not in brain 954: all tissues 955: brain, pancreas, spleen, prostate (no signal liver, peripheral blood leukocytes) 956: liver, kidney, prostate, testis, colon
ATPH1e	3	Chadwick BP, Frischauf AM.	The CD39-like gene family: identification of three new human members (CD39L2, CD39L3, and CD39L4), their murine homologues, and a member of the gene family from Drosophila melanogaster.	Genomics	1998	9676430	IT 953: expressed in placenta, lung, skeletal muscle, kidney, heart but not in brain 954: all tissues 955: brain, pancreas, spleen, prostate (no signal liver, peripheral blood leukocytes) 956: liver, kidney, prostate, testis, colon
B_MANNASEly	0	Alkhayat AH, Kraemer SA, Leipprandt JR, Macek M, Kleijer WJ, Friderici KH.	Human beta-mannosidase cDNA characterization and first identification of a mutation associated with human beta-mannosidosis	Hum Mol Genet	1998	9384606	MANBA encodes the final exoglycosidase in the pathway for N linked oligosaccharide catabolism. This enzyme localizes to the lysosome. Mutations in this gene cause beta-mannosidosis, a lysosomal storage disease that has a wide spectrum of neurological involvement. [RefSeq] Manbap ubiquitously expressed [Alkhayat et al, Hum Mol Genet 1998]
B3GNT11g	3	Isshiki S, Kudo T, Nishihara S, Ikehara Y, Togayachi A, Furuya A, Shitara K, Kubota T, Watanabe M, Kitajima M, Narimatsu H.	Lewis type 1 antigen synthase (beta3Gal-T5) is transcriptionally regulated by homeoproteins.		2003	12855703	localization: golgi - uniprot This gene encodes an enzyme that is a member of the beta-1,3-N-acetylglucosaminyltransferase family. This enzyme is a type II transmembrane protein. It prefers the substrate of lacto-N-neotetraose, and is involved in the biosynthesis of poly-N-acetyllactosamine chains. Two alternatively splicing transcript variants are identified from this gene and encode the same protein product. NJ

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
B3GNT310g	2	Yokoyama-Kobayashi M, Yamaguchi T, Sekine S, Kato S.	Selection of cDNAs encoding putative type II membrane proteins on the cell surface from a human full-length cDNA bank.	Gene	1999	10072769	localization: golgi by uniprot This gene encodes an enzyme that is a member of the beta-1,3-N-acetylglucosaminyltransferase family. This enzyme is a type II transmembrane protein and contains a signal anchor that is not cleaved. It prefers the substrates of lacto-N-tetraose and lacto-N-neotetraose, and is involved in the biosynthesis of poly-N-acetyllactosamine chains and the biosynthesis of the backbone structure of dimeric sialyl Lewis a. It plays dominant roles in L-selectin ligand biosynthesis, lymphocyte homing and lymphocyte trafficking. NJ
B3GNT31g	3	Kolter T, Sandhoff K	Recent advances in the biochemistry of sphingolipidoses	Brain Pathology	1998		Golgi - lumen side - see ref Kolter and Sanhoff; also noted in uniprot This gene encodes an enzyme that is a member of the beta-1,3-N-acetylglucosaminyltransferase family. This enzyme is a type II transmembrane protein and contains a signal anchor that is not cleaved. It prefers the substrates of lacto-N-tetraose and lacto-N-neotetraose, and is involved in the biosynthesis of poly-N-acetyllactosamine chains and the biosynthesis of the backbone structure of dimeric sialyl Lewis a. It plays dominant roles in L-selectin ligand biosynthesis, lymphocyte homing and lymphocyte trafficking. NJ
B3GNT31g	3	Zhou D, Dinter A, Gutierrez Gallego R, Kamerling JP, Vliegenthart JF, Berger EG, Hennet T.	A beta-1,3-N-acetylglucosaminyltransferase with poly-N-acetyllactosamine synthase activity is structurally related to beta-1,3-galactosyltransferases.	Proc Natl Acad Sci	1999		Golgi - lumen side - see ref Kolter and Sanhoff; also noted in uniprot This gene encodes an enzyme that is a member of the beta-1,3-N-acetylglucosaminyltransferase family. This enzyme is a type II transmembrane protein and contains a signal anchor that is not cleaved. It prefers the substrates of lacto-N-tetraose and lacto-N-neotetraose, and is involved in the biosynthesis of poly-N-acetyllactosamine chains and the biosynthesis of the backbone structure of dimeric sialyl Lewis a. It plays dominant roles in L-selectin ligand biosynthesis, lymphocyte homing and lymphocyte trafficking. NJ
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BAAT1x	3	Falany CN, Johnson MR, Barnes S, Diasio RB	Glycine and taurine conugation of bile acids by a single enzyme	Journal of Biological Chemistry	1994		peroxisome: uniprot specificity: muscle, liver NJ
BACCL	3	Suzuki Y, Aoki Y, Ishida Y, Chiba Y, Iwamatsu A, Kishino T, Niikawa N, Matsubara Y, Narisawa K.	Isolation and characterization of mutations in the human holocarboxylase synthetase cDNA.	Nat Genet	1994	7842009	GeneCards noted that location is also mitochondrial.
BACCL	3	Pacheco-Alvarez D, Solorzano-Vargas RS, Del Rio AL.	Biotin in metabolism and its relationship to human disease.	Arch Med Res	2002	12459313	GeneCards noted that location is also mitochondrial.
BAMPPALDOX	1	White WH, Skatrud PL, Xue Z, Toyn JH	Specialization of function among aldehyde dehydrogenases: the ALD2 and ALD3 genes are required for beta-alanine biosynthesis in Saccharomyces cerevisiae	Genetics	2003	12586697	The citation clarifies this reaction in yeast, but only modeling evidence can be included here.
BBHOX	3	Vaz,F.M. , van Gool,S. , Ofman,R. , Ijlst,L. , Wanders,R.J.	Carnitine biosynthesis: identification of the cDNA encoding human gamma-butyrobetaine hydroxylase.		1998	9753662	0
BCDO	3	Wyss A, Wirtz G, Woggon W, Brugger R, Wyss M, Friedlein A, Bachmann H, Hunziker W.	Cloning and expression of beta,beta-carotene 15,15'-dioxygenase.	Biochem Biophys Res Commun	2000	10799297	IT
BCDO	3	Yan W, Jang GF, Haeseleer F, Esumi N, Chang J, Kerrigan M, Campochiaro M, Campochiaro P, Palczewski K, Zack DJ.	Cloning and characterization of a human beta,beta-carotene-15,15'-dioxygenase that is highly expressed in the retinal pigment epithelium.	Genomics	2001	11401432	IT
BDG2HCGHD	1	Daniels LB, Coyle PJ, Chiao YB, Glew RH, Labow RS.	Purification and characterization of a cytosolic broad specificity beta-glucosidase from human liver	J Biol Chem	1981	6796580	Not certain, but seems reasonable there is another enzyme or two, but localization and substrate specificity is much less certain, so they are not included

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
BDHm	3	Marks AR, McIntyre JO, Duncan TM, Erdjument-Bromage H, Tempst P, Fleischer S	Molecular cloning and characterization of (R)-3-hydroxybutyrate dehydrogenase from human heart	J Biol Chem	1992	1639787	- mitochondrial inner membrane [Marks, J Biol Chem 1992], catalytic domain faces matrix [Green, Biochemistry 1996] - gene cloned [Marks J Biol Chem 1992] - has an absolute and specific requirement of phosphatidylcholine [Marks J Biol Chem 1992] - checked over by RS/TV
BDHm	3	Green D, Marks AR, Fleischer S, McIntyre JO	Wild type and mutant human heart (R)-3-hydroxybutyrate dehydrogenase expressed in insect cells	Biochemistry	1996	8679568	- mitochondrial inner membrane [Marks, J Biol Chem 1992], catalytic domain faces matrix [Green, Biochemistry 1996] - gene cloned [Marks J Biol Chem 1992] - has an absolute and specific requirement of phosphatidylcholine [Marks J Biol Chem 1992] - checked over by RS/TV
BETALDHx	3	Chern MK, Pietruszko R.	Human aldehyde dehydrogenase E3 isozyme is a betaine aldehyde dehydrogenase.		1995	7646513	NAD is preferred cofactor; cytosolic location - Chern et. Al. Biochem Biophys Res Commun. 1995 Aug 15;213(2):561-8. mitochondrial location possible PMID:15321791 MM
BETALDHx	3	Craig SA.	Betaine in human nutrition.		2004	15321791	NAD is preferred cofactor; cytosolic location - Chern et. Al. Biochem Biophys Res Commun. 1995 Aug 15;213(2):561-8. mitochondrial location possible PMID:15321791 MM
BHBt	2	Alonso de la Torre SR, Serrano MA, Medina JM.	Carrier-mediated beta-D-hydroxybutyrate transport in brush-border membrane vesicles from rat placenta.	Pediatr Res	1992	1408469	- mechanism of beta-D-hydroxybutyrate transport at brush border membrane of rat placenta is-D-hydroxybutyrate/H+ symport [Alonso de la Torre 1992] - liver mitochondria produce R-beta-hydroxybutyrate; this is released into blood and taken up by peripheral tissueswhich oxidize (R)-hydroxybutyrate back to acetoacetate [Guo 2006]
BHBt	2	Guo K, Lukacik P, Papagrigoriou E, Meier M, Lee WH, Adamski J, Oppermann U.	Characterization of Human DHRS6, an Orphan Short Chain Dehydrogenase/Reductase Enzyme: A NOVEL, CYTOSOLIC TYPE 2 R-beta-HYDROXYBUTYRATE DEHYDROGENASE.	J Biol Chem	2006	16380372	- mechanism of beta-D-hydroxybutyrate transport at brush border membrane of rat placenta is-D-hydroxybutyrate/H+ symport [Alonso de la Torre 1992] - liver mitochondria produce R-beta-hydroxybutyrate; this is released into blood and taken up by peripheral tissueswhich oxidize (R)-hydroxybutyrate back to acetoacetate [Guo 2006]
BHBtm	3	Latruffe N.	Transport of D-beta-hydroxybutyrate across rat liver mitochondrial membranes.	Comp Biochem Physiol B	1987	3427918	- Added by RS/TV - No genes found. - Inner mitochondrial membrane is largely permeable to to bhb. This process which is inhibited by several molecules indicates that this transport is carrier mediated. Two methods of transport are likely as a result of this inhibitory study: (1) like pyruvate/acetoacetate through a monocarboxylate carrier or (2) a dicarboxylate carrier. - It has also been strongly suggested that this translocation process is strongly dependent on pH medium which indicates a H+ symport or an OH- antiport. (Latruffe N. Comp Biochem Physiol B. 1987;88(3):797-802.)
BHMT	3	Sunden SL, Renduchintala MS, Park EI, Miklasz SD, Garrow TA.	Betaine-homocysteine methyltransferase expression in porcine and human tissues and chromosomal localization of the human gene.		1997	9281325	Entrez Gene - Betaine-homocysteine methyltransferase is a cytosolic enzyme that catalyzes the conversion of betaine and homocysteine to dimethylglycine and methionine, respectively. Defects in BHMT could lead to hyperhomocyst(e)inemia,but such a defect has not yet been observed.
BILIRED	0	Saito F, Yamaguchi T, Komuro A, Tobe T, Ikeuchi T, Tomita M, Nakajima H.	Mapping of the newly identified biliverdin-IX beta reductase gene (BLVRB) to human chromosome 19q13.13-->q13.2 by fluorescence in situ hybridization.	Cytogenet Cell Genet	1995	7656592	- Added by RS/TV Stefan Ryter, Free Radical Biology & Medicine, Vol 28, No2, pp. 289-309, 2000. - Cytoplasmic according to GeneCards. - Bilirubin is a lipophilic linear tetrapyrrole, abundant in blood plasma, which occurs uniquely in mammals. It is the final product of heme catabolism, as heme oxygenase (HO) cleaves the heme ring to form the water-soluble biliverdin, which is reduced by biliverdin reductase (BVR) to bilirubin. (Baranano DE, Rao M, Ferris CD, Snyder SH. Proc Natl Acad Sci U S A. 2002 Dec 10;99(25):16093-8. Epub 2002 Nov 27.) - Possible second gene: Blvrb, suspect because it claims to have two different functions. - IT - included blvrb to this GPR IT there might be the possibility that this genes also carries out biliverdin reductase activity in liver cells. Flavin depend enzyme (FMN is more effective than FAD)

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BILIRED	0	Chikuba K, Yubisui T, Shirabe K, Takeshita M.	Cloning and nucleotide sequence of a cDNA of the human erythrocyte NADPH-flavin reductase.	Biochem Biophys Res Commun	1994	8117274	- Added by RS/TV Stefan Ryter, Free Radical Biology & Medicine, Vol 28, No2, pp. 289-309, 2000. - Cytoplasmic according to GeneCards. - Bilirubin is a lipophilic linear tetrapyrrole, abundant in blood plasma, which occurs uniquely in mammals. It is the final product of heme catabolism, as heme oxygenase (HO) cleaves the heme ring to form the water-soluble biliverdin, which is reduced by biliverdin reductase (BVR) to bilirubin. (Baranano DE, Rao M, Ferris CD, Snyder SH. Proc Natl Acad Sci U S A. 2002 Dec 10;99(25):16093-8. Epub 2002 Nov 27.) - Possible second gene: Blvrb, suspect because it claims to have two different functions. - IT - included blvrb to this GPR IT there might be the possibility that this genes also carries out biliverdin reductase activity in liver cells. Flavin depend enzyme (FMN is more effective than FAD)
BILIRED	0	Baranano DE, Rao M, Ferris CD, Snyder SH.	Biliverdin reductase: a major physiologic cytoprotectant.	Proc Natl Acad Sci U S A	2002	12456881	- Added by RS/TV Stefan Ryter, Free Radical Biology & Medicine, Vol 28, No2, pp. 289-309, 2000. - Cytoplasmic according to GeneCards. - Bilirubin is a lipophilic linear tetrapyrrole, abundant in blood plasma, which occurs uniquely in mammals. It is the final product of heme catabolism, as heme oxygenase (HO) cleaves the heme ring to form the water-soluble biliverdin, which is reduced by biliverdin reductase (BVR) to bilirubin. (Baranano DE, Rao M, Ferris CD, Snyder SH. Proc Natl Acad Sci U S A. 2002 Dec 10;99(25):16093-8. Epub 2002 Nov 27.) - Possible second gene: Blvrb, suspect because it claims to have two different functions. - IT - included blvrb to this GPR IT there might be the possibility that this genes also carries out biliverdin reductase activity in liver cells. Flavin depend enzyme (FMN is more effective than FAD)
BMTer_L	3	Takahashi M, Inoue N, Ohishi K, Maeda Y, Nakamura N, Endo Y, Fujita T, Takeda J, Kinoshita T	PIG-B, a membrane protein of the endoplasmic reticulum with a large lumenal domain, is involved in transferring the third mannose of the GPI anchor	EMBO J	1996	8861954	- reaction described in Varki, pg. 136 - endoplasmic reticulum; Dol-P-Man dependent mannosyltransferases [RefSeq] - gene was cloned [Takahashi, EMBO J 1996] - transfers 3rd mannose of GPI anchor [Takahashi, EMBO J 1996]
BPNT	3	Spiegelberg BD, Xiong JP, Smith JJ, Gu RF, York JD.	Cloning and characterization of a mammalian lithium-sensitive bisphosphate 3'-nucleotidase inhibited by inositol 1,4-bisphosphate	J Biol Chem	1999	10224133	from [Spielberg 1999]: - human and mouse cDNA cloned; 92% amino acid sequence identity - human mRNA highly expressed in kidney, liver, pancreas, moderately expressed in heart, lowly expressed in placenta, kidney, brain, lung - enzyme demonstrated 3'-phosphatase activity on PAP and PAPS
BTND1	3	Stanley CM, Hymes J, Wolf B.	Identification of alternatively spliced human biotinidase mRNAs and putative localization of endogenous biotinidase.	Mol Genet Metab	2004	15059618	All this is not really clear to me. Stanley et al, 2004, reported three additional transcripts but they are not included in LocusLink yet. They localized biotinidase activity in cytoplasm. the test for mitochondrial localization seems to be negative. Probable ER localiszation. 686.1 = serum protein, outer membrane associated??? 686.2 = Stanley transcirpt 1 a, present in all tested tissues 686.3 = Stanley transcirpt 1 a, present in all tested tissues 686.4 = Stanley transcirpt 1 c, only expressed in testis due to the fact that 3 out of 5 biotin-dependent enzymes are located in mitochondria it is very likely that biotin-holocarbxylase and biotinidase are located in cytoplasm and mitochondria (Ref: Stanley et al, Pacheco-Alvarez) other splice variants were reported but not in Entrez Gene

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
BTND1n	3	Pispa J.	Animal biotinidase.	Ann Med Exp Biol Fenn	1965	5867120	IT biotin plays a role in regulation of cell cycle (Bender book) as a consequence of biotinylation of histones in the nucleus. Hymes et al (1995) discovered that human biotinidase has biotinyl transferase activity, in which biocytin serves as a biotin donor and histones serve as specific biotin acceptors. (Histones play an important role in the regulation of transcription, translation and packaging of DNA. The biotinyl transferase activity of biotinidase is not included in the model. Therefore, biocytin is only transported in nucleus and one of these two should be included in biomass function. I decided to allow transport of only biocytin since biocytin is transfered to histone (and not biotin) and released from them by proteolysis
BTND1n	3	Hymes J, Fleischhauer K, Wolf B.	Biotinylation of biotinidase following incubation with biocytin.	Clin Chim Acta	1995	7758201	IT biotin plays a role in regulation of cell cycle (Bender book) as a consequence of biotinylation of histones in the nucleus. Hymes et al (1995) discovered that human biotinidase has biotinyl transferase activity, in which biocytin serves as a biotin donor and histones serve as specific biotin acceptors. (Histones play an important role in the regulation of transcription, translation and packaging of DNA. The biotinyl transferase activity of biotinidase is not included in the model. Therefore, biocytin is only transported in nucleus and one of these two should be included in biomass function. I decided to allow transport of only biocytin since biocytin is transfered to histone (and not biotin) and released from them by proteolysis
BTND1n	3	Hymes J, Fleischhauer K, Wolf B.	Biotinylation of histones by human serum biotinidase: assessment of biotinyl-transferase activity in sera from normal individuals and children with biotinidase deficiency.	Biochem Mol Med	1995	8593541	IT biotin plays a role in regulation of cell cycle (Bender book) as a consequence of biotinylation of histones in the nucleus. Hymes et al (1995) discovered that human biotinidase has biotinyl transferase activity, in which biocytin serves as a biotin donor and histones serve as specific biotin acceptors. (Histones play an important role in the regulation of transcription, translation and packaging of DNA. The biotinyl transferase activity of biotinidase is not included in the model. Therefore, biocytin is only transported in nucleus and one of these two should be included in biomass function. I decided to allow transport of only biocytin since biocytin is transfered to histone (and not biotin) and released from them by proteolysis
BTND1n	3	Zempleni J.	Uptake, localization, and noncarboxylase roles of biotin.	Annu Rev Nutr	2005	16011464	IT biotin plays a role in regulation of cell cycle (Bender book) as a consequence of biotinylation of histones in the nucleus. Hymes et al (1995) discovered that human biotinidase has biotinyl transferase activity, in which biocytin serves as a biotin donor and histones serve as specific biotin acceptors. (Histones play an important role in the regulation of transcription, translation and packaging of DNA. The biotinyl transferase activity of biotinidase is not included in the model. Therefore, biocytin is only transported in nucleus and one of these two should be included in biomass function. I decided to allow transport of only biocytin since biocytin is transfered to histone (and not biotin) and released from them by proteolysis
BTND1n	3	Zempleni J., Mock D.M.	Biotin homeostasis during the cell cycle	Nutrition Research Reviews	2001		IT biotin plays a role in regulation of cell cycle (Bender book) as a consequence of biotinylation of histones in the nucleus. Hymes et al (1995) discovered that human biotinidase has biotinyl transferase activity, in which biocytin serves as a biotin donor and histones serve as specific biotin acceptors. (Histones play an important role in the regulation of transcription, translation and packaging of DNA. The biotinyl transferase activity of biotinidase is not included in the model. Therefore, biocytin is only transported in nucleus and one of these two should be included in biomass function. I decided to allow transport of only biocytin since biocytin is transfered to histone (and not biotin) and released from them by proteolysis
BTNDe	3	Cole H, Reynolds TR, Lockyer JM, Buck GA, Denson T, Spence JE, Hymes J, Wolf B.	Human serum biotinidase. cDNA cloning, sequence, and characterization.	J Biol Chem	1994	7509806	IT other splice variants were reported but not in Entrez Gene
BTNDe	3	Cole H, Weremowicz S, Morton CC, Wolf B.	Localization of serum biotinidase (BTD) to human chromosome 3 in band p25.	Genomics	1994	8001986	IT other splice variants were reported but not in Entrez Gene

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BTNt2	3	Daberkow RL, White BR, Cederberg RA, Griffin JB, Zempleni J.	Monocarboxylate transporter 1 mediates biotin uptake in human peripheral blood mononuclear cells.	J Nutr	2003		6566: - isolated [Garcia 1994] - 86% identtity to hamster protein [Garcia 1994] - expressed [Ritzhaupt, Ellis, J Physiol 1998], [Ritzhaupt, Wood, J Physiol et al 1998] - transports butyrate [Ritzhaupt, Ellis, J Physiol 1998] and lactate [Ritzhaupt, Wood, J Physiol et al 1998] - ubiquitous but predominant in colon [Ritzhaupt, Biochem Soc Trans 1998], heart, red muscle [Halestrap 1999] - L-Lactate transport in erythrocytes, cardiac myocytes, and hepatocytes due to proton-linked monocarboxylate transporter (see [Poole 1993] for review) - also transports pyruvate, b-hydroxybutyrate, acetoacetate [Halestrap 2004] - in most tissues MCT1 exports lactate to prevernt fall in cytosolic pH; in sk muscle and heart, MCT1 imports lactate to supply gluconeogenesis and lipogenesis; MCT1 or MCT2 imports lactate in liver, kidney and brain [Halestrap 2004] IT It seems that the transport is reversible since Daberkow et al found that extracellular lactate stimulates efflux from biotin. However, it seems that this biotin transport mediated by MCT1 only takes in lymphoid cells but not into placental (JAr) cells, lu Moreover, it might be that MCT2 is also able to transport biotin
BTNt2m	3	Daberkow RL, White BR, Cederberg RA, Griffin JB, Zempleni J.	Monocarboxylate transporter 1 mediates biotin uptake in human peripheral blood mononuclear cells.	J Nutr	2003	12949353	IT MCT1 transporter location in mito membrane has been confirmed for rat.
BTNt2m	3	Butz CE, McClelland GB, Brooks GA.	MCT1 confirmed in rat striated muscle mitochondria.	J Appl Physiol	2004	15121743	IT MCT1 transporter location in mito membrane has been confirmed for rat.
BTNt3i	3	Prasad PD, Wang H, Kekuda R, Fujita T, Fei YJ, Devoe LD, Leibach FH, Ganapathy V.	Cloning and functional expression of a cDNA encoding a mammalian sodium-dependent vitamin transporter mediating the uptake of pantothenate, biotin, and lipoate.	J Biol Chem	1998	9516450	IT
BTNt3i	3	Wang H, Huang W, Fei YJ, Xia H, Yang-Feng TL, Leibach FH, Devoe LD, Ganapathy V, Prasad PD.	Human placental Na+-dependent multivitamin transporter. Cloning, functional expression, gene structure, and chromosomal localization.	J Biol Chem	1999	10329687	IT
BTNt3i	3	Prasad PD, Wang H, Huang W, Fei YJ, Leibach FH, Devoe LD, Ganapathy V.	Molecular and functional characterization of the intestinal Na+-dependent multivitamin transporter.	Arch Biochem Biophys	1999	10334869	IT
BTNt3i	3	Balamurugan K, Ortiz A, Said HM.	Biotin uptake by human intestinal and liver epithelial cells: role of the SMVT system.	Am J Physiol Gastrointest Liver Physiol	2003	12646417	IT
BTNt3i	3	Balamurugan K, Vaziri ND, Said HM.	Biotin uptake by human proximal tubular epithelial cells: Cellular and molecular aspects.	Am J Physiol Renal Physiol	2005	15561972	IT
BTNt4i	3	Vlasova TI, Stratton SL, Wells AM, Mock NI, Mock DM.	Biotin deficiency reduces expression of SLC19A3, a potential biotin transporter, in leukocytes from human blood.	J Nutr	2005	15623830	IT i am not sure if this transport can be reversible. takes at least place in leukocytes
BUP2	3	Sakamoto T, Sakata SF, Matsuda K, Horikawa Y, Tamaki N.	Expression and properties of human liver beta-ureidopropionase.	J Nutr Sci Vitaminol (Tokyo)	2001	11508704	original rxn (BUP) added by IT changed to BUP2 by MM: 3aib in rxn BUP has been changed to 3aib-D (rxn BUP2) (see OMIM ref below) OMIM: The R enantiomer (old name D-(minus)-BAIB) derives from thymine, the S enantiomer (L-plus-BAIB) from L-valine. Human urine contains R-BAIB almost exclusively (and it is this form that is excreted in excess in the hyper-BAIB trait), whereas the plasma pool is about 80% S-BAIB.
C110CPT2m	2	Verhoeven NM, Wanders RJ, Poll-The BT, Saudubray JM, Jakobs C.	The metabolism of phytanic acid and pristanic acid in man: a review.	J Inherit Metab Dis	1998	9819701	As per Verhoeven J Inher Metab Dis 1998 dmnoncoa must be transfered into mit to undergo 1 round of beta-ox, but fate of 2,6 dimethylheptanoly-CoA is not known! NJ

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C160CPT1	3	Finocchiaro G, Taroni F, Rocchi M, Martin AL, Colombo I, Tarelli GT, DiDonato S.	cDNA cloning, sequence analysis, and chromosomal localization of the gene for human carnitine palmitoyltransferase.	Proc Natl Acad Sci U S A	1991	1988962	- Additional information added by RS/TV J Biol Chem. 2001 Jun 8;276(23):20182-5. Epub 2001 Mar 27 1)GPR association: In order to cross the mitochondrial membranes, long-chain fatty acids are first activated by coenzyme A and then reversibly conjugated with L-carnitine, a reaction that is catalyzed by the enzyme carnitine palmitoyltransferase. CPTase is split into two distinct parts: sequential action of CPT1 (addition of carnitine group to fatty-acid) followed by CPT2 (removal of carnitine group from fatty acid). 2)Differing roles of CPT1 and CPT2: CPT 1is associated with the outer mitochondrial membrane (cytosolic enzyme activity), loses activity upon exposure to strong detergents. CPT 2 is located on the inner mitochondrial membrane, insensitive to malonyl-coa inhibition and exposure to detergent. 3)Isoforms of CPT1: CPT1 exists as three isoforms, each with a different tissue expression. Isoform (a) is expressed primarily in the liver. Isoform (b) is expressed primarily in muscles. Isoform (c) is expressed primarily in the brain. 1 through 3 according to Finocchiaro G, Taroni F, Rocchi M, M Isoform(b) has four splice variants according to Entrez Gene da
C160CPT2	3	Taroni F, Verderio E, Fiorucci S, Cavadini P, Finocchiaro G, Uziel G, Lamantea E, Gellera C, DiDonato S.	Molecular characterization of inherited carnitine palmitoyltransferase II deficiency.	Proc Natl Acad Sci U S A	1992	1528846	J Biol Chem. 2001 Jun 8;276(23):20182-5. Epub 2001 Mar 27 1)GPR association: In order to cross the mitochondrial membranes, long-chain fatty acids are first activated by coenzyme A and then reversibly conjugated with L-carnitine, a reaction that is catalyzed by the enzyme carnitine palmitoyltransferase. CPTase is split into two distinct parts: sequential action of CPT1 (addition of carnitine group to fatty-acid) followed by CPT2 (removal of carnitine group from fatty acid). 2)Differing roles of CPT1 and CPT2: CPT 1is associated with the outer mitochondrial membrane (cytosolic enzyme activity), loses activity upon exposure to strong detergents. CPT 2 is located on the inner mitochondrial membrane, insensitive to malonyl-coa inhibition and exposure to detergent. 3)Isoforms of CPT1: CPT1 exists as three isoforms, each with a different tissue expression. Isoform (a) is expressed primarily in the liver. Isoform (b) is expressed primarily in muscles. Isoform (c) is expressed primarily in the brain. 4) CPT2 does not exist have any tissue-specific isoforms. It see 1 and 2 according to Finocchiaro G, Taroni F, Rocchi M, Marti 3 and 4 according to Taroni F, Verderio E, Fiorucci S, Cavadini
C226CPT2	3	Fraser F, Padovese R, Zammit VA.	Distinct kinetics of carnitine palmitoyltransferase i in contact sites and outer membranes of rat liver mitochondria.	J Biol Chem	2001	11274214	Fraser F, Padovese R, Zammit VA Distinct kinetics of carnitine palmitoyltransferase i in contact sites and outer membranes of rat liver mitochondria J Biol Chem. 2001 Jun 8;276(23):20182-5. Epub 2001 Mar 27 1)GPR association: In order to cross the mitochondrial membranes, long-chain fatty acids are first activated by coenzyme A and then reversibly conjugated with L-carnitine, a reaction that is catalyzed by the enzyme carnitine palmitoyltransferase. CPTase is split into two distinct parts: sequential action of CPT1 (addition of carnitine group to fatty-acid) followed by CPT2 (removal of carnitine group from fatty acid). 2)Differing roles of CPT1 and CPT2: CPT 1is associated with the outer mitochondrial membrane (cytosolic enzyme activity), loses activity upon exposure to strong detergents. CPT 2 is located on the inner mitochondrial membrane, insensitive to malonyl-coa inhibition and exposure to detergent. 3)Isoforms of CPT1: CPT1 exists as three isoforms, each with a different tissue expression. Isoform (a) is expressed primarily in the liver. Isoform (b) is expressed primarily in muscles. Isoform 4) CPT2 does not exist have any tissue-specific isoforms. It see 1 and 2 according to Finocchiaro G, Taroni F, Rocchi M, Marti
C3STDH1Pr	3	Caldas H, Herman GE	NSDHL, an eznyme invovled in cholesterol biosynthesis, traffics through the Golgi and accumulates on ER membranes on the surface of lipid droplets	Human Molecular Genetics	2003		ER - uniprot see refs - particularly Caldas - transport mechanism for steroids from ER -> cytosol: lipid droplets specificity: Brain, heart, liver, lung, kidney, skin and placenta. NSDHL, an enzyme involved in cholesterol synthesis, traffics through the Golgi and accumulates on ER membranes and on the surface of lipid droplets. NAD(P)H steroid dehydrogenase-like protein is localized to lipid droplets NJ

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C3STDH1Pr	3	Konig A, Happle R, Bornholdt D, Engel H, Grzeschik KH	Mutations in the NSDHL gene, encoding a 3-beta-hydroxysteroid dehydrogenase, cause CHILD syndrome	Am J Med Genet	2000		ER - uniprot see refs - particularly Caldas - transport mechanism for steroids from ER -> cytosol: lipid droplets specificity: Brain, heart, liver, lung, kidney, skin and placenta. NSDHL, an enzyme involved in cholesterol synthesis, traffics through the Golgi and accumulates on ER membranes and on the surface of lipid droplets. NAD(P)H steroid dehydrogenase-like protein is localized to lipid droplets NJ
C3STDH1Pr	3	Caldas H, Herman GE	NSDHL, an eznyme invovled in cholesterol biosynthesis, traffics through the Golgi and accumulates on ER membranes on the surface of lipid droplets	Human Molecular Genetics	2003		ER - uniprot see refs - particularly Caldas - transport mechanism for steroids from ER -> cytosol: lipid droplets specificity: Brain, heart, liver, lung, kidney, skin and placenta. NSDHL, an enzyme involved in cholesterol synthesis, traffics through the Golgi and accumulates on ER membranes and on the surface of lipid droplets. NAD(P)H steroid dehydrogenase-like protein is localized to lipid droplets NJ
CAATPS	3	Yu X, Inesi G.	Variable stoichiometric efficiency of Ca2+ and Sr2+ transport by the sarcoplasmic reticulum ATPase.	J Biol Chem	1995	7876199	More famously known for SR subtypes (some of these are also ER membrane see ATP2A family genes (GeneID 487, 488, 489). Plasma membrane CaATP include ATP2B family: 490, 491, 492, 493 Ca/ATP stoichiometry can vary see PMID: 7876199 The protein encoded by this gene belongs to the family of P-type primary ion transport ATPases characterized by the formation of an aspartyl phosphate intermediate during the reaction cycle. These enzymes remove bivalent calcium ions from eukaryotic cells against very large concentration gradients and play a critical role in intracellular calcium homeostasis. The mammalian plasma membrane calcium ATPase isoforms are encoded by at least four separate genes and the diversity of these enzymes is further increased by alternative splicing of transcripts. The expression of different isoforms and splice variants is regulated in a developmental, tissue- and cell type-specific manner, suggesting that these pumps are functionally adapted to the physiological needs of particular cells and tissues. This gene encodes the plasma membrane calcium ATPase isoform 2. Alternatively spliced transcript variants enc NJ
CAATPS	3	Hilfiker H, Strehler-Page MA, Stauffer TP, Carafoli E, Strehler EE.	Structure of the gene encoding the human plasma membrane calcium pump isoform 1.	J Biol Chem	1993	8396145	More famously known for SR subtypes (some of these are also ER membrane see ATP2A family genes (GeneID 487, 488, 489). Plasma membrane CaATP include ATP2B family: 490, 491, 492, 493 Ca/ATP stoichiometry can vary see PMID: 7876199 The protein encoded by this gene belongs to the family of P-type primary ion transport ATPases characterized by the formation of an aspartyl phosphate intermediate during the reaction cycle. These enzymes remove bivalent calcium ions from eukaryotic cells against very large concentration gradients and play a critical role in intracellular calcium homeostasis. The mammalian plasma membrane calcium ATPase isoforms are encoded by at least four separate genes and the diversity of these enzymes is further increased by alternative splicing of transcripts. The expression of different isoforms and splice variants is regulated in a developmental, tissue- and cell type-specific manner, suggesting that these pumps are functionally adapted to the physiological needs of particular cells and tissues. This gene encodes the plasma membrane calcium ATPase isoform 2. Alternatively spliced transcript variants enc NJ
CAMPt	3	Chen ZS, Lee K, Kruh GD.	Transport of cyclic nucleotides and estradiol 17-beta-D-glucuronide by multidrug resistance protein 4. Resistance to 6-mercaptopurine and 6-thioguanine.	J Biol Chem	2001	11447229	IT Chen(2001):ABCC4: cGMP: 2.0 +/- 0.3 pmol/mg/min cAMP:4.1 +/- 0.4 pmol/min/mg Estradiolglc: 102 +/- 16 pmol/min/mg
CAMPt	3	Wielinga PR, van der Heijden I, Reid G, Beijnen JH, Wijnholds J, Borst P.	Characterization of the MRP4- and MRP5-mediated transport of cyclic nucleotides from intact cells.	J Biol Chem	2003	12637526	IT Chen(2001):ABCC4: cGMP: 2.0 +/- 0.3 pmol/mg/min cAMP:4.1 +/- 0.4 pmol/min/mg Estradiolglc: 102 +/- 16 pmol/min/mg
CAMPt	3	Reid G, Wielinga P, Zelcer N, van der Heijden I, Kuil A, de Haas M, Wijnholds J, Borst P.	The human multidrug resistance protein MRP4 functions as a prostaglandin efflux transporter and is inhibited by nonsteroidal antiinflammatory drugs.	Proc Natl Acad Sci U S A	2003	12835412	IT Chen(2001):ABCC4: cGMP: 2.0 +/- 0.3 pmol/mg/min cAMP:4.1 +/- 0.4 pmol/min/mg Estradiolglc: 102 +/- 16 pmol/min/mg

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CAMPt	3	Dazert P, Meissner K, Vogelgesang S, Heydrich B, Eckel L, Bohm M, Warzok R, Kerb R, Brinkmann U, Schaeffeler E, Schwab M, Cascorbi I, Jedlitschky G, Kroemer HK.	Expression and localization of the multidrug resistance protein 5 (MRP5/ABCC5), a cellular export pump for cyclic nucleotides, in human heart.	Am J Pathol	2003	14507663	IT Chen(2001):ABCC4: cGMP: 2.0 +/- 0.3 pmol/mg/min cAMP:4.1 +/- 0.4 pmol/min/mg Estradiolglc: 102 +/- 16 pmol/min/mg
CAMPt	3	Meyer Zu Schwabedissen HE, Grube M, Heydrich B, Linnemann K, Fusch C, Kroemer HK, Jedlitschky G.	Expression, localization, and function of MRP5 (ABCC5), a transporter for cyclic nucleotides, in human placenta and cultured human trophoblasts: effects of gestational age and cellular differentiation.	Am J Pathol	2005	15631998	IT Chen(2001):ABCC4: cGMP: 2.0 +/- 0.3 pmol/mg/min cAMP:4.1 +/- 0.4 pmol/min/mg Estradiolglc: 102 +/- 16 pmol/min/mg
CAt7r	3	Schnetkamp PP.	Na-Ca or Na-Ca-K exchange in rod photoreceptors.		1989	2484986	- encodes a member of the sodium/calcium exchanger integral membrane protein family. Three mammalian isoforms in family 8 have been identified. Na+/Ca2+ exchange proteins are involved in maintaining Ca2+ homeostasis in a wide variety of cell types. - The Na+/Ca2+ exchanger is the dominant cellular Ca2+ efflux mechanism and regulates contractility. - isoform 1 is ubiquitous, 2 and 3 found in brain and skeletal muscle tissue - 6 splice variants for isoform 3 -note: Ca2+/Ca2+, Na+/Na+, Na+/Mg2+, Na+/Ba2+, Na+/Sr2+, and Na+/Ni2+ exchanges have been described, but not significant MM
CAt7r	3	Gabellini,N., Bortoluzzi,S., Danieli,G.A., Carafoli,E.,	The human SLC8A3 gene and the tissue-specific Na+/Ca2+ exchanger 3 isoforms.		2002	12406570	- encodes a member of the sodium/calcium exchanger integral membrane protein family. Three mammalian isoforms in family 8 have been identified. Na+/Ca2+ exchange proteins are involved in maintaining Ca2+ homeostasis in a wide variety of cell types. - The Na+/Ca2+ exchanger is the dominant cellular Ca2+ efflux mechanism and regulates contractility. - isoform 1 is ubiquitous, 2 and 3 found in brain and skeletal muscle tissue - 6 splice variants for isoform 3 -note: Ca2+/Ca2+, Na+/Na+, Na+/Mg2+, Na+/Ba2+, Na+/Sr2+, and Na+/Ni2+ exchanges have been described, but not significant MM
CATm	3	Radi R, Turrens JF, Chang LY, Bush KM, Crapo JD, Freeman BA.	Detection of catalase in rat heart mitochondria.	J Biol Chem	1991	1657986	Proteome Radi R, Turrens JF, Chang LY, Bush KM, Crapo JD, Freeman BA.; Detection of catalase in rat heart mitochondria.; J Biol Chem. 1991 Nov 15;266(32):22028-34. Catalytic Activity: Catalase is an enzyme which catalyzes the decomposition of hydrogen peroxide to oxygen and water. It is found in virtually all aerobic cells and is partly responsible for protecting cells from the toxic effects of hydrogen peroxide. According to F Quan. Nucleic Acids Res. 1986 July 11; 14(13): 5321 5335. Localization: In mammalian tissues found predominantly in liver, kidney, and erythrocytes, while the lowest levels are found in connective tissues. In tissues such as the liver, it is found predominantly in the peroxisome. In mature human erythrocytes, it is found in the cytosol. Catalase has also been found in the mitochondria of cardiac cells. According to F Quan. Nucleic Acids Res. 1986 July 11; 14(13): 5321 5335. Also according to Radi R. J Biol Chem. 1991 Nov 15;266(32):22028-34.

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
CATm	3	Quan F, Korneluk RG, Tropak MB, Gravel RA.	Isolation and characterization of the human catalase gene.	Nucleic Acids Res	1986	3755525	Proteome Radi R, Turrens JF, Chang LY, Bush KM, Crapo JD, Freeman BA.; Detection of catalase in rat heart mitochondria.; J Biol Chem. 1991 Nov 15;266(32):22028-34. Catalytic Activity: Catalase is an enzyme which catalyzes the decomposition of hydrogen peroxide to oxygen and water. It is found in virtually all aerobic cells and is partly responsible for protecting cells from the toxic effects of hydrogen peroxide. According to F Quan. Nucleic Acids Res. 1986 July 11; 14(13): 5321 5335. Localization: In mammalian tissues found predominantly in liver, kidney, and erythrocytes, while the lowest levels are found in connective tissues. In tissues such as the liver, it is found predominantly in the peroxisome. In mature human erythrocytes, it is found in the cytosol. Catalase has also been found in the mitochondria of cardiac cells. According to F Quan. Nucleic Acids Res. 1986 July 11; 14(13): 5321 5335. Also according to Radi R. J Biol Chem. 1991 Nov 15;266(32):22028-34.
CBLATm	3	Dobson CM, Wai T, Leclerc D, Wilson A, Wu X, Dore C, Hudson T, Rosenblatt DS, Gravel RA.	Identification of the gene responsible for the cblA complementation group of vitamin B12-responsive methylmalonic acidemia based on analysis of prokaryotic gene arrangements.	Proc Natl Acad Sci U S A	2002	12438653	IT
CBLATm	3	Carmel R, Green R, Rosenblatt DS, Watkins D.	Update on cobalamin, folate, and homocysteine.	Hematology (Am Soc Hematol Educ Program)	2003	14633777	IT
CBPPer	2	Lueck JD, Nordlie RC.	The utilization of intramitochondrially generated carbamyl phosphate for microsomal glucose 6-phosphate biosynthesis.	FEBS Lett	1972	11946414	- additional activity of glucose-6-phosphate phosphatase [Orten, Human Biochem 1975] - reaction demonstrated in rat liver [Lueck 1972] - reaction produces NH3 & CO2 (not carbamate) according to [Lucius 1993]
CBPS	3	Chen KC, Vannais DB, Jones C, Patterson D, Davidson JN.	Mapping of the gene encoding the multifunctional protein carrying out the first three steps of pyrimidine biosynthesis to human chromosome 2.	Hum Genet	1989	2565865	IT
CBPS	3	Iwahana H, Fujimura M, Ii S, Kondo M, Moritani M, Takahashi Y, Yamaoka T, Yoshimoto K, Itakura M.	Molecular cloning of a human cDNA encoding a trifunctional enzyme of carbamoyl-phosphate synthetase-aspartate transcarbamoylase-dihydroorotase in de Novo pyrimidine synthesis.	Biochem Biophys Res Commun	1996	8619816	IT
CBPSam	3	Uriarte M, Marina A, Ramon-Maiques S, Fita I, Rubio V.	The carbamoyl-phosphate synthetase of Pyrococcus furiosus is enzymologically and structurally a carbamate kinase.	J Biol Chem	1999	10347186	- Infomation added by RS/TV: - Mitochondrial according to entrez Gene Database. - CPSI is highly tissue specific, with function and production limited to the liver and a lesser amount in the intestine. (Summar ML, Hall LD, Eeds AM, Hutcheson HB, Kuo AN, Willis AS, Rubio V, Arvin MK, Schofield JP, Dawson EP.Gene. 2003 Jun 5;311:51-7.) - Catalytic activity specified by GeneCards - Irreversible according to Uriarte M, Marina A, Ramon-Maiques S, Fita I, Rubio V. J Biol Chem. 1999 Jun 4;274(23):16295-303.
CBPSam	3	Summar ML, Hall LD, Eeds AM, Hutcheson HB, Kuo AN, Willis AS, Rubio V, Arvin MK, Schofield JP, Dawson EP.	Characterization of genomic structure and polymorphisms in the human carbamyl phosphate synthetase I gene.	Gene	2003	12853138	- Infomation added by RS/TV: - Mitochondrial according to entrez Gene Database. - CPSI is highly tissue specific, with function and production limited to the liver and a lesser amount in the intestine. (Summar ML, Hall LD, Eeds AM, Hutcheson HB, Kuo AN, Willis AS, Rubio V, Arvin MK, Schofield JP, Dawson EP.Gene. 2003 Jun 5;311:51-7.) - Catalytic activity specified by GeneCards - Irreversible according to Uriarte M, Marina A, Ramon-Maiques S, Fita I, Rubio V. J Biol Chem. 1999 Jun 4;274(23):16295-303.
CBPter	2	Lucius RW, Waddell ID, Burchell A, Nordlie RC	The hepatic glucose-6-phosphatase system in Ehrlich-ascites-tumour-bearing mice	Biochem J	1993	8384451	- rxn catalyzed by T2 beta translocase of glucose-6-phosphatase system [Lucius 1993], [Foster 2002]
CBPter	2	Foster JD, Nordlie RC	The biochemistry and molecular biology of the glucose-6-phosphatase system.	Exp Biol Med (Maywood)	2002	12192101	- rxn catalyzed by T2 beta translocase of glucose-6-phosphatase system [Lucius 1993], [Foster 2002]
CBR1	3	Okita RT, Okita JR.	Prostaglandin-metabolizing enzymes during pregnancy: characterization of NAD(+)-dependent prostaglandin dehydrogenase, carbonyl reductase, and cytochrome P450-dependent prostaglandin omega-hydroxylase.	Crit Rev Biochem Mol Biol	1996	8740524	cytosol - uniprot Carbonyl reductase is one of several monomeric, NADPH-dependent oxidoreductases having wide specificity for carbonyl compounds. This enzyme is widely distributed in human tissues. Another carbonyl reductase gene, CRB3, lies close to this gene on chromosome 21q. Specific rxns for CBR1 found, just general function + chrom mapping has been identified for CBR3 NJ

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
CBR1	3	Watanabe K, Sugawara C, Ono A, Fukuzumi Y, Itakura S, Yamazaki M, Tashiro H, Osoegawa K, Soeda E, Nomura T.	Mapping of a novel human carbonyl reductase, CBR3, and ribosomal pseudogenes to human chromosome 21q22.2.	Genomics	1998	9740676	cytosol - uniprot Carbonyl reductase is one of several monomeric, NADPH-dependent oxidoreductases having wide specificity for carbonyl compounds. This enzyme is widely distributed in human tissues. Another carbonyl reductase gene, CRB3, lies close to this gene on chromosome 21q. Specific rxns for CBR1 found, just general function + chrom mapping has been identified for CBR3 NJ
CDIPTr	3	Lykidis A, Jackson PD, Rock CO, Jackowski S	The role of CDP-diacylglycerol synthetase and phosphatidylinositol synthase activity levels in the regulation of cellular phosphatidylinositol content	Journal of Biological Chemistry	1997		cytoplasmic side of ER - uniprot + refs Reversible reaction as per uniprot catalyzes the biosynthesis of phosphatidylinositol (PtdIns) as well as PtdIns:inositol exchange reaction [see Holub reaction PMID: 2425833]. May thus act to reduce an excessive cellular PtdIns content. The exchange activity is due to the reverse reaction. Widely expressed. Higher expression in adult liver and skeletal muscle, slightly lower levels seen in pancreas, kidney, lung, placenta, brain, heart, leucocyte, colon, small intestine, ovary, testis, prostate, thymus and spleen. In fetus, expressed in kidney, liver, lung and brain. Phosphatidylinositol breakdown products are ubiquitous second messengers that function downstream of many G protein-coupled receptors and tyrosine kinases regulating cell growth, calcium metabolism, and protein kinase C activity. Two enzymes, CDP-diacylglycerol synthase and phosphatidylinositol synthase, are involved in the biosynthesis of phosphatidylinositol. Phosphatidylinositol synthase, a member of the CDP-alcohol phosphatidyl transferase class-I family, is an integral membrane protein found on the cytoplasm NJ
CDS	3	Weeks R, Dowhan W, Shen H, Balantac N, Meengs B, Nudelman E, Leung DW	Isolation and expression of an isoform of human CDP-diacylglycerol synthease cDNA	DNA Cell Biol	1997		ER membrane - cytosolic side - UniProt Expressed in adult tissues such as placenta, brain, small intestine, ovary, testis and prostate. Highly expressed in fetal kidney, lung and brain. Lower level in fetal liver. NJ
CDS	3	Halford S, Dulai KS, Daw SC, Fitzgibbon J, Hunt DM	Isolation and chromosomal localization of two human cdp-diacylglycerol synthase genes	Genomics	1998		ER membrane - cytosolic side - UniProt Expressed in adult tissues such as placenta, brain, small intestine, ovary, testis and prostate. Highly expressed in fetal kidney, lung and brain. Lower level in fetal liver. NJ
CDS	3	Weeks R, Dowhan W, Shen H, Balantac N, Meengs B, Nudelman E, Leung DW	Isolation and expression of an isoform of human CDP-diacylglycerol synthease cDNA	DNA Cell Biol	1997		ER membrane - cytosolic side - UniProt Expressed in adult tissues such as placenta, brain, small intestine, ovary, testis and prostate. Highly expressed in fetal kidney, lung and brain. Lower level in fetal liver. NJ
CDS	3	Halford S, Dulai KS, Daw SC, Fitzgibbon J, Hunt DM	Isolation and chromosomal localization of two human cdp-diacylglycerol synthase genes	Genomics	1998		ER membrane - cytosolic side - UniProt Expressed in adult tissues such as placenta, brain, small intestine, ovary, testis and prostate. Highly expressed in fetal kidney, lung and brain. Lower level in fetal liver. NJ
CEPTC	3	Henneberry AL, McMaster CR	Cloning and expression of a human choline/ethanolaminephosphotransferase: synthesis of phosphatidylcholine and phosphatidylethanolamine	Biochem J	1999		cytosolic/integral membrane protein - Uniprot need to add additional ref for TV CHPT1 NJ
CERK	3	Sugiura M, Kono K, Liu H, Shimizugawa T, Minekura H, Spiegel S, Kohama T.	Ceramide kinase, a novel lipid kinase. Molecular cloning and functional characterization.	J Biol Chem	2002		cytoplasmic - uniprot cloning + biochem activity - see Sugiura ref Catalyzes specifically the phosphorylation of ceramide to form ceramide 1-phosphate. Acts efficiently on natural and analog ceramides (C6, C8, C16 ceramides, and C8-dihydroceramide), to a lesser extent on C2-ceramide and C6-dihydroceramide, but not on other lipids, such as various sphingosines. NJ
CERT1gt	2	van Meer G, Wolthoorn J, Degroote S.	The fate and function of glycosphingolipid glucosylceramide.	Philos Trans R Soc Lond B Biol Sci	2003	12803919	Two transcripts exist - one encodes a kinase that specifically phosphorylates the N-terminal region of the non-collagenous domain of the alpha 3 chain of type IV collagen, known as the Goodpasture antigen. The other isoform (the one encoded here) of this protein is also iPossibly ATP dependent pathway - given confidence level of 2 at this point. See also PMID: 15907394 for review. See PMID: 12803919 for proposed bidirectionality of transport. FUTURE UPDATES: For alternative substrates see PMID: 15596449 NJ

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CERT1gt	2	Hanada K, Kumagai K, Yasuda S, Miura Y, Kawano M, Fukasawa M, Nishijima M.	Molecular machinery for non-vesicular trafficking of ceramide.	Nature	2003	14685229	Two transcripts exist - one encodes a kinase that specifically phosphorylates the N-terminal region of the non-collagenous domain of the alpha 3 chain of type IV collagen, known as the Goodpasture antigen. The other isoform (the one encoded here) of this protein is also iPossibly ATP dependent pathway - given confidence level of 2 at this point. See also PMID: 15907394 for review. See PMID: 12803919 for proposed bidirectionality of transport. FUTURE UPDATES: For alternative substrates see PMID: 15596449 NJ
CERT1gt	2	Kumagai K, Yasuda S, Okemoto K, Nishijima M, Kobayashi S, Hanada K.	CERT mediates intermembrane transfer of various molecular species of ceramides.	J Biol Chem	2005	15596449	Two transcripts exist - one encodes a kinase that specifically phosphorylates the N-terminal region of the non-collagenous domain of the alpha 3 chain of type IV collagen, known as the Goodpasture antigen. The other isoform (the one encoded here) of this protein is also iPossibly ATP dependent pathway - given confidence level of 2 at this point. See also PMID: 15907394 for review. See PMID: 12803919 for proposed bidirectionality of transport. FUTURE UPDATES: For alternative substrates see PMID: 15596449 NJ
CERT1gt	2	Perry RJ, Ridgway ND.	Molecular mechanisms and regulation of ceramide transport.	Biochim Biophys Acta	2005	15907394	Two transcripts exist - one encodes a kinase that specifically phosphorylates the N-terminal region of the non-collagenous domain of the alpha 3 chain of type IV collagen, known as the Goodpasture antigen. The other isoform (the one encoded here) of this protein is also iPossibly ATP dependent pathway - given confidence level of 2 at this point. See also PMID: 15907394 for review. See PMID: 12803919 for proposed bidirectionality of transport. FUTURE UPDATES: For alternative substrates see PMID: 15596449 NJ
CGLYt3(2)	2	Daniel H, Kottra G	The proton oligopeptide cotransporter family SLC15 in physiology and pharmacology	Pflugers Arch	2004	12905028	From PMID 12905028: In contrast, PEPT2 transports neutral substrates with a 2:1 proton to substrate stoichiometry [11] and charged substrates with variable coupling ratios. It was proposed that PEPT2 in brain astrocytes could contribute to brain glutathione metabolism by providing cysteinyl-glycine derived from extracellular glutathione for glial glutathione resynthesis [17]
CHAT	3	Dobransky T, Davis WL, Xiao GH, Rylett RJ.	Expression, purification and characterization of recombinant human choline acetyltransferase: phosphorylation of the enzyme regulates catalytic activity.	Biochem J	2000	10861222	cytosolic and nuclear - uniprot reversibility by uniprot also specificity: CNS/PNS Cholinergic systems are implicated in numerous neurologic functions. Alteration in some cholinergic neurons may account for the disturbances of Alzheimer disease. The protein encoded by this gene synthesizes the neurotransmitter acetylcholine. Alternative splice variants have been found that contain alternative 5' untranslated exons. Three of the four described splice variants encode identical 69 kDa proteins while one variant encodes both the 69 kDa and a larger 82 kDa protein. NJ
CHLP	0	Roberts SJ, Stewart AJ, Sadler PJ, Farquharson C.	Human PHOSPHO1 exhibits high specific phosphoethanolamine and phosphocholine phosphatase activities.	Biochem J	2004	15175005	cytosol - by default, no specific info in lit NJ
CHLPCTD	3	Kent C	Eukaryotic phospholipid biosynthesis	Annu Rev Biochem	1995		cytoplasmic - unitprot NJ - checked by RS/TV NOTE: This reaction was classified under the "Lipid" subsystem in the mitochondrial model.
CHLtm	2	de Ridder JJ.	The uptake of choline by rat liver mitochondria.		1976	10984	-added to allow choline transport from cytosol to mitochondria -choline is an important nutrient in diet (PMID:15640516) -choline transport by rat liver mitochondria demonstrated but mechanism is unclear (PMID:10984) MM

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CHOLATEt	3	Kullak-Ublick GA, Beuers U, Meier PJ, Domdey H, Paumgartner G.	Assignment of the human organic anion transporting polypeptide (OATP) gene to chromosome 12p12 by fluorescence in situ hybridization.	J Hepatol	1996	9007731	Tissue Specificity: SLCO2A1 - ubiquitous SLCO1A2 - brain, kidney, lung, testis, liver SLCO1B1 - liver SLCO1B3 - liver SLCO2B1 - liver, placenta, spleen, lung, kidney, heart, ovary SLCO3A1 - ubiquitously SLCO4A1 - ubiquitously SLCO1C1 - brain, testis May mediate the release of newly synthesized prostaglandins from cells, the transepithelial transport of prostaglandins, and the clearance of prostaglandins from the circulation. NJ
CHOLATEt2	3	Wong MH, Oelkers P, Dawson PA.	Identification of a mutation in the ileal sodium-dependent bile acid transporter gene that abolishes transport activity.	J Biol Chem	1995	7592981	SLC10A1: liver pancreas SLC10A2: ileum, kidney, biliary tract other SLC transporters (A3, A4, A5) have not been biochemically characterized for substrates & cotransporters. SLC10 review in PMID: 12851823 Only SLC10A1 is known to also have estrone-3-sulfate transport capabilites. Only unidirectional (uptake) activity has been shown. See CHOLATEt/GCHOLAt/TCHOLAt for bile acid excretion acitivity. Sodium/bile acid cotransporters are integral membrane glycoproteins that participate in the enterohepatic circulation of bile acids. Two homologous transporters are involved in the reabsorption of bile acids, one absorbing from the intestinal lumen, the bile duct, and the kidney with an apical localization (SLC10A2; MIM 601295), and the other being found in the basolateral membranes of hepatocytes (SLC10A1). NJ
CHOLATEt2	3	Hagenbuch B, Meier PJ.	Molecular cloning, chromosomal localization, and functional characterization of a human liver Na+/bile acid cotransporter.	J Clin Invest	1994	8132774	SLC10A1: liver pancreas SLC10A2: ileum, kidney, biliary tract other SLC transporters (A3, A4, A5) have not been biochemically characterized for substrates & cotransporters. SLC10 review in PMID: 12851823 Only SLC10A1 is known to also have estrone-3-sulfate transport capabilites. Only unidirectional (uptake) activity has been shown. See CHOLATEt/GCHOLAt/TCHOLAt for bile acid excretion acitivity. Sodium/bile acid cotransporters are integral membrane glycoproteins that participate in the enterohepatic circulation of bile acids. Two homologous transporters are involved in the reabsorption of bile acids, one absorbing from the intestinal lumen, the bile duct, and the kidney with an apical localization (SLC10A2; MIM 601295), and the other being found in the basolateral membranes of hepatocytes (SLC10A1). NJ
CHOLATEt2	3	Oelkers P, Kirby LC, Heubi JE, Dawson PA.	Primary bile acid malabsorption caused by mutations in the ileal sodium-dependent bile acid transporter gene (SLC10A2).	J Clin Invest	1997	9109432	SLC10A1: liver pancreas SLC10A2: ileum, kidney, biliary tract other SLC transporters (A3, A4, A5) have not been biochemically characterized for substrates & cotransporters. SLC10 review in PMID: 12851823 Only SLC10A1 is known to also have estrone-3-sulfate transport capabilites. Only unidirectional (uptake) activity has been shown. See CHOLATEt/GCHOLAt/TCHOLAt for bile acid excretion acitivity. Sodium/bile acid cotransporters are integral membrane glycoproteins that participate in the enterohepatic circulation of bile acids. Two homologous transporters are involved in the reabsorption of bile acids, one absorbing from the intestinal lumen, the bile duct, and the kidney with an apical localization (SLC10A2; MIM 601295), and the other being found in the basolateral membranes of hepatocytes (SLC10A1). NJ

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CHOLATEt2	3	Hagenbuch B, Dawson P.	The sodium bile salt cotransport family SLC10.	Pflugers Arch	2004	12851823	SLC10A1: liver pancreas SLC10A2: ileum, kidney, biliary tract other SLC transporters (A3, A4, A5) have not been biochemically characterized for substrates & cotransporters. SLC10 review in PMID: 12851823 Only SLC10A1 is known to also have estrone-3-sulfate transport capabilites. Only unidirectional (uptake) activity has been shown. See CHOLATEt/GCHOLAt/TCHOLAt for bile acid excretion acitivity. Sodium/bile acid cotransporters are integral membrane glycoproteins that participate in the enterohepatic circulation of bile acids. Two homologous transporters are involved in the reabsorption of bile acids, one absorbing from the intestinal lumen, the bile duct, and the kidney with an apical localization (SLC10A2; MIM 601295), and the other being found in the basolateral membranes of hepatocytes (SLC10A1). NJ
CHOLATEt3	3	Kiuchi Y, Suzuki H, Hirohashi T, Tyson CA, Sugiyama Y.	cDNA cloning and inducible expression of human multidrug resistance associated protein 3 (MRP3).	FEBS Lett	1998	9738950	This protein is a member of the MDR/TAP subfamily. Members of the MDR/TAP subfamily are involved in multidrug resistance. The protein encoded by this gene is the major canalicular bile salt export pump in man. Mutations in this gene cause a form of progressive familial intrahepatic cholestases which are a group of inherited disorders with severe cholestatic liver disease from early infancy. NJ
CHOLATEt3	3	Strautnieks SS, Bull LN, Knisely AS, Kocoshis SA, Dahl N, Arnell H, Sokal E, Dahan K, Childs S, Ling V, Tanner MS, Kagalwalla AF, Nemeth A, Pawlowska J, Baker A, Mieli-Vergani G, Freimer NB, Gardiner RM, Thompson RJ.	A gene encoding a liver-specific ABC transporter is mutated in progressive familial intrahepatic cholestasis.	Nat Genet	1998	9806540	This protein is a member of the MDR/TAP subfamily. Members of the MDR/TAP subfamily are involved in multidrug resistance. The protein encoded by this gene is the major canalicular bile salt export pump in man. Mutations in this gene cause a form of progressive familial intrahepatic cholestases which are a group of inherited disorders with severe cholestatic liver disease from early infancy. NJ
CHOLATEt3	3	Uchiumi T, Hinoshita E, Haga S, Nakamura T, Tanaka T, Toh S, Furukawa M, Kawabe T, Wada M, Kagotani K, Okumura K, Kohno K, Akiyama S, Kuwano M.	Isolation of a novel human canalicular multispecific organic anion transporter, cMOAT2/MRP3, and its expression in cisplatin-resistant cancer cells with decreased ATP-dependent drug transport.	Biochem Biophys Res Commun	1998	9813153	This protein is a member of the MDR/TAP subfamily. Members of the MDR/TAP subfamily are involved in multidrug resistance. The protein encoded by this gene is the major canalicular bile salt export pump in man. Mutations in this gene cause a form of progressive familial intrahepatic cholestases which are a group of inherited disorders with severe cholestatic liver disease from early infancy. NJ
CHOLK	3	Activity and tissue distribution of splice variants of alpha6-fucosyltransferase in human embryogenesis.	Martinez-Duncker I, Michalski JC, Bauvy C, Candelier JJ, Mennesson B, Codogno P, Oriol R, Mollicone R.	Glycobiology	2004	14514715	cytosolic - uniport CK has chol and ethal specificity according to RefSeq NJ
CHOLt4	3	Apparsundaram S, Ferguson SM, George AL Jr, Blakely RD	Molecular cloning of a human, hemicholinium-3-sensitive choline transporter	Biochem Biophys Res Commun	2000	11027560	- identified by sequence homology [Apparsundaram 2000] - cloned [Apparsundaram 2000], [Okuda 2000] - expressed in brain regions rich in cholinergic neurons [Apparsundaram 2000], [Okuda 2000] -Na(+)- and Cl(-)-dependent, high-affinity choline uptake [Okuda 2000]; Na+ is cotransported [Okuda 2003]
CHOLt4	3	Okuda T, Haga T.	Functional characterization of the human high-affinity choline transporter	FEBS Lett	2000	11068039	- identified by sequence homology [Apparsundaram 2000] - cloned [Apparsundaram 2000], [Okuda 2000] - expressed in brain regions rich in cholinergic neurons [Apparsundaram 2000], [Okuda 2000] -Na(+)- and Cl(-)-dependent, high-affinity choline uptake [Okuda 2000]; Na+ is cotransported [Okuda 2003]
CHOLt4	3	Okuda T, Haga T	High-affinity choline transporter	Neurochem Res	2003	12675135	- identified by sequence homology [Apparsundaram 2000] - cloned [Apparsundaram 2000], [Okuda 2000] - expressed in brain regions rich in cholinergic neurons [Apparsundaram 2000], [Okuda 2000] -Na(+)- and Cl(-)-dependent, high-affinity choline uptake [Okuda 2000]; Na+ is cotransported [Okuda 2003]

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CHSTEROLSULT	3	Her C, Wood TC, Eichler EE, Mohrenweiser HW, Ramagli LS, Siciliano MJ, Weinshilboum RM.	Human hydroxysteroid sulfotransferase SULT2B1: two enzymes encoded by a single chromosome 19 gene.	Genomics	1998	9799594	cytosolic by swiss-prot see PMID: 9799594, 12145317 Catalyzes the sulfate conjugation of many hormones, neurotransmitters, drugs and xenobiotic compounds. Sulfonation increases the water solubility of most compounds, and therefore their renal excretion, but it can also result in bioactivation to form active metabolites. Sulfates hydroxysteroids like DHEA. Isoform 1 preferentially sulfonates cholesterol, and isoform 2 avidly sulfonates pregnenolone but not cholesterol. NJ
CHSTEROLSULT	3	Fuda H, Lee YC, Shimizu C, Javitt NB, Strott CA.	Mutational analysis of human hydroxysteroid sulfotransferase SULT2B1 isoforms reveals that exon 1B of the SULT2B1 gene produces cholesterol sulfotransferase, whereas exon 1A yields pregnenolone sulfotransferase.	J Biol Chem	2002	12145317	cytosolic by swiss-prot see PMID: 9799594, 12145317 Catalyzes the sulfate conjugation of many hormones, neurotransmitters, drugs and xenobiotic compounds. Sulfonation increases the water solubility of most compounds, and therefore their renal excretion, but it can also result in bioactivation to form active metabolites. Sulfates hydroxysteroids like DHEA. Isoform 1 preferentially sulfonates cholesterol, and isoform 2 avidly sulfonates pregnenolone but not cholesterol. NJ
CHSTEROLt	3	Orso E, Broccardo C, Kaminski WE, Bottcher A, Liebisch G, Drobnik W, Gotz A, Chambenoit O, Diederich W, Langmann T, Spruss T, Luciani MF, Rothe G, Lackner KJ, Chimini G, Schmitz G.	Transport of lipids from golgi to plasma membrane is defective in tangier disease patients and Abc1-deficient mice.	Nat Genet	2000	10655069	IT Gene is also responsiblefor phospholipid efflux orso has shown transport of choline phospholipid
CHSTEROLt	3	Wollmer MA, Streffer JR, Lutjohann D, Tsolaki M, Iakovidou V, Hegi T, Pasch T, Jung HH, Bergmann K, Nitsch RM, Hock C, Papassotiropoulos A.	ABCA1 modulates CSF cholesterol levels and influences the age at onset of Alzheimer's disease.	Neurobiol Aging	2003	12600718	IT Gene is also responsiblefor phospholipid efflux orso has shown transport of choline phospholipid
CHSTEROLt1	2	Zhang M, Liu P, Dwyer NK, Christenson LK, Fujimoto T, Martinez F, Comly M, Hanover JA, Blanchette-Mackie EJ, Strauss JF 3rd.	MLN64 mediates mobilization of lysosomal cholesterol to steroidogenic mitochondria.	J Biol Chem	2002	12070139	Has been shown experimentally to be associated with cholesterol transport from lysosome to mitochondria. The mechanism is also likely to be proton dependent, however the stoichiometry and biochemical details have not yet been elucidated. See PMID: 12070139 for Stard3 (aka MLN64) specific for Stard3 See PMID: 12370263 and PMID: 12770731 for reviews and discussion of STAR transporters NJ
CHSTEROLt1	2	Jefcoate C.	High-flux mitochondrial cholesterol trafficking, a specialized function of the adrenal cortex.	J Clin Invest	2002	12370263	Has been shown experimentally to be associated with cholesterol transport from lysosome to mitochondria. The mechanism is also likely to be proton dependent, however the stoichiometry and biochemical details have not yet been elucidated. See PMID: 12070139 for Stard3 (aka MLN64) specific for Stard3 See PMID: 12370263 and PMID: 12770731 for reviews and discussion of STAR transporters NJ
CHSTEROLt1	2	Strauss JF 3rd, Kishida T, Christenson LK, Fujimoto T, Hiroi H.	START domain proteins and the intracellular trafficking of cholesterol in steroidogenic cells.	Mol Cell Endocrinol	2003	12770731	Has been shown experimentally to be associated with cholesterol transport from lysosome to mitochondria. The mechanism is also likely to be proton dependent, however the stoichiometry and biochemical details have not yet been elucidated. See PMID: 12070139 for Stard3 (aka MLN64) specific for Stard3 See PMID: 12370263 and PMID: 12770731 for reviews and discussion of STAR transporters NJ
CHTNASEe	3	Boot RG, Blommaart EF, Swart E, Ghauharali-van der Vlugt K, Bijl N, Moe C, Place A, Aerts JM	Identification of a novel acidic mammalian chitinase distinct from chitotriosidase	J Biol Chem	2001	11085997	- physiological function is unknown, but enzyme was shown to have chitinase activity in vitro [Boot, J Biol Chem 2001] - abundant in gastrointestinal tract and found to lesser extent in lung [Boot, J Biol Chem 2001], [UniProt] - this mRNA has a 108 bp signal sequence that suggests it is secreted (probable) [Uni-Prot]
CITL	0	Morikawa J, Nishimura Y, Uchida A, Tanaka T	Molecular cloning of novel mouse and human putative citrate lyase beta-subunit	Biochem Biophys Res Commun	2001	11741334	- putative function based on sequence similarity to murine gene [Morikawa et al, Biochem Biophys Res Commun2001] - cytosolic [Devlin, Textbook of biochemistry, 5th ed]

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
CITMCOAHm	2	ADLER J, WANG SF, LARDY HA	The metabolism of itaconic acid by liver mitochondria.	J Biol Chem	1957	13502348	- reaction occurs in rat liver mitochondria [Wang, J Biol Chem 1961] - Itaconate, citraconate, and mesaconate are probably metabolized in the dog, since they could be recovered in the urine to the extent of only 24, 28, and 64 per cent, respectively (see refs in [Adler 1957]) - In guinea pig liver, itaconate is oxidized as rapidly as most members of the tricarboxylic acid cycle, methyl succinate was oxidized 1/6 as fast and mesaconate 1/8 as fast as itaconate [Adler 1957] - the major pathway of itaconate metabolism is its oxidation to pyruvate [Adler 1957]
CITt4_2	3	Pajor AM, Sun N	Functional differences between rabbit and human Na(+)-dicarboxylate cotransporters, NaDC-1 and hNaDC-1.	Am J Physiol	1996	8946005	9058: - cloned [Pajor 1996] - 78% identical to the rabbit and 42% identical to the rat orthologs [Pajor 1996] - low-affinity cotransport of Na+ w/ succinate and citrate [Pajor 1996] - kidney and intestine brush border membranes [Pajor 1996] - Hill coefficient of 2.1 [Pajor, Sun 1996]
CITt4_2	3	Pajor AM	Molecular cloning and functional expression of a sodium-dicarboxylate cotransporter from human kidney	Am J Physiol	1996	8967342	9058: - cloned [Pajor 1996] - 78% identical to the rabbit and 42% identical to the rat orthologs [Pajor 1996] - low-affinity cotransport of Na+ w/ succinate and citrate [Pajor 1996] - kidney and intestine brush border membranes [Pajor 1996] - Hill coefficient of 2.1 [Pajor, Sun 1996]
CITt4_4	3	Inoue K, Zhuang L, Maddox DM, Smith SB, Ganapathy V	Structure, function, and expression pattern of a novel sodium-coupled citrate transporter (NaCT) cloned from mammalian brain	J Biol Chem	2002	12177002	284111: - cloned [Inoue Biochem Biophys Res Commun 2002] - high in liver; moderate in brain, testis [Inoue 2002] - low affinty, cotransports Na+ w/ citrate, no succinate or malate [Inoue Biochem Biophys Res Commun 2002] - 77% sequence identity with rat ortholog [Inoue Biochem Biophys Res Commun 2002] - Na+:citrate stoichiometry couldn't be determined for human NaCT [Inoue Biochem Biophys Res Commun 2002]; assume is the same as rat ortholog (4:1) [Inohue J Biol Chem 2002]
CITt4_4	3	Inoue K, Zhuang L, Ganapathy V	Human Na+ -coupled citrate transporter: primary structure, genomic organization, and transport function	Biochem Biophys Res Commun	2002	12445824	284111: - cloned [Inoue Biochem Biophys Res Commun 2002] - high in liver; moderate in brain, testis [Inoue 2002] - low affinty, cotransports Na+ w/ citrate, no succinate or malate [Inoue Biochem Biophys Res Commun 2002] - 77% sequence identity with rat ortholog [Inoue Biochem Biophys Res Commun 2002] - Na+:citrate stoichiometry couldn't be determined for human NaCT [Inoue Biochem Biophys Res Commun 2002]; assume is the same as rat ortholog (4:1) [Inohue J Biol Chem 2002]
CK	3	Klein SC, Haas RC, Perryman MB, Billadello JJ, Strauss AW.	Regulatory element analysis and structural characterization of the human sarcomeric mitochondrial creatine kinase gene.	J Biol Chem	1991	1917943	- Additional information added by RS/TV: -proteome Mitochondrial creatine kinase comes in two isozymes: Ckmt1.1-m and Ckmt2.1-m according to Entrez gene database. (1) Catalytic Activity: Creatine kinases catalyze the reversible transfer of high energy phosphate from ATP to creatine generating ADP and phosphocreatine. (2) Tissue specificity: Ckmt2.1-m is expressed in only stirated muscle, including heart. Ckmt1.1-m on the other hand was found to be expressed in adult skeletal muscle, ventricle, and to a lesser extent in the small intestine and placenta. All this according to (1) Haas RC, Korenfeld C, Zhang ZF, Perryman B, Roman D, Strauss AW. J Biol Chem. 1989 Feb 15;264(5):2890-7. Erratum in: J Biol Chem 1989 Sep 25;264(27):16332. (2) Klein SC, Haas RC, Perryman MB, Billadello JJ, Strauss AW. J Biol Chem. 1991 Sep 25;266(27):18058-65. Runs forward in mito --SAB

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
CK	3	Haas RC, Korenfeld C, Zhang ZF, Perryman B, Roman D, Strauss AW.	Isolation and characterization of the gene and cDNA encoding human mitochondrial creatine kinase.	J Biol Chem	1989	2914937	- Additional information added by RS/TV: -proteome Mitochondrial creatine kinase comes in two isozymes: Ckmt1.1 m and Ckmt2.1-m according to Entrez gene database. (1) Catalytic Activity: Creatine kinases catalyze the reversible transfer of high energy phosphate from ATP to creatine generating ADP and phosphocreatine. (2) Tissue specificity: Ckmt2.1-m is expressed in only stirated muscle, including heart. Ckmt1.1-m on the other hand was found to be expressed in adult skeletal muscle, ventricle, and to a lesser extent in the small intestine and placenta. All this according to (1) Haas RC, Korenfeld C, Zhang ZF, Perryman B, Roman D, Strauss AW. J Biol Chem. 1989 Feb 15;264(5):2890-7. Erratum in: J Biol Chem 1989 Sep 25;264(27):16332. (2) Klein SC, Haas RC, Perryman MB, Billadello JJ, Strauss AW. J Biol Chem. 1991 Sep 25;266(27):18058-65. Runs forward in mito --SAB
CKc	3	Kaye FJ, McBride OW, Battey JF, Gazdar AF, Sausville EA	Human creatine kinase-B complementary DNA. Nucleotide sequence, gene expression in lung cancer, and chromosomal assignment to two distinct loci	J Clin Invest	1987	2883200	gene and reaction are well-characterized runs backward in cytosol--SAB
CKc	3	Villarreal-Levy G, Ma TS, Kerner SA, Roberts R, Perryman MB	Human creatine kinase: isolation and sequence analysis of cDNA clones for the B subunit, development of subunit specific probes and determination of gene copy number	Biochem Biophys Res Commun	1987	3034271	gene and reaction are well-characterized runs backward in cytosol--SAB
CMPACNAtg	3	Ishida N, Miura N, Yoshioka S, Kawakita M	Molecular cloning and characterization of a novel isoform of the human UDP-galactose transporter, and of related complementary DNAs belonging to the nucleotide-sugar transporter gene family	J Biochem (Tokyo)	1996	9010752	- cloned [Ishida 1996] - Golgi membrane [Ishida 1998] - corrects CMP-Sia knockout phenotype [Ishida 1998] - ubiquitous [Ishida 2004]
CMPACNAtg	3	Ishida N, Ito M, Yoshioka S, Sun-Wada GH, Kawakita M	Functional expression of human golgi CMP-sialic acid transporter in the Golgi complex of a transporter deficient Chinese hamster ovary cell mutant	J Biochem (Tokyo)	1998	9644260	- cloned [Ishida 1996] - Golgi membrane [Ishida 1998] - corrects CMP-Sia knockout phenotype [Ishida 1998] - ubiquitous [Ishida 2004]
CMPACNAtg	3	Ishida N, Kawakita M	Molecular physiology and pathology of the nucleotide sugar transporter family (SLC35)	Pflugers Arch	2004	12759756	- cloned [Ishida 1996] - Golgi membrane [Ishida 1998] - corrects CMP-Sia knockout phenotype [Ishida 1998] - ubiquitous [Ishida 2004]
CMPSAS	2	Munster AK, Eckhardt M, Potvin B, Muhlenhoff M, Stanley P, Gerardy-Schahn R	Mammalian cytidine 5'-monophosphate N-acetylneuraminic acid synthetase: a nuclear protein with evolutionarily conserved structural motifs	Proc Natl Acad Sci U S A	1998	9689047	- murine protein was shown to be predominantly (90%) localized to the nucleus; also localized to cytosol [Munster, PNAS 1998] - reaction shown as irreversible in Varki p. 74, Orten p. 245, Devlin p. 672
CO2tm	3	Balboni E, Lehninger AL.	Entry and exit pathways of CO2 in rat liver mitochondria respiring in a bicarbonate buffer system.	J Biol Chem	1968	3081508	- Added by RS/TV - This article states the following, "this conclusion [of the experiment] is in accord with the generally accepted view that CO2 readily traverses biological membranes, including those of the mitochondrion probably by unmediated physical diffusion". (Balboni E, Lehninger AL. J Biol Chem. 1986 Mar 15;261(8):3563-70.)
COAtl	2	Seetharam B, Alpers DH.	Absorption and transport of cobalamin (vitamin B12).	Annu Rev Nutr	1982	6313022	IT apparently, the lysosomal membrane is permeable for molecules of mol wt 400 or less.(Seetharam, p. 359).
COKECBESr	3	Pindel EV, Kedishvili NY, Abraham TL, Brzezinski MR, Zhang J, Dean RA, Bosron WF	Purification and cloning of a broad substrate specificity human liver carboxylesterase that catalyzes the hydrolysis of cocaine and heroin	J Biol Chem	1997	9169443	CES1 may catalyze a similar, but slightly different, reaction that is not in KEGG apparantly reaction may also proceed nonenzymatically
CORE2GTg	0	Yeh JC, Ong E, Fukuda M	Molecular cloning and expression of a novel beta-1, 6 N-acetylglucosaminyltransferase that forms core 2, core 4, and I branches	J Biol Chem	1999		GCNT1 is a member of the beta-1,6-N-acetylglucosaminyltransferase gene family. It is essential to the formation of Gal beta 1-3(GlcNAc beta 1-6)GalNAc structures and the core 2 O-glycan branch. The gene coding this enzyme was originally mapped to 9q21, but was later localized to 9q13 by another group. [RefSeq] C2GNT3 was identified by BLAST analysis; high levels in the thymus [Schwientek et al, J Biol Chem 2000] Gcnt1p is also referred to as C2GnT-L [Yeh et al, J Biol Chem 1999] Gcnt1p ubiquitously expressed [Yeh et al, J Biol Chem 1999] Gcnt3p expressed in colon, sm intestine, stomach, thyroid, testis, prostate, kidney, pancreas [Yeh et al, J Biol Chem 1999]

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
CORE2GTg	0	Schwientek T, Yeh JC, Levery SB, Keck B, Merkx G, van Kessel AG, Fukuda M, Clausen H	Control of O-glycan branch formation. Molecular cloning and characterization of a novel thymus-associated core 2 beta1, 6-n-acetylglucosaminyltransferase	J Biol Chem	2000	10753916	GCNT1 is a member of the beta-1,6-N-acetylglucosaminyltransferase gene family. It is essential to the formation of Gal beta 1-3(GlcNAc beta 1-6)GalNAc structures and the core 2 O-glycan branch. The gene coding this enzyme was originally mapped to 9q21, but was later localized to 9q13 by another group. [RefSeq] C2GNT3 was identified by BLAST analysis; high levels in the thymus [Schwientek et al, J Biol Chem 2000] Gcnt1p is also referred to as C2GnT-L [Yeh et al, J Biol Chem 1999] Gcnt1p ubiquitously expressed [Yeh et al, J Biol Chem 1999] Gcnt3p expressed in colon, sm intestine, stomach, thyroid, testis, prostate, kidney, pancreas [Yeh et al, J Biol Chem 1999]
CORE3GTg	0	Iwai T, Inaba N, Naundorf A, Zhang Y, Gotoh M, Iwasaki H, Kudo T, Togayachi A, Ishizuka Y, Nakanishi H, Narimatsu H	Molecular cloning and characterization of a novel UDP-GlcNAc:GalNAc-peptide beta1,3-N-acetylglucosaminyltransferase (beta 3Gn-T6), an enzyme synthesizing the core 3 structure of O-glycans	J Biol Chem	2002	11821425	transcript is expressed in stomach, colon, sm intestine, sk muscle, testis [Iwai et al, J Biol Chem 2002]
CPPPGO	2	Kohno H, Furukawa T, Yoshinaga T, Tokunaga R, Taketani S.	Coproporphyrinogen oxidase. Purification, molecular cloning, and induction of mRNA during erythroid differentiation.	J Biol Chem	1995	8407975	- Added by RS/TV Proteome - Coproporphyrinogen III oxidase is a soluble mitochondrial protein that is localized in the intermembrance space within mammalian cells. It catalyzes the sixth step in heme biosynthesis, the conversion of the two propionate groups at positions 2 and 4 of coproporphyrinogen III to two vinyl groups, thus producing protoporphyrinogen IX. - Located in liver cells, also found in the cytosol. (Kohno H, Furukawa T, Yoshinaga T, Tokunaga R, Taketani S. J Biol Chem. 1993 Oct 5;268(28):21359-63.)
CREATtmdiffir	2	Bessman SP, Carpenter CL	The creatine-creatine phosphate energy shuttle	Annu Rev Biochem	1985	3896131	Added to make creatine shuttle. Need to add Biochemical Pathways book citation.
CREATtmdiffir	2	Speer O, Neukomm LJ, Murphy RM, Zanolla E, Schlattner U, Henry H, Snow RJ, Wallimann T	Creatine transporters: a reappraisal	Mol Cell Biochem	2004	14977199	Added to make creatine shuttle. Need to add Biochemical Pathways book citation.
CREATtmdiffir	2		Biochemical pathways : an atlas of biochemistry and molecular biology		1999		Added to make creatine shuttle. Need to add Biochemical Pathways book citation.
CRMPte	2	Baumruker T, Bornancin F, Billich A.	The role of sphingosine and ceramide kinases in inflammatory responses.	Immunol Lett	2005	15585321	Unknown mechanism - may or may not be energy dependent. However these metabolites must be able to be transported intracellularly and exported outside of the cell. NJ
CRNt	3	Verhaagh S, Schweifer N, Barlow DP, Zwart R.	Cloning of the mouse and human solute carrier 22a3 (Slc22a3/SLC22A3) identifies a conserved cluster of three organic cation transporters on mouse chromosome 17 and human 6q26-q27.	Genomics	1999	9933568	specificity: skeletal muscle, kidney, prostate, lung, pancreas, heart, small intestine, adrenal gland, thyroid gland, liver - Koepsell 2004 paper - PMID: 12883891 Km and Ki listed in Koepsell 2003 (in addition to detailed info about localization and other members of organic cation transporters) PMID: 12827517 Polyspecific organic cation transporters in the liver, kidney, intestine, and other organs are critical for elimination of many endogenous small organic cations as well as a wide array of drugs and environmental toxins. The encoded protein is a plasma integral membrane protein which functions both as an organic cation transporter and as a sodium-dependent high affinity carnitine transporter. The encoded protein is involved in the active cellular uptake of carnitine. Mutations in this gene are the cause of systemic primary carnitine deficiency (CDSP), an autosomal recessive disorder manifested early in life by hypoketotic hypoglycemia and acute metabolic decompensation, and later in life by skeletal myopathy or cardiomyopathy. NJ

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CRNt	3	Koepsell H, Schmitt BM, Gorboulev V.	Organic cation transporters.	Rev Physiol Biochem Pharmacol	2003	12827517	specificity: skeletal muscle, kidney, prostate, lung, pancreas, heart, small intestine, adrenal gland, thyroid gland, liver - Koepsell 2004 paper - PMID: 12883891 Km and Ki listed in Koepsell 2003 (in addition to detailed info about localization and other members of organic cation transporters) PMID: 12827517 Polyspecific organic cation transporters in the liver, kidney, intestine, and other organs are critical for elimination of many endogenous small organic cations as well as a wide array of drugs and environmental toxins. The encoded protein is a plasma integral membrane protein which functions both as an organic cation transporter and as a sodium-dependent high affinity carnitine transporter. The encoded protein is involved in the active cellular uptake of carnitine. Mutations in this gene are the cause of systemic primary carnitine deficiency (CDSP), an autosomal recessive disorder manifested early in life by hypoketotic hypoglycemia and acute metabolic decompensation, and later in life by skeletal myopathy or cardiomyopathy. NJ
CRNt	3	Koepsell H, Endou H	The SLC22 drug transporter family	Pflugers Arch	2004	12883891	specificity: skeletal muscle, kidney, prostate, lung, pancreas, heart, small intestine, adrenal gland, thyroid gland, liver - Koepsell 2004 paper - PMID: 12883891 Km and Ki listed in Koepsell 2003 (in addition to detailed info about localization and other members of organic cation transporters) PMID: 12827517 Polyspecific organic cation transporters in the liver, kidney, intestine, and other organs are critical for elimination of many endogenous small organic cations as well as a wide array of drugs and environmental toxins. The encoded protein is a plasma integral membrane protein which functions both as an organic cation transporter and as a sodium-dependent high affinity carnitine transporter. The encoded protein is involved in the active cellular uptake of carnitine. Mutations in this gene are the cause of systemic primary carnitine deficiency (CDSP), an autosomal recessive disorder manifested early in life by hypoketotic hypoglycemia and acute metabolic decompensation, and later in life by skeletal myopathy or cardiomyopathy. NJ
CRNtx	2	Mukherji M, Schofield CJ, Wierzbicki AS, Jansen GA, Wanders RJ, Lloyd MD.	The chemical biology of branched-chain lipid metabolism.	Prog Lipid Res	2003	12814641	Transport of branched chain derivatives from peroxisome to mitochondria. See Mukherji and Wanders for more details. NJ
CSNAT2x	3	Wanders RJ.	Peroxisomes, lipid metabolism, and peroxisomal disorders.	Mol Genet Metab	2004	15464416	For transport of branched fatty acids (initial alpha and beta ox in peroxisome -> partial continuation in mit). See Wanders PMID: 15464416 for further details. -- REVISED GPR, dmnon has specific crn transferase gene and protein. see PMID: 10486279 and PMID: 9469587. Carnitine acetyltransferase (CRAT) is a key enzyme in the metabolic pathway in mitochondria, peroxisomes and endoplasmic reticulum. CRAT catalyzes the reversible transfer of acyl groups from an acyl-CoA thioester to carnitine and regulates the ratio of acylCoA/CoA in the subcellular compartments. Different subcellular localizations of the CRAT mRNAs are thought to result from alternative splicing of the CRAT gene suggested by the divergent sequences in the 5' region of peroxisomal and mitochondrial CRAT cDNAs and the location of an intron where the sequences diverge. Cloning in PMID: 7829107 NJ
CSNATm	3	Lysiak W, Toth PP, Suelter CH, Bieber LL.	Quantitation of the efflux of acylcarnitines from rat heart, brain, and liver mitochondria.	J Biol Chem	1986	3759988	- Additional information added by RS/TV: - CRAT is located in the mitochondria, endoplasmic reticulum, and Kinetic Information: Lysiak W, Toth PP, Suelter CH, Bieber LL. J Biol Chem. 1986 Oct 15;261(29):13698-703 Quantitation of the efflux of acylcarnitines from rat heart, brain, and liver mitochondria Poirier M, Vincent G, Reszko AE, Bouchard B, Kelleher JK, Brunengraber H, Des Rosiers C. Am J Physiol Heart Circ Physiol. 2002 Oct;283(4):H1379-86; Probing the link between citrate and malonyl-CoA in perfused rat hearts
CSNATr	3	Corti O, Finocchiaro G, Rossi E, Zuffardi O, DiDonato S.	Molecular cloning of cDNAs encoding human carnitine acetyltransferase and mapping of the corresponding gene to chromosome 9q34.1.	Genomics	1994	7829107	for reversible cytosolic interconversion between acrn and accoa (for part of peroxisomal FA degradation). see PMID: 11257506 NJ

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CSNATr	3	Ramsay, Gandour, van der Leij	Molecular enzymology of carnitine transfer and transport	Biochim Biophys Acta	2001	11257506	for reversible cytosolic interconversion between acrn and accoa (for part of peroxisomal FA degradation). see PMID: 11257506 NJ
CTPS1	2	Takahashi E, Yamauchi M, Tsuji H, Hitomi A, Meuth M, Hori T.	Chromosome mapping of the human cytidine-5'-triphosphate synthetase (CTPS) gene to band 1p34.1--p34.3 by fluorescence in situ hybridization.	Hum Genet	1991	1959918	IT
CTPS2	3	van Kuilenburg AB, Meinsma R, Vreken P, Waterham HR, van Gennip AH.	Identification of a cDNA encoding an isoform of human CTP synthetase.	Biochim Biophys Acta	2000	10899599	Entrez genes said that reactions is with glutamine as well as orten IT
CYANSTm	3	Horowitz PM, Butler M, McClure GD Jr.	Reducing sugars can induce the oxidative inactivation of rhodanese.		1992	1429701	Entrez Gene - The product of this gene is a mitochondrial matrix enzyme that is encoded by the nucleus. It may play roles in cyanide detoxification, the formation of iron-sulfur proteins, and the modification of sulfur-containing enzymes. The gene product contains two highly conservative domains (rhodanese homology domains), suggesting these domains have a common evolutionary origin. MM
CYANSTm	3	Aita N, Ishii K, Akamatsu Y, Ogasawara Y, Tanabe S.	Cloning and expression of human liver rhodanese cDNA.		1997	9070219	Entrez Gene - The product of this gene is a mitochondrial matrix enzyme that is encoded by the nucleus. It may play roles in cyanide detoxification, the formation of iron-sulfur proteins, and the modification of sulfur-containing enzymes. The gene product contains two highly conservative domains (rhodanese homology domains), suggesting these domains have a common evolutionary origin. MM
CYSGLTH	3	Oshima RG, Rhead WJ, Thoene JG, Schneider JA.	Cystine metabolism in human fibroblasts. Comparison of normal, cystinotic, and gamma-glutamylcysteine synethetase-deficient cells.		1976	932033	- enzyme has been identified, but not gene - reaction known to physiologically exist in order for cystine to be converted to cysteine (see references) MM
CYSO	3	Millard J, Parsons RB, Waring RH, Williams AC, Ramsden DB	Expression of cysteine dioxygenase (EC 1.13.11.20) and sulfite oxidase in the human lung: a potential role for sulfate production in the protection from airborne xenobiotica	Mol Pathol	2003	14514920	Reaction and gene are characterized.
CYSTA	2	Akagi R.	Purification and characterization of cysteine aminotransferase from rat liver cytosol.		1982	7113743	- reaction required in cysteine metabolism according to Stipanuk (2004) - aspartate aminotransferase gene associated based on KEGG and rat evidence indicating its activity is similar to cysteine aminotransferase MM
CYSTAm	2	Ubuka T, Umemura S, Yuasa S, Kinuta M, Watanabe K.	Purification and characterization of mitochondrial cysteine aminotransferase from rat liver.		1978	754189	- reaction required in cysteine metabolism according to Stipanuk (2004) - aspartate aminotransferase gene associated based on KEGG and rat evidence indicating its activity is similar to cysteine aminotransferase
CYSTGL	3	Levonen AL, Lapatto R, Saksela M, Raivio KO.	Human cystathionine gamma-lyase: developmental and in vitro expression of two isoforms.		2000	10727430	0
CYSTGL	3	Stipanuk MH	Sulfur amino acid metabolism: pathways for production and removal of homocysteine and cysteine	Annu Rev Nutr	2004	15189131	0
CYSTS	3	Kraus J, Packman S, Fowler B, Rosenberg LE.	Purification and properties of cystathionine beta-synthase from human liver. Evidence for identical subunits.		1978	681363	Entrez Gene - The protein encoded by this gene is involved in the transsulfuration pathway. The first step of this pathway, from homocysteine to cystathionine, is catalyzed by this protein. CBS deficiency can cause homocystinuria which affects many organs and tissues, including the eyes and the skeletal, vascular and central nervous systems. -in the adult strongly expressed in liver and pancreas, some expression in heart and brain, weak expression in lung and kidney. in the fetus, expressed in brain, liver and kidney. -MM
CYSTS	3	Kraus JP, Oliveriusova J, Sokolova J, Kraus E, Vlcek C, de Franchis R	The human cystathionine beta-synthase (CBS) gene: complete sequence, alternative splicing, and polymorphisms.		1998	9790750	Entrez Gene - The protein encoded by this gene is involved in the transsulfuration pathway. The first step of this pathway, from homocysteine to cystathionine, is catalyzed by this protein. CBS deficiency can cause homocystinuria which affects many organs and tissues, including the eyes and the skeletal, vascular and central nervous systems. -in the adult strongly expressed in liver and pancreas, some expression in heart and brain, weak expression in lung and kidney. in the fetus, expressed in brain, liver and kidney. -MM

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CYTD	2	Laliberte J, Momparler RL.	Human cytidine deaminase: purification of enzyme, cloning, and expression of its complementary DNA.	Cancer Res	1994	7923172	IT mRNA found n myoblase and leukemia cell line, bone marrow cells, monocytes, macrophages I did find any report of measurement of enzyme activity AICDA(57379):Activation-induced cysodine deaminase (AID) is a cytosine deaminase that is critical to immunoglobulin hypermutation, class switch recombination, and gene conversion.In the context of hypermutating B cells, AID deaminates cytosine in the DNA of immunoglobulin genes, leading to the accumulation of mutations in the variable regions. --> most enzyme is in cytoplasm but can also be found in nucleus.
CYTD	2	Saccone S, Besati C, Andreozzi L, Della Valle G, Garattini E, Terao M.	Assignment of the human cytidine deaminase (CDA) gene to chromosome 1 band p35-p36.2.	Genomics	1994	8001985	IT mRNA found n myoblase and leukemia cell line, bone marrow cells, monocytes, macrophages I did find any report of measurement of enzyme activity AICDA(57379):Activation-induced cysodine deaminase (AID) is a cytosine deaminase that is critical to immunoglobulin hypermutation, class switch recombination, and gene conversion.In the context of hypermutating B cells, AID deaminates cytosine in the DNA of immunoglobulin genes, leading to the accumulation of mutations in the variable regions. --> most enzyme is in cytoplasm but can also be found in nucleus.
CYTD	2	Kuhn K, Bertling WM, Emmrich F.	Cloning of a functional cDNA for human cytidine deaminase (CDD) and its use as a marker of monocyte/macrophage differentiation.	Biochem Biophys Res Commun	1993	8422236	IT mRNA found n myoblase and leukemia cell line, bone marrow cells, monocytes, macrophages I did find any report of measurement of enzyme activity AICDA(57379):Activation-induced cysodine deaminase (AID) is a cytosine deaminase that is critical to immunoglobulin hypermutation, class switch recombination, and gene conversion.In the context of hypermutating B cells, AID deaminates cytosine in the DNA of immunoglobulin genes, leading to the accumulation of mutations in the variable regions. --> most enzyme is in cytoplasm but can also be found in nucleus.
CYTD	2	Ge Y, Jensen TL, Stout ML, Flatley RM, Grohar PJ, Ravindranath Y, Matherly LH, Taub JW.	The role of cytidine deaminase and GATA1 mutations in the increased cytosine arabinoside sensitivity of Down syndrome myeloblasts and leukemia cell lines.	Cancer Res	2004	14744791	IT mRNA found n myoblase and leukemia cell line, bone marrow cells, monocytes, macrophages I did find any report of measurement of enzyme activity AICDA(57379):Activation-induced cysodine deaminase (AID) is a cytosine deaminase that is critical to immunoglobulin hypermutation, class switch recombination, and gene conversion.In the context of hypermutating B cells, AID deaminates cytosine in the DNA of immunoglobulin genes, leading to the accumulation of mutations in the variable regions. --> most enzyme is in cytoplasm but can also be found in nucleus.
CYTD	2	Brar SS, Watson M, Diaz M.	Activation-induced cytosine deaminase (AID) is actively exported out of the nucleus but retained by the induction of DNA breaks.	J Biol Chem	2004	15087440	IT mRNA found n myoblase and leukemia cell line, bone marrow cells, monocytes, macrophages I did find any report of measurement of enzyme activity AICDA(57379):Activation-induced cysodine deaminase (AID) is a cytosine deaminase that is critical to immunoglobulin hypermutation, class switch recombination, and gene conversion.In the context of hypermutating B cells, AID deaminates cytosine in the DNA of immunoglobulin genes, leading to the accumulation of mutations in the variable regions. --> most enzyme is in cytoplasm but can also be found in nucleus.
CYTDt4	3	Gray JH, Owen RP, Giacomini KM.	The concentrative nucleoside transporter family, SLC28.		2004	12856181	IT Tissue distribution: SLC28A1 (CNT1): Liver, kidney, small intestine, (epitheloa apical membrane) SLC28A2 (CNT2): kidney (apical membrane), liver, heart, brain, plcaenta, pancreas, skeletal muscle, colon, rectum, small intestine SLC28A3 (CNT3): pancreas, trachea, bone marrow and mammary gland, intestine, lung, placenta, prostrate, testis, liver
CYTK1	3	Van Rompay AR, Johansson M, Karlsson A.	Phosphorylation of deoxycytidine analog monophosphates by UMP-CMP kinase: molecular characterization of the human enzyme.	Mol Pharmacol	1999	10462544	IT
CYTK1	3	Liou JY, Dutschman GE, Lam W, Jiang Z, Cheng YC.	Characterization of human UMP/CMP kinase and its phosphorylation of D- and L-form deoxycytidine analogue monophosphates.	Cancer Res	2002	11912132	IT

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D3AIBTm	3	Kakimoto Y, Taniguchi K, Sano I.	D-beta-aminoisobutyrate:pyruvate aminotransferase in mammalian liver and excretion of beta-aminoisobutyrate by man.		1969	5773299	OMIM: Human urine contains R-BAIB almost exclusively (and it is this form that is excreted in excess in the hyper-BAIB trait), whereas the plasma pool is about 80% S-BAIB. As reviewed by Scriver and Perry (1989), the 'defect' is an impairment of R-BAIB catabolism due to deficient activity of a pyruvate-requiring transaminase, D-beta-aminoisobutyrate:pyruvate aminotransferase MM
DADNK	3	Hurley MC, Palella TD, Fox IH.	Human placental deoxyadenosine and deoxyguanosine phosphorylating activity.	J Biol Chem	1983	6317685	reaction was included during gap filling. i could not identify a gene for this reaction, however, its activity has been observed/studied in/from human placenta cells IT
DAGK_hs	3	Tang W, Bunting M, Zimmerman GA, McIntyre TM, Prescott SM	Molecular cloning of a novel human diacylglycerol kinase highly selective for arachidonate-containing substrates	Journal of Biological Chemistry	1996		cytoplasmic and nuclear - uniport many different genes, some have different isoforms, some are ubiquitous and others are tissue specific - dependent on substrate (different gene products have different specificities different fatty acid chains. NJ
DARGOp	3	D'Aniello A, Vetere A, Petrucelli L	Further study on the specificity of D-amino acid oxidase and D-aspartate oxidase and time course for complete oxidation of D-amino acids	Comp Biochem Physiol B	1993	8103425	Slow rate according to second citation.
DARGOp	3	Vanoni MA, Cosma A, Mazzeo D, Mattevi A, Todone F, Curti B	Limited proteolysis and X-ray crystallography reveal the origin of substrate specificity and of the rate-limiting product release during oxidation of D-amino acids catalyzed by mammalian D-amino acid oxidase	Biochemistry	1997	9153402	Slow rate according to second citation.
DASCBR	3	Lundberg M, Johansson C, Chandra J, Enoksson M, Jacobsson G, Ljung J, Johansson M, Holmgren A.	Cloning and expression of a novel human glutaredoxin (Grx2) with mitochondrial and nuclear isoforms	J Biol Chem	2001	11297543	TV (6/1/2005) Grx1 and Grx2 appear to primarily act on cys residue of proteins, but Lundberg also found that they can reduce dehydroascobic acid. It's not clear what the enzyme uses as reducing agent.
DASPO1p	3	Amery L, Brees C, Baes M, Setoyama C, Miura R, Mannaerts GP, Van Veldhoven PP.	C-terminal tripeptide Ser-Asn-Leu (SNL) of human D-aspartate oxidase is a functional peroxisome-targeting signal.		1998	9820813	Entrez Gene - The protein encoded by this gene is a peroxisomal flavoprotein that catalyzes the oxidative deamination of D-aspartate and N-methyl D-aspartate. Flavin adenine dinucleotide or 6-hydroxyflavin adenine dinucleotide can serve as the cofactor in this reaction. Two transcript variants encoding different isoforms have been found for this gene. **did not include deamination of N-methyl D-aspartate. Could not find another reaction that either transports or synthesizes it. Found references stating that there is a receptor for this compound, but not metabolism MM
DASPO1p	3	Zaar K, Kost HP, Schad A, Volkl A, Baumgart E, Fahimi HD.	Cellular and subcellular distribution of D-aspartate oxidase in human and rat brain.		2002	12209855	Entrez Gene - The protein encoded by this gene is a peroxisomal flavoprotein that catalyzes the oxidative deamination of D-aspartate and N-methyl D-aspartate. Flavin adenine dinucleotide or 6-hydroxyflavin adenine dinucleotide can serve as the cofactor in this reaction. Two transcript variants encoding different isoforms have been found for this gene. **did not include deamination of N-methyl D-aspartate. Could not find another reaction that either transports or synthesizes it. Found references stating that there is a receptor for this compound, but not metabolism MM
DCIm	2	Partanen ST, Novikov DK, Popov AN, Mursula AM, Hiltunen JK, Wierenga RK.	The 1.3 A crystal structure of human mitochondrial Delta3-Delta2-enoyl-CoA isomerase shows a novel mode of binding for the fatty acyl group.	J Mol Biol	2004	15351645	mitochondrial matrix: Uniprot (RefSeq) Function: Partanen et al (PMID: 15351645) This gene encodes a member of the hydratase/isomerase superfamily. The protein encoded is a key mitochondrial enzyme involved in beta-oxidation of unsaturated fatty acids. It catalyzes the transformation of 3-cis and 3-trans-enoyl-CoA esters arising during the stepwise degradation of cis-, mono-, and polyunsaturated fatty acids to the 2-trans-enoyl-CoA intermediates. Alternatively spliced transcript variants have been described, but their full-length nature has not been determined. NJ
DCK1m	3	Cheng YC, Domin B, Lee LS.	Human deoxycytidine kinase. Purification and characterization of the cytoplasmic and mitochondrial isozymes derived from blast cells of acute myelocytic leukemia patients.	Biochim Biophys Acta	1977	265735	reaction was included during gap filling process. could not find gene for mitochondrial recation (1633 is only responsible for nuclear protein based on gene cards). I could only get abstract of reference - but since they used cells from leukemia patient it should be nicely human data mitochondrial version acts on deoxycytidine and deoxythymidine. only with ATP highest activity observed. IT

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DCK1n	3	Turk B, Awad R, Usova EV, Bjork I, Eriksson S.	A pre-steady-state kinetic analysis of substrate binding to human recombinant deoxycytidine kinase: a model for nucleoside kinase action.	Biochemistry	1999	10387103	seems also react with dADO but much slower --> rxns not included yet IT
DCMPDA	2	Weiner KX, Ciesla J, Jaffe AB, Ketring R, Maley F, Maley GF.	Chromosomal location and structural organization of the human deoxycytidylate deaminase gene.	J Biol Chem	1995	7642519	IT
DCMPDA	2	Weiner KX, Weiner RS, Maley F, Maley GF.	Primary structure of human deoxycytidylate deaminase and overexpression of its functional protein in Escherichia coli.	J Biol Chem	1993	7685356	IT
DCT	3	Yokoyama K, Suzuki H, Yasumoto K, Tomita Y, Shibahara S	Molecular cloning and functional analysis of a cDNA coding for human DOPAchrome tautomerase/tyrosinase-related protein-2	Biochim Biophys Acta	1994	8148378	Textbook reaction.
DDPGAm	2	MAITRA U, DEKKER EE	PURIFICATION AND PROPERTIES OF RAT LIVER 2-KETO-4-HYDROXYGLUTARATE ALDOLASE	J Biol Chem	1964	14193832	Reaction noted in citation, but no gene information could be found. - 4-hydroxy-2-ketoglutarate is cleaved by the mitochondrial enzyme 4-hydroxy-2-ketoglutarate aldolase to produce pyruvate and glyoxylate [Holmes 1998] - in rat, this enzyme is found in liver and kidney [Maitra 1964] - isolated mouse liver mitochondria produced glyoxylate from hydroxyproline [Knight 2005]
DESAT16_2	3	Wang Y, Kurdi-Haidar B, Oram JF.	LXR-mediated activation of macrophage stearoyl-CoA desaturase generates unsaturated fatty acids that destabilize ABCA1.	J Lipid Res	2004	14967823	ER localization: outer membrane. Not well characterized in literature (poor data to specifiy inner vs outer membrane). Acts on 16C and 18C see PMID: 14967823 (Wang Y, Kurdi-Haidar B, Oram JF.) Electron carrier is NAD as per texts (future articles in primary literature may provide more specifics. NJ
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DESAT16_2	3	Horrobin DF	Omega-6 Essential Fatty Acids		1990		ER localization: outer membrane. Not well characterized in literature (poor data to specifiy inner vs outer membrane). Acts on 16C and 18C see PMID: 14967823 (Wang Y, Kurdi-Haidar B, Oram JF.) Electron carrier is NAD as per texts (future articles in primary literature may provide more specifics. NJ

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DESAT16_2	3	Pereira SL, Leonard AE, Mukerji P	Recent advances in the study of fatty acid desaturases from animals and lower eukaryotes	Prostaglandins Leukotrienes and Essential Fatty Acids	2003		ER localization: outer membrane. Not well characterized in literature (poor data to specifiy inner vs outer membrane). Acts on 16C and 18C see PMID: 14967823 (Wang Y, Kurdi-Haidar B, Oram JF.) Electron carrier is NAD as per texts (future articles in primary literature may provide more specifics. NJ
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DESAT16_2	3	Pereira SL, Leonard AE, Mukerji P	Recent advances in the study of fatty acid desaturases from animals and lower eukaryotes	Prostaglandins Leukotrienes and Essential Fatty Acids	2003		ER localization: outer membrane. Not well characterized in literature (poor data to specifiy inner vs outer membrane). Acts on 16C and 18C see PMID: 14967823 (Wang Y, Kurdi-Haidar B, Oram JF.) Electron carrier is NAD as per texts (future articles in primary literature may provide more specifics. NJ
DESAT18_6	3	Cho HP, Nakamura MT, Clarke SD	Cloning, expression, and nutritional regulation of the mammalian delta-6 desaturase	The Journal of Biological Chemistry	1999		ER localization: outer membrane. Not well characterized in literature (poor data to specifiy inner vs outer membrane). NJ
DESAT20_1	3	Cho HP, Nakamura M, Clarke SD	Cloning, expression, and fatty acid regulation of the human delta-5 desaturase	The Journal of Biological Chemistry	1999		ER localization: outer membrane. Not well characterized in literature (poor data to specifiy inner vs outer membrane). NJ
DESAT22_1p	3	Sprecher H	An update on the pathways of polyunsaturated fatty acid metabolism	Curr Opn in Clinical Nutrition and Metabolic Care	1999		no gene identified specifically yet for delta 4 desaturase activity peroxisomal localization (inner side) - see mx refs: Sprecher "An update ... pathways of polyunsaturated fatty acid metabolism" (PMID: 8847474) adrn and dcsptn1 are n-6 fatty acids NJ
DESAT22_1p	3	Ferdinandusse S, Denis S, Mooijer PAW, Zhang Z, Reddy JK, Spector AA, Wanders RJA	Identification of the peroxisomal beta-oxidation enzymes involved in the biosynthesis of docosahexaenoic acid	Journal of Lipid Research	2001		no gene identified specifically yet for delta 4 desaturase activity peroxisomal localization (inner side) - see mx refs: Sprecher "An update ... pathways of polyunsaturated fatty acid metabolism" (PMID: 8847474) adrn and dcsptn1 are n-6 fatty acids NJ
DESAT22_1p	3	Sprecher H	An update on the pathways of polyunsaturated fatty acid metabolism	Curr Opn in Clinical Nutrition and Metabolic Care	1999		no gene identified specifically yet for delta 4 desaturase activity peroxisomal localization (inner side) - see mx refs: Sprecher "An update ... pathways of polyunsaturated fatty acid metabolism" (PMID: 8847474) adrn and dcsptn1 are n-6 fatty acids NJ
DESAT22_1p	3	Ferdinandusse S, Denis S, Mooijer PAW, Zhang Z, Reddy JK, Spector AA, Wanders RJA	Identification of the peroxisomal beta-oxidation enzymes involved in the biosynthesis of docosahexaenoic acid	Journal of Lipid Research	2001		no gene identified specifically yet for delta 4 desaturase activity peroxisomal localization (inner side) - see mx refs: Sprecher "An update ... pathways of polyunsaturated fatty acid metabolism" (PMID: 8847474) adrn and dcsptn1 are n-6 fatty acids NJ
DGNSKm	3	Johansson M, Karlsson A.	Cloning and expression of human deoxyguanosine kinase cDNA.	Proc Natl Acad Sci U S A	1996	8692979	IT

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DGSNtm	2	Watkins LF, Lewis RA.	The metabolism of deoxyguanosine in mitochondria. Characterization of the uptake process.	Mol Cell Biochem	1987	3696164	transport has been characterized in rat but not in human. however, has to take place since deoxynucleoside precursor have to be transported in mito for mt DNA synthesis IT
DHAAt1r	3	Wilson JX	Regulation of Vitamin C Transport	Annu Rev Nutr	2004	15705056	see [Wilson 2004], [Ball 2004] for comprehensive review of DHAA transport 6513: - major substrates are Glc, Gal, Man, GlcN [Uldry, 2004], [Uldry, 2002], DHAA [Ball 2004] - facilitated diffusion [Uldry, 2004] - primarily expressed in erythrocytes, brain, blood brain barrier, blood-tissue barrier [Uldry, 2004], [Maher, 1994] - cloned, cDNA isolated [Mueckler, 1985] - not expressed in normal hepatocytes, but induced during cancer [Flier, 1987] 6515: - major substrates are Glc (high affinity), Gal, Man, Xyl, maltose, dehydroascorbic acid [Uldry, Pflugers Arch 2004] - protein localized to brain (neurons), testis (spermatozoa) [Haber, Endocrinology 1993], [Uldry, Pflugers Arch 2004], sk muscle (slow twitch fibers) [Stuart, Metabolism 1999], platelets (alpha-granules) [Heijen, J Cell Biol 1997] - cDNA was cloned [Kayano, J Biol Chem 1988] 6517: - transports Glc, GlcN, dehydroascorbic acid [Uldry, Pflugers Arch 2004] - protein localized to adipose tissue (brown and white), sk and cardiac muscle [Uldry, Pflugers Arch 2004] - insulin binding, exercise stimulate translocation of GLUT4 ve - cDNA was cloned [Fukumoto, J Biol Chem 1989]
DHAPA	3	Thai TP, Heid H, Rackwitz HR, Hunziker A, Gorgas K, Just WW.	Ether lipid biosynthesis: isolation and molecular characterization of human dihydroxyacetonephosphate acyltransferase.	FEBS Lett	1997	9459311	mitochondrial and ER localization. ER localization on outer membrane -> effectively cytosolic. NJ
DHCR71r	3	Moebius FF, Fitzky BU, Lee, JN, Paik YK, Glossmann H	Molecular cloning and expression of the human delta-7-sterol reductase	PNAS	1998		ER - specificity: Most abundant in adrenal gland, liver, testis, and brain. NJ
DHCR72r	3	Correa-Cerro LS, Porter FD.	3beta-hydroxysterol Delta7-reductase and the Smith-Lemli-Opitz syndrome.	Mol Genet Metab	2005	15670717	ER - specificity: Most abundant in adrenal gland, liver, testis, and brain. Moebius ref (seq and cloning) see PMID: 9465114 Marijanovic ref PMID: 12829805 see also PMID: 15670717 for review NJ
DHCRD1	3	Cadena DL, Kurten RC, Gill GN.	The product of the MLD gene is a member of the membrane fatty acid desaturase family: overexpression of MLD inhibits EGF receptor biosynthesis.	Biochemistry	1997	9188692	cytoplasmic (assumed cyt side of ER) - uniprot Varki supports cytoplasmic side of ER or Golgi - chpa 9, p116 NJ
DHDPBMTm	3	Jonassen T, Clarke CF.	Isolation and functional expression of human COQ3, a gene encoding a methyltransferase required for ubiquinone biosynthesis.	J Biol Chem	2000	10777520	IT
DHEASULT	3	Otterness DM, Wieben ED, Wood TC, Watson WG, Madden BJ, McCormick DJ, Weinshilboum RM.	Human liver dehydroepiandrosterone sulfotransferase: molecular cloning and expression of cDNA.	Mol Pharmacol	1992	1588921	cytosolic - uniport and refs TISSUE SPECIFICITY: Liver, adrenal and at lower level in the kidney. Is present in human fetus in higher level in the adrenal than the liver and the kidney. Estrogens present in maternal circulation is predominantly derived from fetal dehydroepiandosterone sulfate which is hydrolyzed and metabolized to estrogens in placenta. Sulfotransferase enzymes catalyze the sulfate conjugation of many hormones, neurotransmitters, drugs, and xenobiotic compounds. These cytosolic enzymes are different in their tissue distributions and substrate specificities. The gene structure (number and length of exons) is similar among family members. This gene is primarily expressed in liver and adrenal tissues where the encoded protein sulfates steroids and bile acids. - It is also known that Sult1e1 catalyzes this reaction according to Table 2 in Glatt H, et al. Mutat Res. 2001 Oct 1;482(1-2):27-40. Review. (RS/TV) NJ

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
DHEASULT	3	Glatt H, Boeing H, Engelke CE, Ma L, Kuhlow A, Pabel U, Pomplun D, Teubner W, Meinl W.	Human cytosolic sulphotransferases: genetics, characteristics, toxicological aspects.	Mutat Res	2001	11535246	cytosolic - uniport and refs TISSUE SPECIFICITY: Liver, adrenal and at lower level in the kidney. Is present in human fetus in higher level in the adrenal than the liver and the kidney. Estrogens present in maternal circulation is predominantly derived from fetal dehydroepiandosterone sulfate which is hydrolyzed and metabolized to estrogens in placenta. Sulfotransferase enzymes catalyze the sulfate conjugation of many hormones, neurotransmitters, drugs, and xenobiotic compounds. These cytosolic enzymes are different in their tissue distributions and substrate specificities. The gene structure (number and length of exons) is similar among family members. This gene is primarily expressed in liver and adrenal tissues where the encoded protein sulfates steroids and bile acids. - It is also known that Sult1e1 catalyzes this reaction according to Table 2 in Glatt H, et al. Mutat Res. 2001 Oct 1;482(1-2):27-40. Review. (RS/TV) NJ
DHFR	2	Funanage VL, Myoda TT, Moses PA, Cowell HR.	Assignment of the human dihydrofolate reductase gene to the q11----q22 region of chromosome 5.	Mol Cell Biol	1984	6504041	IT cyto? Ball: p 359
DHFR	2	Ball, G.F.M	Vitamins: Their Role in the Human Body		2004		IT cyto? Ball: p 359
DHORD9	3	Bader B, Knecht W, Fries M, Loffler M.	Expression, purification, and characterization of histidine-tagged rat and human flavoenzyme dihydroorotate dehydrogenase.	Protein Expr Purif	1998	9693067	01-27-05 IT based on Bader et al, 1998, Prot. Expr. Purif.,, 13,414-422 (I guess it is ubiquinone but i am not sure) (needs FMN as cofactor) v(enzyme is located in inner-membrane of mitochondria, reaction take place in cytosol, Fig. 8 Rawls)
DHORD9	3	Rawls J, Knecht W, Diekert K, Lill R, Loffler M.	Requirements for the mitochondrial import and localization of dihydroorotate dehydrogenase.	Eur J Biochem	2005	10727948	01-27-05 IT based on Bader et al, 1998, Prot. Expr. Purif.,, 13,414-422 (I guess it is ubiquinone but i am not sure) (needs FMN as cofactor) v(enzyme is located in inner-membrane of mitochondria, reaction take place in cytosol, Fig. 8 Rawls)
DHORD9	3	Loffler M, Jockel J, Schuster G, Becker C.	Dihydroorotat-ubiquinone oxidoreductase links mitochondria in the biosynthesis of pyrimidine nucleotides.	Mol Cell Biochem	1997		01-27-05 IT based on Bader et al, 1998, Prot. Expr. Purif.,, 13,414-422 (I guess it is ubiquinone but i am not sure) (needs FMN as cofactor) v(enzyme is located in inner-membrane of mitochondria, reaction take place in cytosol, Fig. 8 Rawls)
DHPM1	3	Hamajima N, Matsuda K, Sakata S, Tamaki N, Sasaki M, Nonaka M.	A novel gene family defined by human dihydropyrimidinase and three related proteins with differential tissue distribution.	Gene	1996	8973361	IT
DMGDHm	3	Binzak BA, Wevers RA, Moolenaar SH	Cloning of dimethylglycine dehydrogenase and a new human inborn error of metabolism, dimethylglycine dehydrogenase deficiency.		2001	1123190	irreversibility according to cited paper Entrez Gene -This gene encodes an enzyme involved in the catabolism of choline, catalyzing the oxidative demethylation of dimethylglycine to form sarcosine. The enzyme is found as a monomer in the mitochondrial matrix, and uses flavin adenine dinucleotide and folate as cofactors. Mutation in this gene causes dimethylglycine dehydrogenase deficiency, characterized by a fishlike body odor, chronic muscle fatigue, and elevated levels of the muscle form of creatine kinase in serum. MM
DMGDHm	3	Binzak,B.A. , Vockley,J.G. , Jenkins,R.B. , Vockley,J.	Structure and analysis of the human dimethylglycine dehydrogenase gene.		2000	10767172	irreversibility according to cited paper Entrez Gene -This gene encodes an enzyme involved in the catabolism of choline, catalyzing the oxidative demethylation of dimethylglycine to form sarcosine. The enzyme is found as a monomer in the mitochondrial matrix, and uses flavin adenine dinucleotide and folate as cofactors. Mutation in this gene causes dimethylglycine dehydrogenase deficiency, characterized by a fishlike body odor, chronic muscle fatigue, and elevated levels of the muscle form of creatine kinase in serum. MM
DMHPTCRNte	2	Libert R, Van Hoof F, Thillaye M, Vincent MF, Nassogne MC, Stroobant V, de Hoffmann E, Schanck A.	Identification of new medium-chain acylcarnitines present in normal human urine	Anal Biochem	1997	9299016	See PMID 9299016. dmhptcrn found in urine. Metabolic fate of corresponding coa (dmhptcoa) is unknown - see PMID 9469587 NJ
DNADDP	2	Funakoshi I, Kato H, Horie K, Yano T, Hori Y, Kobayashi H, Inoue T, Suzuki H, Fukui S, Tsukahara M, et al.	Molecular cloning of cDNAs for human fibroblast nucleotide pyrophosphatase.	Arch Biochem Biophys	1992	1315502	homodimer; membrane protein; broad specificity; in general: a dinucleotide +h2o--> 2 mononucleotides IT
DNAMTn	3	Yen RW, Vertino PM, Nelkin BD, Yu JJ, el-Deiry W, Cumaraswamy A, Lennon GG, Trask BJ, Celano P, Baylin SB.	Isolation and characterization of the cDNA encoding human DNA methyltransferase.		1992	1594447	DNA methylation patterns (cytosine-specific)

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DNAMTn	3	Deloukas,P. , Matthews,L.H. , Ashurst,J.	The DNA sequence and comparative analysis of human chromosome 20.		2001		DNA methylation patterns (cytosine-specific)
DNDPt1m	3	Dolce V, Fiermonte G, Runswick MJ, Palmieri F, Walker JE.	The human mitochondrial deoxynucleotide carrier and its role in the toxicity of nucleoside antivirals.	Proc Natl Acad Sci U S A	2001	11226231	IT
DOGULNO1	2	Simpson GL, Ortwerth BJ	The non-oxidative degradation of ascorbic acid at physiological conditions	Biochim Biophys Acta	2000	10727845	- rxn shown in Fig 2 of [Banhegyi, Fee Radic Mol Biol 1997] - rxn described in [Simpson and Ortwerth, 2000]
DOLASNT_Uer	0	Nakashima T, Sekiguchi T, Kuraoka A, Fukushima K, Shibata Y, Komiyama S, Nishimoto T.	Molecular cloning of a human cDNA encoding a novel protein, DAD1, whose defect causes apoptotic cell death in hamster BHK21 cells.	Mol Cell Biol	1993	8413235	Dad1p ubiquitously expressed [Nakashima et al, Mol Cell Biol 1993] Ddostp ubiquitously expressed [Yamagata et al, Genomics 1997]
DOLASNT_Uer	0	Yamagata T, Tsuru T, Momoi MY, Suwa K, Nozaki Y, Mukasa T, Ohashi H, Fukushima Y, Momoi T	Genome organization of human 48-kDa oligosaccharyltransferase (DDOST)	Genomics	1997	9367678	Dad1p ubiquitously expressed [Nakashima et al, Mol Cell Biol 1993] Ddostp ubiquitously expressed [Yamagata et al, Genomics 1997]
DOLDPP_Ler	0	Helenius J, Aebi M.	Transmembrane movement of dolichol linked carbohydrates during N-glycoprotein biosynthesis in the endoplasmic reticulum	Semin Cell Dev Biol	2002	12137737	occurs in ER lumen Helenius J, Aebi M. Semin Cell Dev Biol. 2002 Jun;13(3):171-8. Putative gene assignment was result of LocusLink search for additional N-glycosylation genes not associated with KEGG maps.
DOLPH_Ler	0	Schenk B, Fernandez F, Waechter CJ.	The ins(ide) and out(side) of dolichyl phosphate biosynthesis and recycling in the endoplasmic reticulum.	Glycobiology	2001	11425794	occurs in ER lumen Schenk B, Fernandez F, Waechter CJ. Glycobiology. 2001 11(5):61-70.
DOLPMT_L	0	Manos EJ, Kim ML, Kassis J, Chang PY, Wells A, Jones DA.	Dolichol-phosphate-mannose-3 (DPM3)/prostin-1 is a novel phospholipase C-gamma regulated gene negatively associated with prostate tumor invasion.	Oncogene	2001	11420690	Dpm3 transcript ubiquitously expressed [Manos et al, Oncogene 2001]
DOPAMT	3	Bertocci B, Miggiano V, Da Prada M, Dembic Z, Lahm HW, Malherbe P	Human catechol-O-methyltransferase: cloning and expression of the membrane-associated form	Proc Natl Acad Sci U S A	1991	1847521	from kegg map
DOPASULT	3	Chapman E, Best MD, Hanson SR, Wong CH.	Sulfotransferases: structure, mechanism, biological activity, inhibition, and synthetic utility.	Angew Chem Int Ed Engl	2004	15293241	- Added by RS/TV - Sulfotransferases (SULT) catalyze the transfer of a sulfuryl group from a donor molecule, PAPS, to a variety of amine and hydroxy substrates as nucleophiles; - All cytosolic according to ref. - Family 1A of the SULT family is known to prefer phenols as substrates: 1) Sult1a1: 4-nitrophenol, dopamine, iodothyronines (e.g. T3), tyramine 2) Sult1a2: 4-nitrophenol, dopamine, 3) Sult1a3: Dopamine, 4-nitrophenol, norepinephrine, tyramine, Based on Table 2 in Glatt H, Boeing H, Engelke CE, Ma L, Kuhlow A, Pabel U, Pomplun D, Teubner W, Meinl W. Mutat Res. 2001 Oct 1;482(1-2):27-40. Review. & Chapman E, Best MD, Hanson SR, Wong CH.Angew Chem Int Ed Engl. 2004 Jul 5;43(27):3526-48. Review. - Tissue Specificity info: 1)Sult1a1: High in liver; present in numerous other tissues such as platelets, placenta, adrenal gland, colon, brain, leukocytes, endometrium, jejunum. 2) Sult1a2: Liver, some bladder tumors 3) Sult1a3: Very high in jejunum and colon; also present in platelets, placenta, brain, leukocytes; neligible in liver.
DPMVDx	3	Iglesias J, Gonzalez-Pacanowska D, Caamano G, Garcia-Peregrin E	Mevalonate 5-pyrophosphate decarboxylase in isolated villus and crypt cells of chick intestine	Lipids	1988		peroxisomal (not cytosolic, contrary to uniprot etc) specificity: Expressed in heart, skeletal muscle, lung, liver, brain, pancreas, kidney and placenta. The enzyme mevalonate pyrophosphate decarboxylase catalyzes the conversion of mevalonate pyrophosphate into isopentenyl pyrophosphate in one of the early steps in cholesterol biosynthesis. It decarboxylates and dehydrates its substrate while hydrolyzing ATP. NJ
DPMVDx	3	Bonanno JB, Edo C, Eswar N, Pieper U, Romanowski MJ, Ilyin V, Gerchman SE, Kycia H, Studier W, Sali A, Burley SK	Structural genomics of enzymes involved in sterol/isoprenoid biosynthesis	Proceedings of the National Academy of Sciences	2001		peroxisomal (not cytosolic, contrary to uniprot etc) specificity: Expressed in heart, skeletal muscle, lung, liver, brain, pancreas, kidney and placenta. The enzyme mevalonate pyrophosphate decarboxylase catalyzes the conversion of mevalonate pyrophosphate into isopentenyl pyrophosphate in one of the early steps in cholesterol biosynthesis. It decarboxylates and dehydrates its substrate while hydrolyzing ATP. NJ
DTMPK	3	Su JY, Sclafani RA.	Molecular cloning and expression of the human deoxythymidylate kinase gene in yeast.	Nucleic Acids Res	1991	2017365	IT in kegg enzyme acts also on dUMP --> not included yet needs Mg2+
DTMPK	3	Huang SH, Tang A, Drisco B, Zhang SQ, Seeger R, Li C, Jong A.	Human dTMP kinase: gene expression and enzymatic activity coinciding with cell cycle progression and cell growth.	DNA Cell Biol	1994	8024690	IT in kegg enzyme acts also on dUMP --> not included yet needs Mg2+

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DURAD	3	Lu ZH, Zhang R, Diasio RB.	Purification and characterization of dihydropyrimidine dehydrogenase from human liver.	J Biol Chem	1992	1512248	01-26-05 IT based on Lu et al., JBC,1992,24,17102-17109 IT homodimer, need 2 FMN, 2 FAD, 33 iron atoms per molecule enzyme It has not been observed that FAD is converted to FMN
DURAD	3	Lu Z, Zhang R, Diasio RB.	Dihydropyrimidine dehydrogenase activity in human peripheral blood mononuclear cells and liver: population characteristics, newly identified deficient patients, and clinical implication in 5-fluorouracil chemotherapy.	Cancer Res	1993	8221682	01-26-05 IT based on Lu et al., JBC,1992,24,17102-17109 IT homodimer, need 2 FMN, 2 FAD, 33 iron atoms per molecule enzyme It has not been observed that FAD is converted to FMN
DUTPDPm	3	Ladner RD, McNulty DE, Carr SA, Roberts GD, Caradonna SJ.	Characterization of distinct nuclear and mitochondrial forms of human deoxyuridine triphosphate nucleotidohydrolase.	J Biol Chem	1996	8631816	Ladner et al, 1996 report that there are to isoforms originating from the same gene but use the 5'exon differently - however in locuslink there is only one transcript noted IT
DUTPDPm	3	Cohen D, Heng HH, Shi XM, McIntosh EM, Tsui LC, Pearlman RE.	Assignment of the human dUTPase gene (DUT) to chromosome 15q15-q21. 1 by fluorescence in situ hybridization.	Genomics	1997	9070952	Ladner et al, 1996 report that there are to isoforms originating from the same gene but use the 5'exon differently - however in locuslink there is only one transcript noted IT
DUTPDPm	3	Tinkelenberg BA, Fazzone W, Lynch FJ, Ladner RD.	Identification of sequence determinants of human nuclear dUTPase isoform localization.	Exp Cell Res	2003	12799180	Ladner et al, 1996 report that there are to isoforms originating from the same gene but use the 5'exon differently - however in locuslink there is only one transcript noted IT
EBP1r	3	Braverman N, Lin P, Moebius FF, Obie C, Moser A, Glossmann H, Wilcox WR, Rimoin DL, Smith M, Kratz L, Kelley RI, Valle D	Mutations in the gene encoding 3-beta-hydroxysteroid delta8, delta7- isomerase cause X-linked dominant Conradi-Hunermann Syndrome	Nature Genetics	1999		ER - uniprot + ref Emopamil-binding protein (EBP) is an integral membrane protein of the endoplasmic reticulum. It is a high affinity binding protein for the antiischemic phenylalkylamine Ca2+ antagonist [3H]emopamil and the photoaffinity label [3H]azidopamil. It is similar to sigma receptors and may be a member of a superfamily of high affinity drug-binding proteins in the endoplasmic reticulum of different tissues. EBP shares structural features with bacterial and eukaryontic drug transporting proteins. It has four putative transmembrane segments and contains two conserved glutamate residues which may be involved in the transport of cationic amphiphilics. Another prominent feature of EBP is its high content of aromatic amino acid residues (>23%) in its transmembrane segments. These aromatic amino acid residues have been suggested to be involved in the drug transport by the P-glycoprotein. Mutations in this gene cause Chondrodysplasia punctata 2 (CDPX2; also known as Conradi-Hunermann syndrome). NJ
ECOAH1m	2	FitzPatrick DR, Germain-Lee E, Valle D.	Isolation and characterization of rat and human cDNAs encoding a novel putative peroxisomal enoyl-CoA hydratase.		1995	7558027	Additional comments by NJ: localization: peroxiosme an mitochondria by similarity - uniprot see PMID: 7558027 for characterization
EGMESTr	2	Probst MR, Beer M, Beer D, Jeno P, Meyer UA, Gasser R	Human liver arylacetamide deacetylase. Molecular cloning of a novel esterase involved in the metabolic activation of arylamine carcinogens with high sequence similarity to hormone-sensitive lipase	J Biol Chem	1994	8063807	this reaction is reasonable, but the gene association is questionable and without good evidence
ENGASE	0	Suzuki T, Yano K, Sugimoto S, Kitajima K, Lennarz WJ, Inoue S, Inoue Y, Emori Y	Endo-beta-N-acetylglucosaminidase, an enzyme involved in processing of free oligosaccharides in the cytosol	Proc Natl Acad Sci U S A	2002	12114544	Suzuki suggests that FLJ21865p is localized to the cytosol because it lacks a signal sequence. [Suzuki et al, PNAS 99(15):9691-6 (2002)] Flj21865 expressed in thymus, spleen, pancreas, kidney, heart, sk muscle, placenta, brain [Suzuki et al, PNAS 2002]
ENMAN3g	0	Roth J, Ziak M, Zuber C.	The role of glucosidase II and endomannosidase in glucose trimming of asparagine-linked oligosaccharides.	Biochimie	2003	12770767	catalyzed by endomannosidase Fig 4 in [Spiro. J. Biol Chem 275(46): pp. 35637-35660 (2000)] Fig 4 in [Roth, Ziak, Zuber. Biochimie 85: pp. 287-294 (2003).
EPCTX	3	Tan SA, Tan LG	Distribution of ciliatine(2-aminoethylphosphonic acid) and phosphonalanine (2-amino-3-phosphonopropionic acid) in human tissues	Clin Physiol Biochem	1989		EPCTX addition by SAB scant evidence of 2ameph in humans - NJ PETHCT: cyt - uniport NJ
EPCTX	3	Lykidis A, Murtis KG, Jackowski S	Cloning and characterization of a second human CTP:Phosphocholine cytidylyltransferase	Journal of Biological Chemistry	1998		EPCTX addition by SAB scant evidence of 2ameph in humans - NJ PETHCT: cyt - uniport NJ
EPCTX	3	Tan SA, Tan LG	Distribution of ciliatine(2-aminoethylphosphonic acid) and phosphonalanine (2-amino-3-phosphonopropionic acid) in human tissues	Clin Physiol Biochem	1989		EPCTX addition by SAB scant evidence of 2ameph in humans - NJ PETHCT: cyt - uniport NJ
EPCTX	3	Lykidis A, Murtis KG, Jackowski S	Cloning and characterization of a second human CTP:Phosphocholine cytidylyltransferase	Journal of Biological Chemistry	1998		EPCTX addition by SAB scant evidence of 2ameph in humans - NJ PETHCT: cyt - uniport NJ

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
ESTRONEGLCt	3	Scheffer GL, Kool M, de Haas M, de Vree JM, Pijnenborg AC, Bosman DK, Elferink RP, van der Valk P, Borst P, Scheper RJ.	Tissue distribution and induction of human multidrug resistant protein 3.	Lab Invest	2002	11850532	ABCC3 - also in hepatocyte and cholangiocytes. a/w pancreatic carcinomas, liver neoplasms. Similar to ABCB11, except also shown to transport estradiol-17-beta-d-glucuronide. Down- and up-regulation of MRP1 (and MRP3) expression can influence cellular folate homeostasis, in particular when cellular retention by polyglutamylation of folates is attenuated. NJ
ESTSULT	3	Aksoy IA, Wood TC, Weinshilboum R.	Human liver estrogen sulfotransferase: identification by cDNA cloning and expression.	Biochem Biophys Res Commun	1994	8185618	cytosolic - uniport and refs TISSUE SPECIFICITY: Liver, intestine and at lower level in the kidney. May also sulfate dehydroepiandrosterone, pregnenolone, ethinylestradiol, equalenin, diethylstilbesterol and 1-naphthol to much smaller degree Sulfotransferase enzymes catalyze the sulfate conjugation of many hormones, neurotransmitters, drugs, and xenobiotic compounds. These cytosolic enzymes are different in their tissue distributions and substrate specificities. The gene structure (number and length of exons) is similar among family members. This gene encodes a protein that transfers a sulfo moiety to and from estrone, which may control levels of estrogen receptors. - It is also known that Sult1a1 is known to catalyze this reaction according to Table 2 in Glatt H, et al. Mutat Res. 2001 Oct 1;482(1-2):27-40. Review. (RS/TV) NJ
ETF	3	Finocchiaro G, Ito M, Ikeda Y, Tanaka K.	Molecular cloning and nucleotide sequence of cDNAs encoding the alpha-subunit of human electron transfer flavoprotein.	J Biol Chem	1988	3170610	- Added by RS/TV - a heterodimer consisting of alpha and beta subunits (Finocchiaro G, Ito M, Ikeda Y, Tanaka K. J Biol Chem. 1988 Oct 25;263(30):15773-80.) - electron-transferring flavoprotein is the physiological electron acceptor from the primary mitochondrial dehydronages such as acyl-CoA dehydrogenases. (Thorpe C, Kim JJ. FASEB J. 1995 Jun;9(9):718-25. Review.) - mitochondrial according to entrez. - beta subunit has two transcriptional variants.
ETF	3	Thorpe C, Kim JJ.	Structure and mechanism of action of the acyl-CoA dehydrogenases.	FASEB J	1995	7601336	- Added by RS/TV - a heterodimer consisting of alpha and beta subunits (Finocchiaro G, Ito M, Ikeda Y, Tanaka K. J Biol Chem. 1988 Oct 25;263(30):15773-80.) - electron-transferring flavoprotein is the physiological electron acceptor from the primary mitochondrial dehydronages such as acyl-CoA dehydrogenases. (Thorpe C, Kim JJ. FASEB J. 1995 Jun;9(9):718-25. Review.) - mitochondrial according to entrez. - beta subunit has two transcriptional variants.
ETFQO	3	Spector EB, Seltzer WK, Goodman SI.	Assignment of electron transfer flavoprotein-ubiquinone oxidoreductase (ETF-QO) to human chromosome 4q33 by fluorescence in situ hybridization and somatic cell hybridization.	Mol Genet Metab	1997	10444348	- Added by RS/TV - Electron transfer flavoprotein-uniquinone oxidoreductase is an iron-sulphur flavoprotein and a component of an electron-transfer system that links 10 different mitochondrial flavoprotein dehydrogenases to the mitochondrial bc1 complex via electron transfer flavoprotein and ubiquinone.(Simkovic M, Degala GD, Eaton SS, Frerman FE. Biochem J. 2002 Jun 15;364(Pt 3):659-67.) - Etfdh.1 is mitochondrial accoridng to Entrez. 84883: - putative function based on significant homology with NADH oxidoreductases/flavoproteins from bacteria to mammalian species (discovered through BLAST searches of the GenBank database). - AMID is associated with the outer membrane of mitochondria and localized in the cytosol.

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ETFQO	3	Simkovic M, Degala GD, Eaton SS, Frerman FE.	Expression of human electron transfer flavoprotein-ubiquinone oxidoreductase from a baculovirus vector kinetic and spectral characterization of the human protein.	Biochem J	2002	12049629	- Added by RS/TV - Electron transfer flavoprotein-uniquinone oxidoreductase is an iron-sulphur flavoprotein and a component of an electron-transfer system that links 10 different mitochondrial flavoprotein dehydrogenases to the mitochondrial bc1 complex via electron transfer flavoprotein and ubiquinone.(Simkovic M, Degala GD, Eaton SS, Frerman FE. Biochem J. 2002 Jun 15;364(Pt 3):659-67.) - Etfdh.1 is mitochondrial accoridng to Entrez. 84883: - putative function based on significant homology with NADH oxidoreductases/flavoproteins from bacteria to mammalian species (discovered through BLAST searches of the GenBank database). - AMID is associated with the outer membrane of mitochondria and localized in the cytosol.
FA120ACPH	3	Chirala SS, Huang WY, Jayakumar A, Sakai K, Wakil SJ.	Animal fatty acid synthase: functional mapping and cloning and expression of the domain I constituent activities.	Proc Natl Acad Sci U S A	1997	9159116	Lumped FAS reactions in current reconstruction, so these reactions won't be used. In future versions if synthesis is unlumped these will be used in simulations. see PMID: 9159116 NJ
FACOAL160i	3	Stanczak H, Stanczak JJ, Singh I.	Chromosomal localization of the human gene for palmitoyl-CoA ligase (FACL1).	Cytogenet Cell Genet	1992	1531127	mitochondrial membrane and peroxisomal membrane. Assuming outer mitochondrial membrane is effectively cytosolic (reaction product will need to be transported into mit if it is to undergo any reactions there). - UniProt - Additional information by RS/TV J Biol Chem. 2001 Jun 8;276(23):20182-5. Epub 2001 Mar 27 ACS results in the conversion of free fatty acid into fatty acyl-CoA esters according to Cao Y. Genomics. 1998 Apr 15;49(2):327-30. Tissue expression and substrate specificity: 1) Acsl1 is highly expressed in highly in liver, adipose tissue, and heart. Acsl6 is a brain-specific subtype of Acsl1. Acsl1 (and consequently Acsl6 which is nearly identical to Acsl2) prefers C10-C18 saturated fatty acids and C16-C20 unsaturated fatty acids. 2) Acsl3 is also highly expressed in the brain. Acsl3 on the other hand prefers C8-C22 saturated fatty acids and C16-C20 unsaturated fatty acids. 3) Acsl4 prefers archidonic acid (20:4) and eicosapentaenoic acid(20:5) as substrates. Human placenta, brain, testis, ovary, spleen, and adrenal cortex all expressed high levels of Acsl4. 4) It is suggested that Acsl5 tends to be expressed in human sma Subcellular localizations: All are expressed to some extent in m Subcellular localizations according to Lewin TM. J Biol Chem. Tissue expression and substrate specificity according to
FACOAL161	3	Mashek DG, Bornfeldt KE, Coleman RA, Berger J, Bernlohr DA, Black P, DiRusso CC, Farber SA, Guo W, Hashimoto N, Khodiyar V, Kuypers FA, Maltais LJ, Nebert DW, Renieri A, Schaffer JE, Stahl A, Watkins PA, Vasiliou V, Yamamoto TT.	Revised nomenclature for the mammalian long-chain acyl-CoA synthetase gene family.	J Lipid Res	2004	15292367	Additional set only added to Acsl1.1 for the time being. For updated nomenclature of Acsl see PMID: 15292367. Reversible reaction due to Keq ~1 - see Reich: Energy metabolism of the cell. ACSL1,3,4,5 noted to occur in Microsomes, outer mitochondrial membrane and peroxisomal membrane. Assuming outer mitochondrial membrane is effectively cytosolic (reaction product will need to be transported into mit if it is to undergo any reactions there). - UniProt NJ
FACOAL161	3	Reich, Sel'kov	Energy metabolism of the cell : a theoretical treatise		1981		Additional set only added to Acsl1.1 for the time being. For updated nomenclature of Acsl see PMID: 15292367. Reversible reaction due to Keq ~1 - see Reich: Energy metabolism of the cell. ACSL1,3,4,5 noted to occur in Microsomes, outer mitochondrial membrane and peroxisomal membrane. Assuming outer mitochondrial membrane is effectively cytosolic (reaction product will need to be transported into mit if it is to undergo any reactions there). - UniProt NJ
FACOAL206	3	Steinberg SJ, Wang SJ, Kim DG, Mihalik J, Watkins PA	Human very-long-chain-acyl-CoA synthetase	Biochemical and biophysical research communications	1999		The protein encoded by this gene is an isozyme of long-chain fatty-acid-coenzyme A ligase family. Although differing in substrate specificity, subcellular localization, and tissue distribution, all isozymes of this family convert free long-chain fatty acids into fatty acyl-CoA esters, and thereby play a key role in lipid biosynthesis and fatty acid degradation. This isozyme activates long-chain, branched-chain and very-long-chain fatty acids containing 22 or more carbons to their CoA derivatives. It is expressed primarily in liver and kidney, and is present in both endoplasmic reticulum and peroxisomes but not in mitochondria. Its decreased peroxisomal enzyme activity is in part responsible for the biochemical pathology in X-linked adrenoleukodystrophy. NJ

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FACOAL40im	3	Bugaut M	Occurrence, absorption and metabolism of short chain fatty acids in the digestive tract of mammals	Comp Biochem Physiol B	1987	3297476	- identification of gene [Fujino, J Biol Chem 2001] - mouse gene was characterized and shown to be localized to mitochondrial matrix [Fujino, J Biol Chem 2001] - reaction described in [Bugaut, Comp Biochem Physiol B 1987]
FACOAL40im	3	Fujino T, Takei YA, Sone H, Ioka RX, Kamataki A, Magoori K, Takahashi S, Sakai J, Yamamoto TT	Molecular identification and characterization of two medium-chain acyl-CoA synthetases, MACS1 and the Sa gene product	J Biol Chem	2001	11470804	- identification of gene [Fujino, J Biol Chem 2001] - mouse gene was characterized and shown to be localized to mitochondrial matrix [Fujino, J Biol Chem 2001] - reaction described in [Bugaut, Comp Biochem Physiol B 1987]
FAEL183	3	Zhang K, Kniazeva M, Han M, Li W, Yu Z, Yang Z, Li Y, Metzker ML, Allikmets R, Zack DJ, Kakuk LE, Lagali PS, Wong PW, MacDonald IM, Sieving PA, Figueroa DJ, Austin CP, Gould RJ, Ayyagari R, Petrukhin K.	A 5-bp deletion in ELOVL4 is associated with two related forms of autosomal dominant macular dystrophy.	Nat Genet	2001	11138005	localization: microsomal - specificty (inner vs outer membrane) not determined so it is assumed to take place on the outer membrane - part of the microsomal elongase/desaturase reactions. Set of 7 elongase genes (ELOVL1-7), the other genes (ELOVL1,2,3,5,6,7) are not as well characterized so gene associations have not yet been made. see PMID: 11138005 for dz association (macular dystrophy) NJ
FAEL183	3	Nakamura MT, Nara TY.	Structure, function, and dietary regulation of delta6, delta5, and delta9 desaturases.	Annu Rev Nutr	2004	15189125	localization: microsomal - specificty (inner vs outer membrane) not determined so it is assumed to take place on the outer membrane - part of the microsomal elongase/desaturase reactions. Set of 7 elongase genes (ELOVL1-7), the other genes (ELOVL1,2,3,5,6,7) are not as well characterized so gene associations have not yet been made. see PMID: 11138005 for dz association (macular dystrophy) NJ
FAH1	3	Palmer CN, Richardson TH, Griffin KJ, Hsu MH, Muerhoff AS, Clark JE, Johnson EF.	Characterization of a cDNA encoding a human kidney, cytochrome P-450 4A fatty acid omega-hydroxylase and the cognate enzyme expressed in Escherichia coli.	Biochim Biophys Acta	1993	7679927	ER integral membrane - assumed to face cytosol This protein localizes to the endoplasmic reticulum and hydroxylates medium-chain fatty acids such as laurate and myristate. NJ
FAH1	3	Imaoka S, Ogawa H, Kimura S, Gonzalez FJ.	Complete cDNA sequence and cDNA-directed expression of CYP4A11, a fatty acid omega-hydroxylase expressed in human kidney.	DNA Cell Biol	1993	8274222	ER integral membrane - assumed to face cytosol This protein localizes to the endoplasmic reticulum and hydroxylates medium-chain fatty acids such as laurate and myristate. NJ
FALDH	3	Uotila L, Koivusalo M	Purification and properties of S-formylglutathione hydrolase from human liver	J Biol Chem	1974	4436331	The degradation of fald is relatively certain. The exact mechanism appears to be well established, but is less certain.
FALDH	3	Engeland K, Hoog JO, Holmquist B, Estonius M, Jornvall H, Vallee BL	Mutation of Arg-115 of human class III alcohol dehydrogenase: a binding site required for formaldehyde dehydrogenase activity and fatty acid activation	Proc Natl Acad Sci U S A	1993	8460164	The degradation of fald is relatively certain. The exact mechanism appears to be well established, but is less certain.
FAOXC160	3	Naito E, Ozasa H, Ikeda Y, Tanaka K.	Molecular cloning and nucleotide sequence of complementary DNAs encoding human short chain acyl-coenzyme A dehydrogenase and the study of the molecular basis of human short chain acyl-coenzyme A dehydrogenase deficiency.	J Clin Invest	1985	2565344	- Added by RS/TV 1) Acyl-Coa dehydrogenases all catalyze a,b-dehydrogenation of acyl-CoA esters and transfer electrons to electron transfer flavoprotein 2) Acads-m and Acadm-m catalyze the first step of B-oxidation cycles for fatty acids with various chain length 3) Acads-m & Acadm-m are located in the mitochondrial matrix 4) Acadm-m is active with acyl chain lengths of C4 to C16. However, Acadm-m and Acads-m exhibits overlap in substrate range (length of fatty acyl chains) 1 through 4 according to Naito E, Ozasa H, Ikeda Y, Tanaka K. Molecular cloning and nucleotide sequence of complementary DNAs encoding human short chain acyl-coenzyme A dehydrogenase and the study of the molecular basis of human short chain acyl-coenzyme A dehydrogenase deficiency. J Clin Invest. 1989 May;83(5):1605-13. PMID: 2565344 Also, Kelly DP, Kim JJ, Billadello JJ, Hainline BE, Chu TW, Strauss AW. Nucleotide sequence of medium-chain acyl-CoA dehydrogenase mRNA and its expression in enzyme-deficient human tissue. Proc Natl Acad Sci U S A. 1987 Jun;84(12):4068-72. PMID: 3035565

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FAOXC160	3	Kelly DP, Kim JJ, Billadello JJ, Hainline BE, Chu TW, Strauss AW	Nucleotide sequence of medium-chain acyl-CoA dehydrogenase mRNA and its expression in enzyme-deficient human tissue.	Proc Natl Acad Sci U S A	1987	3035565	- Added by RS/TV 1) Acyl-Coa dehydrogenases all catalyze a,b-dehydrogenation of acyl-CoA esters and transfer electrons to electron transfer flavoprotein 2) Acads-m and Acadm-m catalyze the first step of B-oxidation cycles for fatty acids with various chain length 3) Acads-m & Acadm-m are located in the mitochondrial matrix 4) Acadm-m is active with acyl chain lengths of C4 to C16. However, Acadm-m and Acads-m exhibits overlap in substrate range (length of fatty acyl chains) 1 through 4 according to Naito E, Ozasa H, Ikeda Y, Tanaka K. Molecular cloning and nucleotide sequence of complementary DNAs encoding human short chain acyl-coenzyme A dehydrogenase and the study of the molecular basis of human short chain acyl-coenzyme A dehydrogenase deficiency. J Clin Invest. 1989 May;83(5):1605-13. PMID: 2565344 Also, Kelly DP, Kim JJ, Billadello JJ, Hainline BE, Chu TW, Strauss AW. Nucleotide sequence of medium-chain acyl-CoA dehydrogenase mRNA and its expression in enzyme-deficient human tissue. Proc Natl Acad Sci U S A. 1987 Jun;84(12):4068-72. PMID: 3035565
FAOXC204	3	Weiping Le, Azfar S. Abbas, Howard Sprecher, Jerry Vockley and Horst Schulz	Long-chain acyl-CoA dehydrogenase is a key enzyme in the mitochondrial [beta]-oxidation of unsaturated fatty acids	Biochimica et Biophysica Acta (BBA) - Molecular and Cell Biology of Lipids	2000		- Added by RS/TV 1) Acyl-Coa dehydrogenases all catalyze a,b-dehydrogenation of acyl-CoA esters and transfer electrons to electron transfer flavoprotein 2) Acads-m and Acadm-m catalyze the first step of B-oxidation cycles for fatty acids with various chain length 3) Acads-m & Acadm-m are located in the mitochondrial matrix 4) Acadm-m is active with acyl chain lengths of C4 to C16. However, Acadm-m and Acads-m exhibits overlap in substrate range (length of fatty acyl chains) 5) Acadl-m is important for the -oxidation of regular fatty acid intermediates that have acyl chains with 10 to 14 carbons, although it accpets substrates with long carbon chains. There is some overlap of the type of substrate it will accept with Acadm m 1 through 4 according to Naito E, Ozasa H, Ikeda Y, Tanaka K. Molecular cloning and nucleotide sequence of complementary DNAs encoding human short chain acyl-coenzyme A dehydrogenase and the study of the molecular basis of human short chain acyl-coenzyme A dehydrogenase deficiency. J Clin Invest. 1989 May;83(5):1605-13. PMID: 2565344 Also, Kelly DP, Kim JJ, Billadello JJ, Hainline BE, Chu TW, Strauss Proc Natl Acad Sci U S A. 1987 Jun;84(12):4068-72.
FAS100COA	3	Wakil SJ.	Fatty acid synthase, a proficient multifunctional enzyme.	Biochemistry	1989	2669958	cytosol: uniprot Fatty acid synthetase catalyzes the formation of long- chain fatty acids from acetyl-CoA, malonyl-CoA and NADPH. This multifunctional protein has 7 catalytic activities and an acyl carrier protein. See PMID: 2669958 for lumped reaction stoichiometry. Specificity: all tissues, but prominent expression in brain, lung, and liver. Structure and substrate specificity: PMID: 15507492. The enzyme encoded by this gene is a multifunctional protein. Its main function is to catalyze the synthesis of palmitate from acetyl-CoA and malonyl-CoA, in the presence of NADPH, into long-chain saturated fatty acids. In some cancer cell lines, this protein has been found to be fused with estrogen receptor-alpha (ER-alpha), in which the N-terminus of FAS is fused in-frame with the C-terminus of ER-alpha. Most tissues produce C16, some tissues produce smaller chains (e.g. C12), hence lumped reaction in addition to stepwise reactions included (see closing sentences of PMID: 2669958). NJ

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FAS100COA	3	Brink J, Ludtke SJ, Yang CY, Gu ZW, Wakil SJ, Chiu W.	Quaternary structure of human fatty acid synthase by electron cryomicroscopy.	Proc Natl Acad Sci	2002	11756679	cytosol: uniprot Fatty acid synthetase catalyzes the formation of long- chain fatty acids from acetyl-CoA, malonyl-CoA and NADPH. This multifunctional protein has 7 catalytic activities and an acyl carrier protein. See PMID: 2669958 for lumped reaction stoichiometry. Specificity: all tissues, but prominent expression in brain, lung, and liver. Structure and substrate specificity: PMID: 15507492. The enzyme encoded by this gene is a multifunctional protein. Its main function is to catalyze the synthesis of palmitate from acetyl-CoA and malonyl-CoA, in the presence of NADPH, into long-chain saturated fatty acids. In some cancer cell lines, this protein has been found to be fused with estrogen receptor-alpha (ER-alpha), in which the N-terminus of FAS is fused in-frame with the C-terminus of ER-alpha. Most tissues produce C16, some tissues produce smaller chains (e.g. C12), hence lumped reaction in addition to stepwise reactions included (see closing sentences of PMID: 2669958). NJ
FAS100COA	3	Chakravarty B, Gu Z, Chirala SS, Wakil SJ, Quiocho FA.	Human fatty acid synthase: structure and substrate selectivity of the thioesterase domain.		2004	15507492	cytosol: uniprot Fatty acid synthetase catalyzes the formation of long- chain fatty acids from acetyl-CoA, malonyl-CoA and NADPH. This multifunctional protein has 7 catalytic activities and an acyl carrier protein. See PMID: 2669958 for lumped reaction stoichiometry. Specificity: all tissues, but prominent expression in brain, lung, and liver. Structure and substrate specificity: PMID: 15507492. The enzyme encoded by this gene is a multifunctional protein. Its main function is to catalyze the synthesis of palmitate from acetyl-CoA and malonyl-CoA, in the presence of NADPH, into long-chain saturated fatty acids. In some cancer cell lines, this protein has been found to be fused with estrogen receptor-alpha (ER-alpha), in which the N-terminus of FAS is fused in-frame with the C-terminus of ER-alpha. Most tissues produce C16, some tissues produce smaller chains (e.g. C12), hence lumped reaction in addition to stepwise reactions included (see closing sentences of PMID: 2669958). NJ
FATP1t	3	Fitscher BA, Riedel HD, Young KC, Stremmel W.	Tissue distribution and cDNA cloning of a human fatty acid transport protein (hsFATP4).	Biochim Biophys Acta	1998	9878842	SLC27A1: heart SLC27A2: kidney SLC27A3: lung SLC27A4: all tissues (ubiquitous) SLC27A5: liver SLC27A6: not well known Specific mechanism unknown - added Na cotransport to make electroneutral transport (mechanism likely involves active prot channels, in contrast to diffusional transport of fatty acids). Specificity of fatty acids not very well known (FATP5t/SLC27A5 transports "very long chain FA"). SLC27A2: The protein encoded by this gene is an isozyme of long-chain fatty-acid-coenzyme A ligase family. Although differing in substrate specificity, subcellular localization, and tissue distribution, all isozymes of this family convert free long-chain fatty acids into fatty acyl-CoA esters, and thereby play a key role in lipid biosynthesis and fatty acid degradation. This isozyme activates long-chain, branched-chain and very-long-chain fatty acids containing 22 or more carbons to their CoA derivatives. It is expressed primarily in liver and kidney, and is present in both endoplasmic reticulum and peroxisomes but not in mitochondria. Its decreased peroxisomal enzyme activity is i SLC27A5: The protein encoded by this gene is an isozyme of v FATP6 is involved in heart LCFA uptake, in which it may play

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FATP1t	3	Stahl A.	A current review of fatty acid transport proteins (SLC27).	Pflugers Arch	2004	12856180	SLC27A1: heart SLC27A2: kidney SLC27A3: lung SLC27A4: all tissues (ubiquitous) SLC27A5: liver SLC27A6: not well known Specific mechanism unknown - added Na cotransport to make electroneutral transport (mechanism likely involves active prot channels, in contrast to diffusional transport of fatty acids). Specificity of fatty acids not very well known (FATP5t/SLC27A5 transports "very long chain FA"). SLC27A2: The protein encoded by this gene is an isozyme of long-chain fatty-acid-coenzyme A ligase family. Although differing in substrate specificity, subcellular localization, and tissue distribution, all isozymes of this family convert free long chain fatty acids into fatty acyl-CoA esters, and thereby play a key role in lipid biosynthesis and fatty acid degradation. This isozyme activates long-chain, branched-chain and very-long-chain fatty acids containing 22 or more carbons to their CoA derivatives. It is expressed primarily in liver and kidney, and is present in both endoplasmic reticulum and peroxisomes but not in mitochondria. Its decreased peroxisomal enzyme activity is i SLC27A5: The protein encoded by this gene is an isozyme of v FATP6 is involved in heart LCFA uptake, in which it may play
FATP1t	3	Pohl J, Ring A, Hermann T, Stremmel W.	Role of FATP in parenchymal cell fatty acid uptake.	Biochim Biophys Acta	2004	15522816	SLC27A1: heart SLC27A2: kidney SLC27A3: lung SLC27A4: all tissues (ubiquitous) SLC27A5: liver SLC27A6: not well known Specific mechanism unknown - added Na cotransport to make electroneutral transport (mechanism likely involves active prot channels, in contrast to diffusional transport of fatty acids). Specificity of fatty acids not very well known (FATP5t/SLC27A5 transports "very long chain FA"). SLC27A2: The protein encoded by this gene is an isozyme of long-chain fatty-acid-coenzyme A ligase family. Although differing in substrate specificity, subcellular localization, and tissue distribution, all isozymes of this family convert free long chain fatty acids into fatty acyl-CoA esters, and thereby play a key role in lipid biosynthesis and fatty acid degradation. This isozyme activates long-chain, branched-chain and very-long-chain fatty acids containing 22 or more carbons to their CoA derivatives. It is expressed primarily in liver and kidney, and is present in both endoplasmic reticulum and peroxisomes but not in mitochondria. Its decreased peroxisomal enzyme activity is i SLC27A5: The protein encoded by this gene is an isozyme of v FATP6 is involved in heart LCFA uptake, in which it may play
FATP4t	3	Steinberg SJ, Wang SJ, McGuinness MC, Watkins PA.	Human liver-specific very-long-chain acyl-coenzyme A synthetase: cDNA cloning and characterization of a second enzymatically active protein.	Mol Genet Metab	1999	10479480	SLC27A1: heart SLC27A2: kidney SLC27A3: lung SLC27A4: all tissues (ubiquitous) SLC27A5: liver SLC27A6: not well known Specific mechanism unknown - added Na cotransport to make electroneutral transport (mechanism likely involves active prot channels, in contrast to diffusional transport of fatty acids). Specificity of fatty acids not very well known (FATP5t/SLC27A5 transports "very long chain FA"). SLC27A2: The protein encoded by this gene is an isozyme of long-chain fatty-acid-coenzyme A ligase family. Although differing in substrate specificity, subcellular localization, and tissue distribution, all isozymes of this family convert free long chain fatty acids into fatty acyl-CoA esters, and thereby play a key role in lipid biosynthesis and fatty acid degradation. This isozyme activates long-chain, branched-chain and very-long-chain fatty acids containing 22 or more carbons to their CoA derivatives. It is expressed primarily in liver and kidney, and is present in both endoplasmic reticulum and peroxisomes but not in mitochondria. Its decreased peroxisomal enzyme activity is i SLC27A5: The protein encoded by this gene is an isozyme of v FATP6 is involved in heart LCFA uptake, in which it may play
FBP	0	Tillmann H, Eschrich K	Isolation and characterization of an allelic cDNA for human muscle fructose-1,6-bisphosphatase	Gene	1998	9678974	2203: - expressed in liver [Genatlas] 8789: - expressed in muscle [Tillmann and Eschrich, Gene 1998]

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FCLTm	2	Tugores A, Magness ST, Brenner DA.	A single promoter directs both housekeeping and erythroid preferential expression of the human ferrochelatase gene.	J Biol Chem	1994	7983009	- Added by RS/TV Proteome - Subcellular location: Bound to the mitochondrial inner membrane in eukaryotic cells with its active site on the matrix side of the membrane, according to Gene Cards. - Added by RS/TV - Catalytic Activity according to Gene Cards: Catalyzes the ferrous insertion into protoporphyrin IX. - Ferrocheletase, the last enzyme of the heme biosynthetic pathway, catalyzes the chelation of ferrous iron and protoporphyrin to form heme. Enzymes participating the heme biosynthetic pathway must be expressed in all cell types to supply the heme required as a co-factor for the respiratory cytochromes. (Tugores A, Magness ST, Brenner DA. J Biol Chem. 1994 Dec 9;269(49):30789-97.)
FCOAH	2	Jansen GA, van den Brink DM, Ofman R, Draghici O, Dacremont G, Wanders RJ.	Identification of pristanal dehydrogenase activity in peroxisomes: conclusive evidence that the complete phytanic acid alpha-oxidation pathway is localized in peroxisomes.	Biochem Biophys Res Commun	2001	11341778	Verhoeven 11591435 and clayton 11356171 See Jansen et al (PMID 11341778) Localization unclear - may be peroxisomal or cytoplasmic - peroxisomal chosen since the next step (oxidation of formate - FDH) is catalyzed by an cytoplasmic enzyme. NJ
FE2t	3	Goswami T, Rolfs A, Hediger MA	Iron transport: emerging roles in health and disease	Biochem Cell Biol	2002	12440707	- this is a lumped reaction representing: (1) iron absorption at the apical membrane intestinal mucosal cells, (2) its secretion and oxidation at the basolateral membrane, (3) binding to transferrin (Tf) and transport in the bloodstream, (4) uptake into heme-producing cells and release of Fe2+ from Tf [Goswami 2002], [Orten 1978] - uptake across apical membrane is mediated by SLC11 family (DCT1, Nramp2) in a voltage-dependent, proton coupled mechanism [Goswami 2002] - export at the basolateral membrane is mediated by IREG1; subsquent pxidation is by hephaestin [Goswami 2002]
FE2tm	2	Lange H, Kispal G, Lill R.	Mechanism of iron transport to the site of heme synthesis inside yeast mitochondria.	J Biol Chem	1999	10383398	- Added by RS/TV - No genes found. - Iron uptake is driven energetically by a membrane potential across the inner membrane but does not require ATP. (Lange H, Kispal G, Lill R. Biol Chem. 1999 Jul 2;274(27):18989-96.) - ABCB10 (ABC-me) appears to play a role in the transport of heme or heme intermediates across the mitochondrial membrane based on indirect experimental observations. See [Chung 2003] for refs.
FE2tm	2	Chung J, Wessling-Resnick M	Molecular mechanisms and regulation of iron transport.	Crit Rev Clin Lab Sci	2003	12755454	- Added by RS/TV - No genes found. - Iron uptake is driven energetically by a membrane potential across the inner membrane but does not require ATP. (Lange H, Kispal G, Lill R. Biol Chem. 1999 Jul 2;274(27):18989-96.) - ABCB10 (ABC-me) appears to play a role in the transport of heme or heme intermediates across the mitochondrial membrane based on indirect experimental observations. See [Chung 2003] for refs.
FE3R2e	3	McKie AT, Barrow D, Latunde-Dada GO, Rolfs A, Sager G, Mudaly E, Mudaly M, Richardson C, Barlow D, Bomford A, Peters TJ, Raja KB, Shirali S, Hediger MA, Farzaneh F, Simpson RJ.	An iron-regulated ferric reductase associated with the absorption of dietary iron	Science	2001	11230685	- stoichiometry uncertain; inferred from EC 1.16.1.7 - Cybrd1 has ascrobic acid binding site; ascorbate also enhances iron absroption; rabbit protein showm to catazlye iron reduction in presence of ascorbate; see refs in [Chung 2003] - Fe3+ reducing avitivity has been isolated from duodenal microvilli membranes and intestinal cell lines; see refs in [Chung 2003] 79901: - cloned [McKie 2001] - reductase activity observed in Xenopus oocytes [McKie 2001] - expressed in brush border membrane of duodenum [Chung 2003]
FPGS	3	McGuire JJ, Russell CA, Balinska M.	Human cytosolic and mitochondrial folylpolyglutamate synthetase are electrophoretically distinct. Expression in antifolate-sensitive and -resistant human cell lines.	J Biol Chem	2000	10777604	IT

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FRDPtr	2	Kovacs WJ, Olivier LM, Krisans SK.	Central role of peroxisomes in isoprenoid biosynthesis.	Prog Lipid Res	2002	12121718	Evidence of flip-flop as mechanism for intracellular transport (PMID: 12840657) discussed in Hamilton. Signifiance of FRDP in particular for IC transport, Krisans et al (PMID: 14713247, PMID: 12121718). NJ
FRDPtr	2	Hamilton JA.	Fast flip-flop of cholesterol and fatty acids in membranes: implications for membrane transport proteins.	Curr Opin Lipidol	2003	12840657	Evidence of flip-flop as mechanism for intracellular transport (PMID: 12840657) discussed in Hamilton. Signifiance of FRDP in particular for IC transport, Krisans et al (PMID: 14713247, PMID: 12121718). NJ
FRUt1r	3	Burant CF, Takeda J, Brot-Laroche E, Bell GI, Davidson NO	Fructose transporter in human spermatozoa and small intestine is GLUT5	J Biol Chem	1992	1634504	6514: - major substrates are Glc (low affinity [Johnson, 1990]), Gal, Fru, Man, GlcN [Uldry, 2004], [Uldry, 2002] - facilitated diffusion [Uldry, Pflugers Arch 2004] - intestine and kidney [Thorens, 1990], liver, pancreatic B cells, islet of Langerhans, brain [Uldry, 2004] - cDNA was cloned [Fukumoto, 1988] - glucose release from hepatocytes has two major pathways: 1) faciliated diffusion through GLUT2 and 2) membrane traffic pathway from ER to extracellular space. There is also a third minor route inwhich glucose re-enters the cytosol to form a pool that slowly diffuses out of the cells [Hosokawa, 2002] - release of glucose by transporters other than GLUT2 is low [Guillam, 1998] 6515: - major substrates are Glc (high affinity), Gal, Man, Xyl, maltose, dehydroascorbic acid [Uldry, 2004] - brain (neurons), testis (spermatozoa) [Haber, 1993], [Uldry, 2004], sk muscle (slow twitch fibers) [Stuart, 1999], platelets (alpha-granules) [Heijen, 1997] - cDNA was cloned [Kayano, 1988] 6518: - transports Fru [Uldry, Pflugers Arch 2004], but not Glc [Burant, 1992] - sm intestine (jejunal region), kidney, sk muscle, adipocytes [U - cDNA was isolated [Kayano,1990] 155184: - gene identified [Joost, 2001] and cloned [Li, 2004] - transports Glc, Fru [Li, 2004]
FRUt1r	3	Kayano T, Burant CF, Fukumoto H, Gould GW, Fan YS, Eddy RL, Byers MG, Shows TB, Seino S, Bell GI	Human facilitative glucose transporters.	J Biol Chem	1990	1695905	6514: - major substrates are Glc (low affinity [Johnson, 1990]), Gal, Fru, Man, GlcN [Uldry, 2004], [Uldry, 2002] - facilitated diffusion [Uldry, Pflugers Arch 2004] - intestine and kidney [Thorens, 1990], liver, pancreatic B cells, islet of Langerhans, brain [Uldry, 2004] - cDNA was cloned [Fukumoto, 1988] - glucose release from hepatocytes has two major pathways: 1) faciliated diffusion through GLUT2 and 2) membrane traffic pathway from ER to extracellular space. There is also a third minor route inwhich glucose re-enters the cytosol to form a pool that slowly diffuses out of the cells [Hosokawa, 2002] - release of glucose by transporters other than GLUT2 is low [Guillam, 1998] 6515: - major substrates are Glc (high affinity), Gal, Man, Xyl, maltose, dehydroascorbic acid [Uldry, 2004] - brain (neurons), testis (spermatozoa) [Haber, 1993], [Uldry, 2004], sk muscle (slow twitch fibers) [Stuart, 1999], platelets (alpha-granules) [Heijen, 1997] - cDNA was cloned [Kayano, 1988] 6518: - transports Fru [Uldry, Pflugers Arch 2004], but not Glc [Burant, 1992] - sm intestine (jejunal region), kidney, sk muscle, adipocytes [U - cDNA was isolated [Kayano,1990] 155184: - gene identified [Joost, 2001] and cloned [Li, 2004] - transports Glc, Fru [Li, 2004]

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FRUt1r	3	Mantych GJ, James DE, Devaskar SU	Jejunal/kidney glucose transporter isoform (Glut-5) is expressed in the human blood-brain barrier	Endocrinology	1993	8419132	6514: - major substrates are Glc (low affinity [Johnson, 1990]), Gal, Fru, Man, GlcN [Uldry, 2004], [Uldry, 2002] - facilitated diffusion [Uldry, Pflugers Arch 2004] - intestine and kidney [Thorens, 1990], liver, pancreatic B cells, islet of Langerhans, brain [Uldry, 2004] - cDNA was cloned [Fukumoto, 1988] - glucose release from hepatocytes has two major pathways: 1) faciliated diffusion through GLUT2 and 2) membrane traffic pathway from ER to extracellular space. There is also a third minor route inwhich glucose re-enters the cytosol to form a pool that slowly diffuses out of the cells [Hosokawa, 2002] - release of glucose by transporters other than GLUT2 is low [Guillam, 1998] 6515: - major substrates are Glc (high affinity), Gal, Man, Xyl, maltose, dehydroascorbic acid [Uldry, 2004] - brain (neurons), testis (spermatozoa) [Haber, 1993], [Uldry, 2004], sk muscle (slow twitch fibers) [Stuart, 1999], platelets (alpha-granules) [Heijen, 1997] - cDNA was cloned [Kayano, 1988] 6518: - transports Fru [Uldry, Pflugers Arch 2004], but not Glc [Burant, 1992] - sm intestine (jejunal region), kidney, sk muscle, adipocytes [U - cDNA was isolated [Kayano,1990] 155184: - gene identified [Joost, 2001] and cloned [Li, 2004] - transports Glc, Fru [Li, 2004]
FTHFCL	3	Anguera MC, Suh JR, Ghandour H, Nasrallah IM, Selhub J, Stover PJ.	Methenyltetrahydrofolate synthetase regulates folate turnover and accumulation.	J Biol Chem	2003	12764149	IT cytoplasm based on GeneCards
FTHFDH	3	Johlin FC, Swain E, Smith C, Tephly TR.	Studies on the mechanism of methanol poisoning: purification and comparison of rat and human liver 10-formyltetrahydrofolate dehydrogenase.	Mol Pharmacol	1989	2733692	IT
FTHFLm	3	Prasannan P, Pike S, Peng K, Shane B, Appling DR	Human mitochondrial C1-tetrahydrofolate synthase: gene structure, tissue distribution of the mRNA, and immunolocalization in Chinese hamster ovary calls	J Biol Chem	2003	12937168	- encodes the mitochondrial isozyme of C1-tetrahydrofolate (THF) synthase, a trifunctional enzyme containing formyl-THF synthetase, methenyl-THF cyclohydrolase, and methylene-THF dehydrogenase activities [Prasannan, J Biol Chem 2003]
FUCASE2e	3	Hopfer RL, Johnson SW, Masserini M, Giuliani A, Alhadeff JA	Hydrolysis of fucosyl-GM1 ganglioside by purified pellet-associated human brain and human liver alpha-L-fucosidases without activator proteins or detergents	Biochem J	1990	2317201	2519: - integral membrane protein on cell surface [Cordero 2001] - accounts for 10-20% of total cellular fucosidase activity [Cordero 2001] - hematopoietic, epithelial, & mesenchimal cells expressed cell surface protein with alpha-l-fucosidase activity [Cordero 2001]; also found in membrane-assoc fraction from brain [Hopfer 1990] and plasma membrane of sperm [Alhadeff 1999] - purified and kinetically characterized [Khunsook 2003]
FUCASE2e	3	Alhadeff JA, Khunsook S, Choowongkomon K, Baney T, Heredia V, Tweedie A, Bean B	Characterization of human semen alpha-L-fucosidases	Mol Hum Reprod	1999	10460218	2519: - integral membrane protein on cell surface [Cordero 2001] - accounts for 10-20% of total cellular fucosidase activity [Cordero 2001] - hematopoietic, epithelial, & mesenchimal cells expressed cell surface protein with alpha-l-fucosidase activity [Cordero 2001]; also found in membrane-assoc fraction from brain [Hopfer 1990] and plasma membrane of sperm [Alhadeff 1999] - purified and kinetically characterized [Khunsook 2003]
FUCASE2e	3	Cordero OJ, Merino A, Paez de la Cadena M, Bugia B, Nogueira M, Vinuela JE, Martinez-Zorzano VS, de Carlos A, Rodriguez-Berrocal FJ	Cell surface human alpha-L-fucosidase	Eur J Biochem	2001	11389735	2519: - integral membrane protein on cell surface [Cordero 2001] - accounts for 10-20% of total cellular fucosidase activity [Cordero 2001] - hematopoietic, epithelial, & mesenchimal cells expressed cell surface protein with alpha-l-fucosidase activity [Cordero 2001]; also found in membrane-assoc fraction from brain [Hopfer 1990] and plasma membrane of sperm [Alhadeff 1999] - purified and kinetically characterized [Khunsook 2003]
FUCASE2e	3	Khunsook S, Bean BS, McGowan SR, Alhadeff JA	Purification and characterization of plasma membrane-associated human sperm alpha-L-fucosidase	Biol Reprod	2003	12604617	2519: - integral membrane protein on cell surface [Cordero 2001] - accounts for 10-20% of total cellular fucosidase activity [Cordero 2001] - hematopoietic, epithelial, & mesenchimal cells expressed cell surface protein with alpha-l-fucosidase activity [Cordero 2001]; also found in membrane-assoc fraction from brain [Hopfer 1990] and plasma membrane of sperm [Alhadeff 1999] - purified and kinetically characterized [Khunsook 2003]

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FUCASE2ly	3	Johnson SW, Alhadeff JA.	Mammalian alpha-L-fucosidases	Comp Biochem Physiol B	1991	1769200	- keratan sulfate chains are released extracellularly by proteolysis; mammalian cells do not have endoglycosidases activity towards keratan sulfate, so chains are broken down sequentially by exoglycosidases and sulfatases in the lysosome [Winchester 19996]; NOTE: extracellular proteolysis is not modeled here, chains are assumed to be linked to only ASn-X-Ser/Thr peptide - the linkage region of keratan sulfate type I is probably degraded by the same set of enzymes used for N-glycan degradation [Winchester 1996] -glycoconjugates contain L-fucose in various alpha-glycosic linkages (a-1,2, a-1,3, a-1,4, a-1,6) primarily to Gal and GlcNAc; appears that only one a-L-fucosidase is responsible for hydrolysis of all linkages [Johnson 1991] 2517: - a-L-fucosidases have been isolated from human brain, kidney, spleen, placenta, liver, epidermis, leucocytes, cultured fibroblasts, serum, and amniotic fluid (see refs in [Johnson 1991]) and seminal plasma [Khunsook 2002] - summary of kinetic properties and substrate specificities of purified enzymes [Johnson 1991], [Khunsook 2002] - cDNA cloned [Occhiodoro 1989], (partial seq cloned by [Fuk
FUCASE2ly	3	Occhiodoro T, Beckmann KR, Morris CP, Hopwood JJ	Human alpha-L-fucosidase: complete coding sequence from cDNA clones	Biochem Biophys Res Commun	1989	2803312	- keratan sulfate chains are released extracellularly by proteolysis; mammalian cells do not have endoglycosidases activity towards keratan sulfate, so chains are broken down sequentially by exoglycosidases and sulfatases in the lysosome [Winchester 19996]; NOTE: extracellular proteolysis is not modeled here, chains are assumed to be linked to only ASn-X-Ser/Thr peptide - the linkage region of keratan sulfate type I is probably degraded by the same set of enzymes used for N-glycan degradation [Winchester 1996] -glycoconjugates contain L-fucose in various alpha-glycosic linkages (a-1,2, a-1,3, a-1,4, a-1,6) primarily to Gal and GlcNAc; appears that only one a-L-fucosidase is responsible for hydrolysis of all linkages [Johnson 1991] 2517: - a-L-fucosidases have been isolated from human brain, kidney, spleen, placenta, liver, epidermis, leucocytes, cultured fibroblasts, serum, and amniotic fluid (see refs in [Johnson 1991]) and seminal plasma [Khunsook 2002] - summary of kinetic properties and substrate specificities of purified enzymes [Johnson 1991], [Khunsook 2002] - cDNA cloned [Occhiodoro 1989], (partial seq cloned by [Fuk
FUCASE2ly	3	Fukushima H, de Wet JR, O'Brien JS	Molecular cloning of a cDNA for human alpha-L-fucosidase	Proc Natl Acad Sci U S A	1985	2983333	- keratan sulfate chains are released extracellularly by proteolysis; mammalian cells do not have endoglycosidases activity towards keratan sulfate, so chains are broken down sequentially by exoglycosidases and sulfatases in the lysosome [Winchester 19996]; NOTE: extracellular proteolysis is not modeled here, chains are assumed to be linked to only ASn-X-Ser/Thr peptide - the linkage region of keratan sulfate type I is probably degraded by the same set of enzymes used for N-glycan degradation [Winchester 1996] -glycoconjugates contain L-fucose in various alpha-glycosic linkages (a-1,2, a-1,3, a-1,4, a-1,6) primarily to Gal and GlcNAc; appears that only one a-L-fucosidase is responsible for hydrolysis of all linkages [Johnson 1991] 2517: - a-L-fucosidases have been isolated from human brain, kidney, spleen, placenta, liver, epidermis, leucocytes, cultured fibroblasts, serum, and amniotic fluid (see refs in [Johnson 1991]) and seminal plasma [Khunsook 2002] - summary of kinetic properties and substrate specificities of purified enzymes [Johnson 1991], [Khunsook 2002] - cDNA cloned [Occhiodoro 1989], (partial seq cloned by [Fuk
FUCASE2ly	3	Khunsook S, Alhadeff JA, Bean BS	Purification and characterization of human seminal plasma alpha-L-fucosidase.	Mol Hum Reprod	2002	11870229	- keratan sulfate chains are released extracellularly by proteolysis; mammalian cells do not have endoglycosidases activity towards keratan sulfate, so chains are broken down sequentially by exoglycosidases and sulfatases in the lysosome [Winchester 19996]; NOTE: extracellular proteolysis is not modeled here, chains are assumed to be linked to only ASn-X-Ser/Thr peptide - the linkage region of keratan sulfate type I is probably degraded by the same set of enzymes used for N-glycan degradation [Winchester 1996] -glycoconjugates contain L-fucose in various alpha-glycosic linkages (a-1,2, a-1,3, a-1,4, a-1,6) primarily to Gal and GlcNAc; appears that only one a-L-fucosidase is responsible for hydrolysis of all linkages [Johnson 1991] 2517: - a-L-fucosidases have been isolated from human brain, kidney, spleen, placenta, liver, epidermis, leucocytes, cultured fibroblasts, serum, and amniotic fluid (see refs in [Johnson 1991]) and seminal plasma [Khunsook 2002] - summary of kinetic properties and substrate specificities of purified enzymes [Johnson 1991], [Khunsook 2002] - cDNA cloned [Occhiodoro 1989], (partial seq cloned by [Fuk

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FUMtm	3	Passarella S, Atlante A, Barile M, Quagliariello E.	Anion transport in rat brain mitochondria: fumarate uptake via the dicarboxylate carrier.	Neurochem Res	1987	3587497	- Added by RS/TV - fumarate and malate share a single carrier to enter mitochondria according to Passarella S, Atlante A, Barile M, Quagliariello E. Related Articles, Links Anion transport in rat brain mitochondria: fumarate uptake via the dicarboxylate carrier. Neurochem Res. 1987 Mar;12(3):255-64.
FUMTSULtm	3	Crompton M, Palmieri F, Capano M, Quagliariello E.	The transport of sulphate and sulphite in rat liver mitochondria.		1974	4441366	SLC25A10 (DIC) transporter facilitates the entry of thiosulphate into mitochondria, where rhodanase and thiosulphate reductase are found (PMID:14598172) biochemical evidence found in rat mitochondria MM
FUT12g	3	Larsen RD, Ernst LK, Nair RP, Lowe JB.	Molecular cloning, sequence, and expression of a human GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase cDNA that can form the H blood group antigen.	Proc Natl Acad Sci U S A	1990	2118655	localization: golgi see PMID 2118655 and swiss-prot. specificity: There are two genes (FUT1 and FUT2) which encode galactoside 2-L-fucosyltransferase. They are expressed in a tissue-specific manner with expression restricted to cells of mesodermal or endodermal origin respectively. Creates a soluble precursor oligosaccharide FuC-alpha ((1,2)Galbeta-) called the H antigen which is an essential substrate for the final step in the soluble A and B antigen synthesis pathway. H and Se enzymes fucosylate the same acceptor substrates but exhibit different Km values. sequence and function: PMID 2118655 NJ
FUT31g	3	Kukowska-Latallo JF, Larsen RD, Nair RP, Lowe JB.	A cloned human cDNA determines expression of a mouse stage-specific embryonic antigen and the Lewis blood group alpha(1,3/1,4)fucosyltransferase.	Genes Dev	1990	1977660	localization: Golgi and PMID: 1977660 and PMID: 12493760 specificity: Highly expressed in stomach, colon, small intestine, lung and kidney and to a lesser extent in salivary gland, bladder, uterus and liver. Swiss-Prot: May catalyze alpha-1,3 and alpha-1,4 glycosidic linkages involved in the expression of Vim-2, Lewis A, Lewis B, sialyl Lewis X and Lewis X/SSEA-1 antigens. May be involved in blood group Lewis determination; Lewis-positive (Le(+)) individuals have an active enzyme while Lewis-negative (Le(-)) individuals have an inactive enzyme. For sequence and cloning see PMID: 1977660. Interesting genotyping and allele freq ref: PMID: 12424536 NJ
FUT31g	3	Cakir B, Pankow JS, Salomaa V, Couper D, Morris TL, Brantley KR, Hiller KM, Heiss G, Weston BW.	Distribution of Lewis (FUT3)genotype and allele: frequencies in a biethnic United States population.	Ann Hematol	2002	12424536	localization: Golgi and PMID: 1977660 and PMID: 12493760 specificity: Highly expressed in stomach, colon, small intestine, lung and kidney and to a lesser extent in salivary gland, bladder, uterus and liver. Swiss-Prot: May catalyze alpha-1,3 and alpha-1,4 glycosidic linkages involved in the expression of Vim-2, Lewis A, Lewis B, sialyl Lewis X and Lewis X/SSEA-1 antigens. May be involved in blood group Lewis determination; Lewis-positive (Le(+)) individuals have an active enzyme while Lewis-negative (Le(-)) individuals have an inactive enzyme. For sequence and cloning see PMID: 1977660. Interesting genotyping and allele freq ref: PMID: 12424536 NJ

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FUT31g	3	Sousa VL, Brito C, Costa T, Lanoix J, Nilsson T, Costa J.	Importance of Cys, Gln, and Tyr from the transmembrane domain of human alpha 3/4 fucosyltransferase III for its localization and sorting in the Golgi of baby hamster kidney cells.	J Biol Chem	2003	12493760	localization: Golgi and PMID: 1977660 and PMID: 12493760 specificity: Highly expressed in stomach, colon, small intestine, lung and kidney and to a lesser extent in salivary gland, bladder, uterus and liver. Swiss-Prot: May catalyze alpha-1,3 and alpha-1,4 glycosidic linkages involved in the expression of Vim-2, Lewis A, Lewis B, sialyl Lewis X and Lewis X/SSEA-1 antigens. May be involved in blood group Lewis determination; Lewis-positive (Le(+)) individuals have an active enzyme while Lewis-negative (Le(-)) individuals have an inactive enzyme. For sequence and cloning see PMID: 1977660. Interesting genotyping and allele freq ref: PMID: 12424536 NJ
FUT91g	3	Kaneko M, Kudo T, Iwasaki H, Ikehara Y, Nishihara S, Nakagawa S, Sasaki K, Shiina T, Inoko H, Saitou N, Narimatsu H.	Alpha1,3-fucosyltransferase IX (Fuc-TIX) is very highly conserved between human and mouse; molecular cloning, characterization and tissue distribution of human Fuc-TIX.	FEBS Lett	1999	10386598	localization: golgi - uniprot specificity: Strongly expressed in forebrain and stomach, lower expression in spleen and peripheral blood leukocytes, and no expression in small intestine, colon, liver, lung, kidney, adrenal cortex or uterus in PMID: 10386598 FUT9 is one of several alpha-3-fucosyltransferases that can catalyze the last step in the biosynthesis of Lewis antigen, the addition of a fucose to precursor polysaccharides. FUT9 synthesizes the LeX oligosaccharide, which is expressed in organ buds progressing in mesenchyma during human embryogenesis.[supplied by OMIM] Transfers a fucose to lacto-N-neotetraose but not to either alpha2,3-sialyl lacto-N-neotetraose or lacto-N-tetraose. Can catalyze the last step in the biosynthesis of Lewis antigen, the addition of a fucose to precursor polysaccharides. NJ
G14T2g	3	Mengle-Gaw L, McCoy-Haman MF, Tiemeier DC	Genomic structure and expression of human beta-1,4-galactosyltransferase	Biochem Biophys Res Commun	1991	1903938	- sequence of biosynthetic pathway reviewed in [Funderburgh, IUBMB Life2002] - scheme for poly-NAcLac extension of core 4 proposed in [Ujita, J Biol Chem 2000] - all have exclusive specificity for UDP-galactose; Golgi apparatus [RefSeq], [UniProt] 2683: - cDNA was isolated [Appert, Biochem Biophys Res Commun 1986], sequence identified [Masri, Biochem Biophys Res Commun 1988], and expressed [Mengle-Gaw, Biochem Biophys Res Commun 1991] - homodimer [UniProt] 8703: - enzyme mainly involved in synthesis of first N-acetyllactosamine unit [RefSeq] - gene was cloned and expressed [Almeida, J Biol Chem 1997] 8704: - synthesizes N-acetyllactosamine in glycolipids and glycoproteins [RefSeq] - gene was cloned and expressed [Almeida, J Biol Chem 1997] 9334: - cDNA was isolated; 37% identity w/ beta-1,4-GalT and 28% with Lymnaea stagnalis beta-1,4-GlcNAcT [Sato, PNAS 1998] B4galt1p expressed in all tissues except brain; B4galt2p heart, muscle, pancreas; B4galt3 and B4galt5 ubiquitously expressed [Lo et al, Glycobiology 1998], [UniProt]

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G14T2g	3	Appert HE, Rutherford TJ, Tarr GE, Wiest JS, Thomford NR, McCorquodale DJ	Isolation of a cDNA coding for human galactosyltransferase	Biochem Biophys Res Commun	1986	3094506	- sequence of biosynthetic pathway reviewed in [Funderburgh, IUBMB Life2002] - scheme for poly-NAcLac extension of core 4 proposed in [Ujita, J Biol Chem 2000] - all have exclusive specificity for UDP-galactose; Golgi apparatus [RefSeq], [UniProt] 2683: - cDNA was isolated [Appert, Biochem Biophys Res Commun 1986], sequence identified [Masri, Biochem Biophys Res Commun 1988], and expressed [Mengle-Gaw, Biochem Biophys Res Commun 1991] - homodimer [UniProt] 8703: - enzyme mainly involved in synthesis of first N-acetyllactosamine unit [RefSeq] - gene was cloned and expressed [Almeida, J Biol Chem 1997] 8704: - synthesizes N-acetyllactosamine in glycolipids and glycoproteins [RefSeq] - gene was cloned and expressed [Almeida, J Biol Chem 1997] 9334: - cDNA was isolated; 37% identity w/ beta-1,4-GalT and 28% with Lymnaea stagnalis beta-1,4-GlcNAcT [Sato, PNAS 1998] B4galt1p expressed in all tissues except brain; B4galt2p heart, muscle, pancreas; B4galt3 and B4galt5 ubiquitously expressed [Lo et al, Glycobiology 1998], [UniProt]
G14T2g	3	Masri KA, Appert HE, Fukuda MN	Identification of the full-length coding sequence for human galactosyltransferase (beta-N-acetylglucosaminide: beta 1,4-galactosyltransferase)	Biochem Biophys Res Commun	1988	3144273	- sequence of biosynthetic pathway reviewed in [Funderburgh, IUBMB Life2002] - scheme for poly-NAcLac extension of core 4 proposed in [Ujita, J Biol Chem 2000] - all have exclusive specificity for UDP-galactose; Golgi apparatus [RefSeq], [UniProt] 2683: - cDNA was isolated [Appert, Biochem Biophys Res Commun 1986], sequence identified [Masri, Biochem Biophys Res Commun 1988], and expressed [Mengle-Gaw, Biochem Biophys Res Commun 1991] - homodimer [UniProt] 8703: - enzyme mainly involved in synthesis of first N-acetyllactosamine unit [RefSeq] - gene was cloned and expressed [Almeida, J Biol Chem 1997] 8704: - synthesizes N-acetyllactosamine in glycolipids and glycoproteins [RefSeq] - gene was cloned and expressed [Almeida, J Biol Chem 1997] 9334: - cDNA was isolated; 37% identity w/ beta-1,4-GalT and 28% with Lymnaea stagnalis beta-1,4-GlcNAcT [Sato, PNAS 1998] B4galt1p expressed in all tissues except brain; B4galt2p heart, muscle, pancreas; B4galt3 and B4galt5 ubiquitously expressed [Lo et al, Glycobiology 1998], [UniProt]

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G14T2g	3	Almeida R, Amado M, David L, Levery SB, Holmes EH, Merkx G, van Kessel AG, Rygaard E, Hassan H, Bennett E, Clausen H	A family of human beta4-galactosyltransferases. Cloning and expression of two novel UDP-galactose:beta-n-acetylglucosamine beta1, 4-galactosyltransferases, beta4Gal-T2 and beta4Gal-T3	J Biol Chem	1997	9405390	- sequence of biosynthetic pathway reviewed in [Funderburgh, IUBMB Life2002] - scheme for poly-NAcLac extension of core 4 proposed in [Ujita, J Biol Chem 2000] - all have exclusive specificity for UDP-galactose; Golgi apparatus [RefSeq], [UniProt] 2683: - cDNA was isolated [Appert, Biochem Biophys Res Commun 1986], sequence identified [Masri, Biochem Biophys Res Commun 1988], and expressed [Mengle-Gaw, Biochem Biophys Res Commun 1991] - homodimer [UniProt] 8703: - enzyme mainly involved in synthesis of first N-acetyllactosamine unit [RefSeq] - gene was cloned and expressed [Almeida, J Biol Chem 1997] 8704: - synthesizes N-acetyllactosamine in glycolipids and glycoproteins [RefSeq] - gene was cloned and expressed [Almeida, J Biol Chem 1997] 9334: - cDNA was isolated; 37% identity w/ beta-1,4-GalT and 28% with Lymnaea stagnalis beta-1,4-GlcNAcT [Sato, PNAS 1998] B4galt1p expressed in all tissues except brain; B4galt2p heart, muscle, pancreas; B4galt3 and B4galt5 ubiquitously expressed [Lo et al, Glycobiology 1998], [UniProt]
G14T2g	3	Sato T, Furukawa K, Bakker H, Van den Eijnden DH, Van Die I.	Molecular cloning of a human cDNA encoding beta-1,4-galactosyltransferase with 37% identity to mammalian UDP-Gal:GlcNAc beta-1,4-galactosyltransferase	Proc Natl Acad Sci U S A	1998	9435216	- sequence of biosynthetic pathway reviewed in [Funderburgh, IUBMB Life2002] - scheme for poly-NAcLac extension of core 4 proposed in [Ujita, J Biol Chem 2000] - all have exclusive specificity for UDP-galactose; Golgi apparatus [RefSeq], [UniProt] 2683: - cDNA was isolated [Appert, Biochem Biophys Res Commun 1986], sequence identified [Masri, Biochem Biophys Res Commun 1988], and expressed [Mengle-Gaw, Biochem Biophys Res Commun 1991] - homodimer [UniProt] 8703: - enzyme mainly involved in synthesis of first N-acetyllactosamine unit [RefSeq] - gene was cloned and expressed [Almeida, J Biol Chem 1997] 8704: - synthesizes N-acetyllactosamine in glycolipids and glycoproteins [RefSeq] - gene was cloned and expressed [Almeida, J Biol Chem 1997] 9334: - cDNA was isolated; 37% identity w/ beta-1,4-GalT and 28% with Lymnaea stagnalis beta-1,4-GlcNAcT [Sato, PNAS 1998] B4galt1p expressed in all tissues except brain; B4galt2p heart, muscle, pancreas; B4galt3 and B4galt5 ubiquitously expressed [Lo et al, Glycobiology 1998], [UniProt]

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G14T2g	3	Funderburgh JL	Keratan sulfate biosynthesis	IUBMB Life	2002	12512857	- sequence of biosynthetic pathway reviewed in [Funderburgh, IUBMB Life2002] - scheme for poly-NAcLac extension of core 4 proposed in [Ujita, J Biol Chem 2000] - all have exclusive specificity for UDP-galactose; Golgi apparatus [RefSeq], [UniProt] 2683: - cDNA was isolated [Appert, Biochem Biophys Res Commun 1986], sequence identified [Masri, Biochem Biophys Res Commun 1988], and expressed [Mengle-Gaw, Biochem Biophys Res Commun 1991] - homodimer [UniProt] 8703: - enzyme mainly involved in synthesis of first N-acetyllactosamine unit [RefSeq] - gene was cloned and expressed [Almeida, J Biol Chem 1997] 8704: - synthesizes N-acetyllactosamine in glycolipids and glycoproteins [RefSeq] - gene was cloned and expressed [Almeida, J Biol Chem 1997] 9334: - cDNA was isolated; 37% identity w/ beta-1,4-GalT and 28% with Lymnaea stagnalis beta-1,4-GlcNAcT [Sato, PNAS 1998] B4galt1p expressed in all tissues except brain; B4galt2p heart, muscle, pancreas; B4galt3 and B4galt5 ubiquitously expressed [Lo et al, Glycobiology 1998], [UniProt]
G14Tg	3	Lo NW, Shaper JH, Pevsner J, Shaper NL.	The expanding beta 4-galactosyltransferase gene family: messages from the databanks	Glycobiology	1998	9597550	membrane-bound glycoproteins that appear to have exclusive specificity for the donor substrate UDP-galactose; all transfer galactose in a beta1,4 linkage to similar acceptor sugars: GlcNAc, Glc, and Xyl. As type II membrane proteins, they have an N-terminal hydrophobic signal sequence that directs the protein to the Golgi apparatus and which then remains uncleaved to function as a transmembrane anchor. By sequence similarity, the beta4GalTs form four groups: beta4GalT1 and beta4GalT2, beta4GalT3 and beta4GalT4, beta4GalT5 and beta4GalT6, and beta4GalT7. B4GALT1 is unique among the beta4GalT genes because it encodes an enzyme that participates both in glycoconjugate and lactose biosynthesis. For the first activity, the enzyme adds galactose to N-acetylglucosamine residues that are either monosaccharides or the nonreducing ends of glycoprotein carbohydrate chains. The two enzymatic forms result from alternate transcription initiation sites and post-translational processing. Two transcripts, which differ only at the 5' end, wit B4GALT3 encodes an enzyme that may be mainly involved in The enzyme encoded by B4GALT2 synthesizes N-acetyllactosa
G14Tg	3	Amado M, Almeida R, Carneiro F, Levery ST, Holmes EH, Nomoto M, Hollingsworth MA, Hassan H, Schwientek T, Nielsen PA, Bennett EP, Clausen H	A family of human beta3-galactosyltransferases	The Journal of Biological Chemistry	1998		membrane-bound glycoproteins that appear to have exclusive specificity for the donor substrate UDP-galactose; all transfer galactose in a beta1,4 linkage to similar acceptor sugars: GlcNAc, Glc, and Xyl. As type II membrane proteins, they have an N-terminal hydrophobic signal sequence that directs the protein to the Golgi apparatus and which then remains uncleaved to function as a transmembrane anchor. By sequence similarity, the beta4GalTs form four groups: beta4GalT1 and beta4GalT2, beta4GalT3 and beta4GalT4, beta4GalT5 and beta4GalT6, and beta4GalT7. B4GALT1 is unique among the beta4GalT genes because it encodes an enzyme that participates both in glycoconjugate and lactose biosynthesis. For the first activity, the enzyme adds galactose to N-acetylglucosamine residues that are either monosaccharides or the nonreducing ends of glycoprotein carbohydrate chains. The two enzymatic forms result from alternate transcription initiation sites and post-translational processing. Two transcripts, which differ only at the 5' end, wit B4GALT3 encodes an enzyme that may be mainly involved in The enzyme encoded by B4GALT2 synthesizes N-acetyllactosa
G3PD1	3	Menaya J, Gonzalez-Manchon C, Parrilla R, Ayuso MS.	Molecular cloning, sequencing and expression of a cDNA encoding a human liver NAD-dependent alpha glycerol-3-phosphate dehydrogenase.	Biochim Biophys Acta	1995	7772607	cytoplasm - uniprot cloning, seq, biochem act - Menaya ref NJ NCD pointed out that GLYC3P -> DHAP directionality needed for glycogenolysis in the cytosol. Rev direction supported by Salway text and Brisson review (PMID: 11385633).

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
G3PD1	3	Brisson D, Vohl MC, St-Pierre J, Hudson TJ, Gaudet D.	Glycerol: a neglected variable in metabolic processes?	Bioessays	2001	11385633	cytoplasm - uniprot cloning, seq, biochem act - Menaya ref NJ NCD pointed out that GLYC3P -> DHAP directionality needed for glycogenolysis in the cytosol. Rev direction supported by Salway text and Brisson review (PMID: 11385633).
G3PD1	3	Salway, JG	Metabolism at a Glance, 2nd ed		1999		cytoplasm - uniprot cloning, seq, biochem act - Menaya ref NJ NCD pointed out that GLYC3P -> DHAP directionality needed for glycogenolysis in the cytosol. Rev direction supported by Salway text and Brisson review (PMID: 11385633).
G3PD2m	2	Ferrer J, Aoki M, Behn P, Nestorowicz A, Riggs A, Permutt MA.	Mitochondrial glycerol-3-phosphate dehydrogenase. Cloning of an alternatively spliced human islet-cell cDNA, tissue distribution, physical mapping, and identification of a polymorphic genetic marker.	Diabetes	1996	8549872	- Added by RS/TV - mitochondrial according to GeneCards - FAD dependent according to GeneCards - Tissue Expression: human pancreatic islets and other tissues (Ferrer J, Aoki M, Behn P, Nestorowicz A, Riggs A, Permutt MA. Diabetes. 1996 Feb;45(2):262-6.) Compartmentation of FAD/FADH2 in mit matrix, but glyc3p/dhap in cytosol noted by NCD as per Brisson (11385633).
G5SADs	2	Hu CA, Lin WW, Obie C, Valle D	Molecular enzymology of mammalian Delta1-pyrroline-5-carboxylate synthase. Alternative splice donor utilization generates isoforms with different sensitivity to ornithine inhibition	J Biol Chem	1999	10037775	KEGG says "non enzymatic" under R03314 citation describes it as "nonenzymatic equibibrium"
G6PDA	3	Shevchenko V, Hogben M, Ekong R, Parrington J, Lai FA	The human glucosamine-6-phosphate deaminase gene: cDNA cloning and expression, genomic organization and chromosomal localization	Gene	1998	9714720	- cloning and expression of 10007 [Shevchenko, Gene 1998] - shown as irreversible in Figure 6.1 on p74 of Varki - high-energy requiring tissues such as neurona and transporting epithelial cells in kidney and intestine use this enzyme to generate f6p for glycolysis; enzyme is essentially absent from liver where other sources of energy are available [Varki, p. 77-8]
G6PDA	3	Varki, Cummings, Esko, Freeze, Hart, Marth	Essentials of Glycobiology		1999		- cloning and expression of 10007 [Shevchenko, Gene 1998] - shown as irreversible in Figure 6.1 on p74 of Varki - high-energy requiring tissues such as neurona and transporting epithelial cells in kidney and intestine use this enzyme to generate f6p for glycolysis; enzyme is essentially absent from liver where other sources of energy are available [Varki, p. 77-8]
G6PDH1er	3	Barash V, Erlich T, Bashan N.	Microsomal hexose-6-phosphate and 6-phosphogluconate dehydrogenases in extrahepatic tissues: human placenta and pig kidney cortex.	Biochem Int	1990	2156506	9563: - can use NAD or NADP [UniProt] - oxidizes glucose-6-phosphate and glucose, as well as other hexose-6-phosphates [UniProt] -shows activity with other hexose-6-phosphates, especially galactose-6-phosphate [RefSeq] - not found in red cells [RefSeq] - endoplasmic reticulum lumen [UniProt], [Clarke 2003] - cDNA isolated and cloned [Mason 1999] - hexose-6-phosphate dehydrogenase isolated from human placental microsomes [Barash 1990]
G6PDH1er	3	Mason PJ, Stevens D, Diez A, Knight SW, Scopes DA, Vulliamy TJ.	Human hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) encoded at 1p36: coding sequence and expression.	Blood Cells Mol Dis	1999	10349511	9563: - can use NAD or NADP [UniProt] - oxidizes glucose-6-phosphate and glucose, as well as other hexose-6-phosphates [UniProt] -shows activity with other hexose-6-phosphates, especially galactose-6-phosphate [RefSeq] - not found in red cells [RefSeq] - endoplasmic reticulum lumen [UniProt], [Clarke 2003] - cDNA isolated and cloned [Mason 1999] - hexose-6-phosphate dehydrogenase isolated from human placental microsomes [Barash 1990]
G6PDH1er	3	Clarke JL, Mason PJ	Murine hexose-6-phosphate dehydrogenase: a bifunctional enzyme with broad substrate specificity and 6-phosphogluconolactonase activity.	Arch Biochem Biophys	2003	12831846	9563: - can use NAD or NADP [UniProt] - oxidizes glucose-6-phosphate and glucose, as well as other hexose-6-phosphates [UniProt] -shows activity with other hexose-6-phosphates, especially galactose-6-phosphate [RefSeq] - not found in red cells [RefSeq] - endoplasmic reticulum lumen [UniProt], [Clarke 2003] - cDNA isolated and cloned [Mason 1999] - hexose-6-phosphate dehydrogenase isolated from human placental microsomes [Barash 1990]

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G6PPer	3	Lei KJ, Shelly LL, Pan CJ, Sidbury JB, Chou JY	Mutations in the glucose-6-phosphatase gene that cause glycogen storage disease type 1a	Science	1993	8211187	- enzyme is found in liver, kidney, intestine, but NOT muscle [Orten, Human Biochem 1975] 2538: -integral to ER membrane [LocusLink] - may be hydrolase and translocase [UniProt] - active site faces ER lumen [Pan et al, J Biol Chem 1998] - also known as G6Pase alpha [Lei, Science 1993], [Shelly, J Biol Chem 1993] - expressed in liver, kidney, intestine (gluconeogenic tissues) [Nordlie and Sukalski, The Enzymes of Biological Membranes 1985], [Orten, Human Biochem 1975] 57818: - also known as islet-specific glucose-6-phosphatase-related protein (IGRP) -specific to pancreatic B islet cells [Arden, Diabetes 1999], [Martin, J Biol Chem 2001] - active site in ER [Shieh, FEBS Lett 2004] 92579: - also known as G6Pase-related protein - ubiquitously distributed [Martin, J Mol Endocrinol 2002], [Shieh, J Biol Chem 2003], [Guione, FEBS Lett 2003]
G6PPer	3	Shelly LL, Lei KJ, Pan CJ, Sakata SF, Ruppert S, Schutz G, Chou JY.	Isolation of the gene for murine glucose-6-phosphatase, the enzyme deficient in glycogen storage disease type 1A	J Biol Chem	1993	8407995	- enzyme is found in liver, kidney, intestine, but NOT muscle [Orten, Human Biochem 1975] 2538: -integral to ER membrane [LocusLink] - may be hydrolase and translocase [UniProt] - active site faces ER lumen [Pan et al, J Biol Chem 1998] - also known as G6Pase alpha [Lei, Science 1993], [Shelly, J Biol Chem 1993] - expressed in liver, kidney, intestine (gluconeogenic tissues) [Nordlie and Sukalski, The Enzymes of Biological Membranes 1985], [Orten, Human Biochem 1975] 57818: - also known as islet-specific glucose-6-phosphatase-related protein (IGRP) -specific to pancreatic B islet cells [Arden, Diabetes 1999], [Martin, J Biol Chem 2001] - active site in ER [Shieh, FEBS Lett 2004] 92579: - also known as G6Pase-related protein - ubiquitously distributed [Martin, J Mol Endocrinol 2002], [Shieh, J Biol Chem 2003], [Guione, FEBS Lett 2003]
G6PPer	3	Pan CJ, Lei KJ, Annabi B, Hemrika W, Chou JY	Transmembrane topology of glucose-6-phosphatase.	J Biol Chem	1998	9497333	- enzyme is found in liver, kidney, intestine, but NOT muscle [Orten, Human Biochem 1975] 2538: -integral to ER membrane [LocusLink] - may be hydrolase and translocase [UniProt] - active site faces ER lumen [Pan et al, J Biol Chem 1998] - also known as G6Pase alpha [Lei, Science 1993], [Shelly, J Biol Chem 1993] - expressed in liver, kidney, intestine (gluconeogenic tissues) [Nordlie and Sukalski, The Enzymes of Biological Membranes 1985], [Orten, Human Biochem 1975] 57818: - also known as islet-specific glucose-6-phosphatase-related protein (IGRP) -specific to pancreatic B islet cells [Arden, Diabetes 1999], [Martin, J Biol Chem 2001] - active site in ER [Shieh, FEBS Lett 2004] 92579: - also known as G6Pase-related protein - ubiquitously distributed [Martin, J Mol Endocrinol 2002], [Shieh, J Biol Chem 2003], [Guione, FEBS Lett 2003]

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G6PPer	3	Arden SD, Zahn T, Steegers S, Webb S, Bergman B, O'Brien RM, Hutton JC.	Molecular cloning of a pancreatic islet-specific glucose-6-phosphatase catalytic subunit-related protein.	Diabetes	1999	10078553	- enzyme is found in liver, kidney, intestine, but NOT muscle [Orten, Human Biochem 1975] 2538: -integral to ER membrane [LocusLink] - may be hydrolase and translocase [UniProt] - active site faces ER lumen [Pan et al, J Biol Chem 1998] - also known as G6Pase alpha [Lei, Science 1993], [Shelly, J Biol Chem 1993] - expressed in liver, kidney, intestine (gluconeogenic tissues) [Nordlie and Sukalski, The Enzymes of Biological Membranes 1985], [Orten, Human Biochem 1975] 57818: - also known as islet-specific glucose-6-phosphatase-related protein (IGRP) -specific to pancreatic B islet cells [Arden, Diabetes 1999], [Martin, J Biol Chem 2001] - active site in ER [Shieh, FEBS Lett 2004] 92579: - also known as G6Pase-related protein - ubiquitously distributed [Martin, J Mol Endocrinol 2002], [Shieh, J Biol Chem 2003], [Guione, FEBS Lett 2003]
G6PPer	3	Martin CC, Bischof LJ, Bergman B, Hornbuckle LA, Hilliker C, Frigeri C, Wahl D, Svitek CA, Wong R, Goldman JK, Oeser JK, Lepretre F, Froguel P, O'Brien RM, Hutton JC.	Cloning and characterization of the human and rat islet-specific glucose-6-phosphatase catalytic subunit-related protein (IGRP) genes.	J Biol Chem	2001	11297555	- enzyme is found in liver, kidney, intestine, but NOT muscle [Orten, Human Biochem 1975] 2538: -integral to ER membrane [LocusLink] - may be hydrolase and translocase [UniProt] - active site faces ER lumen [Pan et al, J Biol Chem 1998] - also known as G6Pase alpha [Lei, Science 1993], [Shelly, J Biol Chem 1993] - expressed in liver, kidney, intestine (gluconeogenic tissues) [Nordlie and Sukalski, The Enzymes of Biological Membranes 1985], [Orten, Human Biochem 1975] 57818: - also known as islet-specific glucose-6-phosphatase-related protein (IGRP) -specific to pancreatic B islet cells [Arden, Diabetes 1999], [Martin, J Biol Chem 2001] - active site in ER [Shieh, FEBS Lett 2004] 92579: - also known as G6Pase-related protein - ubiquitously distributed [Martin, J Mol Endocrinol 2002], [Shieh, J Biol Chem 2003], [Guione, FEBS Lett 2003]
G6PPer	3	Martin CC, Oeser JK, Svitek CA, Hunter SI, Hutton JC, O'Brien RM	Identification and characterization of a human cDNA and gene encoding a ubiquitously expressed glucose-6-phosphatase catalytic subunit-related protein.	J Mol Endocrinol	2002	12370122	- enzyme is found in liver, kidney, intestine, but NOT muscle [Orten, Human Biochem 1975] 2538: -integral to ER membrane [LocusLink] - may be hydrolase and translocase [UniProt] - active site faces ER lumen [Pan et al, J Biol Chem 1998] - also known as G6Pase alpha [Lei, Science 1993], [Shelly, J Biol Chem 1993] - expressed in liver, kidney, intestine (gluconeogenic tissues) [Nordlie and Sukalski, The Enzymes of Biological Membranes 1985], [Orten, Human Biochem 1975] 57818: - also known as islet-specific glucose-6-phosphatase-related protein (IGRP) -specific to pancreatic B islet cells [Arden, Diabetes 1999], [Martin, J Biol Chem 2001] - active site in ER [Shieh, FEBS Lett 2004] 92579: - also known as G6Pase-related protein - ubiquitously distributed [Martin, J Mol Endocrinol 2002], [Shieh, J Biol Chem 2003], [Guione, FEBS Lett 2003]

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G6PPer	3	Guionie O, Clottes E, Stafford K, Burchell A.	Identification and characterisation of a new human glucose-6-phosphatase isoform	FEBS Lett	2003	12965222	- enzyme is found in liver, kidney, intestine, but NOT muscle [Orten, Human Biochem 1975] 2538: -integral to ER membrane [LocusLink] - may be hydrolase and translocase [UniProt] - active site faces ER lumen [Pan et al, J Biol Chem 1998] - also known as G6Pase alpha [Lei, Science 1993], [Shelly, J Biol Chem 1993] - expressed in liver, kidney, intestine (gluconeogenic tissues) [Nordlie and Sukalski, The Enzymes of Biological Membranes 1985], [Orten, Human Biochem 1975] 57818: - also known as islet-specific glucose-6-phosphatase-related protein (IGRP) -specific to pancreatic B islet cells [Arden, Diabetes 1999], [Martin, J Biol Chem 2001] - active site in ER [Shieh, FEBS Lett 2004] 92579: - also known as G6Pase-related protein - ubiquitously distributed [Martin, J Mol Endocrinol 2002], [Shieh, J Biol Chem 2003], [Guione, FEBS Lett 2003]
G6PPer	3	Shieh JJ, Pan CJ, Mansfield BC, Chou JY.	A glucose-6-phosphate hydrolase, widely expressed outside the liver, can explain age-dependent resolution of hypoglycemia in glycogen storage disease type Ia.	J Biol Chem	2003	13129915	- enzyme is found in liver, kidney, intestine, but NOT muscle [Orten, Human Biochem 1975] 2538: -integral to ER membrane [LocusLink] - may be hydrolase and translocase [UniProt] - active site faces ER lumen [Pan et al, J Biol Chem 1998] - also known as G6Pase alpha [Lei, Science 1993], [Shelly, J Biol Chem 1993] - expressed in liver, kidney, intestine (gluconeogenic tissues) [Nordlie and Sukalski, The Enzymes of Biological Membranes 1985], [Orten, Human Biochem 1975] 57818: - also known as islet-specific glucose-6-phosphatase-related protein (IGRP) -specific to pancreatic B islet cells [Arden, Diabetes 1999], [Martin, J Biol Chem 2001] - active site in ER [Shieh, FEBS Lett 2004] 92579: - also known as G6Pase-related protein - ubiquitously distributed [Martin, J Mol Endocrinol 2002], [Shieh, J Biol Chem 2003], [Guione, FEBS Lett 2003]
G6PPer	3	Shieh JJ, Pan CJ, Mansfield BC, Chou JY	The islet-specific glucose-6-phosphatase-related protein, implicated in diabetes, is a glycoprotein embedded in the endoplasmic reticulum membrane	FEBS Lett	2004	15044018	- enzyme is found in liver, kidney, intestine, but NOT muscle [Orten, Human Biochem 1975] 2538: -integral to ER membrane [LocusLink] - may be hydrolase and translocase [UniProt] - active site faces ER lumen [Pan et al, J Biol Chem 1998] - also known as G6Pase alpha [Lei, Science 1993], [Shelly, J Biol Chem 1993] - expressed in liver, kidney, intestine (gluconeogenic tissues) [Nordlie and Sukalski, The Enzymes of Biological Membranes 1985], [Orten, Human Biochem 1975] 57818: - also known as islet-specific glucose-6-phosphatase-related protein (IGRP) -specific to pancreatic B islet cells [Arden, Diabetes 1999], [Martin, J Biol Chem 2001] - active site in ER [Shieh, FEBS Lett 2004] 92579: - also known as G6Pase-related protein - ubiquitously distributed [Martin, J Mol Endocrinol 2002], [Shieh, J Biol Chem 2003], [Guione, FEBS Lett 2003]

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
G6PPer	3	Nordlie, R.C. and Sukalski, K.A.	The Enzymes of Biological Membranes		1985		- enzyme is found in liver, kidney, intestine, but NOT muscle [Orten, Human Biochem 1975] 2538: -integral to ER membrane [LocusLink] - may be hydrolase and translocase [UniProt] - active site faces ER lumen [Pan et al, J Biol Chem 1998] - also known as G6Pase alpha [Lei, Science 1993], [Shelly, J Biol Chem 1993] - expressed in liver, kidney, intestine (gluconeogenic tissues) [Nordlie and Sukalski, The Enzymes of Biological Membranes 1985], [Orten, Human Biochem 1975] 57818: - also known as islet-specific glucose-6-phosphatase-related protein (IGRP) -specific to pancreatic B islet cells [Arden, Diabetes 1999], [Martin, J Biol Chem 2001] - active site in ER [Shieh, FEBS Lett 2004] 92579: - also known as G6Pase-related protein - ubiquitously distributed [Martin, J Mol Endocrinol 2002], [Shieh, J Biol Chem 2003], [Guione, FEBS Lett 2003]
G6Pter	3	Gerin I, Veiga-da-Cunha M, Achouri Y, Collet JF, Van Schaftingen E	Sequence of a putative glucose 6-phosphate translocase, mutated in glycogen storage disease type Ib	FEBS Lett	1997	9428641	2542: - encodes a reversible glucose-6-phosphate transporter [van Schaftingen and Gerin, Biochem J 2002] - cloned [Gerin 1997] - highly expressed in human liver, kidney, haematopoietcs prgenitor cells [Ihara 2000] - 20-26% identity to E. coli G6P transporters [Gerin 1997] - ER target sequence [Gerin 1997] - brain/heart/sk muscle isoform transports G6P into ER lumen [Lin 2000]
G6Pter	3	Ihara K, Nomura A, Hikino S, Takada H, Hara T	Quantitative analysis of glucose-6-phosphate translocase gene expression in various human tissues and haematopoietic progenitor cells	J Inherit Metab Dis	2000	11032333	2542: - encodes a reversible glucose-6-phosphate transporter [van Schaftingen and Gerin, Biochem J 2002] - cloned [Gerin 1997] - highly expressed in human liver, kidney, haematopoietcs prgenitor cells [Ihara 2000] - 20-26% identity to E. coli G6P transporters [Gerin 1997] - ER target sequence [Gerin 1997] - brain/heart/sk muscle isoform transports G6P into ER lumen [Lin 2000]
G6Pter	3	Lin B, Pan CJ, Chou JY	Human variant glucose-6-phosphate transporter is active in microsomal transport	Hum Genet	2000	11140953	2542: - encodes a reversible glucose-6-phosphate transporter [van Schaftingen and Gerin, Biochem J 2002] - cloned [Gerin 1997] - highly expressed in human liver, kidney, haematopoietcs prgenitor cells [Ihara 2000] - 20-26% identity to E. coli G6P transporters [Gerin 1997] - ER target sequence [Gerin 1997] - brain/heart/sk muscle isoform transports G6P into ER lumen [Lin 2000]
G6Pter	3	van Schaftingen E, Gerin I	The glucose-6-phopsphatase system	Biochem J	2002	11879177	2542: - encodes a reversible glucose-6-phosphate transporter [van Schaftingen and Gerin, Biochem J 2002] - cloned [Gerin 1997] - highly expressed in human liver, kidney, haematopoietcs prgenitor cells [Ihara 2000] - 20-26% identity to E. coli G6P transporters [Gerin 1997] - ER target sequence [Gerin 1997] - brain/heart/sk muscle isoform transports G6P into ER lumen [Lin 2000]
GACMTRc	3	Pegg AE, Nagarajan S, Naficy S, Ganem B	Role of unsaturated derivatives of spermidine as substrates for spermine synthase and in supporting growth of SV-3T3 cells	Biochem J	1991	2001229	Well-established function
GAL3ST11	3	Honke K, Tsuda M, Hirahara Y, Ishii A, Makita A, Wada Y.	Molecular cloning and expression of cDNA encoding human 3'-phosphoadenylylsulfate:galactosylceramide 3'-sulfotransferase.	J Biol Chem	1997	9030544	Golgi - lumen side - see ref Kolter and Sanhoff; also noted in uniprot Sulfonation, an important step in the metabolism of many drugs, xenobiotics, hormones, and neurotransmitters, is catalyzed by sulfotransferases. The product of this gene is galactosylceramide sulfotransferase which catalyzes the conversion between 3'-phosphoadenylylsulfate + a galactosylceramide to adenosine 3',5'-bisphosphate + galactosylceramide sulfate. Activity of this sulfotransferase is enhanced in renal cell carcinoma. NJ

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
GALASE1ly	3	Glossl J, Truppe W, Kresse H	Purification and properties of N-acetylgalactosamine 6-sulphate sulphatase from human placenta	Biochem J	1979	39554	- two distinct forms of lysosomal complex purified from human placenta: CathA/GAL/SIAL/GALNS and CathA/GAL [Pshezhetsky 2001], [Ostrowska 2003]; average ratio btwn CathA/GAL/SIAL/GALNS and CathA/GAL complexes is 1:10 [Pshezhetsky 2001] 2720: - cleaves terminal beta-1,4- or beta-1,3- linked galactose from GM1-ganglioside, GA1 ganglioside, lactosylceramide, asialofetuin, galactose-containing oligosaccharides, keratan sulfate [Pshezhetsky 2001] - pH optimum is 4.5-4.75 [Pshezhetsky 2001] - most abundant in liver, kidney, skin, blood cells [Pshezhetsky 2001] - cloned and expressed in COS cells [Oshima 1988] - cDNA isolated [Yamamoto 1990] 4758: - hydrolyzes terminal sialic acids of glycolipids and glycopeptides [Pshezhetsky 2001] - pH optimum 4.2 [Pshezhetsky 2001] - cloned an expressed in fibroblasts [Pshezhetsky 1997],[Bonten 1996] and COS-7 cells [Milner 1997] 2588: - purified from human placenta [Glossl 1979], [Lim & Horwitz 1981], [Masue1991] and human liver [Bielicki 1991], recombinant protein purified from CHO cells [Bielicki 1995] - kinetic characterization [Bielicki 1991], [Masue1991], [Bielic - could desulfate acetylgalactosamine 6-sulphate (from chondroitin-6-sulfate) or galactose 6-sulphate glucosamine 6-sulphate residues in keratan sulfate or heparan su - cloned and expressed in deficient fibroblasts [Tomatsu 1991]
GALASE1ly	3	Tomatsu S, Fukuda S, Masue M, Sukegawa K, Fukao T, Yamagishi A, Hori T, Iwata H, Ogawa T, Nakashima Y, et al	Morquio disease: isolation, characterization and expression of full-length cDNA for human N-acetylgalactosamine-6-sulfate sulfatase	Biochem Biophys Res Commun	1991	1755850	- two distinct forms of lysosomal complex purified from human placenta: CathA/GAL/SIAL/GALNS and CathA/GAL [Pshezhetsky 2001], [Ostrowska 2003]; average ratio btwn CathA/GAL/SIAL/GALNS and CathA/GAL complexes is 1:10 [Pshezhetsky 2001] 2720: - cleaves terminal beta-1,4- or beta-1,3- linked galactose from GM1-ganglioside, GA1 ganglioside, lactosylceramide, asialofetuin, galactose-containing oligosaccharides, keratan sulfate [Pshezhetsky 2001] - pH optimum is 4.5-4.75 [Pshezhetsky 2001] - most abundant in liver, kidney, skin, blood cells [Pshezhetsky 2001] - cloned and expressed in COS cells [Oshima 1988] - cDNA isolated [Yamamoto 1990] 4758: - hydrolyzes terminal sialic acids of glycolipids and glycopeptides [Pshezhetsky 2001] - pH optimum 4.2 [Pshezhetsky 2001] - cloned an expressed in fibroblasts [Pshezhetsky 1997],[Bonten 1996] and COS-7 cells [Milner 1997] 2588: - purified from human placenta [Glossl 1979], [Lim & Horwitz 1981], [Masue1991] and human liver [Bielicki 1991], recombinant protein purified from CHO cells [Bielicki 1995] - kinetic characterization [Bielicki 1991], [Masue1991], [Bielic - could desulfate acetylgalactosamine 6-sulphate (from chondroitin-6-sulfate) or galactose 6-sulphate glucosamine 6-sulphate residues in keratan sulfate or heparan su - cloned and expressed in deficient fibroblasts [Tomatsu 1991]
GALASE1ly	3	Masue M, Sukegawa K, Orii T, Hashimoto T	N-acetylgalactosamine-6-sulfate sulfatase in human placenta: purification and characteristics	J Biochem (Tokyo)	1991	1794986	- two distinct forms of lysosomal complex purified from human placenta: CathA/GAL/SIAL/GALNS and CathA/GAL [Pshezhetsky 2001], [Ostrowska 2003]; average ratio btwn CathA/GAL/SIAL/GALNS and CathA/GAL complexes is 1:10 [Pshezhetsky 2001] 2720: - cleaves terminal beta-1,4- or beta-1,3- linked galactose from GM1-ganglioside, GA1 ganglioside, lactosylceramide, asialofetuin, galactose-containing oligosaccharides, keratan sulfate [Pshezhetsky 2001] - pH optimum is 4.5-4.75 [Pshezhetsky 2001] - most abundant in liver, kidney, skin, blood cells [Pshezhetsky 2001] - cloned and expressed in COS cells [Oshima 1988] - cDNA isolated [Yamamoto 1990] 4758: - hydrolyzes terminal sialic acids of glycolipids and glycopeptides [Pshezhetsky 2001] - pH optimum 4.2 [Pshezhetsky 2001] - cloned an expressed in fibroblasts [Pshezhetsky 1997],[Bonten 1996] and COS-7 cells [Milner 1997] 2588: - purified from human placenta [Glossl 1979], [Lim & Horwitz 1981], [Masue1991] and human liver [Bielicki 1991], recombinant protein purified from CHO cells [Bielicki 1995] - kinetic characterization [Bielicki 1991], [Masue1991], [Bielic - could desulfate acetylgalactosamine 6-sulphate (from chondroitin-6-sulfate) or galactose 6-sulphate glucosamine 6-sulphate residues in keratan sulfate or heparan su - cloned and expressed in deficient fibroblasts [Tomatsu 1991]

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GALASE1ly	3	Bielicki J, Hopwood JJ	Human liver N-acetylgalactosamine 6-sulphatase. Purification and characterization	Biochem J	1991	1953646	- two distinct forms of lysosomal complex purified from human placenta: CathA/GAL/SIAL/GALNS and CathA/GAL [Pshezhetsky 2001], [Ostrowska 2003]; average ratio btwn CathA/GAL/SIAL/GALNS and CathA/GAL complexes is 1:10 [Pshezhetsky 2001] 2720: - cleaves terminal beta-1,4- or beta-1,3- linked galactose from GM1-ganglioside, GA1 ganglioside, lactosylceramide, asialofetuin, galactose-containing oligosaccharides, keratan sulfate [Pshezhetsky 2001] - pH optimum is 4.5-4.75 [Pshezhetsky 2001] - most abundant in liver, kidney, skin, blood cells [Pshezhetsky 2001] - cloned and expressed in COS cells [Oshima 1988] - cDNA isolated [Yamamoto 1990] 4758: - hydrolyzes terminal sialic acids of glycolipids and glycopeptides [Pshezhetsky 2001] - pH optimum 4.2 [Pshezhetsky 2001] - cloned an expressed in fibroblasts [Pshezhetsky 1997],[Bonten 1996] and COS-7 cells [Milner 1997] 2588: - purified from human placenta [Glossl 1979], [Lim & Horwitz 1981], [Masue1991] and human liver [Bielicki 1991], recombinant protein purified from CHO cells [Bielicki 1995] - kinetic characterization [Bielicki 1991], [Masue1991], [Bielic - could desulfate acetylgalactosamine 6-sulphate (from chondroitin-6-sulfate) or galactose 6-sulphate glucosamine 6-sulphate residues in keratan sulfate or heparan su - cloned and expressed in deficient fibroblasts [Tomatsu 1991]
GALASE1ly	3	Yamamoto Y, Hake CA, Martin BM, Kretz KA, Ahern-Rindell AJ, Naylor SL, Mudd M, O'Brien JS	Isolation, characterization, and mapping of a human acid beta-galactosidase cDNA	DNA Cell Biol	1990	2111707	- two distinct forms of lysosomal complex purified from human placenta: CathA/GAL/SIAL/GALNS and CathA/GAL [Pshezhetsky 2001], [Ostrowska 2003]; average ratio btwn CathA/GAL/SIAL/GALNS and CathA/GAL complexes is 1:10 [Pshezhetsky 2001] 2720: - cleaves terminal beta-1,4- or beta-1,3- linked galactose from GM1-ganglioside, GA1 ganglioside, lactosylceramide, asialofetuin, galactose-containing oligosaccharides, keratan sulfate [Pshezhetsky 2001] - pH optimum is 4.5-4.75 [Pshezhetsky 2001] - most abundant in liver, kidney, skin, blood cells [Pshezhetsky 2001] - cloned and expressed in COS cells [Oshima 1988] - cDNA isolated [Yamamoto 1990] 4758: - hydrolyzes terminal sialic acids of glycolipids and glycopeptides [Pshezhetsky 2001] - pH optimum 4.2 [Pshezhetsky 2001] - cloned an expressed in fibroblasts [Pshezhetsky 1997],[Bonten 1996] and COS-7 cells [Milner 1997] 2588: - purified from human placenta [Glossl 1979], [Lim & Horwitz 1981], [Masue1991] and human liver [Bielicki 1991], recombinant protein purified from CHO cells [Bielicki 1995] - kinetic characterization [Bielicki 1991], [Masue1991], [Bielic - could desulfate acetylgalactosamine 6-sulphate (from chondroitin-6-sulfate) or galactose 6-sulphate glucosamine 6-sulphate residues in keratan sulfate or heparan su - cloned and expressed in deficient fibroblasts [Tomatsu 1991]
GALASE1ly	3	Oshima A, Tsuji A, Nagao Y, Sakuraba H, Suzuki Y.	Cloning, sequencing, and expression of cDNA for human beta-galactosidase.	Biochem Biophys Res Commun	1988	3143362	- two distinct forms of lysosomal complex purified from human placenta: CathA/GAL/SIAL/GALNS and CathA/GAL [Pshezhetsky 2001], [Ostrowska 2003]; average ratio btwn CathA/GAL/SIAL/GALNS and CathA/GAL complexes is 1:10 [Pshezhetsky 2001] 2720: - cleaves terminal beta-1,4- or beta-1,3- linked galactose from GM1-ganglioside, GA1 ganglioside, lactosylceramide, asialofetuin, galactose-containing oligosaccharides, keratan sulfate [Pshezhetsky 2001] - pH optimum is 4.5-4.75 [Pshezhetsky 2001] - most abundant in liver, kidney, skin, blood cells [Pshezhetsky 2001] - cloned and expressed in COS cells [Oshima 1988] - cDNA isolated [Yamamoto 1990] 4758: - hydrolyzes terminal sialic acids of glycolipids and glycopeptides [Pshezhetsky 2001] - pH optimum 4.2 [Pshezhetsky 2001] - cloned an expressed in fibroblasts [Pshezhetsky 1997],[Bonten 1996] and COS-7 cells [Milner 1997] 2588: - purified from human placenta [Glossl 1979], [Lim & Horwitz 1981], [Masue1991] and human liver [Bielicki 1991], recombinant protein purified from CHO cells [Bielicki 1995] - kinetic characterization [Bielicki 1991], [Masue1991], [Bielic - could desulfate acetylgalactosamine 6-sulphate (from chondroitin-6-sulfate) or galactose 6-sulphate glucosamine 6-sulphate residues in keratan sulfate or heparan su - cloned and expressed in deficient fibroblasts [Tomatsu 1991]

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GALASE1ly	3	Lim CT, Horwitz AL	Purification and properties of human N-acetylgalactosamine-6-sulfate sulfatase	Biochim Biophys Acta	1981	7213753	- two distinct forms of lysosomal complex purified from human placenta: CathA/GAL/SIAL/GALNS and CathA/GAL [Pshezhetsky 2001], [Ostrowska 2003]; average ratio btwn CathA/GAL/SIAL/GALNS and CathA/GAL complexes is 1:10 [Pshezhetsky 2001] 2720: - cleaves terminal beta-1,4- or beta-1,3- linked galactose from GM1-ganglioside, GA1 ganglioside, lactosylceramide, asialofetuin, galactose-containing oligosaccharides, keratan sulfate [Pshezhetsky 2001] - pH optimum is 4.5-4.75 [Pshezhetsky 2001] - most abundant in liver, kidney, skin, blood cells [Pshezhetsky 2001] - cloned and expressed in COS cells [Oshima 1988] - cDNA isolated [Yamamoto 1990] 4758: - hydrolyzes terminal sialic acids of glycolipids and glycopeptides [Pshezhetsky 2001] - pH optimum 4.2 [Pshezhetsky 2001] - cloned an expressed in fibroblasts [Pshezhetsky 1997],[Bonten 1996] and COS-7 cells [Milner 1997] 2588: - purified from human placenta [Glossl 1979], [Lim & Horwitz 1981], [Masue1991] and human liver [Bielicki 1991], recombinant protein purified from CHO cells [Bielicki 1995] - kinetic characterization [Bielicki 1991], [Masue1991], [Bielic - could desulfate acetylgalactosamine 6-sulphate (from chondroitin-6-sulfate) or galactose 6-sulphate glucosamine 6-sulphate residues in keratan sulfate or heparan su - cloned and expressed in deficient fibroblasts [Tomatsu 1991]
GALASE1ly	3	Bielicki J, Fuller M, Guo XH, Morris CP, Hopewood JJ, Anson DS	Expression, purification and characterization of recombinant human N-acetylgalactosamine-6-sulphatase	Biochem J	1995	7575473	- two distinct forms of lysosomal complex purified from human placenta: CathA/GAL/SIAL/GALNS and CathA/GAL [Pshezhetsky 2001], [Ostrowska 2003]; average ratio btwn CathA/GAL/SIAL/GALNS and CathA/GAL complexes is 1:10 [Pshezhetsky 2001] 2720: - cleaves terminal beta-1,4- or beta-1,3- linked galactose from GM1-ganglioside, GA1 ganglioside, lactosylceramide, asialofetuin, galactose-containing oligosaccharides, keratan sulfate [Pshezhetsky 2001] - pH optimum is 4.5-4.75 [Pshezhetsky 2001] - most abundant in liver, kidney, skin, blood cells [Pshezhetsky 2001] - cloned and expressed in COS cells [Oshima 1988] - cDNA isolated [Yamamoto 1990] 4758: - hydrolyzes terminal sialic acids of glycolipids and glycopeptides [Pshezhetsky 2001] - pH optimum 4.2 [Pshezhetsky 2001] - cloned an expressed in fibroblasts [Pshezhetsky 1997],[Bonten 1996] and COS-7 cells [Milner 1997] 2588: - purified from human placenta [Glossl 1979], [Lim & Horwitz 1981], [Masue1991] and human liver [Bielicki 1991], recombinant protein purified from CHO cells [Bielicki 1995] - kinetic characterization [Bielicki 1991], [Masue1991], [Bielic - could desulfate acetylgalactosamine 6-sulphate (from chondroitin-6-sulfate) or galactose 6-sulphate glucosamine 6-sulphate residues in keratan sulfate or heparan su - cloned and expressed in deficient fibroblasts [Tomatsu 1991]
GALASE1ly	3	Bonten E, van der Spoel A, Fornerod M, Grosveld G, d'Azzo A	Characterization of human lysosomal neuraminidase defines the molecular basis of the metabolic storage disorder sialidosis.	Genes Dev	1996	8985184	- two distinct forms of lysosomal complex purified from human placenta: CathA/GAL/SIAL/GALNS and CathA/GAL [Pshezhetsky 2001], [Ostrowska 2003]; average ratio btwn CathA/GAL/SIAL/GALNS and CathA/GAL complexes is 1:10 [Pshezhetsky 2001] 2720: - cleaves terminal beta-1,4- or beta-1,3- linked galactose from GM1-ganglioside, GA1 ganglioside, lactosylceramide, asialofetuin, galactose-containing oligosaccharides, keratan sulfate [Pshezhetsky 2001] - pH optimum is 4.5-4.75 [Pshezhetsky 2001] - most abundant in liver, kidney, skin, blood cells [Pshezhetsky 2001] - cloned and expressed in COS cells [Oshima 1988] - cDNA isolated [Yamamoto 1990] 4758: - hydrolyzes terminal sialic acids of glycolipids and glycopeptides [Pshezhetsky 2001] - pH optimum 4.2 [Pshezhetsky 2001] - cloned an expressed in fibroblasts [Pshezhetsky 1997],[Bonten 1996] and COS-7 cells [Milner 1997] 2588: - purified from human placenta [Glossl 1979], [Lim & Horwitz 1981], [Masue1991] and human liver [Bielicki 1991], recombinant protein purified from CHO cells [Bielicki 1995] - kinetic characterization [Bielicki 1991], [Masue1991], [Bielic - could desulfate acetylgalactosamine 6-sulphate (from chondroitin-6-sulfate) or galactose 6-sulphate glucosamine 6-sulphate residues in keratan sulfate or heparan su - cloned and expressed in deficient fibroblasts [Tomatsu 1991]

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GALASE1ly	3	Milner CM, Smith SV, Carrillo MB, Taylor GL, Hollinshead M, Campbell RD	Identification of a sialidase encoded in the human major histocompatibility complex	J Biol Chem	1997	9020182	- two distinct forms of lysosomal complex purified from human placenta: CathA/GAL/SIAL/GALNS and CathA/GAL [Pshezhetsky 2001], [Ostrowska 2003]; average ratio btwn CathA/GAL/SIAL/GALNS and CathA/GAL complexes is 1:10 [Pshezhetsky 2001] 2720: - cleaves terminal beta-1,4- or beta-1,3- linked galactose from GM1-ganglioside, GA1 ganglioside, lactosylceramide, asialofetuin, galactose-containing oligosaccharides, keratan sulfate [Pshezhetsky 2001] - pH optimum is 4.5-4.75 [Pshezhetsky 2001] - most abundant in liver, kidney, skin, blood cells [Pshezhetsky 2001] - cloned and expressed in COS cells [Oshima 1988] - cDNA isolated [Yamamoto 1990] 4758: - hydrolyzes terminal sialic acids of glycolipids and glycopeptides [Pshezhetsky 2001] - pH optimum 4.2 [Pshezhetsky 2001] - cloned an expressed in fibroblasts [Pshezhetsky 1997],[Bonten 1996] and COS-7 cells [Milner 1997] 2588: - purified from human placenta [Glossl 1979], [Lim & Horwitz 1981], [Masue1991] and human liver [Bielicki 1991], recombinant protein purified from CHO cells [Bielicki 1995] - kinetic characterization [Bielicki 1991], [Masue1991], [Bielic - could desulfate acetylgalactosamine 6-sulphate (from chondroitin-6-sulfate) or galactose 6-sulphate glucosamine 6-sulphate residues in keratan sulfate or heparan su - cloned and expressed in deficient fibroblasts [Tomatsu 1991]
GALASE1ly	3	Pshezhetsky AV, Richard C, Michaud L, Igdoura S, Wang S, Elsliger MA, Qu J, Leclerc D, Gravel R, Dallaire L, Potier M	Cloning, expression and chromosomal mapping of human lysosomal sialidase and characterization of mutations in sialidosis	Nat Genet	1997	9054950	- two distinct forms of lysosomal complex purified from human placenta: CathA/GAL/SIAL/GALNS and CathA/GAL [Pshezhetsky 2001], [Ostrowska 2003]; average ratio btwn CathA/GAL/SIAL/GALNS and CathA/GAL complexes is 1:10 [Pshezhetsky 2001] 2720: - cleaves terminal beta-1,4- or beta-1,3- linked galactose from GM1-ganglioside, GA1 ganglioside, lactosylceramide, asialofetuin, galactose-containing oligosaccharides, keratan sulfate [Pshezhetsky 2001] - pH optimum is 4.5-4.75 [Pshezhetsky 2001] - most abundant in liver, kidney, skin, blood cells [Pshezhetsky 2001] - cloned and expressed in COS cells [Oshima 1988] - cDNA isolated [Yamamoto 1990] 4758: - hydrolyzes terminal sialic acids of glycolipids and glycopeptides [Pshezhetsky 2001] - pH optimum 4.2 [Pshezhetsky 2001] - cloned an expressed in fibroblasts [Pshezhetsky 1997],[Bonten 1996] and COS-7 cells [Milner 1997] 2588: - purified from human placenta [Glossl 1979], [Lim & Horwitz 1981], [Masue1991] and human liver [Bielicki 1991], recombinant protein purified from CHO cells [Bielicki 1995] - kinetic characterization [Bielicki 1991], [Masue1991], [Bielic - could desulfate acetylgalactosamine 6-sulphate (from chondroitin-6-sulfate) or galactose 6-sulphate glucosamine 6-sulphate residues in keratan sulfate or heparan su - cloned and expressed in deficient fibroblasts [Tomatsu 1991]
GALASE1ly	3	Pshezhetsky AV, Ashmarina M	Lysosomal multienzyme complex: biochemistry, genetics, and molecular pathophysiology.	Prog Nucleic Acid Res Mol Biol	2001	11550799	- two distinct forms of lysosomal complex purified from human placenta: CathA/GAL/SIAL/GALNS and CathA/GAL [Pshezhetsky 2001], [Ostrowska 2003]; average ratio btwn CathA/GAL/SIAL/GALNS and CathA/GAL complexes is 1:10 [Pshezhetsky 2001] 2720: - cleaves terminal beta-1,4- or beta-1,3- linked galactose from GM1-ganglioside, GA1 ganglioside, lactosylceramide, asialofetuin, galactose-containing oligosaccharides, keratan sulfate [Pshezhetsky 2001] - pH optimum is 4.5-4.75 [Pshezhetsky 2001] - most abundant in liver, kidney, skin, blood cells [Pshezhetsky 2001] - cloned and expressed in COS cells [Oshima 1988] - cDNA isolated [Yamamoto 1990] 4758: - hydrolyzes terminal sialic acids of glycolipids and glycopeptides [Pshezhetsky 2001] - pH optimum 4.2 [Pshezhetsky 2001] - cloned an expressed in fibroblasts [Pshezhetsky 1997],[Bonten 1996] and COS-7 cells [Milner 1997] 2588: - purified from human placenta [Glossl 1979], [Lim & Horwitz 1981], [Masue1991] and human liver [Bielicki 1991], recombinant protein purified from CHO cells [Bielicki 1995] - kinetic characterization [Bielicki 1991], [Masue1991], [Bielic - could desulfate acetylgalactosamine 6-sulphate (from chondroitin-6-sulfate) or galactose 6-sulphate glucosamine 6-sulphate residues in keratan sulfate or heparan su - cloned and expressed in deficient fibroblasts [Tomatsu 1991]

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GALC	3	Luzi P, Rafi MA, Wenger DA.	Structure and organization of the human galactocerebrosidase (GALC) gene.	Genomics	1995	7601472	lysosomal - uniprot and luzi ref biochem act + localization by luzi ref Galactosylceramidase (GALC) is a lysosomal enzyme that hydrolyzes several galactolipids. GALC deficiency is associated with Krabbe disease (globoid cell leukodystrophy). The gene is about 60 kb in length and consists of 17 exons. This gene contains ten GC-box-like sequences within the promoter region but no typical TATA box. This feature is also characteristic of other lysosomal protein encoding genes. Highest level of activity in testes compared to brain, kidney, placenta and liver. Can also be found in urine. NJ
GALGT1	3	Nagata Y, Yamashiro S, Yodoi J, Lloyd KO, Shiku H, Furukawa K.	Expression cloning of beta 1,4 N-acetylgalactosaminyltransferase cDNAs that determine the expression of GM2 and GD2 gangliosides.	J Biol Chem	1992	1601877	Golgi - lumen side - see ref Kolter and Sanhoff; also noted in uniprot Involved in the biosynthesis of gangliosides GM2, GD2 and GA2. GM2 and GD2 gangliosides are sialic acid-containing glycosphingolipids expressed in some normal tissues such as brain and in various tumors such as neuroblastomas, astrocytomas, and malignant melanomas. NJ
GALGT1	3	Furukawa K, Soejima H, Niikawa N, Shiku H.	Genomic organization and chromosomal assignment of the human beta1, 4-N-acetylgalactosaminyltransferase gene. Identification of multiple transcription units.	J Biol Chem	1996	8702839	Golgi - lumen side - see ref Kolter and Sanhoff; also noted in uniprot Involved in the biosynthesis of gangliosides GM2, GD2 and GA2. GM2 and GD2 gangliosides are sialic acid-containing glycosphingolipids expressed in some normal tissues such as brain and in various tumors such as neuroblastomas, astrocytomas, and malignant melanomas. NJ
GALNACT1g	3	Uyama T, Kitagawa H, Tamura Ji J, Sugahara K	Molecular cloning and expression of human chondroitin N-acetylgalactosaminyltransferase: the key enzyme for chain initiation and elongation of chondroitin/dermatan sulfate on the protein linkage region tetrasaccharide shared by heparin/heparan sulfate	J Biol Chem	2002	11788602	- Golgi localization [Silbert, IUBMB LIfe 2002] 55454: - exhibits both GalNAcT-I and GalNAcT-II activity, but mainly participates in elongation, not initiation [Sato, J Biol Chem 2003] - gene identified by BLAST; cDNA isolated [Sato, J Biol Chem 2003] - ubiquitous, but most highly expressed in the small intestine, leukocytes, and spleen [Sato, J Biol Chem 2003] 55790: - identified based on sequence homology [Uyama, J Biol Chem 2002], [Gotoh, J Biol Chem 2002] - exhibits both GalNAcT-I and GalNAcT-II activity, but mainly participates in initiation, not elongation [Uyama, J Biol Chem 2002], [Sato, J Biol Chem 2003], [Gotoh, J Biol Chem 2002] - ubiquitously expressed [Uyama, J Biol Chem 2002], but highly expressed in thyroid and placenta [Gotoh, J Biol Chem 2002]
GALNACT1g	3	Gotoh M, Sato T, Akashima T, Iwasaki H, Kameyama A, Mochizuki H, Yada T, Inaba N, Zhang Y, Kikuchi N, Kwon YD, Togayachi A, Kudo T, Nishihara S, Watanabe H, Kimata K, Narimatsu H	Enzymatic synthesis of chondroitin with a novel chondroitin sulfate N-acetylgalactosaminyltransferase that transfers N-acetylgalactosamine to glucuronic acid in initiation and elongation of chondroitin sulfate synthesis	J Biol Chem	2002	12163485	- Golgi localization [Silbert, IUBMB LIfe 2002] 55454: - exhibits both GalNAcT-I and GalNAcT-II activity, but mainly participates in elongation, not initiation [Sato, J Biol Chem 2003] - gene identified by BLAST; cDNA isolated [Sato, J Biol Chem 2003] - ubiquitous, but most highly expressed in the small intestine, leukocytes, and spleen [Sato, J Biol Chem 2003] 55790: - identified based on sequence homology [Uyama, J Biol Chem 2002], [Gotoh, J Biol Chem 2002] - exhibits both GalNAcT-I and GalNAcT-II activity, but mainly participates in initiation, not elongation [Uyama, J Biol Chem 2002], [Sato, J Biol Chem 2003], [Gotoh, J Biol Chem 2002] - ubiquitously expressed [Uyama, J Biol Chem 2002], but highly expressed in thyroid and placenta [Gotoh, J Biol Chem 2002]

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GALNACT1g	3	Sato T, Gotoh M, Kiyohara K, Akashima T, Iwasaki H, Kameyama A, Mochizuki H, Yada T, Inaba N, Togayachi A, Kudo T, Asada M, Watanabe H, Imamura T, Kimata K, Narimatsu H	Differential roles of two N-acetylgalactosaminyltransferases, CSGalNAcT-1, and a novel enzyme, CSGalNAcT-2. Initiation and elongation in synthesis of chondroitin sulfate	J Biol Chem	2003	12446672	- Golgi localization [Silbert, IUBMB LIfe 2002] 55454: - exhibits both GalNAcT-I and GalNAcT-II activity, but mainly participates in elongation, not initiation [Sato, J Biol Chem 2003] - gene identified by BLAST; cDNA isolated [Sato, J Biol Chem 2003] - ubiquitous, but most highly expressed in the small intestine, leukocytes, and spleen [Sato, J Biol Chem 2003] 55790: - identified based on sequence homology [Uyama, J Biol Chem 2002], [Gotoh, J Biol Chem 2002] - exhibits both GalNAcT-I and GalNAcT-II activity, but mainly participates in initiation, not elongation [Uyama, J Biol Chem 2002], [Sato, J Biol Chem 2003], [Gotoh, J Biol Chem 2002] - ubiquitously expressed [Uyama, J Biol Chem 2002], but highly expressed in thyroid and placenta [Gotoh, J Biol Chem 2002]
GALNTg	0	Cheng L, Tachibana K, Zhang Y, Guo J, Kahori Tachibana K, Kameyama A, Wang H, Hiruma T, Iwasaki H, Togayachi A, Kudo T, Narimatsu H	Characterization of a novel human UDP-GalNAc transferase, pp-GalNAc-T10	FEBS Lett	2002		Golgi apparatus by catalyzing the transfer of GalNAc to serine and threonine residues on target proteins. They are characterized by an N-terminal transmembrane domain, a stem region, a lumenal catalytic domain containing a GT1 motif and Gal/GalNAc transferase motif, and a C-terminal ricin/lectin-like domain. GalNAc-Ts have different, but overlapping, substrate specificities and patterns of expression. GALNT6p is capable of glycosylating fibronectin peptide in vitro and is expressed in a fibroblast cell line, indicating that it may be involved in the synthesis of oncofetal fibronectin. Transcript variants of GALNT1 utilize alternative polyA signals which have been described in the literature. GALNT9 is expressed specifically in the brain, with highest expression in the cerebellum. GALNT8 has two main isoforms, the larger of which is ubiquitously distributed, and the smaller of which is primarily expressed in th e heart, kidney, liver, and placenta. [White et al. Gene 246 (1-2): 347-356 (2000)] Following expression in insect cells, recombinant GALNT10 sh GALNT7p shows exclusive specificity for partially GalNAc-gly References for tissue distributions:
GALNTg	0	Ten Hagen KG, Hagen FK, Balys MM, Beres TM, Van Wuyckhuyse B, Tabak LA	Cloning and expression of a novel, tissue specifically expressed member of the UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase family.	J Biol Chem	1998	9765313	Golgi apparatus by catalyzing the transfer of GalNAc to serine and threonine residues on target proteins. They are characterized by an N-terminal transmembrane domain, a stem region, a lumenal catalytic domain containing a GT1 motif and Gal/GalNAc transferase motif, and a C-terminal ricin/lectin-like domain. GalNAc-Ts have different, but overlapping, substrate specificities and patterns of expression. GALNT6p is capable of glycosylating fibronectin peptide in vitro and is expressed in a fibroblast cell line, indicating that it may be involved in the synthesis of oncofetal fibronectin. Transcript variants of GALNT1 utilize alternative polyA signals which have been described in the literature. GALNT9 is expressed specifically in the brain, with highest expression in the cerebellum. GALNT8 has two main isoforms, the larger of which is ubiquitously distributed, and the smaller of which is primarily expressed in th e heart, kidney, liver, and placenta. [White et al. Gene 246 (1-2): 347-356 (2000)] Following expression in insect cells, recombinant GALNT10 sh GALNT7p shows exclusive specificity for partially GalNAc-gly References for tissue distributions:

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GALNTg	0	White KE, Lorenz B, Evans WE, Meitinger T, Strom TM, Econs MJ	Molecular cloning of a novel human UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase, GalNAc-T8, and analysis as a candidate autosomal dominant hypophosphatemic rickets (ADHR) gene.	Gene	2000	10767557	Golgi apparatus by catalyzing the transfer of GalNAc to serine and threonine residues on target proteins. They are characterized by an N-terminal transmembrane domain, a stem region, a lumenal catalytic domain containing a GT1 motif and Gal/GalNAc transferase motif, and a C-terminal ricin/lectin-like domain. GalNAc-Ts have different, but overlapping, substrate specificities and patterns of expression. GALNT6p is capable of glycosylating fibronectin peptide in vitro and is expressed in a fibroblast cell line, indicating that it may be involved in the synthesis of oncofetal fibronectin. Transcript variants of GALNT1 utilize alternative polyA signals which have been described in the literature. GALNT9 is expressed specifically in the brain, with highest expression in the cerebellum. GALNT8 has two main isoforms, the larger of which is ubiquitously distributed, and the smaller of which is primarily expressed in th e heart, kidney, liver, and placenta. [White et al. Gene 246 (1-2): 347-356 (2000)] Following expression in insect cells, recombinant GALNT10 sh GALNT7p shows exclusive specificity for partially GalNAc-gly References for tissue distributions:
GALNTg	0	Wang H, Tachibana K, Zhang Y, Iwasaki H, Kameyama A, Cheng L, Guo J, Hiruma T, Togayachi A, Kudo T, Kikuchi N, Narimatsu H	Cloning and characterization of a novel UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase, pp-GalNAc-T14.	Biochem Biophys Res Commun	2003	12507512	Golgi apparatus by catalyzing the transfer of GalNAc to serine and threonine residues on target proteins. They are characterized by an N-terminal transmembrane domain, a stem region, a lumenal catalytic domain containing a GT1 motif and Gal/GalNAc transferase motif, and a C-terminal ricin/lectin-like domain. GalNAc-Ts have different, but overlapping, substrate specificities and patterns of expression. GALNT6p is capable of glycosylating fibronectin peptide in vitro and is expressed in a fibroblast cell line, indicating that it may be involved in the synthesis of oncofetal fibronectin. Transcript variants of GALNT1 utilize alternative polyA signals which have been described in the literature. GALNT9 is expressed specifically in the brain, with highest expression in the cerebellum. GALNT8 has two main isoforms, the larger of which is ubiquitously distributed, and the smaller of which is primarily expressed in th e heart, kidney, liver, and placenta. [White et al. Gene 246 (1-2): 347-356 (2000)] Following expression in insect cells, recombinant GALNT10 sh GALNT7p shows exclusive specificity for partially GalNAc-gly References for tissue distributions:
GALNTg	0	Ten Hagen KG, Fritz TA, Tabak LA.	All in the family: the UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferases	Glycobiology	2003	12634319	Golgi apparatus by catalyzing the transfer of GalNAc to serine and threonine residues on target proteins. They are characterized by an N-terminal transmembrane domain, a stem region, a lumenal catalytic domain containing a GT1 motif and Gal/GalNAc transferase motif, and a C-terminal ricin/lectin-like domain. GalNAc-Ts have different, but overlapping, substrate specificities and patterns of expression. GALNT6p is capable of glycosylating fibronectin peptide in vitro and is expressed in a fibroblast cell line, indicating that it may be involved in the synthesis of oncofetal fibronectin. Transcript variants of GALNT1 utilize alternative polyA signals which have been described in the literature. GALNT9 is expressed specifically in the brain, with highest expression in the cerebellum. GALNT8 has two main isoforms, the larger of which is ubiquitously distributed, and the smaller of which is primarily expressed in th e heart, kidney, liver, and placenta. [White et al. Gene 246 (1-2): 347-356 (2000)] Following expression in insect cells, recombinant GALNT10 sh GALNT7p shows exclusive specificity for partially GalNAc-gly References for tissue distributions:

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
GALNTg	0	Cheng L, Tachibana K, Iwasaki H, Kameyama A, Zhang Y, Kubota T, Hiruma T, Tachibana K, Kudo T, Guo JM, Narimatsu H	Characterization of a novel human UDP-GalNAc transferase, pp-GalNAc-T15	FEBS Lett	2004	15147861	Golgi apparatus by catalyzing the transfer of GalNAc to serine and threonine residues on target proteins. They are characterized by an N-terminal transmembrane domain, a stem region, a lumenal catalytic domain containing a GT1 motif and Gal/GalNAc transferase motif, and a C-terminal ricin/lectin-like domain. GalNAc-Ts have different, but overlapping, substrate specificities and patterns of expression. GALNT6p is capable of glycosylating fibronectin peptide in vitro and is expressed in a fibroblast cell line, indicating that it may be involved in the synthesis of oncofetal fibronectin. Transcript variants of GALNT1 utilize alternative polyA signals which have been described in the literature. GALNT9 is expressed specifically in the brain, with highest expression in the cerebellum. GALNT8 has two main isoforms, the larger of which is ubiquitously distributed, and the smaller of which is primarily expressed in th e heart, kidney, liver, and placenta. [White et al, Gene 246 (1-2): 347-356 (2000)] Following expression in insect cells, recombinant GALNT10 sh GALNT7p shows exclusive specificity for partially GalNAc-gly References for tissue distributions:
GALOR	2	Leslie ND	Insights into the pathogenesis of galactosemia.	Annu Rev Nutr	2003	12704219	- galactitol production is a dead end pathway, and the product is poorly diffusable [Leslie, Annu Rev Nutr 2003], elevated levels can cause cataracts [Champe, Biochemistry 2005] - enzyme is present in liver, kidney, retina, lens, nerve tissue, seminal vesicles, and ovaries [Champe, Biochemistry 2005] - reaction is physiologically unimportant unless galactose levels are high [Champe, Biochemistry 2005]
GALT	0	Leslie ND, Immerman EB, Flach JE, Florez M, Fridovich-Keil JL, Elsas LJ	The human galactose-1-phosphate uridyltransferase gene	Genomics	1992	1427861	- UTP-hexose-1-phosphate uridylyltransferase activity [Leslie et al, Genomics 1992]
GALT2g	3	Bai X, Zhou D, Brown JR, Crawford BE, Hennet T, Esko JD	Biosynthesis of the linkage region of glycosaminoglycans: cloning and activity of galactosyltransferase II, the sixth member of the beta 1,3-galactosyltransferase family (beta 3GalT6)	J Biol Chem	2001	11551958	- Golgi lumen [Bai, J Biol Chem 2001], [Silbert, IUBMB LIfe 2002] - identification of galactosyltransferase II activity [Bai, J Biol Chem 2001] - cDNA was cloned and expressed [Bai, J Biol Chem 2001] - broad expression in human tissues [Bai, J Biol Chem 2001]
GALTg	3	Almeida R, Levery SB, Mandel U, Kresse H, Schwientek T, Bennett EP, Clausen H	Cloning and expression of a proteoglycan UDP-galactose:beta-xylose beta1,4-galactosyltransferase I. A seventh member of the human beta4-galactosyltransferase gene family	J Biol Chem	1999	1073568	- attaches first Gal in tetrasaccharide linkage region of chondroitin / heparan sulfate [RefSeq] - Golgi membrane protein [UniProt], [Silbert, IUBMB Life 2002] - High expression in heart, pancreas and liver, medium in placenta and kidney, low in brain, skeletal muscle and lung [UniProt] - cDNA identified by BLAST and expressed [Okajima, J Biol Chem 1999], [Almeida, J Biol Chem 1999] - gene has 38% homology to C. elegans SQV-3 [Okajima, J Biol Chem 1999]
GALTg	3	Okajima T, Yoshida K, Kondo T, Furukawa K	Human homolog of Caenorhabditis elegans sqv-3 gene is galactosyltransferase I involved in the biosynthesis of the glycosaminoglycan-protein linkage region of proteoglycans	J Biol Chem	1999	10438455	- attaches first Gal in tetrasaccharide linkage region of chondroitin / heparan sulfate [RefSeq] - Golgi membrane protein [UniProt], [Silbert, IUBMB Life 2002] - High expression in heart, pancreas and liver, medium in placenta and kidney, low in brain, skeletal muscle and lung [UniProt] - cDNA identified by BLAST and expressed [Okajima, J Biol Chem 1999], [Almeida, J Biol Chem 1999] - gene has 38% homology to C. elegans SQV-3 [Okajima, J Biol Chem 1999]
GAO1	3	Kanamori A, Nakayama J, Fukuda MN, Stallcup WB, Sasaki K, Fukuda M, Hirabayashi Y	Expression cloning and characterization of a cDNA encoding a novel membrane protein required for the formation of O-acetylated ganglioside: A putative acetyl-CoA-transporter	Proc Natl Acad Sci	1997		activity in cytoplasm - refseq expression in ER (probable) Kanamori et al ref - assumed outer membrane of ER seq homology initially determined as transporter, also found to have O-acetyl activity on gangliosides. NJ
GASNASE3ly	3	Ikonen E, Baumann M, Gron K, Syvanen AC, Enomaa N, Halila R, Aula P, Peltonen L	Aspartylglucosaminuria: cDNA encoding human aspartylglucosaminidase and the missense mutation causing the disease.	EMBO J	1991	1703489	175: - isolated from human placenta [Fisher 1990], fetal liver cDNA library [Ikonen 1991] - cloned [Fisher 1990], [Ikonen 1991] - expressed in monkey COS-1 cells [Ikonen 1991] - requires a free a-amino and carboxyl group on the Asn and any L-fucose at the 6-position of GlcNAc must be removed prior to GlcNAc-Asn hydrolysis [Fisher 1990] - 86% of residues identical in overlapping regions of human and mouse cDNA clones [Fisher 1990] - native protein is a heterodimer; single gene encodes both heavy and light chains [Tollersrud 1994]

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GASNASE3ly	3	Fisher KJ, Tollersrud OK, Aronson NN Jr	Cloning and sequence analysis of a cDNA for human glycosylasparaginase. A single gene encodes the subunits of this lysosomal amidase	FEBS Lett	1990	2401370	175: - isolated from human placenta [Fisher 1990], fetal liver cDNA library [Ikonen 1991] - cloned [Fisher 1990], [Ikonen 1991] - expressed in monkey COS-1 cells [Ikonen 1991] - requires a free a-amino and carboxyl group on the Asn and any L-fucose at the 6-position of GlcNAc must be removed prior to GlcNAc-Asn hydrolysis [Fisher 1990] - 86% of residues identical in overlapping regions of human and mouse cDNA clones [Fisher 1990] - native protein is a heterodimer; single gene encodes both heavy and light chains [Tollersrud 1994]
GASNASE3ly	3	Tollersrud OK, Heiskanen T, Peltonen L	Human leucocyte glycosylasparaginase is an alpha/beta-heterodimer of 19 kDa alpha-subunit and 17 and 18 kDa beta-subunit.	Biochem J	1994	8002961	175: - isolated from human placenta [Fisher 1990], fetal liver cDNA library [Ikonen 1991] - cloned [Fisher 1990], [Ikonen 1991] - expressed in monkey COS-1 cells [Ikonen 1991] - requires a free a-amino and carboxyl group on the Asn and any L-fucose at the 6-position of GlcNAc must be removed prior to GlcNAc-Asn hydrolysis [Fisher 1990] - 86% of residues identical in overlapping regions of human and mouse cDNA clones [Fisher 1990] - native protein is a heterodimer; single gene encodes both heavy and light chains [Tollersrud 1994]
GBA	0	Schmitz M, Alfalah M, Aerts JM, Naim HY, Zimmer KP.	Impaired trafficking of mutants of lysosomal glucocerebrosidase in Gaucher's disease.	Int J Biochem Cell Biol	2005	15982918	This gene encodes a lysosomal membrane protein that cleaves the beta-glucosidic linkage of glycosylceramide, an intermediate in glycolipid metabolism. Mutations in this gene cause Gaucher disease, a lysosomal storage disease characterized by an accumulation of glucocerebrosides. A related pseudogene is approximately 12 kb downstream of this gene on chromosome 1. Alternative splicing results in multiple transcript variants encoding the same protein. NJ
GBAl	3	Orvisky E, Park JK, Parker A, Walker JM, Martin BM, Stubblefield BK, Uyama E, Tayebi N, Sidransky E.	The identification of eight novel glucocerebrosidase (GBA) mutations in patients with Gaucher disease.	Hum Mutat	2002	11933202	lysosomal - uniprot cytosolic form also exists - berrin ref: Substrate (aglycone) specificity of human cytosolic beta-glucosidase. Biochem J. 2003 Jul 1;373(Pt 1):41-8. This gene encodes a lysosomal membrane protein that cleaves the beta-glucosidic linkage of glycosylceramide, an intermediate in glycolipid metabolism. Mutations in this gene cause Gaucher disease, a lysosomal storage disease characterized by an accumulation of glucocerebrosides. A related pseudogene is approximately 12 kb downstream of this gene on chromosome 1. Alternative splicing results in multiple transcript variants encoding the same protein. NJ
GBAl	3	Berrin JG, Czjzek M, Kroon PA, McLauchlan WR, Puigserver A, Williamson G, Juge N.	Substrate (aglycone) specificity of human cytosolic beta-glucosidase.	Biochem J	2003	12667141	lysosomal - uniprot cytosolic form also exists - berrin ref: Substrate (aglycone) specificity of human cytosolic beta-glucosidase. Biochem J. 2003 Jul 1;373(Pt 1):41-8. This gene encodes a lysosomal membrane protein that cleaves the beta-glucosidic linkage of glycosylceramide, an intermediate in glycolipid metabolism. Mutations in this gene cause Gaucher disease, a lysosomal storage disease characterized by an accumulation of glucocerebrosides. A related pseudogene is approximately 12 kb downstream of this gene on chromosome 1. Alternative splicing results in multiple transcript variants encoding the same protein. NJ
GBAl	3	Tettamanti G, Bassi R, Viani P, Riboni L	Salvage pathways in glycosphingolipid metabolism	Biochimie	2003		lysosomal - uniprot cytosolic form also exists - berrin ref: Substrate (aglycone) specificity of human cytosolic beta-glucosidase. Biochem J. 2003 Jul 1;373(Pt 1):41-8. This gene encodes a lysosomal membrane protein that cleaves the beta-glucosidic linkage of glycosylceramide, an intermediate in glycolipid metabolism. Mutations in this gene cause Gaucher disease, a lysosomal storage disease characterized by an accumulation of glucocerebrosides. A related pseudogene is approximately 12 kb downstream of this gene on chromosome 1. Alternative splicing results in multiple transcript variants encoding the same protein. NJ

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GBGT1	3	Xu H, Storch T, Yu M, Elliott SP, Haslam DB.	haracterization of the human Forssman synthetase gene. An evolving association between glycolipid synthesis and host-microbial interactions.	J Biol Chem	1999	10506200	Golgi - lumen side - see ref Kolter and Sandhoff; also noted in uniprot no direct biochem evidence - see xu ref This gene encodes a member of the histo-blood group ABO gene family that encodes glycosyltransferases with related but distinct substrate specificity. This protein plays a role in synthesizing Forssman glycolipid (FG), a member of the globoseries glycolipid family. Human cells do not normally produce FG but produce the precursor glycolipids globotriaosylceramide and globoside. This protein may be involved in the tropism and binding of pathogenic organisms. NJ
GCALDD	2	Brent J	Current management of ethylene glycol poisoning	Drugs	2001	11434452	- reaction catalyzed by aldehyde dehydrogenase [Brent, Drugs 2001] - reaction is essentially irreversible in vivo [Poore 1998] - several liver enzymes can catalyze this rxn (see refs in [Poore 1998]) - this rxn is primarily catalyzed by the mitochondrial isozyme, particularly at low levels of acetaldehyde (see refs in [Poore 1998])
GCCcm	3	Lee HH, Kim do J, Ahn HJ, Ha JY, Suh SW.	Crystal structure of T-protein of the glycine cleavage system. Cofactor binding, insights into H-protein recognition, and molecular basis for understanding nonketotic hyperglycinemia.		2004	15355973	0
GCNTg	3	Bierhuizen MF, Mattei MG, Fukuda M.	Expression of the developmental I antigen by a cloned human cDNA encoding a member of a beta-1,6-N-acetylglucosaminyltransferase gene family.	Genes Dev	1993	8449405	specificity: In the adult, highly expressed in prostate and to a lesser extent in small intestine and colon. Barely detected in heart, brain, kidkey and pancreas. No expression in placenta, lung, liver, skeletal muscle, spleen, thymus, testis, ovary and peripheral blood leukocytes. In fetus, highly expressed in brain and to a lesser extent in lung and kidney. Barely detected in liver. The enzyme encoded by this gene is responsible for the formation of the blood group I antigen. The i and I antigens are determined by linear and branched poly-N-acetyllactosaminoglycans, respectively. During embryonic development in human erythrocytes, the fetal i antigen is replaced by the adult I antigen as the result of the appearance of a beta-1,6-N-acetylglucosaminyltransferase, the I-branching enzyme. This gene encodes the I-branching enzyme that converts the linear form into the branched form. Defects in this gene have been associated with adult i blood group phenotype. Several transcript variants encoding different isoforms have been described. Branching enzyme that converts linear into branched poly-N-ac Introduces the blood group I antigen during embryonic develop
GCNTg	3	Pras E, Raz J, Yahalom V, Frydman M, Garzozi HJ, Pras E, Hejtmancik JF.	A nonsense mutation in the glucosaminyl (N-acetyl) transferase 2 gene (GCNT2): association with autosomal recessive congenital cataracts.	Invest Ophthalmol Vis Sci	2004	15161861	specificity: In the adult, highly expressed in prostate and to a lesser extent in small intestine and colon. Barely detected in heart, brain, kidkey and pancreas. No expression in placenta, lung, liver, skeletal muscle, spleen, thymus, testis, ovary and peripheral blood leukocytes. In fetus, highly expressed in brain and to a lesser extent in lung and kidney. Barely detected in liver. The enzyme encoded by this gene is responsible for the formation of the blood group I antigen. The i and I antigens are determined by linear and branched poly-N-acetyllactosaminoglycans, respectively. During embryonic development in human erythrocytes, the fetal i antigen is replaced by the adult I antigen as the result of the appearance of a beta-1,6-N-acetylglucosaminyltransferase, the I-branching enzyme. This gene encodes the I-branching enzyme that converts the linear form into the branched form. Defects in this gene have been associated with adult i blood group phenotype. Several transcript variants encoding different isoforms have been described. Branching enzyme that converts linear into branched poly-N-ac Introduces the blood group I antigen during embryonic develop
GDPFUCtg	3	Luhn K, Wild MK, Eckhardt M, Gerardy-Schahn R, Vestweber D	The gene defective in leukocyte adhesion deficiency II encodes a putative GDP-fucose transporter	Nat Genet	2001	11326279	- isolated; restored fucosylation in mutant cells [Lubke 2001] - 55% identity to C. elegans ortholog [Luhn 2001] - cloned [Luhn 2001] - Golgi [Luhn 2001]
GDPFUCtg	3	Lubke T, Marquardt T, Etzioni A, Hartmann E, von Figura K, Korner C	Complementation cloning identifies CDG-IIc, a new type of congenital disorders of glycosylation, as a GDP-fucose transporter deficiency	Nat Genet	2001	11326280	- isolated; restored fucosylation in mutant cells [Lubke 2001] - 55% identity to C. elegans ortholog [Luhn 2001] - cloned [Luhn 2001] - Golgi [Luhn 2001]
GF6PTA	3	McKnight GL, Mudri SL, Mathewes SL, Traxinger RR, Marshall S, Sheppard PO, O'Hara PJ.	Molecular cloning, cDNA sequence, and bacterial expression of human glutamine:fructose-6-phosphate amidotransferase.		1992	1460020	- shown as irreversible in Devlin p. 672, 676 and Orten p. 243, Varki p. 74 [however, transaminase reactions are typically reversible] - sequence data - GFPT1 and GFPT2 - biochemical data - GFPT1 -cytosol based on GeneCards

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GF6PTA	3	Oki T, Yamazaki K, Kuromitsu J, Okada M, Tanaka I.	cDNA cloning and mapping of a novel subtype of glutamine:fructose-6-phosphate amidotransferase (GFAT2) in human and mouse.		1999	10198162	- shown as irreversible in Devlin p. 672, 676 and Orten p. 243, Varki p. 74 [however, transaminase reactions are typically reversible] - sequence data - GFPT1 and GFPT2 - biochemical data - GFPT1 -cytosol based on GeneCards
GF6PTA	3	Broschat KO, Gorka C, Page JD, Martin-Berger CL, Davies MS, Huang Hc HC, Gulve EA, Salsgiver WJ, Kasten TP.	Kinetic characterization of human glutamine-fructose 6-phosphate amidotransferase I: potent feedback inhibition by glucosamine 6-phosphate.		2002	11842094	- shown as irreversible in Devlin p. 672, 676 and Orten p. 243, Varki p. 74 [however, transaminase reactions are typically reversible] - sequence data - GFPT1 and GFPT2 - biochemical data - GFPT1 -cytosol based on GeneCards
GGH-7THFl	3	Chandler CJ, Wang TT, Halsted CH.	Pteroylpolyglutamate hydrolase from human jejunal brush borders. Purification and characterization.	J Biol Chem	1986	2867095	IT
GGH-7THFl	3	Rhee MS, Lindau-Shepard B, Chave KJ, Galivan J, Ryan TJ.	Characterization of human cellular gamma-glutamyl hydrolase.	Mol Pharmacol	1998	9614206	IT
GGLUCT	3	York MJ, Crossley MJ, Hyslop SJ, Fisher ML, Kuchel PW	gamma-Glutamylcyclotransferase: inhibition by D-beta-aminoglutaryl-L-alanine and analysis of the solvent kinetic isotope effect	Eur J Biochem	1989	2570694	also may work with other amino acids probably the reaction is standard, although there is little information about the gene
GGNG	3	Barbetti F, Rocchi M, Bossolasco M, Cordera R, Sbraccia P, Finelli P, Consalez GG.	The human skeletal muscle glycogenin gene: cDNA, tissue expression and chromosomal localization	Biochem Biophys Res Commun	1996	8602861	- glycogenin self glucosylates, forming a primer for glycogen synthesis [Devlin, Texbook of Biochem, 2001] -two known forms of glycogenin, expressed in different tissues [Mu, J Biol Chem 1997], [Mu, J Biol Chem 1998] -pathway reviewed in Lomako, Biochim Biophys Acta 2004
GGNG	3	Mu J, Roach PJ	Characterization of human glycogenin-2, a self-glucosylating initiator of liver glycogen metabolism	J Biol Chem	1998	9857012	- glycogenin self glucosylates, forming a primer for glycogen synthesis [Devlin, Texbook of Biochem, 2001] -two known forms of glycogenin, expressed in different tissues [Mu, J Biol Chem 1997], [Mu, J Biol Chem 1998] -pathway reviewed in Lomako, Biochim Biophys Acta 2004
GGNG	3	Mu J, Skurat AV, Roach PJ	Glycogenin-2, a novel self-glucosylating protein involved in liver glycogen biosynthesis	J Biol Chem	1997		- glycogenin self glucosylates, forming a primer for glycogen synthesis [Devlin, Texbook of Biochem, 2001] -two known forms of glycogenin, expressed in different tissues [Mu, J Biol Chem 1997], [Mu, J Biol Chem 1998] -pathway reviewed in Lomako, Biochim Biophys Acta 2004
GHMT2rm	3	Garrow TA, Brenner AA, Whitehead VM, Chen XN, Duncan RG, Korenberg JR, Shane B.	Cloning of human cDNAs encoding mitochondrial and cytosolic serine hydroxymethyltransferases and chromosomal localization.		1993	8505317	reversible according to Lehninger (4th ed., p.844) - humans have a cytosolic and mitochondrial isoform of serine (glycine) hydroxymethyltransferase [Poore 1998] - experiments w/ CHO cells indicate that the mitochondrial enzyme participates in the conversion of serine to glycine whereas the cytoplasmic enzyme may primarily act in the reverse reaction [Narkewicz 1996] - in the liver, the conversion is largely in the direction of glycine to serine (see refs in [Poore 1998])
GHMT2rm	3	Narkewicz MR, Sauls SD, Tjoa SS, Teng C, Fennessey PV	Evidence for intracellular partitioning of serine and glycine metabolism in Chinese hamster ovary cells	Biochem J	1996	8611185	reversible according to Lehninger (4th ed., p.844) - humans have a cytosolic and mitochondrial isoform of serine (glycine) hydroxymethyltransferase [Poore 1998] - experiments w/ CHO cells indicate that the mitochondrial enzyme participates in the conversion of serine to glycine whereas the cytoplasmic enzyme may primarily act in the reverse reaction [Narkewicz 1996] - in the liver, the conversion is largely in the direction of glycine to serine (see refs in [Poore 1998])
GHMT2rm	3	Poore RE, Hurst CH, Assimos DG, Holmes RP	Pathways of hepatic oxalate synthesis and their regulation	Am J Physiol	1997	9038835	reversible according to Lehninger (4th ed., p.844) - humans have a cytosolic and mitochondrial isoform of serine (glycine) hydroxymethyltransferase [Poore 1998] - experiments w/ CHO cells indicate that the mitochondrial enzyme participates in the conversion of serine to glycine whereas the cytoplasmic enzyme may primarily act in the reverse reaction [Narkewicz 1996] - in the liver, the conversion is largely in the direction of glycine to serine (see refs in [Poore 1998])
GK1	3	Brady WA, Kokoris MS, Fitzgibbon M, Black ME.	Cloning, characterization, and modeling of mouse and human guanylate kinases.	J Biol Chem	1996	8663313	IT

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GLACO	2	Marsh CA	Biosynthesis of D-glucaric acid in mammals: a free-radical mechanism?	Carbohydr Res	1986	3779687	- A cytosolic liver enzyme, with NAD+ as co-substrate, has been found12 to produce D-glucaric acid from D-ghicurono-6,3-lactone. However, studies of the enzyme, purified from rat liver, established that this glucuronolactone dehydrogenase was an aldehyde dehydrogenase of wide specificity [Marsh, Carb Res 1986] - glucaric acid seems to be a dead end metabolite [Marsh, Carb Res 1986]
GLAl	3	Bishop DF, Kornreich R, Desnick RJ	Structural organization of the human alpha-galactosidase A gene: further evidence for the absence of a 3' untranslated region	Proc Natl Acad Sci U S A	1988	2836863	lysosomal - uniprot Look -> great article: [Fabry's disease (alpha-galactosidase-A deficiency): physiopathology, clinical signs, and genetic aspects] J Soc Biol. 2002;196(2):161-73. Review. --> can't read because it's French (consult IT) Lam ref - SNP study w/ pts w/ Fabry's dz NJ - cloned [Bishop 1998] - alpha-galactosidase has been purified from human placenta, [11.] liver cells, [12.] spleen cells, [13.] plasma, [13.] and fibroblasts; [14.] recombinant enzyme has been produced in Escherichia coli bacterial cells,[15.] COS monkey cells, [16.] CHO cells, [17.] baculovirus-infected Sf9 insect cells, [18. and 19.] Pichia pastoris yeast cells,[20.] transduced human bone marrow cells, [21.] (refs are from [Garman 2004])
GLAl	3	Lam CW, Mak YT, Lo YM, Tong SF, To KF, Lai FM.	Molecular genetic analysis of a Chinese patient with Fabry disease.	Chin Med J (Engl)	2000	11775551	lysosomal - uniprot Look -> great article: [Fabry's disease (alpha-galactosidase-A deficiency): physiopathology, clinical signs, and genetic aspects] J Soc Biol. 2002;196(2):161-73. Review. --> can't read because it's French (consult IT) Lam ref - SNP study w/ pts w/ Fabry's dz NJ - cloned [Bishop 1998] - alpha-galactosidase has been purified from human placenta, [11.] liver cells, [12.] spleen cells, [13.] plasma, [13.] and fibroblasts; [14.] recombinant enzyme has been produced in Escherichia coli bacterial cells,[15.] COS monkey cells, [16.] CHO cells, [17.] baculovirus-infected Sf9 insect cells, [18. and 19.] Pichia pastoris yeast cells,[20.] transduced human bone marrow cells, [21.] (refs are from [Garman 2004])
GLAl	3	Ishii S, Nakao S, Minamikawa-Tachino R, Desnick RJ, Fan JQ.	Alternative splicing in the alpha-galactosidase A gene: increased exon inclusion results in the Fabry cardiac phenotype.	Am J Hum Genet	2002	11828341	lysosomal - uniprot Look -> great article: [Fabry's disease (alpha-galactosidase-A deficiency): physiopathology, clinical signs, and genetic aspects] J Soc Biol. 2002;196(2):161-73. Review. --> can't read because it's French (consult IT) Lam ref - SNP study w/ pts w/ Fabry's dz NJ - cloned [Bishop 1998] - alpha-galactosidase has been purified from human placenta, [11.] liver cells, [12.] spleen cells, [13.] plasma, [13.] and fibroblasts; [14.] recombinant enzyme has been produced in Escherichia coli bacterial cells,[15.] COS monkey cells, [16.] CHO cells, [17.] baculovirus-infected Sf9 insect cells, [18. and 19.] Pichia pastoris yeast cells,[20.] transduced human bone marrow cells, [21.] (refs are from [Garman 2004])
GLAl	3	Garman SC, Garboczi DN.	The molecular defect leading to Fabry disease: structure of human alpha-galactosidase.	J Mol Biol	2004	15003450	lysosomal - uniprot Look -> great article: [Fabry's disease (alpha-galactosidase-A deficiency): physiopathology, clinical signs, and genetic aspects] J Soc Biol. 2002;196(2):161-73. Review. --> can't read because it's French (consult IT) Lam ref - SNP study w/ pts w/ Fabry's dz NJ - cloned [Bishop 1998] - alpha-galactosidase has been purified from human placenta, [11.] liver cells, [12.] spleen cells, [13.] plasma, [13.] and fibroblasts; [14.] recombinant enzyme has been produced in Escherichia coli bacterial cells,[15.] COS monkey cells, [16.] CHO cells, [17.] baculovirus-infected Sf9 insect cells, [18. and 19.] Pichia pastoris yeast cells,[20.] transduced human bone marrow cells, [21.] (refs are from [Garman 2004])
GLBRAN	3	Thon VJ, Khalil M, Cannon JF	Isolation of human glycogen branching enzyme cDNAs by screening complementation in yeast.	J Biol Chem	1993	8463281	- forms alpha 1,6- glucosidic linkages [RefSeq] -most highly expressed in liver and muscle [RefSeq] - see Devlin p. 650

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
GLCAASE1ly	3	Oshima A, Kyle JW, Miller RD, Hoffmann JW, Powell PP, Grubb JH, Sly WS, Tropak M, Guise KS, Gravel RA	Cloning, sequencing, and expression of cDNA for human beta-glucuronidase	Proc Natl Acad Sci U S A	1987	3468507	2990: - isolated and expressed in E. coli [Guise 1985] - isolation from human liver and kinetic characterization [Ho 1985] -cloned and expressed in COS cells [Oshima 1987]
GLCAASE1ly	3	Guise KS, Korneluk RG, Waye J, Lamhonwah AM, Quan F, Palmer R, Ganschow RE, Sly WS, Gravel RA	Isolation and expression in Escherichia coli of a cDNA clone encoding human beta-glucuronidase	Gene	1985	3924735	2990: - isolated and expressed in E. coli [Guise 1985] - isolation from human liver and kinetic characterization [Ho 1985] -cloned and expressed in COS cells [Oshima 1987]
GLCAASE1ly	3	Ho YC, Ho LH, Ho KJ	Human hepatic beta-glucuronidase: an enzyme kinetic study	Enzyme	1985	3987656	2990: - isolated and expressed in E. coli [Guise 1985] - isolation from human liver and kinetic characterization [Ho 1985] -cloned and expressed in COS cells [Oshima 1987]
GLCAE2g	3	Li JP, Gong F, El Darwish K, Jalkanen M, Lindahl U	Characterization of the D-glucuronyl C5-epimerase involved in the biosynthesis of heparin and heparan sulfate	J Biol Chem	2001	11274177	- has > 96% identity to mouse and bovine cDNAs [Li, J Biol Chem 2001] - gene identified by BLAST and cloned [Crawford, J Biol Chem 2001] - reaction is effectively irreversible in vivo [Hagner-McWhirter, J Biol Chem 2004] - ubiquitously expressed [Sugahara, IUBMB Life 2002] - Golgi (based on mouse protein's localization) [UniProt], [Crawford, J Biol Chem 2001]
GLCAE2g	3	Crawford BE, Olson SK, Esko JD, Pinhal MA	Cloning, Golgi localization, and enzyme activity of the full-length heparin/heparan sulfate-glucuronic acid C5-epimerase	J Biol Chem	2001	11279150	- has > 96% identity to mouse and bovine cDNAs [Li, J Biol Chem 2001] - gene identified by BLAST and cloned [Crawford, J Biol Chem 2001] - reaction is effectively irreversible in vivo [Hagner-McWhirter, J Biol Chem 2004] - ubiquitously expressed [Sugahara, IUBMB Life 2002] - Golgi (based on mouse protein's localization) [UniProt], [Crawford, J Biol Chem 2001]
GLCAE2g	3	Hagner-McWhirter A, Li JP, Oscarson S, Lindahl U	Irreversible glucuronyl C5-epimerization in the biosynthesis of heparan sulfate.	J Biol Chem	2004	14718527	- has > 96% identity to mouse and bovine cDNAs [Li, J Biol Chem 2001] - gene identified by BLAST and cloned [Crawford, J Biol Chem 2001] - reaction is effectively irreversible in vivo [Hagner-McWhirter, J Biol Chem 2004] - ubiquitously expressed [Sugahara, IUBMB Life 2002] - Golgi (based on mouse protein's localization) [UniProt], [Crawford, J Biol Chem 2001]
GLCAT2g	3	Kitagawa H, Uyama T, Sugahara K	Molecular cloning and expression of a human chondroitin synthase	J Biol Chem	2001	11514575	- Golgi localization [Silbert, IUBMB LIfe 2002] 54480: - gene was cloned and characterized [Gotoh, J Biol Chem 2002] - has only GlcA-T activity [Gotoh, J Biol Chem 2002] - ubiquitously expressed, most highly expressed in the placenta, small intestine, and pancreas [Gotoh, J Biol Chem 2002] 22856: - gene was cloned and expressed [Kitagawa, J Biol Chem 2001] - has GlcA-T and GalNAc-T activities [Kitagawa, J Biol Chem 2001] - ubiquitously expressed [Kitagawa, J Biol Chem 2001] - requires concomitant expression of chondroitin polymerizing factor (79586) [Kitagawa, J Biol Chem 2003] - 79586 & 22856 form a protein complex [Kitagawa, J Biol Chem 2003] 79586: - gene was cloned and expressed [Yada, J Biol Chem 2003] - has GlcA-T and GalNAc-T activities [Yada, J Biol Chem 2003] - ubiquitously expressed, but highly expressed in the pancreas, ovary, placenta, small intestine, and stomach [Yada, J Biol Chem 2003] 337876: - cloned and characterized [Yada, J Biol Chem 2003] - has GlcA-T and GalNAc-T activities [Yada, J Biol Chem 2003] - ubiquitously expressed [Yada, J Biol Chem 2003]

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GLCAT2g	3	Gotoh M, Yada T, Sato T, Akashima T, Iwasaki H, Mochizuki H, Inaba N, Togayachi A, Kudo T, Watanabe H, Kimata K, Narimatsu H	Molecular cloning and characterization of a novel chondroitin sulfate glucuronyltransferase that transfers glucuronic acid to N-acetylgalactosamine	J Biol Chem	2002	12145278	- Golgi localization [Silbert, IUBMB LIfe 2002] 54480: - gene was cloned and characterized [Gotoh, J Biol Chem 2002] - has only GlcA-T activity [Gotoh, J Biol Chem 2002] - ubiquitously expressed, most highly expressed in the placenta, small intestine, and pancreas [Gotoh, J Biol Chem 2002] 22856: - gene was cloned and expressed [Kitagawa, J Biol Chem 2001] - has GlcA-T and GalNAc-T activities [Kitagawa, J Biol Chem 2001] - ubiquitously expressed [Kitagawa, J Biol Chem 2001] - requires concomitant expression of chondroitin polymerizing factor (79586) [Kitagawa, J Biol Chem 2003] - 79586 & 22856 form a protein complex [Kitagawa, J Biol Chem 2003] 79586: - gene was cloned and expressed [Yada, J Biol Chem 2003] - has GlcA-T and GalNAc-T activities [Yada, J Biol Chem 2003] - ubiquitously expressed, but highly expressed in the pancreas, ovary, placenta, small intestine, and stomach [Yada, J Biol Chem 2003] 337876: - cloned and characterized [Yada, J Biol Chem 2003] - has GlcA-T and GalNAc-T activities [Yada, J Biol Chem 2003] - ubiquitously expressed [Yada, J Biol Chem 2003]
GLCAT2g	3	Kitagawa H, Izumikawa T, Uyama T, Sugahara K	Molecular cloning of a chondroitin polymerizing factor that cooperates with chondroitin synthase for chondroitin polymerization	J Biol Chem	2003	12716890	- Golgi localization [Silbert, IUBMB LIfe 2002] 54480: - gene was cloned and characterized [Gotoh, J Biol Chem 2002] - has only GlcA-T activity [Gotoh, J Biol Chem 2002] - ubiquitously expressed, most highly expressed in the placenta, small intestine, and pancreas [Gotoh, J Biol Chem 2002] 22856: - gene was cloned and expressed [Kitagawa, J Biol Chem 2001] - has GlcA-T and GalNAc-T activities [Kitagawa, J Biol Chem 2001] - ubiquitously expressed [Kitagawa, J Biol Chem 2001] - requires concomitant expression of chondroitin polymerizing factor (79586) [Kitagawa, J Biol Chem 2003] - 79586 & 22856 form a protein complex [Kitagawa, J Biol Chem 2003] 79586: - gene was cloned and expressed [Yada, J Biol Chem 2003] - has GlcA-T and GalNAc-T activities [Yada, J Biol Chem 2003] - ubiquitously expressed, but highly expressed in the pancreas, ovary, placenta, small intestine, and stomach [Yada, J Biol Chem 2003] 337876: - cloned and characterized [Yada, J Biol Chem 2003] - has GlcA-T and GalNAc-T activities [Yada, J Biol Chem 2003] - ubiquitously expressed [Yada, J Biol Chem 2003]

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GLCAT2g	3	Yada T, Gotoh M, Sato T, Shionyu M, Go M, Kaseyama H, Iwasaki H, Kikuchi N, Kwon YD, Togayachi A, Kudo T, Watanabe H, Narimatsu H, Kimata K	Chondroitin sulfate synthase-2. Molecular cloning and characterization of a novel human glycosyltransferase homologous to chondroitin sulfate glucuronyltransferase, which has dual enzymatic activities	J Biol Chem	2003	12761225	- Golgi localization [Silbert, IUBMB LIfe 2002] 54480: - gene was cloned and characterized [Gotoh, J Biol Chem 2002] - has only GlcA-T activity [Gotoh, J Biol Chem 2002] - ubiquitously expressed, most highly expressed in the placenta, small intestine, and pancreas [Gotoh, J Biol Chem 2002] 22856: - gene was cloned and expressed [Kitagawa, J Biol Chem 2001] - has GlcA-T and GalNAc-T activities [Kitagawa, J Biol Chem 2001] - ubiquitously expressed [Kitagawa, J Biol Chem 2001] - requires concomitant expression of chondroitin polymerizing factor (79586) [Kitagawa, J Biol Chem 2003] - 79586 & 22856 form a protein complex [Kitagawa, J Biol Chem 2003] 79586: - gene was cloned and expressed [Yada, J Biol Chem 2003] - has GlcA-T and GalNAc-T activities [Yada, J Biol Chem 2003] - ubiquitously expressed, but highly expressed in the pancreas, ovary, placenta, small intestine, and stomach [Yada, J Biol Chem 2003] 337876: - cloned and characterized [Yada, J Biol Chem 2003] - has GlcA-T and GalNAc-T activities [Yada, J Biol Chem 2003] - ubiquitously expressed [Yada, J Biol Chem 2003]
GLCAT2g	3	Yada T, Sato T, Kaseyama H, Gotoh M, Iwasaki H, Kikuchi N, Kwon YD, Togayachi A, Kudo T, Watanabe H, Narimatsu H, Kimata K	Chondroitin sulfate synthase-3. Molecular cloning and characterization	J Biol Chem	2003	12907687	- Golgi localization [Silbert, IUBMB LIfe 2002] 54480: - gene was cloned and characterized [Gotoh, J Biol Chem 2002] - has only GlcA-T activity [Gotoh, J Biol Chem 2002] - ubiquitously expressed, most highly expressed in the placenta, small intestine, and pancreas [Gotoh, J Biol Chem 2002] 22856: - gene was cloned and expressed [Kitagawa, J Biol Chem 2001] - has GlcA-T and GalNAc-T activities [Kitagawa, J Biol Chem 2001] - ubiquitously expressed [Kitagawa, J Biol Chem 2001] - requires concomitant expression of chondroitin polymerizing factor (79586) [Kitagawa, J Biol Chem 2003] - 79586 & 22856 form a protein complex [Kitagawa, J Biol Chem 2003] 79586: - gene was cloned and expressed [Yada, J Biol Chem 2003] - has GlcA-T and GalNAc-T activities [Yada, J Biol Chem 2003] - ubiquitously expressed, but highly expressed in the pancreas, ovary, placenta, small intestine, and stomach [Yada, J Biol Chem 2003] 337876: - cloned and characterized [Yada, J Biol Chem 2003] - has GlcA-T and GalNAc-T activities [Yada, J Biol Chem 2003] - ubiquitously expressed [Yada, J Biol Chem 2003]
GLCAT6g	3	Ahn J, Ludecke HJ, Lindow S, Horton WA, Lee B, Wagner MJ, Horsthemke B, Wells DE	Cloning of the putative tumour suppressor gene for hereditary multiple exostoses (EXT1)	Nat Genet	1995	7550340	- 2131, 2132 form a hetero-oligomeric complex in the Golgi [UniProt],[McCormick, PNAS 2000], [Kobayashi, Biochem Biophys Res Commun 2000]; complex has significantly higher activity in vitro than EXT1 or EXT2 alone, suggesting it is the predominant form in vivo [McCormick, PNAS 2000] 2131: - gene was cloned [Ahn, Nat Genet 1995] - human EXT1 was used to complement mouse knockout [McCormick, Nat Genet 1998] - ubiquitous [UniProt] 2132: - gene was isolated and characterized [Stickens, Nat Genet 1996] - bovine protein has both GlcNAc and GlcA transferase activities [Lind, J Biol Chem 1998] - ubiquitous [UniProt]

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GLCAT6g	3	Stickens D, Clines G, Burbee D, Ramos P, Thomas S, Hogue D, Hecht JT, Lovett M, Evans GA	The EXT2 multiple exostoses gene defines a family of putative tumour suppressor genes	Nat Genet	1996	8782816	- 2131, 2132 form a hetero-oligomeric complex in the Golgi [UniProt],[McCormick, PNAS 2000], [Kobayashi, Biochem Biophys Res Commun 2000]; complex has significantly higher activity in vitro than EXT1 or EXT2 alone, suggesting it is the predominant form in vivo [McCormick, PNAS 2000] 2131: - gene was cloned [Ahn, Nat Genet 1995] - human EXT1 was used to complement mouse knockout [McCormick, Nat Genet 1998] - ubiquitous [UniProt] 2132: - gene was isolated and characterized [Stickens, Nat Genet 1996] - bovine protein has both GlcNAc and GlcA transferase activities [Lind, J Biol Chem 1998] - ubiquitous [UniProt]
GLCAT6g	3	McCormick C, Leduc Y, Martindale D, Mattison K, Esford LE, Dyer AP, Tufaro F	The putative tumour suppressor EXT1 alters the expression of cell-surface heparan sulfate	Nat Genet	1998	9620772	- 2131, 2132 form a hetero-oligomeric complex in the Golgi [UniProt],[McCormick, PNAS 2000], [Kobayashi, Biochem Biophys Res Commun 2000]; complex has significantly higher activity in vitro than EXT1 or EXT2 alone, suggesting it is the predominant form in vivo [McCormick, PNAS 2000] 2131: - gene was cloned [Ahn, Nat Genet 1995] - human EXT1 was used to complement mouse knockout [McCormick, Nat Genet 1998] - ubiquitous [UniProt] 2132: - gene was isolated and characterized [Stickens, Nat Genet 1996] - bovine protein has both GlcNAc and GlcA transferase activities [Lind, J Biol Chem 1998] - ubiquitous [UniProt]
GLCAT6g	3	Lind T, Tufaro F, McCormick C, Lindahl U, Lidholt K	The putative tumor suppressors EXT1 and EXT2 are glycosyltransferases required for the biosynthesis of heparan sulfate	J Biol Chem	1998	9756849	- 2131, 2132 form a hetero-oligomeric complex in the Golgi [UniProt],[McCormick, PNAS 2000], [Kobayashi, Biochem Biophys Res Commun 2000]; complex has significantly higher activity in vitro than EXT1 or EXT2 alone, suggesting it is the predominant form in vivo [McCormick, PNAS 2000] 2131: - gene was cloned [Ahn, Nat Genet 1995] - human EXT1 was used to complement mouse knockout [McCormick, Nat Genet 1998] - ubiquitous [UniProt] 2132: - gene was isolated and characterized [Stickens, Nat Genet 1996] - bovine protein has both GlcNAc and GlcA transferase activities [Lind, J Biol Chem 1998] - ubiquitous [UniProt]
GLCAT6g	3	McCormick C, Duncan G, Goutsos KT, Tufaro F	The putative tumor suppressors EXT1 and EXT2 form a stable complex that accumulates in the Golgi apparatus and catalyzes the synthesis of heparan sulfate	Proc Natl Acad Sci U S A	2000	10639137	- 2131, 2132 form a hetero-oligomeric complex in the Golgi [UniProt],[McCormick, PNAS 2000], [Kobayashi, Biochem Biophys Res Commun 2000]; complex has significantly higher activity in vitro than EXT1 or EXT2 alone, suggesting it is the predominant form in vivo [McCormick, PNAS 2000] 2131: - gene was cloned [Ahn, Nat Genet 1995] - human EXT1 was used to complement mouse knockout [McCormick, Nat Genet 1998] - ubiquitous [UniProt] 2132: - gene was isolated and characterized [Stickens, Nat Genet 1996] - bovine protein has both GlcNAc and GlcA transferase activities [Lind, J Biol Chem 1998] - ubiquitous [UniProt]
GLCAT6g	3	Kobayashi S, Morimoto K, Shimizu T, Takahashi M, Kurosawa H, Shirasawa T	Association of EXT1 and EXT2, hereditary multiple exostoses gene products, in Golgi apparatus	Biochem Biophys Res Commun	2000	10679296	- 2131, 2132 form a hetero-oligomeric complex in the Golgi [UniProt],[McCormick, PNAS 2000], [Kobayashi, Biochem Biophys Res Commun 2000]; complex has significantly higher activity in vitro than EXT1 or EXT2 alone, suggesting it is the predominant form in vivo [McCormick, PNAS 2000] 2131: - gene was cloned [Ahn, Nat Genet 1995] - human EXT1 was used to complement mouse knockout [McCormick, Nat Genet 1998] - ubiquitous [UniProt] 2132: - gene was isolated and characterized [Stickens, Nat Genet 1996] - bovine protein has both GlcNAc and GlcA transferase activities [Lind, J Biol Chem 1998] - ubiquitous [UniProt]

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GLCATg	3	Kitagawa H, Tone Y, Tamura J, Neumann KW, Ogawa T, Oka S, Kawasaki T, Sugahara K	Molecular cloning and expression of glucuronyltransferase I involved in the biosynthesis of the glycosaminoglycan-protein linkage region of proteoglycans	J Biol Chem	1998	9506957	- Golgi localization [Silbert, IUBMB LIfe 2002] 135152: - transfers a GlcA to terminal Gal residue in linkage region of chondroitin / heparan sulfate [RefSeq], [UniProt] - Golgi [UniProt] - Expressed in the trachea, retina, spinal cord, hippocampus and other brain regions, and, at lower levels, in testis and ovary [UniProt], [Marcus, J Hum Genet 2002] - gene identified via BLAST; 89% homology to rat protein [Marcus, J Hum Genet 2002] 26229: - transfers a GlcA to terminal Gal residue in linkage region of chondroitin / heparan sulfate [RefSeq], [UniProt], [Kitagawa, J Biol Chem 1998] - Golgi [UniProt] - Ubiquitous (but weakly expresed in all tissues examined) [UniProt] - gene was cloned and expressed [Kitagawa, J Biol Chem 1998] - 43% identity to rat protein [Kitagawa, J Biol Chem 1998] 27087: - Golgi [UniProt] - transfers a GlcA to terminal Gal residue in linkage region of chondroitin / heparan sulfate [UniProt] - mainly expressed in the brain [UniProt], [Mitsumoto, Genomics 2000] - cDNA was isolated [Mitsumoto, Genomics 2000] - 98% identical to rat protein [Mitsumoto, Genomics 2000]
GLCATg	3	Mitsumoto Y, Oka S, Sakuma H, Inazawa J, Kawasaki T	Cloning and chromosomal mapping of human glucuronyltransferase involved in biosynthesis of the HNK-1 carbohydrate epitope	Genomics	2000	10783264	- Golgi localization [Silbert, IUBMB LIfe 2002] 135152: - transfers a GlcA to terminal Gal residue in linkage region of chondroitin / heparan sulfate [RefSeq], [UniProt] - Golgi [UniProt] - Expressed in the trachea, retina, spinal cord, hippocampus and other brain regions, and, at lower levels, in testis and ovary [UniProt], [Marcus, J Hum Genet 2002] - gene identified via BLAST; 89% homology to rat protein [Marcus, J Hum Genet 2002] 26229: - transfers a GlcA to terminal Gal residue in linkage region of chondroitin / heparan sulfate [RefSeq], [UniProt], [Kitagawa, J Biol Chem 1998] - Golgi [UniProt] - Ubiquitous (but weakly expresed in all tissues examined) [UniProt] - gene was cloned and expressed [Kitagawa, J Biol Chem 1998] - 43% identity to rat protein [Kitagawa, J Biol Chem 1998] 27087: - Golgi [UniProt] - transfers a GlcA to terminal Gal residue in linkage region of chondroitin / heparan sulfate [UniProt] - mainly expressed in the brain [UniProt], [Mitsumoto, Genomics 2000] - cDNA was isolated [Mitsumoto, Genomics 2000] - 98% identical to rat protein [Mitsumoto, Genomics 2000]
GLCATg	3	Marcos I, Galan JJ, Borrego S, Antinolo G	Cloning, characterization, and chromosome mapping of the human GlcAT-S gene	J Hum Genet	2002	12522689	- Golgi localization [Silbert, IUBMB LIfe 2002] 135152: - transfers a GlcA to terminal Gal residue in linkage region of chondroitin / heparan sulfate [RefSeq], [UniProt] - Golgi [UniProt] - Expressed in the trachea, retina, spinal cord, hippocampus and other brain regions, and, at lower levels, in testis and ovary [UniProt], [Marcus, J Hum Genet 2002] - gene identified via BLAST; 89% homology to rat protein [Marcus, J Hum Genet 2002] 26229: - transfers a GlcA to terminal Gal residue in linkage region of chondroitin / heparan sulfate [RefSeq], [UniProt], [Kitagawa, J Biol Chem 1998] - Golgi [UniProt] - Ubiquitous (but weakly expresed in all tissues examined) [UniProt] - gene was cloned and expressed [Kitagawa, J Biol Chem 1998] - 43% identity to rat protein [Kitagawa, J Biol Chem 1998] 27087: - Golgi [UniProt] - transfers a GlcA to terminal Gal residue in linkage region of chondroitin / heparan sulfate [UniProt] - mainly expressed in the brain [UniProt], [Mitsumoto, Genomics 2000] - cDNA was isolated [Mitsumoto, Genomics 2000] - 98% identical to rat protein [Mitsumoto, Genomics 2000]

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GLCNACASE1ly	3	Sasaki T, Sukegawa K, Masue M, Fukuda S, Tomatsu S, Orii T	Purification and partial characterization of alpha-N-acetylglucosaminidase from human liver	J Biochem (Tokyo)	1991	1783617	- cleaves terminal N-acetylglucosamine in heparan sulfate [Winchester 1996] 4669: - purified from human liver [Sasaki 1991] - cloned and expressed in CHO cells [Weber 1996]
GLCNACASE1ly	3	Weber B, Blanch L, Clements PR, Scott HS, Hopwood JJ	Cloning and expression of the gene involved in Sanfilippo B syndrome (mucopolysaccharidosis III B)	Hum Mol Genet	1996	8776591	- cleaves terminal N-acetylglucosamine in heparan sulfate [Winchester 1996] 4669: - purified from human liver [Sasaki 1991] - cloned and expressed in CHO cells [Weber 1996]
GLCNACASE1ly	3	Winchester BG	Lysosomal metabolism of glycoconjugates	Subcell Biochem	1996	8993162	- cleaves terminal N-acetylglucosamine in heparan sulfate [Winchester 1996] 4669: - purified from human liver [Sasaki 1991] - cloned and expressed in CHO cells [Weber 1996]
GLCNACDASg	3	Dixon J, Loftus SK, Gladwin AJ, Scambler PJ, Wasmuth JJ, Dixon MJ	Cloning of the human heparan sulfate-N-deacetylase/N-sulfotransferase gene from the Treacher Collins syndrome candidate region at 5q32-q33.1	Genomics	1995	7601448	- N-deacetylase/ N-sulfotransferase acts on a subset of GlcNAc residues in a cluster along the chain [Varki, Glycobiology 1999] - enzyme rapidly deacetylates then sulfates, but some of the deacetylated GlcN residues can escape sulfation [Varki, Glycobiology 1999] 3340: - gene was cloned [Dixon, Genomics 1995], [Humphries, Biochem J 1997] - ubiquitous, but expression most abundant in heart, liver, pancreas [UniProt], [Humphries, Biochem J 1997] - Golgi [UniProt], [Humphries, Biochem J 1997] - N-sulfation and N-deacetylation of glucosamine in heparan sulfate [UniProt] - characterization of N-deacetylase activity [van den Born, Glycobiology 2003] - NDST1 & NDST2 have similar ratios of deactylase and sulfotransferase activities [Aikawa, J Biol Chem 2001] 8509: - gene was cloned [Humphries, Biochem J 1998] - 94% similar to mouse homolog [Humphries, Biochem J 1998] - characterization of N-deacetylase activity [van den Born, Glycobiology 2003] - Golgi [UniProt] - ubiquitously expressed [Sugahara, IUBMB Liife 2002] 9348: - gene was cloned and expressed [Aikawa, J Biol Chem 1999] - N-sulfation and N-deacetylation of glucosamine in heparan su - highly expressed in brain, liver, kidney [Aikawa, J Biol Chem
GLCNACDASg	3	Humphries DE, Sullivan BM, Aleixo MD, Stow JL	Localization of human heparan glucosaminyl N-deacetylase/N-sulphotransferase to the trans-Golgi network.	Biochem J	1997	9230113	- N-deacetylase/ N-sulfotransferase acts on a subset of GlcNAc residues in a cluster along the chain [Varki, Glycobiology 1999] - enzyme rapidly deacetylates then sulfates, but some of the deacetylated GlcN residues can escape sulfation [Varki, Glycobiology 1999] 3340: - gene was cloned [Dixon, Genomics 1995], [Humphries, Biochem J 1997] - ubiquitous, but expression most abundant in heart, liver, pancreas [UniProt], [Humphries, Biochem J 1997] - Golgi [UniProt], [Humphries, Biochem J 1997] - N-sulfation and N-deacetylation of glucosamine in heparan sulfate [UniProt] - characterization of N-deacetylase activity [van den Born, Glycobiology 2003] - NDST1 & NDST2 have similar ratios of deactylase and sulfotransferase activities [Aikawa, J Biol Chem 2001] 8509: - gene was cloned [Humphries, Biochem J 1998] - 94% similar to mouse homolog [Humphries, Biochem J 1998] - characterization of N-deacetylase activity [van den Born, Glycobiology 2003] - Golgi [UniProt] - ubiquitously expressed [Sugahara, IUBMB Liife 2002] 9348: - gene was cloned and expressed [Aikawa, J Biol Chem 1999] - N-sulfation and N-deacetylation of glucosamine in heparan su - highly expressed in brain, liver, kidney [Aikawa, J Biol Chem

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
GLCNACDASg	3	Humphries DE, Lanciotti J, Karlinsky JB	cDNA cloning, genomic organization and chromosomal localization of human heparan glucosaminyl N-deacetylase/N-sulphotransferase-2	Biochem J	1998	9601056	6-O-deacetylase/ N-sulfotransferase acts on a subset of GlcNAc residues in a cluster along the chain [Varki, Glycobiology 1999] - enzyme rapidly deacetylates then sulfates, but some of the deacetylated GlcN residues can escape sulfation [Varki, Glycobiology 1999] 3340: - gene was cloned [Dixon, Genomics 1995], [Humphries, Biochem J 1997] - ubiquitous, but expression most abundant in heart, liver, pancreas [UniProt], [Humphries, Biochem J 1997] - Golgi [UniProt], [Humphries, Biochem J 1997] - N-sulfation and N-deacetylation of glucosamine in heparan sulfate [UniProt] - characterization of N-deacetylase activity [van den Born, Glycobiology 2003] - NDST1 & NDST2 have similar ratios of deactylase and sulfotransferase activities [Aikawa, J Biol Chem 2001] 8509: - gene was cloned [Humphries, Biochem J 1998] - 94% similar to mouse homolog [Humphries, Biochem J 1998] - characterization of N-deacetylase activity [van den Born, Glycobiology 2003] - Golgi [UniProt] - ubiquitously expressed [Sugahara, IUBMB Liife 2002] 9348: - gene was cloned and expressed [Aikawa, J Biol Chem 1999] - N-sulfation and N-deacetylation of glucosamine in heparan su - highly expressed in brain, liver, kidney [Aikawa, J Biol Chem
GLCNACDASg	3	Aikawa J, Esko JD	Molecular cloning and expression of a third member of the heparan sulfate/heparin GlcNAc N-deacetylase/ N-sulfotransferase family	J Biol Chem	1999	9915799	6-O-deacetylase/ N-sulfotransferase acts on a subset of GlcNAc residues in a cluster along the chain [Varki, Glycobiology 1999] - enzyme rapidly deacetylates then sulfates, but some of the deacetylated GlcN residues can escape sulfation [Varki, Glycobiology 1999] 3340: - gene was cloned [Dixon, Genomics 1995], [Humphries, Biochem J 1997] - ubiquitous, but expression most abundant in heart, liver, pancreas [UniProt], [Humphries, Biochem J 1997] - Golgi [UniProt], [Humphries, Biochem J 1997] - N-sulfation and N-deacetylation of glucosamine in heparan sulfate [UniProt] - characterization of N-deacetylase activity [van den Born, Glycobiology 2003] - NDST1 & NDST2 have similar ratios of deactylase and sulfotransferase activities [Aikawa, J Biol Chem 2001] 8509: - gene was cloned [Humphries, Biochem J 1998] - 94% similar to mouse homolog [Humphries, Biochem J 1998] - characterization of N-deacetylase activity [van den Born, Glycobiology 2003] - Golgi [UniProt] - ubiquitously expressed [Sugahara, IUBMB Liife 2002] 9348: - gene was cloned and expressed [Aikawa, J Biol Chem 1999] - N-sulfation and N-deacetylation of glucosamine in heparan su - highly expressed in brain, liver, kidney [Aikawa, J Biol Chem
GLCNACDASg	3	Aikawa J, Grobe K, Tsujimoto M, Esko JD	Multiple isozymes of heparan sulfate/heparin GlcNAc N-deacetylase/GlcN N-sulfotransferase. Structure and activity of the fourth member, NDST4	J Biol Chem	2001	11087757	6-O-deacetylase/ N-sulfotransferase acts on a subset of GlcNAc residues in a cluster along the chain [Varki, Glycobiology 1999] - enzyme rapidly deacetylates then sulfates, but some of the deacetylated GlcN residues can escape sulfation [Varki, Glycobiology 1999] 3340: - gene was cloned [Dixon, Genomics 1995], [Humphries, Biochem J 1997] - ubiquitous, but expression most abundant in heart, liver, pancreas [UniProt], [Humphries, Biochem J 1997] - Golgi [UniProt], [Humphries, Biochem J 1997] - N-sulfation and N-deacetylation of glucosamine in heparan sulfate [UniProt] - characterization of N-deacetylase activity [van den Born, Glycobiology 2003] - NDST1 & NDST2 have similar ratios of deactylase and sulfotransferase activities [Aikawa, J Biol Chem 2001] 8509: - gene was cloned [Humphries, Biochem J 1998] - 94% similar to mouse homolog [Humphries, Biochem J 1998] - characterization of N-deacetylase activity [van den Born, Glycobiology 2003] - Golgi [UniProt] - ubiquitously expressed [Sugahara, IUBMB Liife 2002] 9348: - gene was cloned and expressed [Aikawa, J Biol Chem 1999] - N-sulfation and N-deacetylation of glucosamine in heparan su - highly expressed in brain, liver, kidney [Aikawa, J Biol Chem

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GLCNACDASg	3	van den Born J, Pikas DS, Pisa BJ, Eriksson I, Kjellen L, Berden JH	Antibody-based assay for N-deacetylase activity of heparan sulfate/heparin N-deacetylase/N-sulfotransferase (NDST): novel characteristics of NDST-1 and -2	Glycobiology	2003	12634318	- N-deacetylase/ N-sulfotransferase acts on a subset of GlcNAc residues in a cluster along the chain [Varki, Glycobiology 1999] - enzyme rapidly deacetylates then sulfates, but some of the deacetylated GlcN residues can escape sulfation [Varki, Glycobiology 1999] 3340: - gene was cloned [Dixon, Genomics 1995], [Humphries, Biochem J 1997] - ubiquitous, but expression most abundant in heart, liver, pancreas [UniProt], [Humphries, Biochem J 1997] - Golgi [UniProt], [Humphries, Biochem J 1997] - N-sulfation and N-deacetylation of glucosamine in heparan sulfate [UniProt] - characterization of N-deacetylase activity [van den Born, Glycobiology 2003] - NDST1 & NDST2 have similar ratios of deactylase and sulfotransferase activities [Aikawa, J Biol Chem 2001] 8509: - gene was cloned [Humphries, Biochem J 1998] - 94% similar to mouse homolog [Humphries, Biochem J 1998] - characterization of N-deacetylase activity [van den Born, Glycobiology 2003] - Golgi [UniProt] - ubiquitously expressed [Sugahara, IUBMB Liife 2002] 9348: - gene was cloned and expressed [Aikawa, J Biol Chem 1999] - N-sulfation and N-deacetylation of glucosamine in heparan su - highly expressed in brain, liver, kidney [Aikawa, J Biol Chem
GLCNACT1g	3	Wuyts W, Van Hul W, Hendrickx J, Speleman F, Wauters J, De Boulle K, Van Roy N, Van Agtmael T, Bossuyt P, Willems PJ	Identification and characterization of a novel member of the EXT gene family, EXTL2	Eur J Hum Genet	1997	9450183	- 2135 and 2137 both have GlcNAc-T1 activity 2135: - listed as ER localization, but has been modeled as Golgi since syhtnesis of linkage region and most other reactions occur there [UniProt],[Sugahara, IUBMB Life 2002] - transfers GalNAc in beta-1,4- linkages [UniProt],[Sugahara, IUBMB Life 2002] - ubiquitous [UniProt], [Wuyts, Eur J Hum Genet 1997], [Saito, Biochem Biophy Res Commun 1998] - gene was identified [Wuyts, Eur J Hum Genet 1997], [Saito, Biochem Biophy Res Commun 1998] - isolated enzyme; recombinantly expressed, identified alpha1, 4-N-acetylhexosaminyltransferase activity [Kitagawa, J Biol Chem 1999] 2317: - listed as ER localization, but has been modeled as Golgi since syhtnesis of linkage region and most other reactions occur there [UniProt],[Sugahara, IUBMB Life 2002] - transfers GalNAc in beta-1,4- linkages [UniProt],[Sugahara, IUBMB Life 2002] - has both GlcNAc-TI and TII activities (initiation and elongation) [Sugahara, IUBMB Life 2002], [Kim, PNAS 2001] - ubiquitous [UniProt], [Saito, Biochem Biophy Res Commun 1998] - gene was identified [Van Hul, Genomics 1998], [Saito, Bioch
GLCNACT1g	3	Kitagawa H, Shimakawa H, Sugahara K.	The tumor suppressor EXT-like gene EXTL2 encodes an alpha1, 4-N-acetylhexosaminyltransferase that transfers N-acetylgalactosamine and N-acetylglucosamine to the common glycosaminoglycan protein linkage region.	J Biol Chem	1999	10318803	- 2135 and 2137 both have GlcNAc-T1 activity 2135: - listed as ER localization, but has been modeled as Golgi since syhtnesis of linkage region and most other reactions occur there [UniProt],[Sugahara, IUBMB Life 2002] - transfers GalNAc in beta-1,4- linkages [UniProt],[Sugahara, IUBMB Life 2002] - ubiquitous [UniProt], [Wuyts, Eur J Hum Genet 1997], [Saito, Biochem Biophy Res Commun 1998] - gene was identified [Wuyts, Eur J Hum Genet 1997], [Saito, Biochem Biophy Res Commun 1998] - isolated enzyme; recombinantly expressed, identified alpha1, 4-N-acetylhexosaminyltransferase activity [Kitagawa, J Biol Chem 1999] 2317: - listed as ER localization, but has been modeled as Golgi since syhtnesis of linkage region and most other reactions occur there [UniProt],[Sugahara, IUBMB Life 2002] - transfers GalNAc in beta-1,4- linkages [UniProt],[Sugahara, IUBMB Life 2002] - has both GlcNAc-TI and TII activities (initiation and elongation) [Sugahara, IUBMB Life 2002], [Kim, PNAS 2001] - ubiquitous [UniProt], [Saito, Biochem Biophy Res Commun 1998] - gene was identified [Van Hul, Genomics 1998], [Saito, Bioch

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GLCNACT2g	3	Wise CA, Clines GA, Massa H, Trask BJ, Lovett M	Identification and localization of the gene for EXTL, a third member of the multiple exostoses gene family	Genome Res	1997	9037597	- 2131, 2132 form a hetero-oligomeric complex in the Golgi [UniProt],[McCormick, PNAS 2000], [Kobayashi, Biochem Biophys Res Commun 2000]; complex has significantly higher activity in vitro than EXT1 or EXT2 alone, suggesting it is the predominant form in vivo [McCormick, PNAS 2000] 2131: - gene was cloned [Ahn, Nat Genet 1995] - human EXT1 was used to complement mouse knockout [McCormick, Nat Genet 1998] - ubiquitous [UniProt] 2132: - gene was isolated and characterized [Stickens, Nat Genet 1996] - bovine protein has both GlcNAc and GlcA transferase activities [Lind, J Biol Chem 1998] - ubiquitous [UniProt] 2317: - listed as ER localization, but has been modeled as Golgi since syhtnesis of linkage region and most other reactions occur there [UniProt],[Sugahara, IUBMB Life 2002] - transfers GalNAc in beta-1,4- linkages [UniProt],[Sugahara, IUBMB Life 2002] - has both GlcNAc-TI and TII activities (initiation and elongation) [Sugahara, IUBMB Life 2002], [Kim, PNAS 2001] - ubiquitous [UniProt], [Saito, Biochem Biophy Res Commun 1998] - gene was identified [Van Hul, Genomics 1998], [Saito, Bioch 2134: - only has GlcNAcT-II activity (elongation) [Sugahara, IUBMB - gene was identified and characterized [Wise, Genome Res 199
GLCNACT2g	3	Saito T, Seki N, Yamauchi M, Tsuji S, Hayashi A, Kozuma S, Hori T	Structure, chromosomal location, and expression profile of EXTR1 and EXTR2, new members of the multiple exostoses gene family	Biochem Biophys Res Commun	1998	9473480	- 2131, 2132 form a hetero-oligomeric complex in the Golgi [UniProt],[McCormick, PNAS 2000], [Kobayashi, Biochem Biophys Res Commun 2000]; complex has significantly higher activity in vitro than EXT1 or EXT2 alone, suggesting it is the predominant form in vivo [McCormick, PNAS 2000] 2131: - gene was cloned [Ahn, Nat Genet 1995] - human EXT1 was used to complement mouse knockout [McCormick, Nat Genet 1998] - ubiquitous [UniProt] 2132: - gene was isolated and characterized [Stickens, Nat Genet 1996] - bovine protein has both GlcNAc and GlcA transferase activities [Lind, J Biol Chem 1998] - ubiquitous [UniProt] 2317: - listed as ER localization, but has been modeled as Golgi since syhtnesis of linkage region and most other reactions occur there [UniProt],[Sugahara, IUBMB Life 2002] - transfers GalNAc in beta-1,4- linkages [UniProt],[Sugahara, IUBMB Life 2002] - has both GlcNAc-TI and TII activities (initiation and elongation) [Sugahara, IUBMB Life 2002], [Kim, PNAS 2001] - ubiquitous [UniProt], [Saito, Biochem Biophy Res Commun 1998] - gene was identified [Van Hul, Genomics 1998], [Saito, Bioch 2134: - only has GlcNAcT-II activity (elongation) [Sugahara, IUBMB - gene was identified and characterized [Wise, Genome Res 199
GLCNACT2g	3	Van Hul W, Wuyts W, Hendrickx J, Speleman F, Wauters J, De Boulle K, Van Roy N, Bossuyt P, Willems PJ	Identification of a third EXT-like gene (EXTL3) belonging to the EXT gene family	Genomics	1998	9479495	- 2131, 2132 form a hetero-oligomeric complex in the Golgi [UniProt],[McCormick, PNAS 2000], [Kobayashi, Biochem Biophys Res Commun 2000]; complex has significantly higher activity in vitro than EXT1 or EXT2 alone, suggesting it is the predominant form in vivo [McCormick, PNAS 2000] 2131: - gene was cloned [Ahn, Nat Genet 1995] - human EXT1 was used to complement mouse knockout [McCormick, Nat Genet 1998] - ubiquitous [UniProt] 2132: - gene was isolated and characterized [Stickens, Nat Genet 1996] - bovine protein has both GlcNAc and GlcA transferase activities [Lind, J Biol Chem 1998] - ubiquitous [UniProt] 2317: - listed as ER localization, but has been modeled as Golgi since syhtnesis of linkage region and most other reactions occur there [UniProt],[Sugahara, IUBMB Life 2002] - transfers GalNAc in beta-1,4- linkages [UniProt],[Sugahara, IUBMB Life 2002] - has both GlcNAc-TI and TII activities (initiation and elongation) [Sugahara, IUBMB Life 2002], [Kim, PNAS 2001] - ubiquitous [UniProt], [Saito, Biochem Biophy Res Commun 1998] - gene was identified [Van Hul, Genomics 1998], [Saito, Bioch 2134: - only has GlcNAcT-II activity (elongation) [Sugahara, IUBMB - gene was identified and characterized [Wise, Genome Res 199

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GLCNACT2g	3	Kim BT, Kitagawa H, Tamura J, Saito T, Kusche-Gullberg M, Lindahl U, Sugahara K	Human tumor suppressor EXT gene family members EXTL1 and EXTL3 encode alpha 1,4- N-acetylglucosaminyltransferases that likely are involved in heparan sulfate/ heparin biosynthesis	Proc Natl Acad Sci U S A	2001	11390981	- 2131, 2132 form a hetero-oligomeric complex in the Golgi [UniProt],[McCormick, PNAS 2000], [Kobayashi, Biochem Biophys Res Commun 2000]; complex has significantly higher activity in vitro than EXT1 or EXT2 alone, suggesting it is the predominant form in vivo [McCormick, PNAS 2000] 2131: - gene was cloned [Ahn, Nat Genet 1995] - human EXT1 was used to complement mouse knockout [McCormick, Nat Genet 1998] - ubiquitous [UniProt] 2132: - gene was isolated and characterized [Stickens, Nat Genet 1996] - bovine protein has both GlcNAc and GlcA transferase activities [Lind, J Biol Chem 1998] - ubiquitous [UniProt] 2317: - listed as ER localization, but has been modeled as Golgi since syhtnesis of linkage region and most other reactions occur there [UniProt],[Sugahara, IUBMB Life 2002] - transfers GalNAc in beta-1,4- linkages [UniProt],[Sugahara, IUBMB Life 2002] - has both GlcNAc-TI and TII activities (initiation and elongation) [Sugahara, IUBMB Life 2002], [Kim, PNAS 2001] - ubiquitous [UniProt], [Saito, Biochem Biophy Res Commun 1998] - gene was identified [Van Hul, Genomics 1998], [Saito, Bioch 2134: - only has GlcNAcT-II activity (elongation) [Sugahara, IUBMB - gene was identified and characterized [Wise, Genome Res 199
GLCNACT2g	3	Sugahara K, Kitagawa H	Heparin and heparan sulfate biosynthesis	IUBMB Life	2002	12512855	- 2131, 2132 form a hetero-oligomeric complex in the Golgi [UniProt],[McCormick, PNAS 2000], [Kobayashi, Biochem Biophys Res Commun 2000]; complex has significantly higher activity in vitro than EXT1 or EXT2 alone, suggesting it is the predominant form in vivo [McCormick, PNAS 2000] 2131: - gene was cloned [Ahn, Nat Genet 1995] - human EXT1 was used to complement mouse knockout [McCormick, Nat Genet 1998] - ubiquitous [UniProt] 2132: - gene was isolated and characterized [Stickens, Nat Genet 1996] - bovine protein has both GlcNAc and GlcA transferase activities [Lind, J Biol Chem 1998] - ubiquitous [UniProt] 2317: - listed as ER localization, but has been modeled as Golgi since syhtnesis of linkage region and most other reactions occur there [UniProt],[Sugahara, IUBMB Life 2002] - transfers GalNAc in beta-1,4- linkages [UniProt],[Sugahara, IUBMB Life 2002] - has both GlcNAc-TI and TII activities (initiation and elongation) [Sugahara, IUBMB Life 2002], [Kim, PNAS 2001] - ubiquitous [UniProt], [Saito, Biochem Biophy Res Commun 1998] - gene was identified [Van Hul, Genomics 1998], [Saito, Bioch 2134: - only has GlcNAcT-II activity (elongation) [Sugahara, IUBMB - gene was identified and characterized [Wise, Genome Res 199
GLCt1r	3	Thorens B, Cheng ZQ, Brown D, Lodish HF	Liver glucose transporter: a basolateral protein in hepatocytes and intestine and kidney cells	Am J Physiol	1990	1701966	simple diffusion 6513: - transports Glc, Gal, Man, GlcN [Uldry 2004], [Uldry 2002] - RBC, brain [Maher 1994] - cloned [Mueckler 1985] - not expressed in normal hepatocytes; induced during cancer [Flier 1987] 6514: - transports Glc (low affinity [Johnson 1990]), Gal, Fru, Man, GlcN [Uldry 2004], [Uldry 2002] - intest and kidney [Thorens 1990], liver, panc B cells, Langerhans, brain [Uldry 2004] - cloned [Fukumoto 1988] - primary GLUT for Glc release in hepatocytes [Hosokawa 2002], [Guillam 1998] 6515: - transports Glc (high), Gal, Man, Xyl, Malt, DHA [Uldry 2004] - brain, testis [Haber 1993], [Uldry 2004], sk muscle [Stuart 1999], platelets [Heijen 1997] - cloned [Kayano 1988] 6517: - cDNA was cloned [Fukumoto 1989] - transports Glc, GlcN, DHA; adipose (brown & white), sk and cardiac muscle; insulin, exercise stimulate translocation of GLUT4 vesicles to cell surface [Uldry 2004] 11182: - cDNA was cloned [Doege 2000] - transports Glc; brain, spleen, WBC; activity only demonstrated in liposomes [Udry 2004] 155184: - gene identified [Joost 2001]

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GLCt1r	3	Johnson JH, Newgard CB, Milburn JL, Lodish HF, Thorens B	The high Km glucose transporter of islets of Langerhans is functionally similar to the low affinity transporter of liver and has an identical primary sequence	J Biol Chem	1990	2182619	simple diffusion 6513: - transports Glc, Gal, Man, GlcN [Uldry 2004], [Uldry 2002] - RBC, brain [Maher 1994] - cloned [Mueckler 1985] - not expressed in normal hepatocytes; induced during cancer [Flier 1987] 6514: - transports Glc (low affinity [Johnson 1990]), Gal, Fru, Man, GlcN [Uldry 2004], [Uldry 2002] - intest and kidney [Thorens 1990], liver, panc B cells, Langerhans, brain [Uldry 2004] - cloned [Fukumoto 1988] - primary GLUT for Glc release in hepatocytes [Hosokawa 2002], [Guillam 1998] 6515: - transports Glc (high), Gal, Man, Xyl, Malt, DHA [Uldry 2004] - brain, testis [Haber 1993], [Uldry 2004], sk muscle [Stuart 1999], platelets [Heijen 1997] - cloned [Kayano 1988] 6517: - cDNA was cloned [Fukumoto 1989] - transports Glc, GlcN, DHA; adipose (brown & white), sk and cardiac muscle; insulin, exercise stimulate translocation of GLUT4 vesicles to cell surface [Uldry 2004] 11182: - cDNA was cloned [Doege 2000] - transports Glc; brain, spleen, WBC; activity only demonstrated in liposomes [Udry 2004] 155184: - gene identified [Joost 2001]
GLCt1r	3	Fukumoto H, Kayano T, Buse JB, Edwards Y, Pilch PF, Bell GI, Seino S	Cloning and characterization of the major insulin-responsive glucose transporter expressed in human skeletal muscle and other insulin-responsive tissues	J Biol Chem	1989	2656669	simple diffusion 6513: - transports Glc, Gal, Man, GlcN [Uldry 2004], [Uldry 2002] - RBC, brain [Maher 1994] - cloned [Mueckler 1985] - not expressed in normal hepatocytes; induced during cancer [Flier 1987] 6514: - transports Glc (low affinity [Johnson 1990]), Gal, Fru, Man, GlcN [Uldry 2004], [Uldry 2002] - intest and kidney [Thorens 1990], liver, panc B cells, Langerhans, brain [Uldry 2004] - cloned [Fukumoto 1988] - primary GLUT for Glc release in hepatocytes [Hosokawa 2002], [Guillam 1998] 6515: - transports Glc (high), Gal, Man, Xyl, Malt, DHA [Uldry 2004] - brain, testis [Haber 1993], [Uldry 2004], sk muscle [Stuart 1999], platelets [Heijen 1997] - cloned [Kayano 1988] 6517: - cDNA was cloned [Fukumoto 1989] - transports Glc, GlcN, DHA; adipose (brown & white), sk and cardiac muscle; insulin, exercise stimulate translocation of GLUT4 vesicles to cell surface [Uldry 2004] 11182: - cDNA was cloned [Doege 2000] - transports Glc; brain, spleen, WBC; activity only demonstrated in liposomes [Udry 2004] 155184: - gene identified [Joost 2001]

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GLCt1r	3	Flier JS, Mueckler MM, Usher P, Lodish HF	Elevated levels of glucose transport and transporter messenger RNA are induced by ras or src oncogenes	Science	1987	3103217	simple diffusion 6513: - transports Glc, Gal, Man, GlcN [Uldry 2004], [Uldry 2002] - RBC, brain [Maher 1994] - cloned [Mueckler 1985] - not expressed in normal hepatocytes; induced during cancer [Flier 1987] 6514: - transports Glc (low affinity [Johnson 1990]), Gal, Fru, Man, GlcN [Uldry 2004], [Uldry 2002] - intest and kidney [Thorens 1990], liver, panc B cells, Langerhans, brain [Uldry 2004] - cloned [Fukumoto 1988] - primary GLUT for Glc release in hepatocytes [Hosokawa 2002], [Guillam 1998] 6515: - transports Glc (high), Gal, Man, Xyl, Malt, DHA [Uldry 2004] - brain, testis [Haber 1993], [Uldry 2004], sk muscle [Stuart 1999], platelets [Heijen 1997] - cloned [Kayano 1988] 6517: - cDNA was cloned [Fukumoto 1989] - transports Glc, GlcN, DHA; adipose (brown & white), sk and cardiac muscle; insulin, exercise stimulate translocation of GLUT4 vesicles to cell surface [Uldry 2004] 11182: - cDNA was cloned [Doege 2000] - transports Glc; brain, spleen, WBC; activity only demonstrated in liposomes [Udry 2004] 155184: - gene identified [Joost 2001]
GLCt1r	3	Fukumoto H, Seino S, Imura H, Seino Y, Eddy RL, Fukushima Y, Byers MG, Shows TB, Bell GI	Sequence, tissue distribution, and chromosomal localization of mRNA encoding a human glucose transporter-like protein	Proc Natl Acad Sci U S A	1988	3399500	simple diffusion 6513: - transports Glc, Gal, Man, GlcN [Uldry 2004], [Uldry 2002] - RBC, brain [Maher 1994] - cloned [Mueckler 1985] - not expressed in normal hepatocytes; induced during cancer [Flier 1987] 6514: - transports Glc (low affinity [Johnson 1990]), Gal, Fru, Man, GlcN [Uldry 2004], [Uldry 2002] - intest and kidney [Thorens 1990], liver, panc B cells, Langerhans, brain [Uldry 2004] - cloned [Fukumoto 1988] - primary GLUT for Glc release in hepatocytes [Hosokawa 2002], [Guillam 1998] 6515: - transports Glc (high), Gal, Man, Xyl, Malt, DHA [Uldry 2004] - brain, testis [Haber 1993], [Uldry 2004], sk muscle [Stuart 1999], platelets [Heijen 1997] - cloned [Kayano 1988] 6517: - cDNA was cloned [Fukumoto 1989] - transports Glc, GlcN, DHA; adipose (brown & white), sk and cardiac muscle; insulin, exercise stimulate translocation of GLUT4 vesicles to cell surface [Uldry 2004] 11182: - cDNA was cloned [Doege 2000] - transports Glc; brain, spleen, WBC; activity only demonstrated in liposomes [Udry 2004] 155184: - gene identified [Joost 2001]

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GLCt1r	3	Mueckler M, Caruso C, Baldwin SA, Panico M, Blench I, Morris HR, Allard WJ, Lienhard GE, Lodish HF	Sequence and structure of a human glucose transporter	Science	1985	3839598	simple diffusion 6513: - transports Glc, Gal, Man, GlcN [Uldry 2004], [Uldry 2002] - RBC, brain [Maher 1994] - cloned [Mueckler 1985] - not expressed in normal hepatocytes; induced during cancer [Flier 1987] 6514: - transports Glc (low affinity [Johnson 1990]), Gal, Fru, Man, GlcN [Uldry 2004], [Uldry 2002] - intest and kidney [Thorens 1990], liver, panc B cells, Langerhans, brain [Uldry 2004] - cloned [Fukumoto 1988] - primary GLUT for Glc release in hepatocytes [Hosokawa 2002], [Guillam 1998] 6515: - transports Glc (high), Gal, Man, Xyl, Malt, DHA [Uldry 2004] - brain, testis [Haber 1993], [Uldry 2004], sk muscle [Stuart 1999], platelets [Heijen 1997] - cloned [Kayano 1988] 6517: - cDNA was cloned [Fukumoto 1989] - transports Glc, GlcN, DHA; adipose (brown & white), sk and cardiac muscle; insulin, exercise stimulate translocation of GLUT4 vesicles to cell surface [Uldry 2004] 11182: - cDNA was cloned [Doege 2000] - transports Glc; brain, spleen, WBC; activity only demonstrated in liposomes [Udry 2004] 155184: - gene identified [Joost 2001]
GLCt1r	3	Maher F, Vannucci SJ, Simpson IA	Glucose transporter proteins in brain	FASEB J	1994	7926364	simple diffusion 6513: - transports Glc, Gal, Man, GlcN [Uldry 2004], [Uldry 2002] - RBC, brain [Maher 1994] - cloned [Mueckler 1985] - not expressed in normal hepatocytes; induced during cancer [Flier 1987] 6514: - transports Glc (low affinity [Johnson 1990]), Gal, Fru, Man, GlcN [Uldry 2004], [Uldry 2002] - intest and kidney [Thorens 1990], liver, panc B cells, Langerhans, brain [Uldry 2004] - cloned [Fukumoto 1988] - primary GLUT for Glc release in hepatocytes [Hosokawa 2002], [Guillam 1998] 6515: - transports Glc (high), Gal, Man, Xyl, Malt, DHA [Uldry 2004] - brain, testis [Haber 1993], [Uldry 2004], sk muscle [Stuart 1999], platelets [Heijen 1997] - cloned [Kayano 1988] 6517: - cDNA was cloned [Fukumoto 1989] - transports Glc, GlcN, DHA; adipose (brown & white), sk and cardiac muscle; insulin, exercise stimulate translocation of GLUT4 vesicles to cell surface [Uldry 2004] 11182: - cDNA was cloned [Doege 2000] - transports Glc; brain, spleen, WBC; activity only demonstrated in liposomes [Udry 2004] 155184: - gene identified [Joost 2001]

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
GLCt1r	3	Guillam MT, Burcelin R, Thorens B	Normal hepatic glucose production in the absence of GLUT2 reveals an alternative pathway for glucose release from hepatocytes	Proc Natl Acad Sci U S A	1998	9770484	simple diffusion 6513: - transports Glc, Gal, Man, GlcN [Uldry 2004], [Uldry 2002] - RBC, brain [Maher 1994] - cloned [Mueckler 1985] - not expressed in normal hepatocytes; induced during cancer [Flier 1987] 6514: - transports Glc (low affinity [Johnson 1990]), Gal, Fru, Man, GlcN [Uldry 2004], [Uldry 2002] - intest and kidney [Thorens 1990], liver, panc B cells, Langerhans, brain [Uldry 2004] - cloned [Fukumoto 1988] - primary GLUT for Glc release in hepatocytes [Hosokawa 2002], [Guillam 1998] 6515: - transports Glc (high), Gal, Man, Xyl, Malt, DHA [Uldry 2004] - brain, testis [Haber 1993], [Uldry 2004], sk muscle [Stuart 1999], platelets [Heijen 1997] - cloned [Kayano 1988] 6517: - cDNA was cloned [Fukumoto 1989] - transports Glc, GlcN, DHA; adipose (brown & white), sk and cardiac muscle; insulin, exercise stimulate translocation of GLUT4 vesicles to cell surface [Uldry 2004] 11182: - cDNA was cloned [Doege 2000] - transports Glc; brain, spleen, WBC; activity only demonstrated in liposomes [Udry 2004] 155184: - gene identified [Joost 2001]
GLCt1r	3	Doege H, Schurmann A, Bahrenberg G, Brauers A, Joost HG	GLUT8, a novel member of the sugar transport facilitator family with glucose transport activity	J Biol Chem	2000	10821868	simple diffusion 6513: - transports Glc, Gal, Man, GlcN [Uldry 2004], [Uldry 2002] - RBC, brain [Maher 1994] - cloned [Mueckler 1985] - not expressed in normal hepatocytes; induced during cancer [Flier 1987] 6514: - transports Glc (low affinity [Johnson 1990]), Gal, Fru, Man, GlcN [Uldry 2004], [Uldry 2002] - intest and kidney [Thorens 1990], liver, panc B cells, Langerhans, brain [Uldry 2004] - cloned [Fukumoto 1988] - primary GLUT for Glc release in hepatocytes [Hosokawa 2002], [Guillam 1998] 6515: - transports Glc (high), Gal, Man, Xyl, Malt, DHA [Uldry 2004] - brain, testis [Haber 1993], [Uldry 2004], sk muscle [Stuart 1999], platelets [Heijen 1997] - cloned [Kayano 1988] 6517: - cDNA was cloned [Fukumoto 1989] - transports Glc, GlcN, DHA; adipose (brown & white), sk and cardiac muscle; insulin, exercise stimulate translocation of GLUT4 vesicles to cell surface [Uldry 2004] 11182: - cDNA was cloned [Doege 2000] - transports Glc; brain, spleen, WBC; activity only demonstrated in liposomes [Udry 2004] 155184: - gene identified [Joost 2001]

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GLCt1r	3	Phay JE, Hussain HB, Moley JF	Cloning and expression analysis of a novel member of the facilitative glucose transporter family, SLC2A9 (GLUT9)	Genomics	2000	10860667	simple diffusion 6513: - transports Glc, Gal, Man, GlcN [Uldry 2004], [Uldry 2002] - RBC, brain [Maher 1994] - cloned [Mueckler 1985] - not expressed in normal hepatocytes; induced during cancer [Flier 1987] 6514: - transports Glc (low affinity [Johnson 1990]), Gal, Fru, Man, GlcN [Uldry 2004], [Uldry 2002] - intest and kidney [Thorens 1990], liver, panc B cells, Langerhans, brain [Uldry 2004] - cloned [Fukumoto 1988] - primary GLUT for Glc release in hepatocytes [Hosokawa 2002], [Guillam 1998] 6515: - transports Glc (high), Gal, Man, Xyl, Malt, DHA [Uldry 2004] - brain, testis [Haber 1993], [Uldry 2004], sk muscle [Stuart 1999], platelets [Heijen 1997] - cloned [Kayano 1988] 6517: - cDNA was cloned [Fukumoto 1989] - transports Glc, GlcN, DHA; adipose (brown & white), sk and cardiac muscle; insulin, exercise stimulate translocation of GLUT4 vesicles to cell surface [Uldry 2004] 11182: - cDNA was cloned [Doege 2000] - transports Glc; brain, spleen, WBC; activity only demonstrated in liposomes [Udry 2004] 155184: - gene identified [Joost 2001]
GLCt1r	3	Carayannopoulos MO, Chi MM, Cui Y, Pingsterhaus JM, McKnight RA, Mueckler M, Devaskar SU, Moley KH	GLUT8 is a glucose transporter responsible for insulin-stimulated glucose uptake in the blastocyst	Proc Natl Acad Sci U S A	2000	10860996	simple diffusion 6513: - transports Glc, Gal, Man, GlcN [Uldry 2004], [Uldry 2002] - RBC, brain [Maher 1994] - cloned [Mueckler 1985] - not expressed in normal hepatocytes; induced during cancer [Flier 1987] 6514: - transports Glc (low affinity [Johnson 1990]), Gal, Fru, Man, GlcN [Uldry 2004], [Uldry 2002] - intest and kidney [Thorens 1990], liver, panc B cells, Langerhans, brain [Uldry 2004] - cloned [Fukumoto 1988] - primary GLUT for Glc release in hepatocytes [Hosokawa 2002], [Guillam 1998] 6515: - transports Glc (high), Gal, Man, Xyl, Malt, DHA [Uldry 2004] - brain, testis [Haber 1993], [Uldry 2004], sk muscle [Stuart 1999], platelets [Heijen 1997] - cloned [Kayano 1988] 6517: - cDNA was cloned [Fukumoto 1989] - transports Glc, GlcN, DHA; adipose (brown & white), sk and cardiac muscle; insulin, exercise stimulate translocation of GLUT4 vesicles to cell surface [Uldry 2004] 11182: - cDNA was cloned [Doege 2000] - transports Glc; brain, spleen, WBC; activity only demonstrated in liposomes [Udry 2004] 155184: - gene identified [Joost 2001]

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GLCt1r	3	Doege H, Bocianski A, Joost HG, Schurmann A	Activity and genomic organization of human glucose transporter 9 (GLUT9), a novel member of the family of sugar-transport facilitators predominantly expressed in brain and leucocytes	Biochem J	2000	10970791	simple diffusion 6513: - transports Glc, Gal, Man, GlcN [Uldry 2004], [Uldry 2002] - RBC, brain [Maher 1994] - cloned [Mueckler 1985] - not expressed in normal hepatocytes; induced during cancer [Flier 1987] 6514: - transports Glc (low affinity [Johnson 1990]), Gal, Fru, Man, GlcN [Uldry 2004], [Uldry 2002] - intest and kidney [Thorens 1990], liver, panc B cells, Langerhans, brain [Uldry 2004] - cloned [Fukumoto 1988] - primary GLUT for Glc release in hepatocytes [Hosokawa 2002], [Guillam 1998] 6515: - transports Glc (high), Gal, Man, Xyl, Malt, DHA [Uldry 2004] - brain, testis [Haber 1993], [Uldry 2004], sk muscle [Stuart 1999], platelets [Heijen 1997] - cloned [Kayano 1988] 6517: - cDNA was cloned [Fukumoto 1989] - transports Glc, GlcN, DHA; adipose (brown & white), sk and cardiac muscle; insulin, exercise stimulate translocation of GLUT4 vesicles to cell surface [Uldry 2004] 11182: - cDNA was cloned [Doege 2000] - transports Glc; brain, spleen, WBC; activity only demonstrated in liposomes [Udry 2004] 155184: - gene identified [Joost 2001]
GLCt1r	3	McVie-Wylie AJ, Lamson DR, Chen YT	Molecular cloning of a novel member of the GLUT family of transporters, SLC2a10 (GLUT10), localized on chromosome 20q13.1: a candidate gene for NIDDM susceptibility	Genomics	2001	11247674	simple diffusion 6513: - transports Glc, Gal, Man, GlcN [Uldry 2004], [Uldry 2002] - RBC, brain [Maher 1994] - cloned [Mueckler 1985] - not expressed in normal hepatocytes; induced during cancer [Flier 1987] 6514: - transports Glc (low affinity [Johnson 1990]), Gal, Fru, Man, GlcN [Uldry 2004], [Uldry 2002] - intest and kidney [Thorens 1990], liver, panc B cells, Langerhans, brain [Uldry 2004] - cloned [Fukumoto 1988] - primary GLUT for Glc release in hepatocytes [Hosokawa 2002], [Guillam 1998] 6515: - transports Glc (high), Gal, Man, Xyl, Malt, DHA [Uldry 2004] - brain, testis [Haber 1993], [Uldry 2004], sk muscle [Stuart 1999], platelets [Heijen 1997] - cloned [Kayano 1988] 6517: - cDNA was cloned [Fukumoto 1989] - transports Glc, GlcN, DHA; adipose (brown & white), sk and cardiac muscle; insulin, exercise stimulate translocation of GLUT4 vesicles to cell surface [Uldry 2004] 11182: - cDNA was cloned [Doege 2000] - transports Glc; brain, spleen, WBC; activity only demonstrated in liposomes [Udry 2004] 155184: - gene identified [Joost 2001]

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GLCt1r	3	Doege H, Bocianski A, Scheepers A, Axer H, Eckel J, Joost HG, Schurmann A	Characterization of human glucose transporter (GLUT) 11 (encoded by SLC2A11), a novel sugar-transport facilitator specifically expressed in heart and skeletal muscle	Biochem J	2001	11583593	simple diffusion 6513: - transports Glc, Gal, Man, GlcN [Uldry 2004], [Uldry 2002] - RBC, brain [Maher 1994] - cloned [Mueckler 1985] - not expressed in normal hepatocytes; induced during cancer [Flier 1987] 6514: - transports Glc (low affinity [Johnson 1990]), Gal, Fru, Man, GlcN [Uldry 2004], [Uldry 2002] - intest and kidney [Thorens 1990], liver, panc B cells, Langerhans, brain [Uldry 2004] - cloned [Fukumoto 1988] - primary GLUT for Glc release in hepatocytes [Hosokawa 2002], [Guillam 1998] 6515: - transports Glc (high), Gal, Man, Xyl, Malt, DHA [Uldry 2004] - brain, testis [Haber 1993], [Uldry 2004], sk muscle [Stuart 1999], platelets [Heijen 1997] - cloned [Kayano 1988] 6517: - cDNA was cloned [Fukumoto 1989] - transports Glc, GlcN, DHA; adipose (brown & white), sk and cardiac muscle; insulin, exercise stimulate translocation of GLUT4 vesicles to cell surface [Uldry 2004] 11182: - cDNA was cloned [Doege 2000] - transports Glc; brain, spleen, WBC; activity only demonstrated in liposomes [Udry 2004] 155184: - gene identified [Joost 2001]
GLCt1r	3	Dawson PA, Mychaleckyj JC, Fossey SC, Mihic SJ, Craddock AL, Bowden DW	Sequence and functional analysis of GLUT10: a glucose transporter in the Type 2 diabetes-linked region of chromosome 20q12-13.1	Mol Genet Metab	2001	11592815	simple diffusion 6513: - transports Glc, Gal, Man, GlcN [Uldry 2004], [Uldry 2002] - RBC, brain [Maher 1994] - cloned [Mueckler 1985] - not expressed in normal hepatocytes; induced during cancer [Flier 1987] 6514: - transports Glc (low affinity [Johnson 1990]), Gal, Fru, Man, GlcN [Uldry 2004], [Uldry 2002] - intest and kidney [Thorens 1990], liver, panc B cells, Langerhans, brain [Uldry 2004] - cloned [Fukumoto 1988] - primary GLUT for Glc release in hepatocytes [Hosokawa 2002], [Guillam 1998] 6515: - transports Glc (high), Gal, Man, Xyl, Malt, DHA [Uldry 2004] - brain, testis [Haber 1993], [Uldry 2004], sk muscle [Stuart 1999], platelets [Heijen 1997] - cloned [Kayano 1988] 6517: - cDNA was cloned [Fukumoto 1989] - transports Glc, GlcN, DHA; adipose (brown & white), sk and cardiac muscle; insulin, exercise stimulate translocation of GLUT4 vesicles to cell surface [Uldry 2004] 11182: - cDNA was cloned [Doege 2000] - transports Glc; brain, spleen, WBC; activity only demonstrated in liposomes [Udry 2004] 155184: - gene identified [Joost 2001]

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GLCt1r	3	Joost HG, Thorens B	The extended GLUT-family of sugar/polyol transport facilitators: nomenclature, sequence characteristics, and potential function of its novel members (review)	Mol Membr Biol	2001	11780753	simple diffusion 6513: - transports Glc, Gal, Man, GlcN [Uldry 2004], [Uldry 2002] - RBC, brain [Maher 1994] - cloned [Mueckler 1985] - not expressed in normal hepatocytes; induced during cancer [Flier 1987] 6514: - transports Glc (low affinity [Johnson 1990]), Gal, Fru, Man, GlcN [Uldry 2004], [Uldry 2002] - intest and kidney [Thorens 1990], liver, panc B cells, Langerhans, brain [Uldry 2004] - cloned [Fukumoto 1988] - primary GLUT for Glc release in hepatocytes [Hosokawa 2002], [Guillam 1998] 6515: - transports Glc (high), Gal, Man, Xyl, Malt, DHA [Uldry 2004] - brain, testis [Haber 1993], [Uldry 2004], sk muscle [Stuart 1999], platelets [Heijen 1997] - cloned [Kayano 1988] 6517: - cDNA was cloned [Fukumoto 1989] - transports Glc, GlcN, DHA; adipose (brown & white), sk and cardiac muscle; insulin, exercise stimulate translocation of GLUT4 vesicles to cell surface [Uldry 2004] 11182: - cDNA was cloned [Doege 2000] - transports Glc; brain, spleen, WBC; activity only demonstrated in liposomes [Udry 2004] 155184: - gene identified [Joost 2001]
GLCt1r	3	Rogers S, Macheda ML, Docherty SE, Carty MD, Henderson MA, Soeller WC, Gibbs EM, James DE, Best JD	Identification of a novel glucose transporter-like protein-GLUT-12	Am J Physiol Endocrinol Metab	2002	11832379	simple diffusion 6513: - transports Glc, Gal, Man, GlcN [Uldry 2004], [Uldry 2002] - RBC, brain [Maher 1994] - cloned [Mueckler 1985] - not expressed in normal hepatocytes; induced during cancer [Flier 1987] 6514: - transports Glc (low affinity [Johnson 1990]), Gal, Fru, Man, GlcN [Uldry 2004], [Uldry 2002] - intest and kidney [Thorens 1990], liver, panc B cells, Langerhans, brain [Uldry 2004] - cloned [Fukumoto 1988] - primary GLUT for Glc release in hepatocytes [Hosokawa 2002], [Guillam 1998] 6515: - transports Glc (high), Gal, Man, Xyl, Malt, DHA [Uldry 2004] - brain, testis [Haber 1993], [Uldry 2004], sk muscle [Stuart 1999], platelets [Heijen 1997] - cloned [Kayano 1988] 6517: - cDNA was cloned [Fukumoto 1989] - transports Glc, GlcN, DHA; adipose (brown & white), sk and cardiac muscle; insulin, exercise stimulate translocation of GLUT4 vesicles to cell surface [Uldry 2004] 11182: - cDNA was cloned [Doege 2000] - transports Glc; brain, spleen, WBC; activity only demonstrated in liposomes [Udry 2004] 155184: - gene identified [Joost 2001]

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GLCt1r	3	Hosokawa M, Thorens B	Glucose release from GLUT2-null hepatocytes: characterization of a major and a minor pathway	Am J Physiol Endocrinol Metab	2002	11882499	simple diffusion 6513: - transports Glc, Gal, Man, GlcN [Uldry 2004], [Uldry 2002] - RBC, brain [Maher 1994] - cloned [Mueckler 1985] - not expressed in normal hepatocytes; induced during cancer [Flier 1987] 6514: - transports Glc (low affinity [Johnson 1990]), Gal, Fru, Man, GlcN [Uldry 2004], [Uldry 2002] - intest and kidney [Thorens 1990], liver, panc B cells, Langerhans, brain [Uldry 2004] - cloned [Fukumoto 1988] - primary GLUT for Glc release in hepatocytes [Hosokawa 2002], [Guillam 1998] 6515: - transports Glc (high), Gal, Man, Xyl, Malt, DHA [Uldry 2004] - brain, testis [Haber 1993], [Uldry 2004], sk muscle [Stuart 1999], platelets [Heijen 1997] - cloned [Kayano 1988] 6517: - cDNA was cloned [Fukumoto 1989] - transports Glc, GlcN, DHA; adipose (brown & white), sk and cardiac muscle; insulin, exercise stimulate translocation of GLUT4 vesicles to cell surface [Uldry 2004] 11182: - cDNA was cloned [Doege 2000] - transports Glc; brain, spleen, WBC; activity only demonstrated in liposomes [Udry 2004] 155184: - gene identified [Joost 2001]
GLCt1r	3	Uldry M, Ibberson M, Hosokawa M, Thorens B	GLUT2 is a high affinity glucosamine transporter	FEBS Lett	2002	12135767	simple diffusion 6513: - transports Glc, Gal, Man, GlcN [Uldry 2004], [Uldry 2002] - RBC, brain [Maher 1994] - cloned [Mueckler 1985] - not expressed in normal hepatocytes; induced during cancer [Flier 1987] 6514: - transports Glc (low affinity [Johnson 1990]), Gal, Fru, Man, GlcN [Uldry 2004], [Uldry 2002] - intest and kidney [Thorens 1990], liver, panc B cells, Langerhans, brain [Uldry 2004] - cloned [Fukumoto 1988] - primary GLUT for Glc release in hepatocytes [Hosokawa 2002], [Guillam 1998] 6515: - transports Glc (high), Gal, Man, Xyl, Malt, DHA [Uldry 2004] - brain, testis [Haber 1993], [Uldry 2004], sk muscle [Stuart 1999], platelets [Heijen 1997] - cloned [Kayano 1988] 6517: - cDNA was cloned [Fukumoto 1989] - transports Glc, GlcN, DHA; adipose (brown & white), sk and cardiac muscle; insulin, exercise stimulate translocation of GLUT4 vesicles to cell surface [Uldry 2004] 11182: - cDNA was cloned [Doege 2000] - transports Glc; brain, spleen, WBC; activity only demonstrated in liposomes [Udry 2004] 155184: - gene identified [Joost 2001]

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GLCt1r	3	Macheda ML, Williams ED, Best JD, Wlodek ME, Rogers S	Expression and localisation of GLUT1 and GLUT12 glucose transporters in the pregnant and lactating rat mammary gland	Cell Tissue Res	2003	12483288	simple diffusion 6513: - transports Glc, Gal, Man, GlcN [Uldry 2004], [Uldry 2002] - RBC, brain [Maher 1994] - cloned [Mueckler 1985] - not expressed in normal hepatocytes; induced during cancer [Flier 1987] 6514: - transports Glc (low affinity [Johnson 1990]), Gal, Fru, Man, GlcN [Uldry 2004], [Uldry 2002] - intest and kidney [Thorens 1990], liver, panc B cells, Langerhans, brain [Uldry 2004] - cloned [Fukumoto 1988] - primary GLUT for Glc release in hepatocytes [Hosokawa 2002], [Guillam 1998] 6515: - transports Glc (high), Gal, Man, Xyl, Malt, DHA [Uldry 2004] - brain, testis [Haber 1993], [Uldry 2004], sk muscle [Stuart 1999], platelets [Heijen 1997] - cloned [Kayano 1988] 6517: - cDNA was cloned [Fukumoto 1989] - transports Glc, GlcN, DHA; adipose (brown & white), sk and cardiac muscle; insulin, exercise stimulate translocation of GLUT4 vesicles to cell surface [Uldry 2004] 11182: - cDNA was cloned [Doege 2000] - transports Glc; brain, spleen, WBC; activity only demonstrated in liposomes [Udry 2004] 155184: - gene identified [Joost 2001]
GLCt1r	3	Wu X, Freeze HH	GLUT14, a duplicon of GLUT3, is specifically expressed in testis as alternative splice forms	Genomics	2002	12504846	simple diffusion 6513: - transports Glc, Gal, Man, GlcN [Uldry 2004], [Uldry 2002] - RBC, brain [Maher 1994] - cloned [Mueckler 1985] - not expressed in normal hepatocytes; induced during cancer [Flier 1987] 6514: - transports Glc (low affinity [Johnson 1990]), Gal, Fru, Man, GlcN [Uldry 2004], [Uldry 2002] - intest and kidney [Thorens 1990], liver, panc B cells, Langerhans, brain [Uldry 2004] - cloned [Fukumoto 1988] - primary GLUT for Glc release in hepatocytes [Hosokawa 2002], [Guillam 1998] 6515: - transports Glc (high), Gal, Man, Xyl, Malt, DHA [Uldry 2004] - brain, testis [Haber 1993], [Uldry 2004], sk muscle [Stuart 1999], platelets [Heijen 1997] - cloned [Kayano 1988] 6517: - cDNA was cloned [Fukumoto 1989] - transports Glc, GlcN, DHA; adipose (brown & white), sk and cardiac muscle; insulin, exercise stimulate translocation of GLUT4 vesicles to cell surface [Uldry 2004] 11182: - cDNA was cloned [Doege 2000] - transports Glc; brain, spleen, WBC; activity only demonstrated in liposomes [Udry 2004] 155184: - gene identified [Joost 2001]

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GLCt1r	3	Rogers S, Chandler JD, Clarke AL, Petrou S, Best JD	Glucose transporter GLUT12-functional characterization in Xenopus laevis oocytes	Biochem Biophys Res Commun	2003	12914765	simple diffusion 6513: - transports Glc, Gal, Man, GlcN [Uldry 2004], [Uldry 2002] - RBC, brain [Maher 1994] - cloned [Mueckler 1985] - not expressed in normal hepatocytes; induced during cancer [Flier 1987] 6514: - transports Glc (low affinity [Johnson 1990]), Gal, Fru, Man, GlcN [Uldry 2004], [Uldry 2002] - intest and kidney [Thorens 1990], liver, panc B cells, Langerhans, brain [Uldry 2004] - cloned [Fukumoto 1988] - primary GLUT for Glc release in hepatocytes [Hosokawa 2002], [Guillam 1998] 6515: - transports Glc (high), Gal, Man, Xyl, Malt, DHA [Uldry 2004] - brain, testis [Haber 1993], [Uldry 2004], sk muscle [Stuart 1999], platelets [Heijen 1997] - cloned [Kayano 1988] 6517: - cDNA was cloned [Fukumoto 1989] - transports Glc, GlcN, DHA; adipose (brown & white), sk and cardiac muscle; insulin, exercise stimulate translocation of GLUT4 vesicles to cell surface [Uldry 2004] 11182: - cDNA was cloned [Doege 2000] - transports Glc; brain, spleen, WBC; activity only demonstrated in liposomes [Udry 2004] 155184: - gene identified [Joost 2001]
GLCt1r	3	Augustin R, Carayannopoulos MO, Dowd LO, Phay JE, Moley JF, Moley KH	Identification and characterization of human glucose transporter-like protein-9 (GLUT9): alternative splicing alters trafficking	J Biol Chem	2004	14739288	simple diffusion 6513: - transports Glc, Gal, Man, GlcN [Uldry 2004], [Uldry 2002] - RBC, brain [Maher 1994] - cloned [Mueckler 1985] - not expressed in normal hepatocytes; induced during cancer [Flier 1987] 6514: - transports Glc (low affinity [Johnson 1990]), Gal, Fru, Man, GlcN [Uldry 2004], [Uldry 2002] - intest and kidney [Thorens 1990], liver, panc B cells, Langerhans, brain [Uldry 2004] - cloned [Fukumoto 1988] - primary GLUT for Glc release in hepatocytes [Hosokawa 2002], [Guillam 1998] 6515: - transports Glc (high), Gal, Man, Xyl, Malt, DHA [Uldry 2004] - brain, testis [Haber 1993], [Uldry 2004], sk muscle [Stuart 1999], platelets [Heijen 1997] - cloned [Kayano 1988] 6517: - cDNA was cloned [Fukumoto 1989] - transports Glc, GlcN, DHA; adipose (brown & white), sk and cardiac muscle; insulin, exercise stimulate translocation of GLUT4 vesicles to cell surface [Uldry 2004] 11182: - cDNA was cloned [Doege 2000] - transports Glc; brain, spleen, WBC; activity only demonstrated in liposomes [Udry 2004] 155184: - gene identified [Joost 2001]

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GLCt1r	3	Li Q, Manolescu A, Ritzel M, Yao S, Slugoski M, Young JD, Chen XZ, Cheeseman CI	Cloning and functional characterization of the human GLUT7 isoform SLC2A7 from the small intestine	Am J Physiol Gastrointest Liver Physiol	2004	15033637	simple diffusion 6513: - transports Glc, Gal, Man, GlcN [Uldry 2004], [Uldry 2002] - RBC, brain [Maher 1994] - cloned [Mueckler 1985] - not expressed in normal hepatocytes; induced during cancer [Flier 1987] 6514: - transports Glc (low affinity [Johnson 1990]), Gal, Fru, Man, GlcN [Uldry 2004], [Uldry 2002] - intest and kidney [Thorens 1990], liver, panc B cells, Langerhans, brain [Uldry 2004] - cloned [Fukumoto 1988] - primary GLUT for Glc release in hepatocytes [Hosokawa 2002], [Guillam 1998] 6515: - transports Glc (high), Gal, Man, Xyl, Malt, DHA [Uldry 2004] - brain, testis [Haber 1993], [Uldry 2004], sk muscle [Stuart 1999], platelets [Heijen 1997] - cloned [Kayano 1988] 6517: - cDNA was cloned [Fukumoto 1989] - transports Glc, GlcN, DHA; adipose (brown & white), sk and cardiac muscle; insulin, exercise stimulate translocation of GLUT4 vesicles to cell surface [Uldry 2004] 11182: - cDNA was cloned [Doege 2000] - transports Glc; brain, spleen, WBC; activity only demonstrated in liposomes [Udry 2004] 155184: - gene identified [Joost 2001]
GLCt2r	3	Wells RG, Pajor AM, Kanai Y, Turk E, Wright EM, Hediger MA	Cloning of a human kidney cDNA with similarity to the sodium-glucose cotransporter	Am J Physiol	1992	1415574	0
GLCt2r	3	Kanai Y, Lee WS, You G, Brown D, Hediger MA	The human kidney low affinity Na+/glucose cotransporter SGLT2. Delineation of the major renal reabsorptive mechanism for D-glucose	J Clin Invest	1994	8282810	0
GLCt2r	3	Wright EM	Renal Na(+)-glucose cotransporters	Am J Physiol Renal Physiol	2001	11133510	0
GLCt4	3	van den Heuvel LP, Assink K, Willemsen M, Monnens L	Autosomal recessive renal glucosuria attributable to a mutation in the sodium glucose cotransporter (SGLT2).	Hum Genet	2002	12436245	6524: - cloned [Wells 1992] - transports Glc/Na+ (low affinity) at a 1:1 ratio [Kanai 1994] - renal cortex [Wright 2001] - major transporter involved in reabsorption of glc from glomrtular filtrate [Van de Heuvel 2002] 6526: - cloned [Kwon 1992], [Berry 1995] - kidney, brain, placenta, pancreas, heart, skeletal muscle, lung [Berry 1995] - Na+/myo-inositol cotransport; also transports other sugars (incl glc) with low affinity [Hager 1995], [Kwon 1992] - plasma membrane; see [Wright 2004] for refs - transports Na+ in the absence of sugar [Wright, Physiology 2004] 125206: - function inferred from electronic annotation [GO] - kidney (rabbit ortholog); see [Wright 2004] for refs 159963: - function inferred from electronic annotation [GO]
GLCt4_2	3	Tazawa S, Yamato T, Fujikura H, Hiratochi M, Itoh F, Tomae M, Takemura Y, Maruyama H, Sugiyama T, Wakamatsu A, Isogai T, Isaji M	SLC5A9/SGLT4, a new Na+-dependent glucose transporter, is an essential transporter for mannose, 1,5-anhydro-D-glucitol, and fructose	Life Sci	2005	15607332	- glc is transported against concentration gradient, typically into the cell [Champe, Biochemistry 2005] - occurs in epithelial cels of the intestine, renal tubules, and choroid plexus [Champe, Biochemistry 2005] 6523: -cloned [Hediger 1989] - cotransports Glc/2 Na+, Gal/2 Na+ [Quick 2001] - H+ can replace Na+ [Hirayama 1994] - behaves as urea channel in the absence of substrates; cotransports urea under substrate-transporting conditions [Leung 2000] - Na+ transport occurs by a saturable uniport mechanism; water permeation is through a low conductance water channel [Loo 1999] - brush border membrane [Wright 1994] - plasma membrane; see [Wright 2004] for refs 200010: - cloned and characterized [Tazawa 2005] - mainly sm intestine & kidney, also liver, lung, brain [Tazawa 2005] - transports D-mannose (Man) >> D-glucose (Glc) > D-fructose (Fru) = 1,5-anhydro-D-glucitol (1,5AG) > D-galactose (Gal) [Tazawa 2005]

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
GLCtg	3	Haney PM	Glucose transport in lactation	Adv Exp Med Biol	2004	15384581	Glc passes across Golgi membrane into Golgi lumen by GLUT 1 [Haney 2004] - GLUT1 is the only known glucose transporter isoform expressed in mammary gland [Haney 2004] original ref was WL Hurley's website on Lactation Biology, Dept of Animal Sciences, Univ of Illinois, Urbana-Champaign. He cites Kuhn, Ch 6 in Mepham, 1983, Biochem of Lactation, Elsevier http://classes.aces.uiuc.edu/AnSci308/lactosesynthesis.html
GLCtly	2	Pisoni RL, Thoene JG	The transport systems of mammalian lysosomes	Biochim Biophys Acta	1991	1751541	- function has only been characterized in rat liver lysosomes (see refs in [Pisoni 1991]) - D-glucose, D-galactose, D-mannose, and L-fucose are known substrates [Lloyd 1996] - D-xylose is also recognized by the carrier, but passive diffusion may be the predominant mode of efflux [Lloyd 1996]
GLCtly	2	Lloyd JB	Metabolite efflux and influx across the lysosome membrane	Subcell Biochem	1996	8993166	- function has only been characterized in rat liver lysosomes (see refs in [Pisoni 1991]) - D-glucose, D-galactose, D-mannose, and L-fucose are known substrates [Lloyd 1996] - D-xylose is also recognized by the carrier, but passive diffusion may be the predominant mode of efflux [Lloyd 1996]
GLCURtly	3	Mancini GM, de Jonge HR, Galjaard H, Verheijen FW.	Characterization of a proton-driven carrier for sialic acid in the lysosomal membrane. Evidence for a group-specific transport system for acidic monosaccharides.	J Biol Chem	1989	2768261	H symport with sialic acid (precursors) into lysososome. See PMID: 2768261for biochem characterization and PMID: 10581036 for discussion of particular SNPs with sialic acid storage diseases. Sialic acid storage disorders (due to transporter mutations) require import and export e.g. PMID: 2768266 - hence made reversible. NJ
GLCURtly	3	Verheijen FW, Verbeek E, Aula N, Beerens CE, Havelaar AC, Joosse M, Peltonen L, Aula P, Galjaard H, van der Spek PJ, Mancini GM.	A new gene, encoding an anion transporter, is mutated in sialic acid storage diseases.	Nat Genet	1999	10581036	H symport with sialic acid (precursors) into lysososome. See PMID: 2768261for biochem characterization and PMID: 10581036 for discussion of particular SNPs with sialic acid storage diseases. Sialic acid storage disorders (due to transporter mutations) require import and export e.g. PMID: 2768266 - hence made reversible. NJ
GLDBRAN	3	Yang BZ, Ding JH, Enghild JJ, Bao Y, Chen YT	Molecular cloning and nucleotide sequence of cDNA encoding human muscle glycogen debranching enzyme	J Biol Chem	1992	1374391	- see Devlin p. 648 - Variants 1, 5, and 6 are present in both liver and muscle, whereas variants 2, 3, and 4 occur in muscle [RefSeq]
GLGNS1	2	Lomako J, Lomako WM, Whelan WJ	Glycogenin: the primer for mammalian and yeast glycogen synthesis	Biochim Biophys Acta	2004	15238248	-glycogenin and glycogen synthase form a complex [Lomako, Biochim Biophys Acta 2004] -see pathway in Fig 2 of Lomako, Biochim Biophys Acta 2004 - see Devlin p.652
GLNS	2	Gibbs CS, Campbell KE, Wilson RH.	Sequence of a human glutamine synthetase cDNA.		1987	2888076	cytosolic - Reactome irreversible reaction - Reactome and "common knowledge" that synthetase reactions are typically irreversible
GLPASE1	3	Newgard CB, Littman DR, van Genderen C, Smith M, Fletterick RJ	Human brain glycogen phosphorylase. Cloning, sequence analysis, chromosomal mapping, tissue expression, and comparison with the human liver and muscle isozymes	J Biol Chem	1988	3346228	- see Devlin p. 648 5834: - found predominantly in the brain [RefSeq]
GLUCYS	3	Gipp JJ, Bailey HH, Mulcahy RT.	Cloning and sequencing of the cDNA for the light subunit of human liver gamma-glutamylcysteine synthetase and relative mRNA levels for heavy and light subunits in human normal tissues.	Biochem Biophys Res Commun	1995	7826375	- Added by RS/TV Meister, A, Mitochondrial changes associated with glutathione deficiency, Biochimica et Biophysica Acta 1271 (1995) 35-42. 1) Catalytic activity specified by GeneCards. 2) Glutamate-cysteine ligase (GCL) is a rate-limiting enzyme for GSH synthesis (cytosol) Intracellular gamma-glutamylcystein synthetase can be dissociated into two subunits: a heavy(Gclc.1), catalytic subunit and a light(Gclm.1), regulatory subunit. 3) While enzymatic activity was found to some extent in all tissues, gamma-glutamylcystein synthetase activity has been reported with highest levels of expression commonly being found in liver and kidney. All this according to Gipp JJ, Bailey HH, Mulcahy RT. Biochem Biophys Res Commun. 1995 Jan 17;206(2):584-9.

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
GLUDC	3	Karlsen AE, Hagopian WA, Grubin CE, Dube S, Disteche CM, Adler DA, Barmeier H, Mathewes S, Grant FJ, Foster D, et al.	Cloning and primary structure of a human islet isoform of glutamic acid decarboxylase from chromosome 10.		1991	1924293	Entrez gene - This gene encodes one of several forms of glutamic acid decarboxylase, identified as a major autoantigen in insulin-dependent diabetes. The enzyme encoded is responsible for catalyzing the production of gamma-aminobutyric acid from L-glutamic acid. A pathogenic role for this enzyme has been identified in the human pancreas since it has been identified as an autoantigen and an autoreactive T cell target in insulin-dependent diabetes. This gene may also play a role in the stiff man syndrome. Deficiency in this enzyme has been shown to lead to pyridoxine dependency with seizures. Alternative splicing of this gene results in two products, the predominant 67-kD form and a less-frequent 25-kD form
GLUDC	3	Bu DF, Tobin AJ.	The exon-intron organization of the genes (GAD1 and GAD2) encoding two human glutamate decarboxylases (GAD67 and GAD65) suggests that they derive from a common ancestral GAD.		1994	8088791	Entrez gene - This gene encodes one of several forms of glutamic acid decarboxylase, identified as a major autoantigen in insulin-dependent diabetes. The enzyme encoded is responsible for catalyzing the production of gamma-aminobutyric acid from L-glutamic acid. A pathogenic role for this enzyme has been identified in the human pancreas since it has been identified as an autoantigen and an autoreactive T cell target in insulin-dependent diabetes. This gene may also play a role in the stiff man syndrome. Deficiency in this enzyme has been shown to lead to pyridoxine dependency with seizures. Alternative splicing of this gene results in two products, the predominant 67-kD form and a less-frequent 25-kD form
GLUDxm	3	Mavrothalassitis G, Tzimagiorgis G, Mitsialis A, Zannis V, Plaitakis A, Papamatheakis J, Moschonas N.	Isolation and characterization of cDNA clones encoding human liver glutamate dehydrogenase: evidence for a small gene family.	Proc Natl Acad Sci U S A	1988	3368458	Reversible reaction, Mitochondrial matrix - Fang et al. Biochem. J. (2002) 363 (81 87) - Additional information added by RS/TV: mitochondrial according to GeneCards 1) Glutamate dehydrogenase is known to catalyze the reversible oxidative deamination of L-glutamate to akg using NAD and/or NADP as cofactors according to G Mavrothalassitis, G Tzimagiorgis, A Mitsialis, V Zannis, A Plaitakis, J Papamatheakis, and N Moschonas. Isolation and characterization of cDNA clones encoding human liver glutamate dehydrogenase: evidence for a small gene family. Proc Natl Acad Sci U S A. 1988 May;85(10):3494-8. PMID: 3368458 2) Glutamate dehydrogenase exists in two isoforms. Glud1.1-m is considered to be housekeeping (localization description) according to Zaganas I, Spanaki C, Karpusas M, Plaitakis A. Substitution of Ser for Arg-443 in the regulatory domain of human housekeeping (GLUD1) glutamate dehydrogenase virtually abolishes basal activity and markedly alters the activation of the enzyme by ADP and L-leucine. J Biol Chem. 2002 Nov 29;277(48):46552-8. Epub 2002 Sep 24. PMID: 12324473
GLUDxm	3	Zaganas I, Spanaki C, Karpusas M, Plaitakis A.	Substitution of Ser for Arg-443 in the regulatory domain of human housekeeping (GLUD1) glutamate dehydrogenase virtually abolishes basal activity and markedly alters the activation of the enzyme by ADP and L-leucine.	J Biol Chem	2002	12324473	Reversible reaction, Mitochondrial matrix - Fang et al. Biochem. J. (2002) 363 (81 87) - Additional information added by RS/TV: mitochondrial according to GeneCards 1) Glutamate dehydrogenase is known to catalyze the reversible oxidative deamination of L-glutamate to akg using NAD and/or NADP as cofactors according to G Mavrothalassitis, G Tzimagiorgis, A Mitsialis, V Zannis, A Plaitakis, J Papamatheakis, and N Moschonas. Isolation and characterization of cDNA clones encoding human liver glutamate dehydrogenase: evidence for a small gene family. Proc Natl Acad Sci U S A. 1988 May;85(10):3494-8. PMID: 3368458 2) Glutamate dehydrogenase exists in two isoforms. Glud1.1-m is considered to be housekeeping (localization description) according to Zaganas I, Spanaki C, Karpusas M, Plaitakis A. Substitution of Ser for Arg-443 in the regulatory domain of human housekeeping (GLUD1) glutamate dehydrogenase virtually abolishes basal activity and markedly alters the activation of the enzyme by ADP and L-leucine. J Biol Chem. 2002 Nov 29;277(48):46552-8. Epub 2002 Sep 24. PMID: 12324473

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GLUDxm	3	Jie FANG , Betty Y. L. HSU , Courtney M. MACMULLEN , Mortimer PONCZ , Thomas J. SMITH and Charles A. STANLEY	Expression, purification and characterization of human glutamate dehydrogenase (GDH) allosteric regulatory mutations		2002		Reversible reaction, Mitochondrial matrix - Fang et al. Biochem. J. (2002) 363 (81 87) - Additional information added by RS/TV: mitochondrial according to GeneCards 1) Glutamate dehydrogenase is known to catalyze the reversible oxidative deamination of L-glutamate to akg using NAD and/or NADP as cofactors according to G Mavrothalassitis, G Tzimagiorgis, A Mitsialis, V Zannis, A Plaitakis, J Papamatheakis, and N Moschonas. Isolation and characterization of cDNA clones encoding human liver glutamate dehydrogenase: evidence for a small gene family. Proc Natl Acad Sci U S A. 1988 May;85(10):3494-8. PMID: 3368458 2) Glutamate dehydrogenase exists in two isoforms. Glud1.1-m is considered to be housekeeping (localization description) according to Zaganas I, Spanaki C, Karpusas M, Plaitakis A. Substitution of Ser for Arg-443 in the regulatory domain of human housekeeping (GLUD1) glutamate dehydrogenase virtually abolishes basal activity and markedly alters the activation of the enzyme by ADP and L-leucine. J Biol Chem. 2002 Nov 29;277(48):46552-8. Epub 2002 Sep 24. PMID: 12324473
GluForTx	3	Hilton JF, Christensen KE, Watkins D, Raby BA, Renaud Y, de la Luna S, Estivill X, MacKenzie RE, Hudson TJ, Rosenblatt DS	The molecular basis of glutamate formiminotransferase deficiency	Hum Mutat	2003	12815595	This enzyme is likely responsible for the second most common inborn error of folate metabolism.
GLUNm	3	Holcomb T, Taylor L, Trohkimoinen J, Curthoys NP.	Isolation, characterization and expression of a human brain mitochondrial glutaminase cDNA.		2000	10719215	-2 isozymes, one expressed mainly in kidney and brain, the other in the liver - Aledo et. al. Mamm Genome. 2000 Dec;11(12):1107-10. -mitochondrial matrix- Holcomb et al. Brain Res Mol Brain Res. 2000 Mar 10;76(1):56-63. and Reactome -irreversible according to Reactome -genetic data - Zacharias et al. Cell Biochem Funct. 2003 Mar;21(1):81-4.
GLUNm	3	Zacharias DP, Lima MM, Souza AL Jr, de Abranches Oliveira Santos ID, Enokiara M, Michalany N, Curi R.	Human cutaneous melanoma expresses a significant phosphate-dependent glutaminase activity: a comparison with the surrounding skin of the same patient.		2003	12579526	-2 isozymes, one expressed mainly in kidney and brain, the other in the liver - Aledo et. al. Mamm Genome. 2000 Dec;11(12):1107-10. -mitochondrial matrix- Holcomb et al. Brain Res Mol Brain Res. 2000 Mar 10;76(1):56-63. and Reactome -irreversible according to Reactome -genetic data - Zacharias et al. Cell Biochem Funct. 2003 Mar;21(1):81-4.
GLUNm	3	Aledo JC, Gomez-Fabre PM, Olalla L, Marquez J.	Identification of two human glutaminase loci and tissue-specific expression of the two related genes.		2005		-2 isozymes, one expressed mainly in kidney and brain, the other in the liver - Aledo et. al. Mamm Genome. 2000 Dec;11(12):1107-10. -mitochondrial matrix- Holcomb et al. Brain Res Mol Brain Res. 2000 Mar 10;76(1):56-63. and Reactome -irreversible according to Reactome -genetic data - Zacharias et al. Cell Biochem Funct. 2003 Mar;21(1):81-4.
GLUPRT	3	Iwahana H, Oka J, Mizusawa N, Kudo E, Ii S, Yoshimoto K, Holmes EW, Itakura M.	Molecular cloning of human amidophosphoribosyltransferase.	Biochem Biophys Res Commun	1993	8380692	I could not find any infos about compartiment, however, the HPRD database said nucleus. This info is based on paper of Chen et al, 1997. But they found only a nuclear protein that regulates the expression of PPAT but they did not mentioned where PPAt is located. IT
GLUPRT	3	Chen S, Nagy PL, Zalkin H	Role of NRF-1 in bidirectional transcription of the human GPAT-AIRC purine biosynthesis locus.	Nucleic Acids Res	1997	9108165	I could not find any infos about compartiment, however, the HPRD database said nucleus. This info is based on paper of Chen et al, 1997. But they found only a nuclear protein that regulates the expression of PPAT but they did not mentioned where PPAt is located. IT
GLUt6	3	Kanai Y, Hediger MA	The glutamate/neutral amino acid transporter family SLC1: molecular, physiological and pharmacological aspects	Pflugers Arch	2004	14530974	The high affinity glutamate transporters mediate transport of l-Glu, l-Asp and d-Asp, accompanied by the cotransport of 3 Na+ and 1 H+, and the countertransport of 1 K+ from PMID 14530974

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GLUVESSEC	3	Bai L, Xu H, Collins JF, Ghishan FK	Molecular and functional analysis of a novel neuronal vesicular glutamate transporter	J Biol Chem	2001	11432869	This is a lumped reaction. The most precise description is that h is transported from the cytosol into a vesicle with an ATP-dependent transporter, and then the h gradient used with an antiport to drive glutamate transport from the cytosol into the vesicle. The vesicle fuses with the membrane and dumps the glutamate outside the cell. From PMID 12811560: The three VGLUT isoforms exhibit saturable glutamate transport with a Km~1 mM that is driven primarily by the electrical component (Dy) of the proton electrochemical gradient across the vesicle membrane: valinomycin, a K+ ionophore that dissipates Dy reduces transport to a greater extent than nigericin, a H+-K+- exchanging ionophore that dissipates the pH gradient [6, 9, 17, 18, 19, 24, 37, 40, 41, 42, 44]. From PMID 15383652: In addition to this intrinsic dependency on the transmembrane electrochemical gradient, the transport rate can also be modulated by alterations in the rate of ATP hydrolysis and its coupling to H+ translocation. A recent detailed analysis of current-voltage relationships in the absence and presence of sev
GLUVESSEC	3	Wagner CA, Finberg KE, Breton S, Marshansky V, Brown D, Geibel JP	Renal vacuolar H+-ATPase	Physiol Rev	2004	15383652	This is a lumped reaction. The most precise description is that h is transported from the cytosol into a vesicle with an ATP-dependent transporter, and then the h gradient used with an antiport to drive glutamate transport from the cytosol into the vesicle. The vesicle fuses with the membrane and dumps the glutamate outside the cell. From PMID 12811560: The three VGLUT isoforms exhibit saturable glutamate transport with a Km~1 mM that is driven primarily by the electrical component (Dy) of the proton electrochemical gradient across the vesicle membrane: valinomycin, a K+ ionophore that dissipates Dy reduces transport to a greater extent than nigericin, a H+-K+- exchanging ionophore that dissipates the pH gradient [6, 9, 17, 18, 19, 24, 37, 40, 41, 42, 44]. From PMID 15383652: In addition to this intrinsic dependency on the transmembrane electrochemical gradient, the transport rate can also be modulated by alterations in the rate of ATP hydrolysis and its coupling to H+ translocation. A recent detailed analysis of current-voltage relationships in the absence and presence of sev
GLXO1	3	Holmes RP	Pharmacological approaches in the treatment of primary hyperoxaluria	J Nephrol	1998	9604807	- described in Devlin, p. 795, Orten p. 316 -catalyzed by lactate dehydrogenase [Holmes, J Urol 1998], [Holmes, J Nerphol 1998], [Pirulli, J Nephrol 2003] - cytoplasm [Holmes, J Urol 1998] - lactate dehydrogenase catalyzes the bulk of glyoxylate -> oxalate conversion in vivo as the concentrations of glycolate and lactate in hepatocytes will inhibit the glycolate oxidase catalyzed reaction [Poore 1997]
GLXO1	3	Holmes RP, Assimos DG	Glyoxylate synthesis, and its modulation and influence on oxalate synthesis	J Urol	1998	9783918	- described in Devlin, p. 795, Orten p. 316 -catalyzed by lactate dehydrogenase [Holmes, J Urol 1998], [Holmes, J Nerphol 1998], [Pirulli, J Nephrol 2003] - cytoplasm [Holmes, J Urol 1998] - lactate dehydrogenase catalyzes the bulk of glyoxylate -> oxalate conversion in vivo as the concentrations of glycolate and lactate in hepatocytes will inhibit the glycolate oxidase catalyzed reaction [Poore 1997]
GLXO1	3	Pirulli D, Marangella M, Amoroso A	Primary hyperoxaluria: genotype-phenotype correlation	J Nephrol	2003	12768081	- described in Devlin, p. 795, Orten p. 316 -catalyzed by lactate dehydrogenase [Holmes, J Urol 1998], [Holmes, J Nerphol 1998], [Pirulli, J Nephrol 2003] - cytoplasm [Holmes, J Urol 1998] - lactate dehydrogenase catalyzes the bulk of glyoxylate -> oxalate conversion in vivo as the concentrations of glycolate and lactate in hepatocytes will inhibit the glycolate oxidase catalyzed reaction [Poore 1997]
GLXtp	1	Baker PR, Cramer SD, Kennedy M, Assimos DG, Holmes RP.	Glycolate and glyoxylate metabolism in HepG2 cells.		2004	15240345	- reaction proposed in Fig 6 of [Baker 2004]
GLYAMDTRc	3	Isbrandt D, von Figura K	Cloning and sequence analysis of human guanidinoacetate N-methyltransferase cDNA	Biochim Biophys Acta	1995	8547310	Introduction of first citation states function from another paper from 1973.
GLYATm	2	Edgar,A.J. , Polak,J.M.	Molecular cloning of the human and murine 2-amino-3-ketobutyrate coenzyme A ligase cDNAs.		2000	10712613	0

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GLYBtm	2	Porter RK, Scott JM, Brand MD.	Characterization of betaine efflux from rat liver mitochondria.		1993	8443213	-added to allow glyb transport from mitochondria to cytosol -glyb diffuses across rat liver mitochondrial membrane to cytosol (PMID:8443213) -needed this rxn to fill gap since glyb is used by rxn BHMT in the cytosol MM
GLYCLTDy	3	Taylor SW, Fahy E, Zhang B, Glenn GM, Warnock DE, Wiley S, Murphy AN, Gaucher SP, Capaldi RA, Gibson BW, Ghosh SS	Characterization of the human heart mitochondrial proteome	Nat Biotechnol	2003	1252411	- ubiquitous [RefSeq], [UniProt] - has hydroxy-pyruvate reductase, glyoxylate reductase and D-glycerate dehydrogenase enzymatic activities [RefSeq], [UniProt] - uses NADPH as coenzyme [Van Schaftingen, Eur J Biochem 1989] - cellular localization uncertain, but glyoxylate reductase activity seems to be present in both cytosol and mitochondria - mitochondrial glyoxylate dehydrogenase was identified in human heart proteomic data [Taylor 2003] - HepG2 mitochondria have glyoxylate reductase acticity similar to that found in cell homogenates, suggesting that the cytosol and mitochondria have equivalent activities [Baker 2004]
GLYCLTDy	3	Van Schaftingen E, Draye JP, Van Hoof F	Coenzyme specificity of mammalian liver D-glycerate dehydrogenase	Eur J Biochem	1989	2689175	- ubiquitous [RefSeq], [UniProt] - has hydroxy-pyruvate reductase, glyoxylate reductase and D-glycerate dehydrogenase enzymatic activities [RefSeq], [UniProt] - uses NADPH as coenzyme [Van Schaftingen, Eur J Biochem 1989] - cellular localization uncertain, but glyoxylate reductase activity seems to be present in both cytosol and mitochondria - mitochondrial glyoxylate dehydrogenase was identified in human heart proteomic data [Taylor 2003] - HepG2 mitochondria have glyoxylate reductase acticity similar to that found in cell homogenates, suggesting that the cytosol and mitochondria have equivalent activities [Baker 2004]
GLYC-St	1	Petrarulo M, Vitale C, Facchini P, Marangella M	Biochemical approach to diagnosis and differentiation of primary hyperoxalurias: an update	J Nephrol	1998	9604805	- L-glycerate is virtually absent from urine of healthy individuals [Petrarulo 1998] (presumably because it is not produced in detectable quantities) - Patients with primary hyperoxaluria type 2 overproduce L-glycerate (mutation in glyoxylate reductase/hydroxypyruvate reductase gene leaves lactate dehydrogenase as only enzyme available to metabolize hydroxypyruvate) and as a result L-glycerate is detectable in plasma and urine [Petrarulo 1998] - Note that this rxn should not be necessary in healthy people since the rxn producing L-glycerate (HPYRR2x) should essentially be "off"
GLYCt	2	Kuriyama H, Kawamoto S, Ishida N, Ohno I, Mita S, Matsuzawa Y, Matsubara K, Okubo K	Molecular cloning and expression of a novel human aquaporin from adipose tissue with glycerol permeability	Biochem Biophys Res Commun	1997	9405233	- glycerol is released during hydrolysis of triacylglycerols in adipose tissue and delivered to the liver by the blood [Champe, Biochemistry 2005] - is is taken up aquaglyceroporins that transport glycerol as well as water [Biochem Biophys Res Commun 1997]
GLYCTO1p	3	Ushijima Y	Identity of aliphatic L- -hydroxyacid oxidase and glycolate oxidase from rat livers	Arch Biochem Biophys	1973	4705431	- reaction is essentially irreversible under in vivo conditions [Poore 1998] - rat liver glycolate oxidase has 10x higher affinity for glycolate than glyoxylate [Ushijima 1973] 51179: - peroxisome [RefSeq], [UniProt], [Jones, J Biol Chem 2000] - liver and kidney [RefSeq], [UniProt], [Jones, J Biol Chem 2000] 54363: - peroxisome [RefSeq], [UniProt], [Jones, J Biol Chem 2000] - liver and pancreas [RefSeq], [UniProt], [Jones, J Biol Chem 2000] - most active on glycolate [RefSeq], [UniProt], [Jones, J Biol Chem 2000]

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GLYCTO1p	3	Jones JM, Morrell JC, Gould SJ	Identification and characterization of HAOX1, HAOX2, and HAOX3, three human peroxisomal 2-hydroxy acid oxidases	J Biol Chem	2000	10777549	- reaction is essentially irreversible under in vivo conditions [Poore 1998] - rat liver glycolate oxidase has 10x higher affinity for glycolate than glyoxylate [Ushijima 1973] 51179: - peroxisome [RefSeq], [UniProt], [Jones, J Biol Chem 2000] - liver and kidney [RefSeq], [UniProt], [Jones, J Biol Chem 2000] 54363: - peroxisome [RefSeq], [UniProt], [Jones, J Biol Chem 2000] - liver and pancreas [RefSeq], [UniProt], [Jones, J Biol Chem 2000] - most active on glycolate [RefSeq], [UniProt], [Jones, J Biol Chem 2000]
GLYK	3	Sargent CA, Young C, Marsh S, Ferguson-Smith MA, Affara NA.	The glycerol kinase gene family: structure of the Xp gene, and related intronless retroposons.	Hum Mol Genet	1994	7987308	Bound to the mitochondrial surface or cytoplasmic. In sperm and fetal tissues, the majority of the enzyme is bound to mitochondria, but in adult tissues, such as liver found in the cytoplasm. see Sargent refs for different types Highly expressed in the liver, kidney and testis. Isoforms 2 (GK2) and 3(GKP3) are expressed specifically in testis and fetal liver, but not in the adult liver. NJ - adipocytes lack glycerol kinase [Champe, Biochemistry 2005] - ~50% similarity btwn human and E. coli GK proteins [Hurley 1993]
GLYK	3	Hurley JH, Faber HR, Worthylake D, Meadow ND, Roseman S, Pettigrew DW, Remington SJ	Structure of the regulatory complex of Escherichia coli IIIGlc with glycerol kinase	Science	1993	8430315	Bound to the mitochondrial surface or cytoplasmic. In sperm and fetal tissues, the majority of the enzyme is bound to mitochondria, but in adult tissues, such as liver found in the cytoplasm. see Sargent refs for different types Highly expressed in the liver, kidney and testis. Isoforms 2 (GK2) and 3(GKP3) are expressed specifically in testis and fetal liver, but not in the adult liver. NJ - adipocytes lack glycerol kinase [Champe, Biochemistry 2005] - ~50% similarity btwn human and E. coli GK proteins [Hurley 1993]
GLYK	3	Voet D, Voet JG	Biochemistry		1995		Bound to the mitochondrial surface or cytoplasmic. In sperm and fetal tissues, the majority of the enzyme is bound to mitochondria, but in adult tissues, such as liver found in the cytoplasm. see Sargent refs for different types Highly expressed in the liver, kidney and testis. Isoforms 2 (GK2) and 3(GKP3) are expressed specifically in testis and fetal liver, but not in the adult liver. NJ - adipocytes lack glycerol kinase [Champe, Biochemistry 2005] - ~50% similarity btwn human and E. coli GK proteins [Hurley 1993]

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GLYK	3	Murray RK, Granner DK, Mayes PA, Rodwell VW	Harper's Biochemistry		1999		Bound to the mitochondrial surface or cytoplasmic. In sperm and fetal tissues, the majority of the enzyme is bound to mitochondria, but in adult tissues, such as liver found in the cytoplasm. see Sargent refs for different types Highly expressed in the liver, kidney and testis. Isoforms 2 (GK2) and 3(GKP3) are expressed specifically in testis and fetal liver, but not in the adult liver. NJ - adipocytes lack glycerol kinase [Champe, Biochemistry 2005] - ~50% similarity btwn human and E. coli GK proteins [Hurley 1993]
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GLYK	3	Guo W, Worley K, Adams V, Mason J, Sylvester-Jackson D, Zhang Y, Towbin JA, Fogt DD, Madu S, Wheeler DA, McCabe ERB	Genomic scanning for expressed sequences in Xp21 identifies the glycerol kinase gene	Nature Genetics	1993		Bound to the mitochondrial surface or cytoplasmic. In sperm and fetal tissues, the majority of the enzyme is bound to mitochondria, but in adult tissues, such as liver found in the cytoplasm. see Sargent refs for different types Highly expressed in the liver, kidney and testis. Isoforms 2 (GK2) and 3(GKP3) are expressed specifically in testis and fetal liver, but not in the adult liver. NJ - adipocytes lack glycerol kinase [Champe, Biochemistry 2005] - ~50% similarity btwn human and E. coli GK proteins [Hurley 1993]
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GLYOX	3	Ridderstrom M, Saccucci F, Hellman U, Bergman T, Principato G, Mannervik B	Molecular cloning, heterologous expression, and characterization of human glyoxalase II	J Biol Chem	1996	8550579	3029: - hydrolyzes S-D- lactoyl-glutathione to form glutathione and D-lactic acid [UniProt] - cloned & expressed in E. coli; recombinant enzyme had full catalytic activity and kinetic parameters indistinguishable from those of the native enzyme purified from human erythrocytes [Ridderstrom 1996] - gene encodes both a cytosolic enzyme and a mitochondrial matrix enzyme [Cordell 2004] 84264: - hydrolyzes S-D- lactoyl-glutathione to form glutathione and D-lactic acid [UniProt] - function inferred from electronic annotation [GO]; protein has been assigned EC number
GLYOX	3	Cordell PA, Futers TS, Grant PJ, Pease RJ	The Human hydroxyacylglutathione hydrolase (HAGH) gene encodes both cytosolic and mitochondrial forms of glyoxalase II.	J Biol Chem	2004	15117945	3029: - hydrolyzes S-D- lactoyl-glutathione to form glutathione and D-lactic acid [UniProt] - cloned & expressed in E. coli; recombinant enzyme had full catalytic activity and kinetic parameters indistinguishable from those of the native enzyme purified from human erythrocytes [Ridderstrom 1996] - gene encodes both a cytosolic enzyme and a mitochondrial matrix enzyme [Cordell 2004] 84264: - hydrolyzes S-D- lactoyl-glutathione to form glutathione and D-lactic acid [UniProt] - function inferred from electronic annotation [GO]; protein has been assigned EC number
GLYtm	3	Benavides J, Garcia ML, Lopez-Lahoya J, Ugarte M, Valdivieso F.	Glycine transport in rat brain and liver mitochondria.	Biochim Biophys Acta	1980	7388024	- Added by RS/TV - No genes found. - The data presented in this report demonstrate that glycine is taken up by brain and liver mitochondria by a carrier-mediated process without requiring energy. (Benavides J, Garcia ML, Lopez-Lahoya J, Ugarte M, Valdivieso F. Biochim Biophys Acta. 1980 Jun 6;598(3):588-94.)

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GLYVESSEC	3	Gasnier B	The SLC32 transporter, a key protein for the synaptic release of inhibitory amino acids	Pflugers Arch	2004	12750892	This represents the vesiclar secretion of the compound. The reaction is written as a net secretion reaction--the ATP would actually drive a proton pump, creating a gradient that is used to concentrate a compound in a secretory vesicle. from PMID 12750892: There is evidence that glycine is also translocated [3, 19], in agreement with previous studies showing that GABA and glycine compete for uptake into synaptic vesicles [2, 5]. Similar data suggest that b-alanine is another substrate [5]. Although not proven, a 1:1 stoichiometry of H+ and amino acid is usually postulated and would concentrate enough transmitter in the vesicles because of the high cytosolic concentration of GABA and glycine at nerve terminals. This abundance is also consistent with the low affinity of VIAAT for its substrates (~5 and ~25 mM for GABA and glycine, respectively [15]). From PMID 15383652: In addition to this intrinsic dependency on the transmembrane electrochemical gradient, the transport rate can also be modulated by alterations in the rate of ATP hydrolysis and its coupling to H+ translocation. A recent detailed analysis of curr
GMPR	3	Murano I, Tsukahara M, Kajii T, Yoshida A.	Mapping of the human guanosine monophosphate reductase gene (GMPR) to chromosome 6p23 by fluorescence in situ hybridization.	Genomics	1994	8188226	0
GMPR	3	Deng Y, Wang Z, Ying K, Gu S, Ji C, Huang Y, Gu X, Wang Y, Xu Y, Li Y, Xie Y, Mao Y.	NADPH-dependent GMP reductase isoenzyme of human (GMPR2). Expression, purification, and kinetic properties.	Int J Biochem Cell Biol	2002	12009299	0
GMPS2	3	Nakamura J, Lou L.	Biochemical characterization of human GMP synthetase.	J Biol Chem	1995	7706277	IT GeneCards: needs MG2+ homodimer
GND	3	Tsui SK, Chan JY, Waye MM, Fung KP, Lee CY	Identification of a cDNA encoding 6-phosphogluconate dehydrogenase from a human heart cDNA library.	Biochem Genet	1996	8978909	5226: - cDNA isolated from adult heart library [Tsui 1996] - 94.2% identity to sheep aa seq [Tsui 1996]
GNMT	3	Chen YM, Chen LY, Wong FH, Lee CM, Chang TJ, Yang-Feng TL.	Genomic structure, expression, and chromosomal localization of the human glycine N-methyltransferase gene.		2000	10843803	abundant in liver cytosolic according to GeneCards
GNMT	3	Luka Z, Cerone R, Phillips JA 3rd, Mudd HS, Wagner C.	Mutations in human glycine N-methyltransferase give insights into its role in methionine metabolism.		2002	11810299	abundant in liver cytosolic according to GeneCards
GPIAT	3	Murakami Y, Siripanyapinyo U, Hong Y, Kang JY, Ishihara S, Nakakuma H, Maeda Y, Kinoshita T	PIG-W is critical for inositol acylation but not for flipping of glycosylphosphatidylinositol-anchor	Mol Biol Cell	2003	14517336	- identification, cloning and expression of gene [Murakami, Mol Biol Cell 2003] - knockout was complemented by S. cerevisiae and S. pombe homologs [Murakami, Mol Biol Cell 2003] - enzyme is localized in ER membrane but reaction takes place on cytosolic side [Murakami, Mol Biol Cell 2003]
GPIDAer	3	Tanaka S, Maeda Y, Tashima Y, Kinoshita T	Inositol deacylation of glycosylphosphatidylinositol-anchored proteins is mediated by mammalian PGAP1 and yeast Bst1p	J Biol Chem	2004	14734546	- gene was cloned, encodes an ER-associated GPI inositol-deacylase [Tanaka, J Biol Chem 2004] - inositol deacylation occurs in the ER soon after GPI-anchor attachment; as a result, the acyl group is usually absent from GPI-anchored proteins on the cell surface [Tanaka, J Biol Chem 2004] - this is an important step for efficient transport of GPI-anchored proteins from the ER to the Golgi [Tanaka, J Biol Chem 2004] - note: the inositol remains acylated in human erythrocytes [Tanaka, J Biol Chem 2004]
GPIMTer_L	3	Maeda Y, Watanabe R, Harris CL, Hong Y, Ohishi K, Kinoshita K, Kinoshita T	PIG-M transfers the first mannose to glycosylphosphatidylinositol on the lumenal side of the ER	EMBO J	2001	11226175	93183: - transfers the first mannose to GPI on the lumenal side of the endoplasmic reticulum [RefSeq] - identification of gene for cell line defective in activity [Maeda, EMBO J 2001] - gene has 38 and 35% similarity w/ C. elegans and S. cerevisiae, respectively [Maeda, EMBO J 2001] - catalytic domain on luminal side [Maeda, EMBO J 2001] 54965: - gene was cloned; has 77% identify to rat homolog [Ashida, Mol Biol Cell 2005] - associates w/ and stabilizes PIG-M [Ashida, Mol Biol Cell 2005]
GPIMTer_L	3	Ashida H, Hong Y, Murakami Y, Shishioh N, Sugimoto N, Kim YU, Maeda Y, Kinoshita T	Mammalian PIG-X and yeast Pbn1p are the essential components of glycosylphosphatidylinositol-mannosyltransferase I	Mol Biol Cell	2005	15635094	93183: - transfers the first mannose to GPI on the lumenal side of the endoplasmic reticulum [RefSeq] - identification of gene for cell line defective in activity [Maeda, EMBO J 2001] - gene has 38 and 35% similarity w/ C. elegans and S. cerevisiae, respectively [Maeda, EMBO J 2001] - catalytic domain on luminal side [Maeda, EMBO J 2001] 54965: - gene was cloned; has 77% identify to rat homolog [Ashida, Mol Biol Cell 2005] - associates w/ and stabilizes PIG-M [Ashida, Mol Biol Cell 2005]

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GTHO	2	Kelner MJ, Montoya MA.	Structural organization of the human glutathione reductase gene: determination of correct cDNA sequence and identification of a mitochondrial leader sequence.	Biochem Biophys Res Commun	2000	10708558	-biochemically shown to have both cytosolic and mitochondrial forms (see citation)
GTHOm	2	Tramer F, Caponecchia L, Sgro P, Martinelli M, Sandri G, Panfili E, Lenzi A, Gandini L.	Native specific activity of glutathione peroxidase (GPx-1), phospholipid hydroperoxide glutathione peroxidase (PHGPx) and glutathione reductase (GR) does not differ between normo- and hypomotile human sperm samples.	Int J Androl	2004	15149466	-biochemically shown to have both cytosolic and mitochondrial forms (see citation) - additional information added by RS/TV 1) Mitochondrial & cytosol enzyme. 2) Glutathione reductase is a major component of cellular defense mechanisms against oxidative injury. according to Kelner MJ, Montoya MA. Biochem Biophys Res Commun. 2000 Mar 16;269(2):366-8. 3) Catalytic activity: Glutathione reductase is often considered the 'ancillary' enzyme necessary for restoring oxidized glutathione at the expense of the NADPH/NADP+ couple according to Tramer F, Caponecchia L, Sgro P, Martinelli M, Sandri G, Panfili E, Lenzi A, Gandini L. Int J Androl. 2004 Apr;27(2):88-93.
GTHP	3	Metzler, David E	Biochemistry : the chemical reactions of living cells 2 ed vol 1		2001		TV (6/1/2005) Rabilloud, 2002 Peroxiredoxins are a class of enzymes, similar to glutathione peroxidase, reduces perodixes to either alcohol or water. Its substrates are not specific, and since we don't have other ROS other than h2o2, I used h2o2 as a representative. Additional unique characteristic of this enz is that its cys residue gets oxidized, and later is supposedly reduced by thioredoxin. The reduction by thioredoxin is speculative based on yeast.
GTHPe	3	Takahashi K, Avissar N, Whitin J, Cohen H.	Purification and characterization of human plasma glutathione peroxidase: a selenoglycoprotein distinct from the known cellular enzyme	Arch Biochem Biophys	1987	3619451	0
GTHPm	3	Borchert A, Savaskan NE, Kuhn H.	Regulation of expression of the phospholipid hydroperoxide/sperm nucleus glutathione peroxidase gene. Tissue-specific expression pattern and identification of functional cis- and trans-regulatory elements.	J Biol Chem	2003	12427732	- Additional information added by RS/TV: 1) Shlafer M, Myers CL, Adkins S.; Mitochondrial hydrogen peroxide generation and activities of glutathione peroxidase and superoxide dismutase following global ischemia.; J Mol Cell Cardiol. 1987 Dec;19(12):1195-206. 2) Mitochondrial & cytoplasmic according to gene cards. 3) The production of ROS is regulated by a number of antioxidant enzymes within the mitochondria. Which include phospholipid hydroperoxide glutathione peroxidase. (Mitochondrial) 4) Glutathione peroxidases (GPx)1 constitute a family of antioxidative enzymes that are capable of reducing organic and inorganic hydroperoxides to the corresponding hydroxy compounds utilizing glutathione or other hydrogen donors as reducing equivalents. 5) Gpx4 is expressed in small small amounts in many cells and tissues, but at much higher levels in testis. 6) Gpx 4 is also known to reside in the cytoplasm. All this according to Borchert A, Savaskan NE, Kuhn H.J Biol Chem. 2003 Jan 24;278(4):2571-80. Epub 2002 Nov 08.
GTHRDt	2	J Mårtensson, J C Lai, and A Meister	High-affinity transport of glutathione is part of a multicomponent system essential for mitochondrial function.	Proc Natl Acad Sci U S A	1990		- Added by RS/TV - No genes found as of yet for this transporter. - findings strongly indicate a multicomponent transport system that includes a high-affinity component that functions at very low external GSH levels (J Mårtensson, J C Lai, and A Meister. Proc Natl Acad Sci U S A. 1990 September; 87(18): 7185 7189.)
GTHS	3	Dinescu A, Cundari TR, Bhansali VS, Luo JL, Anderson ME.	Function of conserved residues of human glutathione synthetase: implications for the ATP-grasp enzymes.	J Biol Chem	2004	14990577	- Extra information added by RS/TV: -Meister, A, Mitochondrial changes associated with glutathione deficiency, Biochimica et Biophysica Acta 1271 (1995) 35-42. - Gluthione synthetase catalyzes the second and final step in the biosynthesis of gluthione from gamma-glutamylcysteine and glycine in an ATP dependent manner. - Cytosolic enzyme (gluthione is predominantly found in the cytosol) All according to Dinescu A, Cundari TR, Bhansali VS, Luo JL, Anderson ME. J Biol Chem. 2004 May 21;279(21):22412-21. Epub 2004 Feb 27.

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GTMLTe	3	Hultberg B, Hultberg M	High glutathione turnover in human cell lines revealed by acivicin inhibition of gamma-glutamyltranspeptidase and the effects of thiol-reactive metals during acivicin inhibition	Clin Chim Acta	2004	15469854	parallel reaction and transport may work with other amino acids also intracellular ala-L assumed but is the least certain part of this reaction
GTPCI	3	Thony B, Auerbach G, Blau N.	Tetrahydrobiopterin biosynthesis, regeneration and functions.	Biochem J	2000	10727395	IT
GUACYC	3	Giuili G, Scholl U, Bulle F, Guellaen G.	Molecular cloning of the cDNAs coding for the two subunits of soluble guanylyl cyclase from human brain.	FEBS Lett	1992	1352257	Potthast et al 2004 has measured activity for 4882 4881: retina, heart, kindey, others? Gucy1A3B2.1 less active than Gucy1A3B3.1 but functional heterodimer (Zaebl et al, 1998) from 2977 there is an alternative, non-functional spliceform that can inhibit the function of the heterodimer. cDNA 2977 isolated from fetal brain 2984: testis, ovary, lower expression in kidney (sugaware et al 1995) - has a extracellular domain - precursor has been found in ER (Ghanekar et al, 2004) 2986:olfactory sensory neurons and retina (Yang et al, 1996)
GUACYC	3	Arden KC, Viars CS, Weiss S, Argentin S, Nemer M.	Localization of the human B-type natriuretic peptide precursor (NPPB) gene to chromosome 1p36.	Genomics	1995	7601467	Potthast et al 2004 has measured activity for 4882 4881: retina, heart, kindey, others? Gucy1A3B2.1 less active than Gucy1A3B3.1 but functional heterodimer (Zaebl et al, 1998) from 2977 there is an alternative, non-functional spliceform that can inhibit the function of the heterodimer. cDNA 2977 isolated from fetal brain 2984: testis, ovary, lower expression in kidney (sugaware et al 1995) - has a extracellular domain - precursor has been found in ER (Ghanekar et al, 2004) 2986:olfactory sensory neurons and retina (Yang et al, 1996)
GUACYC	3	Sugawara T, Holt JA, Driscoll D, Strauss JF 3rd, Lin D, Miller WL, Patterson D, Clancy KP, Hart IM, Clark BJ, et al.	Human steroidogenic acute regulatory protein: functional activity in COS-1 cells, tissue-specific expression, and mapping of the structural gene to 8p11.2 and a pseudogene to chromosome 13.	Proc Natl Acad Sci U S A	1995	7761400	Potthast et al 2004 has measured activity for 4882 4881: retina, heart, kindey, others? Gucy1A3B2.1 less active than Gucy1A3B3.1 but functional heterodimer (Zaebl et al, 1998) from 2977 there is an alternative, non-functional spliceform that can inhibit the function of the heterodimer. cDNA 2977 isolated from fetal brain 2984: testis, ovary, lower expression in kidney (sugaware et al 1995) - has a extracellular domain - precursor has been found in ER (Ghanekar et al, 2004) 2986:olfactory sensory neurons and retina (Yang et al, 1996)
GUACYC	3	Lowe DG, Dizhoor AM, Liu K, Gu Q, Spencer M, Laura R, Lu L, Hurley JB.	Cloning and expression of a second photoreceptor-specific membrane retina guanylyl cyclase (RetGC), RetGC-2.	Proc Natl Acad Sci U S A	1995	7777544	Potthast et al 2004 has measured activity for 4882 4881: retina, heart, kindey, others? Gucy1A3B2.1 less active than Gucy1A3B3.1 but functional heterodimer (Zaebl et al, 1998) from 2977 there is an alternative, non-functional spliceform that can inhibit the function of the heterodimer. cDNA 2977 isolated from fetal brain 2984: testis, ovary, lower expression in kidney (sugaware et al 1995) - has a extracellular domain - precursor has been found in ER (Ghanekar et al, 2004) 2986:olfactory sensory neurons and retina (Yang et al, 1996)
GUACYC	3	Pardhasaradhi K, Kutty RK, Gentleman S, Krishna G.	Expression of mRNA for atrial natriuretic peptide receptor guanylate cyclase (ANPRA) in human retina.	Cell Mol Neurobiol	1994	7954658	Potthast et al 2004 has measured activity for 4882 4881: retina, heart, kindey, others? Gucy1A3B2.1 less active than Gucy1A3B3.1 but functional heterodimer (Zaebl et al, 1998) from 2977 there is an alternative, non-functional spliceform that can inhibit the function of the heterodimer. cDNA 2977 isolated from fetal brain 2984: testis, ovary, lower expression in kidney (sugaware et al 1995) - has a extracellular domain - precursor has been found in ER (Ghanekar et al, 2004) 2986:olfactory sensory neurons and retina (Yang et al, 1996)
GUACYC	3	Yang RB, Fulle HJ, Garbers DL.	Chromosomal localization and genomic organization of genes encoding guanylyl cyclase receptors expressed in olfactory sensory neurons and retina.	Genomics	1996	8838319	Potthast et al 2004 has measured activity for 4882 4881: retina, heart, kindey, others? Gucy1A3B2.1 less active than Gucy1A3B3.1 but functional heterodimer (Zaebl et al, 1998) from 2977 there is an alternative, non-functional spliceform that can inhibit the function of the heterodimer. cDNA 2977 isolated from fetal brain 2984: testis, ovary, lower expression in kidney (sugaware et al 1995) - has a extracellular domain - precursor has been found in ER (Ghanekar et al, 2004) 2986:olfactory sensory neurons and retina (Yang et al, 1996)

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GUACYC	3	Kelsell RE, Evans K, Gregory CY, Moore AT, Bird AC, Hunt DM.	Localisation of a gene for dominant cone-rod dystrophy (CORD6) to chromosome 17p.	Hum Mol Genet	1997	9097965	Potthast et al 2004 has measured activity for 4882 4881: retina, heart, kindey, others? Gucy1A3B2.1 less active than Gucy1A3B3.1 but functional heterodimer (Zaebl et al, 1998) from 2977 there is an alternative, non-functional spliceform that can inhibit the function of the heterodimer. cDNA 2977 isolated from fetal brain 2984: testis, ovary, lower expression in kidney (sugaware et al 1995) - has a extracellular domain - precursor has been found in ER (Ghanekar et al, 2004) 2986:olfactory sensory neurons and retina (Yang et al, 1996)
GUACYC	3	Zabel U, Weeger M, La M, Schmidt HH.	Human soluble guanylate cyclase: functional expression and revised isoenzyme family.	Biochem J	1998	9742212	Potthast et al 2004 has measured activity for 4882 4881: retina, heart, kindey, others? Gucy1A3B2.1 less active than Gucy1A3B3.1 but functional heterodimer (Zaebl et al, 1998) from 2977 there is an alternative, non-functional spliceform that can inhibit the function of the heterodimer. cDNA 2977 isolated from fetal brain 2984: testis, ovary, lower expression in kidney (sugaware et al 1995) - has a extracellular domain - precursor has been found in ER (Ghanekar et al, 2004) 2986:olfactory sensory neurons and retina (Yang et al, 1996)
GUACYC	3	Malterer A, Gupta G, Danziger RS.	Assignment of GUCY1B2, the human homologue of a candidate gene for hypertension, to chromosome bands 13q14.2-->q14.3 by in situ hybridization.	Cytogenet Cell Genet	1999	10449911	Potthast et al 2004 has measured activity for 4882 4881: retina, heart, kindey, others? Gucy1A3B2.1 less active than Gucy1A3B3.1 but functional heterodimer (Zaebl et al, 1998) from 2977 there is an alternative, non-functional spliceform that can inhibit the function of the heterodimer. cDNA 2977 isolated from fetal brain 2984: testis, ovary, lower expression in kidney (sugaware et al 1995) - has a extracellular domain - precursor has been found in ER (Ghanekar et al, 2004) 2986:olfactory sensory neurons and retina (Yang et al, 1996)
GUACYC	3	Behrends S, Vehse K.	The beta(2) subunit of soluble guanylyl cyclase contains a human-specific frameshift and is expressed in gastric carcinoma.	Biochem Biophys Res Commun	2000	10777682	Potthast et al 2004 has measured activity for 4882 4881: retina, heart, kindey, others? Gucy1A3B2.1 less active than Gucy1A3B3.1 but functional heterodimer (Zaebl et al, 1998) from 2977 there is an alternative, non-functional spliceform that can inhibit the function of the heterodimer. cDNA 2977 isolated from fetal brain 2984: testis, ovary, lower expression in kidney (sugaware et al 1995) - has a extracellular domain - precursor has been found in ER (Ghanekar et al, 2004) 2986:olfactory sensory neurons and retina (Yang et al, 1996)
GUACYC	3	Payne AM, Morris AG, Downes SM, Johnson S, Bird AC, Moore AT, Bhattacharya SS, Hunt DM.	Clustering and frequency of mutations in the retinal guanylate cyclase (GUCY2D) gene in patients with dominant cone-rod dystrophies.	J Med Genet	2001	11565546	Potthast et al 2004 has measured activity for 4882 4881: retina, heart, kindey, others? Gucy1A3B2.1 less active than Gucy1A3B3.1 but functional heterodimer (Zaebl et al, 1998) from 2977 there is an alternative, non-functional spliceform that can inhibit the function of the heterodimer. cDNA 2977 isolated from fetal brain 2984: testis, ovary, lower expression in kidney (sugaware et al 1995) - has a extracellular domain - precursor has been found in ER (Ghanekar et al, 2004) 2986:olfactory sensory neurons and retina (Yang et al, 1996)
GUACYC	3	Koptides M, Mean R, Stavrou C, Pierides A, Demetriou K, Nakayama T, Hildebrandt F, Fuchshuber A, Deltas CC.	Novel NPR1 polymorphic variants and its exclusion as a candidate gene for medullary cystic kidney disease (ADMCKD) type 1.	Mol Cell Probes	2001	11851379	Potthast et al 2004 has measured activity for 4882 4881: retina, heart, kindey, others? Gucy1A3B2.1 less active than Gucy1A3B3.1 but functional heterodimer (Zaebl et al, 1998) from 2977 there is an alternative, non-functional spliceform that can inhibit the function of the heterodimer. cDNA 2977 isolated from fetal brain 2984: testis, ovary, lower expression in kidney (sugaware et al 1995) - has a extracellular domain - precursor has been found in ER (Ghanekar et al, 2004) 2986:olfactory sensory neurons and retina (Yang et al, 1996)

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GUACYC	3	Ghanekar Y, Chandrashaker A, Tatu U, Visweswariah SS.	Glycosylation of the receptor guanylate cyclase C: role in ligand binding and catalytic activity.	Biochem J	2004	14748740	Potthast et al 2004 has measured activity for 4882 4881: retina, heart, kindey, others? Gucy1A3B2.1 less active than Gucy1A3B3.1 but functional heterodimer (Zaebl et al, 1998) from 2977 there is an alternative, non-functional spliceform that can inhibit the function of the heterodimer. cDNA 2977 isolated from fetal brain 2984: testis, ovary, lower expression in kidney (sugaware et al 1995) - has a extracellular domain - precursor has been found in ER (Ghanekar et al, 2004) 2986:olfactory sensory neurons and retina (Yang et al, 1996)
GUACYC	3	Potthast R, Abbey-Hosch SE, Antos LK, Marchant JS, Kuhn M, Potter LR.	Calcium-dependent dephosphorylation mediates the hyperosmotic and lysophosphatidic acid-dependent inhibition of natriuretic peptide receptor-B/guanylyl cyclase-B.	J Biol Chem	2004	15371450	Potthast et al 2004 has measured activity for 4882 4881: retina, heart, kindey, others? Gucy1A3B2.1 less active than Gucy1A3B3.1 but functional heterodimer (Zaebl et al, 1998) from 2977 there is an alternative, non-functional spliceform that can inhibit the function of the heterodimer. cDNA 2977 isolated from fetal brain 2984: testis, ovary, lower expression in kidney (sugaware et al 1995) - has a extracellular domain - precursor has been found in ER (Ghanekar et al, 2004) 2986:olfactory sensory neurons and retina (Yang et al, 1996)
GUAD	3	Yuan G, Bin JC, McKay DJ, Snyder FF.	Cloning and characterization of human guanine deaminase. Purification and partial amino acid sequence of the mouse protein.	J Biol Chem	1999	10075721	homodimer binds 1 zinc per subunit IT
GULLACter	1	Banhegyi G, Mandl J	The hepatic glycogenoreticular system	Pathol Oncol Res	2001	11458272	- gulonolactone may possibly be transported into the ER; suggested by [Banhegyi 2001]
H2CO3D	0	Sly WS, Hu PY	Human carbonic anhydrases and carbonic anhydrase deficiencies	Annu Rev Biochem	1995	7574487	[759.1]: cytosolic; 5 to 6 times more abundant than CA2 in human erythrocytes; expressed in epithelium of the large intestine, corneal epithelium, lens, ciliary body epithelium, sweat glands, adipose tissue, myoepithelial cells, neutrophils and zona glomerulosa cells of adrenal gland (Sly WS, Hu PY. Annu Rev Biochem. 1995;64:375-401. Review.) [760.1]: cytosolic; expression - see paper, has very specific expression data (Sly WS, Hu PY. Annu Rev Biochem. 1995;64:375-401. Review.) [761.1]: cytosolic; expression: skeletal muscle (type I fiber red skeletal muscle), adipose tissue (Sly WS, Hu PY. Annu Rev Biochem. 1995;64:375-401. Review.) [762.1]: CA IV is glycosylphosphatidyl-inositol-anchored membrane isozyme (GPI- linked); expressed: kidney, lung, colon, brain; (Sly WS, Hu PY. Annu Rev Biochem. 1995;64:375-401. Review.) & (Fleming RE, et al. J Clin Invest. 1995 Dec;96(6):2907-13) [766.1, 766.2]: CA7 is a cytosolic enzyme. The mRNA is primarily expressed in the cytosol of the salivary glands. Functional role remains speculative. (Sly WS, Hu PY. Annu Re [768.1]: CA 9 is a transmembrane protein, with the carbonic an [771.1, 771.2]: Type-1 membrane protein; Expressed in normal [23632.1]: Type-1 transmembrane protein; CA 14 is expressed
H2CO3D	0	Parkkila S, Parkkila AK, Saarnio J, Kivela J, Karttunen TJ, Kaunisto K, Waheed A, Sly WS, Tureci O, Virtanen I, Rajaniemi H.	Expression of the membrane-associated carbonic anhydrase isozyme XII in the human kidney and rena tumors	J Histochem Cytochem	2000	11101628	[759.1]: cytosolic; 5 to 6 times more abundant than CA2 in human erythrocytes; expressed in epithelium of the large intestine, corneal epithelium, lens, ciliary body epithelium, sweat glands, adipose tissue, myoepithelial cells, neutrophils and zona glomerulosa cells of adrenal gland (Sly WS, Hu PY. Annu Rev Biochem. 1995;64:375-401. Review.) [760.1]: cytosolic; expression - see paper, has very specific expression data (Sly WS, Hu PY. Annu Rev Biochem. 1995;64:375-401. Review.) [761.1]: cytosolic; expression: skeletal muscle (type I fiber red skeletal muscle), adipose tissue (Sly WS, Hu PY. Annu Rev Biochem. 1995;64:375-401. Review.) [762.1]: CA IV is glycosylphosphatidyl-inositol-anchored membrane isozyme (GPI- linked); expressed: kidney, lung, colon, brain; (Sly WS, Hu PY. Annu Rev Biochem. 1995;64:375-401. Review.) & (Fleming RE, et al. J Clin Invest. 1995 Dec;96(6):2907-13) [766.1, 766.2]: CA7 is a cytosolic enzyme. The mRNA is primarily expressed in the cytosol of the salivary glands. Functional role remains speculative. (Sly WS, Hu PY. Annu Re [768.1]: CA 9 is a transmembrane protein, with the carbonic an [771.1, 771.2]: Type-1 membrane protein; Expressed in normal [23632.1]: Type-1 transmembrane protein; CA 14 is expressed

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H2CO3D	0	Parkkila S, Parkkila AK, Rajaniemi H, Shah GN, Grubb JH, Waheed A, Sly WS.	Expression of membrane-associated carbonic anhydrase XIV on neurons and axons in mouse and human brain	Proc Natl Acad Sci U S A	2001	11172051	Reversible (Entrez) [759.1]: cytosolic; 5 to 6 times more abundant than CA2 in human erythrocytes; expressed in epithelium of the large intestine, corneal epithelium, lens, ciliary body epithelium, sweat glands, adipose tissue, myoepithelial cells, neutrophils and zona glomerulosa cells of adrenal gland (Sly WS, Hu PY. Annu Rev Biochem. 1995;64:375-401. Review.) [760.1]: cytosolic; expression - see paper, has very specific expression data (Sly WS, Hu PY. Annu Rev Biochem. 1995;64:375-401. Review.) [761.1]: cytosolic; expression: skeletal muscle (type I fiber red skeletal muscle), adipose tissue (Sly WS, Hu PY. Annu Rev Biochem. 1995;64:375-401. Review.) [762.1]: CA IV is glycosylphosphatidyl-inositol-anchored membrane isozyme (GPI- linked); expressed: kidney, lung, colon, brain; (Sly WS, Hu PY. Annu Rev Biochem. 1995;64:375-401. Review.) & (Fleming RE, et al. J Clin Invest. 1995 Dec;96(6):2907-13) [766.1, 766.2]: CA7 is a cytosolic enzyme. The mRNA is primarily expressed in the cytosol of the salivary glands. Functional role remains speculative. (Sly WS, Hu PY. Annu Re [768.1]: CA 9 is a transmembrane protein, with the carbonic an [771.1, 771.2]: Type-1 membrane protein; Expressed in normal [23632.1]: Type-1 transmembrane protein; CA 14 is expressed
H2CO3D	0	Wingo T, Tu C, Laipis PJ, Silverman DN.	The catalytic properties of human carbonic anhydrase IX	Biochem Biophys Res Commun	2001	11676494	Reversible (Entrez) [759.1]: cytosolic; 5 to 6 times more abundant than CA2 in human erythrocytes; expressed in epithelium of the large intestine, corneal epithelium, lens, ciliary body epithelium, sweat glands, adipose tissue, myoepithelial cells, neutrophils and zona glomerulosa cells of adrenal gland (Sly WS, Hu PY. Annu Rev Biochem. 1995;64:375-401. Review.) [760.1]: cytosolic; expression - see paper, has very specific expression data (Sly WS, Hu PY. Annu Rev Biochem. 1995;64:375-401. Review.) [761.1]: cytosolic; expression: skeletal muscle (type I fiber red skeletal muscle), adipose tissue (Sly WS, Hu PY. Annu Rev Biochem. 1995;64:375-401. Review.) [762.1]: CA IV is glycosylphosphatidyl-inositol-anchored membrane isozyme (GPI- linked); expressed: kidney, lung, colon, brain; (Sly WS, Hu PY. Annu Rev Biochem. 1995;64:375-401. Review.) & (Fleming RE, et al. J Clin Invest. 1995 Dec;96(6):2907-13) [766.1, 766.2]: CA7 is a cytosolic enzyme. The mRNA is primarily expressed in the cytosol of the salivary glands. Functional role remains speculative. (Sly WS, Hu PY. Annu Re [768.1]: CA 9 is a transmembrane protein, with the carbonic an [771.1, 771.2]: Type-1 membrane protein; Expressed in normal [23632.1]: Type-1 transmembrane protein; CA 14 is expressed
H2CO3D	0	Lehtonen J, Shen B, Vihinen M, Casini A, Scozzafava A, Supuran CT, Parkkila AK, Saarnio J, Kivela AJ, Waheed A, Sly WS, Parkkila S.	Characterization of CA XIII, a novel member of the carbonic anhydrase isozyme family.	J Biol Chem	2004	14600151	Reversible (Entrez) [759.1]: cytosolic; 5 to 6 times more abundant than CA2 in human erythrocytes; expressed in epithelium of the large intestine, corneal epithelium, lens, ciliary body epithelium, sweat glands, adipose tissue, myoepithelial cells, neutrophils and zona glomerulosa cells of adrenal gland (Sly WS, Hu PY. Annu Rev Biochem. 1995;64:375-401. Review.) [760.1]: cytosolic; expression - see paper, has very specific expression data (Sly WS, Hu PY. Annu Rev Biochem. 1995;64:375-401. Review.) [761.1]: cytosolic; expression: skeletal muscle (type I fiber red skeletal muscle), adipose tissue (Sly WS, Hu PY. Annu Rev Biochem. 1995;64:375-401. Review.) [762.1]: CA IV is glycosylphosphatidyl-inositol-anchored membrane isozyme (GPI- linked); expressed: kidney, lung, colon, brain; (Sly WS, Hu PY. Annu Rev Biochem. 1995;64:375-401. Review.) & (Fleming RE, et al. J Clin Invest. 1995 Dec;96(6):2907-13) [766.1, 766.2]: CA7 is a cytosolic enzyme. The mRNA is primarily expressed in the cytosol of the salivary glands. Functional role remains speculative. (Sly WS, Hu PY. Annu Re [768.1]: CA 9 is a transmembrane protein, with the carbonic an [771.1, 771.2]: Type-1 membrane protein; Expressed in normal [23632.1]: Type-1 transmembrane protein; CA 14 is expressed

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H2CO3D	0	Taniuchi K, Nishimori I, Takeuchi T, Fujikawa-Adachi K, Ohtsuki Y, Onishi S.	Developmental expression of carbonic anhydrase-related proteins VIII, X, and XI in the human brain.	Neuroscience	2002		- reversible (Entrez) [759.1]: cytosolic; 5 to 6 times more abundant than CA2 in human erythrocytes; expressed in epithelium of the large intestine, corneal epithelium, lens, ciliary body epithelium, sweat glands, adipose tissue, myoepithelial cells, neutrophils and zona glomerulosa cells of adrenal gland (Sly WS, Hu PY. Annu Rev Biochem. 1995;64:375-401. Review.) [760.1]: cytosolic; expression - see paper, has very specific expression data (Sly WS, Hu PY. Annu Rev Biochem. 1995;64:375-401. Review.) [761.1]: cytosolic; expression: skeletal muscle (type I fiber red skeletal muscle), adipose tissue (Sly WS, Hu PY. Annu Rev Biochem. 1995;64:375-401. Review.) [762.1]: CA IV is glycosylphosphatidyl-inositol-anchored membrane isozyme (GPI- linked); expressed: kidney, lung, colon, brain; (Sly WS, Hu PY. Annu Rev Biochem. 1995;64:375-401. Review.) & (Fleming RE, et al. J Clin Invest. 1995 Dec;96(6):2907-13) [766.1, 766.2]: CA7 is a cytosolic enzyme. The mRNA is primarily expressed in the cytosol of the salivary glands. Functional role remains speculative. (Sly WS, Hu PY. Annu Re [768.1]: CA 9 is a transmembrane protein, with the carbonic an [771.1, 771.2]: Type-1 membrane protein; Expressed in normal [23632.1]: Type-1 transmembrane protein; CA 14 is expressed
H2CO3D	0	Fleming RE, Parkkila S, Parkkila AK, Rajaniemi H, Waheed A, Sly WS.	Carbonic anhydrase IV expression in rat and human gastrointestinal tract regional, cellular, and subcellular localization.	J Clin Invest	1995		- reversible (Entrez) [759.1]: cytosolic; 5 to 6 times more abundant than CA2 in human erythrocytes; expressed in epithelium of the large intestine, corneal epithelium, lens, ciliary body epithelium, sweat glands, adipose tissue, myoepithelial cells, neutrophils and zona glomerulosa cells of adrenal gland (Sly WS, Hu PY. Annu Rev Biochem. 1995;64:375-401. Review.) [760.1]: cytosolic; expression - see paper, has very specific expression data (Sly WS, Hu PY. Annu Rev Biochem. 1995;64:375-401. Review.) [761.1]: cytosolic; expression: skeletal muscle (type I fiber red skeletal muscle), adipose tissue (Sly WS, Hu PY. Annu Rev Biochem. 1995;64:375-401. Review.) [762.1]: CA IV is glycosylphosphatidyl-inositol-anchored membrane isozyme (GPI- linked); expressed: kidney, lung, colon, brain; (Sly WS, Hu PY. Annu Rev Biochem. 1995;64:375-401. Review.) & (Fleming RE, et al. J Clin Invest. 1995 Dec;96(6):2907-13) [766.1, 766.2]: CA7 is a cytosolic enzyme. The mRNA is primarily expressed in the cytosol of the salivary glands. Functional role remains speculative. (Sly WS, Hu PY. Annu Re [768.1]: CA 9 is a transmembrane protein, with the carbonic an [771.1, 771.2]: Type-1 membrane protein; Expressed in normal [23632.1]: Type-1 transmembrane protein; CA 14 is expressed
H2CO3Dm	3	Shah GN, Hewett-Emmett D, Grubb JH, Migas MC, Fleming RE, Waheed A, Sly WS.	Mitochondrial carbonic anhydrase CA VB: differences in tissue distribution and pattern of evolution from those of CA VA suggest distinct physiological roles.	Proc Natl Acad Sci U S A	2000	10677517	- Added by RS/TV Catalytic Activity: The carbonic anhydrases (CAs) are a family of zinc metalloenzymes that catalyze the reversible hydration of CO2 in the reaction CO2 + H2O<--> HCO3- + H+. Both Ca5a.1-m and Ca5b.1-m catalyze this reaction. Tissue Distribution: Ca5a.1-m: Found exclusively in liver tissue. Ca5b.1-m: Found in kidney, liver, muscle, and brain. All according to Shah GN. Proc Natl Acad Sci U S A. 2000 Feb 15;97(4):1677-82.
H2ETer	2	Hong Y, Maeda Y, Watanabe R, Ohishi K, Mishkind M, Riezman H, Kinoshita T	Pig-n, a mammalian homologue of yeast Mcd4p, is involved in transferring phosphoethanolamine to the first mannose of the glycosylphosphatidylinositol	J Biol Chem	1999	10574991	- reaction described in Varki, pg. 136 - expressed in the endoplasmic reticulum and transfers phosphoethanolamine (EtNP) to the first mannose of the GPI anchor [RefSeq] - mouse gene has been cloned [Hong, J Biol Chem 1999]
H2MTer_L	3	Kang JY, Hong Y, Ashida H, Shishioh N, Murakami Y, Morita YS, Maeda Y, Kinoshita T	IG-V involved in transferring the second mannose in glycosylphosphatidylinositol	J Biol Chem	2005	15623507	- reaction described in Varki, pg. 136 - gene was identified and cloned [Kang, J Biol Chem 2005] - Man-GlcN-acyIPI inferred as preferred substrate (based on knockout); may also mannosylate EtNP-Man-GlcN-acyIPI [Kang, J Biol Chem 2005]
H2O2syn	2	Forteza R, Salathe M, Miot F, Forteza R, Conner GE	Regulated hydrogen peroxide production by Duox in human airway epithelial cells	Am J Respir Cell Mol Biol	2005	15677770	This reaction is supported by at least two references. However, it is not absolutely certain that this is the mechanism that these genes use to make H2O2, so physiological evidence is assigned. These genes make H2O2 that is used in the synthesis of the thyroid hormones T3 and T4.
H2O2syn	2	Ameziane-El-Hassani R, Morand S, Boucher JL, Frapart YM, Apostolou D, Agnandji D, Gnidehou S, Ohayon R, Noel-Hudson MS, Francon J, Lalaoui K, Virion A, Dupuy C	Dual Oxidase-2 Has an Intrinsic Ca2+-dependent H2O2-generating Activity	J Biol Chem	2005	15972824	This reaction is supported by at least two references. However, it is not absolutely certain that this is the mechanism that these genes use to make H2O2, so physiological evidence is assigned. These genes make H2O2 that is used in the synthesis of the thyroid hormones T3 and T4.

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H2O2tp	2	Ohno Y, Gallin JI.	Diffusion of extracellular hydrogen peroxide into intracellular compartments of human neutrophils. Studies utilizing the inactivation of myeloperoxidase by hydrogen peroxide and azide.	J Biol Chem	1985	2989289	- extracellular hydrogen peroxide diffuses into intracellular compartments of human neutrophils [Ohno 1985]
H2Ot	3	Hediger MA, Turk E, Wright EM	Homology of the human intestinal Na+/glucose and Escherichia coli Na+/proline cotransporters	Proc Natl Acad Sci U S A	1989	2490366	6523: -cloned [Hediger 1989] - cotransports Glc/2 Na+, Gal/2 Na+ [Quick 2001] - H+ can replace Na+ [Hirayama 1994] - behaves as urea channel in the absence of substrates; cotransports urea under substrate-transporting conditions [Leung 2000] - Na+ transport occurs by a saturable uniport mechanism; water permeation is through a low conductance water channel; approximately 260 water molecules are transported per 2 Na+:1 Glc [Loo 1999] NOTE: it's a point of depate whether water is transported by SLC5A1 or by osmosis - brush border membrane [Wright 1994] - plasma membrane; see [Wright 2004] for refs
H2Ot	3	Hirayama BA, Loo DD, Wright EM.	Protons drive sugar transport through the Na+/glucose cotransporter (SGLT1)	J Biol Chem	1994	8063771	6523: -cloned [Hediger 1989] - cotransports Glc/2 Na+, Gal/2 Na+ [Quick 2001] - H+ can replace Na+ [Hirayama 1994] - behaves as urea channel in the absence of substrates; cotransports urea under substrate-transporting conditions [Leung 2000] - Na+ transport occurs by a saturable uniport mechanism; water permeation is through a low conductance water channel; approximately 260 water molecules are transported per 2 Na+:1 Glc [Loo 1999] NOTE: it's a point of depate whether water is transported by SLC5A1 or by osmosis - brush border membrane [Wright 1994] - plasma membrane; see [Wright 2004] for refs
H2Ot	3	Quick M, Loo DD, Wright EM	Neutralization of a conserved amino acid residue in the human Na+/glucose transporter (hSGLT1) generates a glucose-gated H+ channel	J Biol Chem	2001	11024018	6523: -cloned [Hediger 1989] - cotransports Glc/2 Na+, Gal/2 Na+ [Quick 2001] - H+ can replace Na+ [Hirayama 1994] - behaves as urea channel in the absence of substrates; cotransports urea under substrate-transporting conditions [Leung 2000] - Na+ transport occurs by a saturable uniport mechanism; water permeation is through a low conductance water channel; approximately 260 water molecules are transported per 2 Na+:1 Glc [Loo 1999] NOTE: it's a point of depate whether water is transported by SLC5A1 or by osmosis - brush border membrane [Wright 1994] - plasma membrane; see [Wright 2004] for refs
H2Ot	3	Leung DW, Loo DD, Hirayama BA, Zeuthen T, Wright EM	Urea transport by cotransporters	J Physiol	2000	11034615	6523: -cloned [Hediger 1989] - cotransports Glc/2 Na+, Gal/2 Na+ [Quick 2001] - H+ can replace Na+ [Hirayama 1994] - behaves as urea channel in the absence of substrates; cotransports urea under substrate-transporting conditions [Leung 2000] - Na+ transport occurs by a saturable uniport mechanism; water permeation is through a low conductance water channel; approximately 260 water molecules are transported per 2 Na+:1 Glc [Loo 1999] NOTE: it's a point of depate whether water is transported by SLC5A1 or by osmosis - brush border membrane [Wright 1994] - plasma membrane; see [Wright 2004] for refs
H2Ot	3	Wright EM, Turk E	The sodium/glucose cotransport family SLC5.	Pflugers Arch	2004	12748858	6523: -cloned [Hediger 1989] - cotransports Glc/2 Na+, Gal/2 Na+ [Quick 2001] - H+ can replace Na+ [Hirayama 1994] - behaves as urea channel in the absence of substrates; cotransports urea under substrate-transporting conditions [Leung 2000] - Na+ transport occurs by a saturable uniport mechanism; water permeation is through a low conductance water channel; approximately 260 water molecules are transported per 2 Na+:1 Glc [Loo 1999] NOTE: it's a point of depate whether water is transported by SLC5A1 or by osmosis - brush border membrane [Wright 1994] - plasma membrane; see [Wright 2004] for refs
H2Ot	3	Wright EM, Hirayama BA, Loo DDF, Turk E, Hager K	Intestinal sugar transport		1994		6523: -cloned [Hediger 1989] - cotransports Glc/2 Na+, Gal/2 Na+ [Quick 2001] - H+ can replace Na+ [Hirayama 1994] - behaves as urea channel in the absence of substrates; cotransports urea under substrate-transporting conditions [Leung 2000] - Na+ transport occurs by a saturable uniport mechanism; water permeation is through a low conductance water channel; approximately 260 water molecules are transported per 2 Na+:1 Glc [Loo 1999] NOTE: it's a point of depate whether water is transported by SLC5A1 or by osmosis - brush border membrane [Wright 1994] - plasma membrane; see [Wright 2004] for refs

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H2Otm	3	Calamita G, Ferri D, Gena P, Liquori GE, Cavalier A, Thomas D, Svelto M.	The inner mitochondrial membrane has aquaporin-8 water channels and is highly permeable to water.	J Biol Chem	2005	15749715	- Added by RS/TV - It is suggested that AQP8-mediated water transport may be particularly important for rapid expansions of mitochondrial volume. - Immunoblotting, electron microscopy and biophysical studies show the presence of AQP8. - In this study was found in the rat liver, but also found in the mitochondria of other organs. (Calamita G, Ferri D, Gena P, Liquori GE, Cavalier A, Thomas D, Svelto M. J Biol Chem. 2005 Mar 4)
H4ET3er	3	Inoue N, Kinoshita T, Orii T, Takeda J	Cloning of a human gene, PIG-F, a component of glycosylphosphatidylinositol anchor biosynthesis, by a novel expression cloning strategy	J Biol Chem	1993	8463218	- reaction described in Varki, pg. 136 - PIGF and PIGO transfer ethanolaminephosphate to the third mannose in GPI [RefSeq] - PIGF and PIGO form a complex [UniProt], [Hong, J Biol Chem 2000] 5281: - gene was cloned [Inoue, J Biol Chem 1993] 84720: - mouse gene was cloned [Hong, J Biol Chem 2000]
H4ET3er	3	Hong Y, Maeda Y, Watanabe R, Inoue N, Ohishi K, Kinoshita T	Requirement of PIG-F and PIG-O for transferring phosphoethanolamine to the third mannose in glycosylphosphatidylinositol	J Biol Chem	2000	10781593	- reaction described in Varki, pg. 136 - PIGF and PIGO transfer ethanolaminephosphate to the third mannose in GPI [RefSeq] - PIGF and PIGO form a complex [UniProt], [Hong, J Biol Chem 2000] 5281: - gene was cloned [Inoue, J Biol Chem 1993] 84720: - mouse gene was cloned [Hong, J Biol Chem 2000]
H6'ET2er	3	Shishioh N, Hong Y, Ohishi K, Ashida H, Maeda Y, Kinoshita T	GPI7 is the second partner of PIG-F and involved in modification of glycosylphosphatidylinositol	J Biol Chem	2005	15632136	- reaction described in Varki, pg. 136 - gene was cloned, function inferred from knockout [Shishioh, J Biol Chem 2005] - enzyme complex consisting of GPI7 and PIG-F is involved in the conversion of EtNP-Man-Man-(EtNP)Man-GlcN-(acyl)PI to EtNP-Man-(EtNP)Man-(EtNP)Man-GlcN-(acyl)PI [Shishioh, J Biol Chem 2005]
H8TAer	3	Yu J, Nagarajan S, Knez JJ, Udenfriend S, Chen R, Medof ME	The affected gene underlying the class K glycosylphosphatidylinositol (GPI) surface protein defect codes for the GPI transamidase	Proc Natl Acad Sci U S A	1997	9356492	- minor structure transfered to proteins as GPI anchor [Shishioh, J Biol Chem 2005] - transamidase is complex with GPAA1, PIGK/GPI8, PIGT, PIGU and PIGS [UniProt] 8733: - functions in GPI transfer [RefSeq] - uniquitous expression [UniProt], [Hiroi, FEBS Lett 1998] - gene has been cloned [Hiroi, FEBS Lett 1998] - 25% identity to yeast homolog [Hiroi, FEBS Lett 1998] 10026: - gene was identified [Yu, PNAS 1997] - active site characterized [Meyer, Biochemistry 2000] 94005, 51604: - gene was cloned, demonstrated to be essential to complex [Ohishi, EMBO J 2001] 128869: - gene was cloned, demonstrated to be part of complex [Hong, Mol Biol Cell 2003]
H8TAer	3	Hiroi Y, Komuro I, Chen R, Hosoda T, Mizuno T, Kudoh S, Georgescu SP, Medof ME, Yazaki Y	Molecular cloning of human homolog of yeast GAA1 which is required for attachment of glycosylphosphatidylinositols to proteins	FEBS Lett	1998	9468317	- minor structure transfered to proteins as GPI anchor [Shishioh, J Biol Chem 2005] - transamidase is complex with GPAA1, PIGK/GPI8, PIGT, PIGU and PIGS [UniProt] 8733: - functions in GPI transfer [RefSeq] - uniquitous expression [UniProt], [Hiroi, FEBS Lett 1998] - gene has been cloned [Hiroi, FEBS Lett 1998] - 25% identity to yeast homolog [Hiroi, FEBS Lett 1998] 10026: - gene was identified [Yu, PNAS 1997] - active site characterized [Meyer, Biochemistry 2000] 94005, 51604: - gene was cloned, demonstrated to be essential to complex [Ohishi, EMBO J 2001] 128869: - gene was cloned, demonstrated to be part of complex [Hong, Mol Biol Cell 2003]

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
H8TAer	3	Meyer U, Benghezal M, Imhof I, Conzelmann A	Active site determination of Gpi8p, a caspase-related enzyme required for glycosylphosphatidylinositol anchor addition to proteins	Biochemistry	2000	10727241	- minor structure transfered to proteins as GPI anchor [Shishioh, J Biol Chem 2005] - transamidase is complex with GPAA1, PIGK/GPI8, PIGT, PIGU and PIGS [UniProt] 8733: - functions in GPI transfer [RefSeq] - uniquitous expression [UniProt], [Hiroi, FEBS Lett 1998] - gene has been cloned [Hiroi, FEBS Lett 1998] - 25% identity to yeast homolog [Hiroi, FEBS Lett 1998] 10026: - gene was identified [Yu, PNAS 1997] - active site characterized [Meyer, Biochemistry 2000] 94005, 51604: - gene was cloned, demonstrated to be essential to complex [Ohishi, EMBO J 2001] 128869: - gene was cloned, demonstrated to be part of complex [Hong, Mol Biol Cell 2003]
H8TAer	3	Ohishi K, Inoue N, Kinoshita T	PIG-S and PIG-T, essential for GPI anchor attachment to proteins, form a complex with GAA1 and GPI8	EMBO J	2001	11483512	- minor structure transfered to proteins as GPI anchor [Shishioh, J Biol Chem 2005] - transamidase is complex with GPAA1, PIGK/GPI8, PIGT, PIGU and PIGS [UniProt] 8733: - functions in GPI transfer [RefSeq] - uniquitous expression [UniProt], [Hiroi, FEBS Lett 1998] - gene has been cloned [Hiroi, FEBS Lett 1998] - 25% identity to yeast homolog [Hiroi, FEBS Lett 1998] 10026: - gene was identified [Yu, PNAS 1997] - active site characterized [Meyer, Biochemistry 2000] 94005, 51604: - gene was cloned, demonstrated to be essential to complex [Ohishi, EMBO J 2001] 128869: - gene was cloned, demonstrated to be part of complex [Hong, Mol Biol Cell 2003]
H8TAer	3	Hong Y, Ohishi K, Kang JY, Tanaka S, Inoue N, Nishimura J, Maeda Y, Kinoshita T	Human PIG-U and yeast Cdc91p are the fifth subunit of GPI transamidase that attaches GPI-anchors to proteins	Mol Biol Cell	2003	12802054	- minor structure transfered to proteins as GPI anchor [Shishioh, J Biol Chem 2005] - transamidase is complex with GPAA1, PIGK/GPI8, PIGT, PIGU and PIGS [UniProt] 8733: - functions in GPI transfer [RefSeq] - uniquitous expression [UniProt], [Hiroi, FEBS Lett 1998] - gene has been cloned [Hiroi, FEBS Lett 1998] - 25% identity to yeast homolog [Hiroi, FEBS Lett 1998] 10026: - gene was identified [Yu, PNAS 1997] - active site characterized [Meyer, Biochemistry 2000] 94005, 51604: - gene was cloned, demonstrated to be essential to complex [Ohishi, EMBO J 2001] 128869: - gene was cloned, demonstrated to be part of complex [Hong, Mol Biol Cell 2003]

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HAS2	3	Itano N, Kimata K.	Molecular cloning of human hyaluronan synthase	Biochem Biophys Res Commun	1996	8651928	from [Varki 1999]: - GlcNAc and GlcA are copolymerized from UDP-GlcNAC and UDP-GlcA - synthesis occurs at plasma membrane; assembles from reducing end, causing its extrusion from cell surface - HA synthesizes can polymerize ~100 monosaccharides/sec in vitro from [Itano 2002]: - each HAS protein can independently synthesize HA - HAS2 synthesizes very large HA molecules; smaller molecules synthesized by HAS1, HAS3 - recombinant HAS1 has higher Km for UDP-GlcNAc and UDP-GlcA than HAS2 and HAS3 3036: - clone isolated from human fetal cDNA library [Itano 1996] - 84.4% and 96.0% identity with murine nucleotide sequence and amino acid sequences [Itano 1996]; 22%, 54%, and 92% identity with S. pyogenes, X. laevis, and murine amino acid sequences [Shyjan 1996] - ubiquitous [Itano 1996]; high in ovary; moderate in spleen, thymus, prostate, testes, large intestine, and heart; weak in small intestine [Shyjan 1996] - isolated & expressed in CHO cells [Shyjan 1996] 3037: - cloned and expressed in human 293 and CHO cells [Watanabe 1996] - 55% amino acid identity with Xenopus DG42 and 52% identi 3038: - isolated partial ORF sequence [Spicer 1997] - 99% conservation between human (partial) and mouse amino
HAS2	3	Watanabe K, Yamaguchi Y	Molecular identification of a putative human hyaluronan synthase	J Biol Chem	1996	8798477	from [Varki 1999]: - GlcNAc and GlcA are copolymerized from UDP-GlcNAC and UDP-GlcA - synthesis occurs at plasma membrane; assembles from reducing end, causing its extrusion from cell surface - HA synthesizes can polymerize ~100 monosaccharides/sec in vitro from [Itano 2002]: - each HAS protein can independently synthesize HA - HAS2 synthesizes very large HA molecules; smaller molecules synthesized by HAS1, HAS3 - recombinant HAS1 has higher Km for UDP-GlcNAc and UDP-GlcA than HAS2 and HAS3 3036: - clone isolated from human fetal cDNA library [Itano 1996] - 84.4% and 96.0% identity with murine nucleotide sequence and amino acid sequences [Itano 1996]; 22%, 54%, and 92% identity with S. pyogenes, X. laevis, and murine amino acid sequences [Shyjan 1996] - ubiquitous [Itano 1996]; high in ovary; moderate in spleen, thymus, prostate, testes, large intestine, and heart; weak in small intestine [Shyjan 1996] - isolated & expressed in CHO cells [Shyjan 1996] 3037: - cloned and expressed in human 293 and CHO cells [Watanabe 1996] - 55% amino acid identity with Xenopus DG42 and 52% identi 3038: - isolated partial ORF sequence [Spicer 1997] - 99% conservation between human (partial) and mouse amino
HAS2	3	Shyjan AM, Heldin P, Butcher EC, Yoshino T, Briskin MJ	Functional cloning of the cDNA for a human hyaluronan synthase	J Biol Chem	1996	8798544	from [Varki 1999]: - GlcNAc and GlcA are copolymerized from UDP-GlcNAC and UDP-GlcA - synthesis occurs at plasma membrane; assembles from reducing end, causing its extrusion from cell surface - HA synthesizes can polymerize ~100 monosaccharides/sec in vitro from [Itano 2002]: - each HAS protein can independently synthesize HA - HAS2 synthesizes very large HA molecules; smaller molecules synthesized by HAS1, HAS3 - recombinant HAS1 has higher Km for UDP-GlcNAc and UDP-GlcA than HAS2 and HAS3 3036: - clone isolated from human fetal cDNA library [Itano 1996] - 84.4% and 96.0% identity with murine nucleotide sequence and amino acid sequences [Itano 1996]; 22%, 54%, and 92% identity with S. pyogenes, X. laevis, and murine amino acid sequences [Shyjan 1996] - ubiquitous [Itano 1996]; high in ovary; moderate in spleen, thymus, prostate, testes, large intestine, and heart; weak in small intestine [Shyjan 1996] - isolated & expressed in CHO cells [Shyjan 1996] 3037: - cloned and expressed in human 293 and CHO cells [Watanabe 1996] - 55% amino acid identity with Xenopus DG42 and 52% identi 3038: - isolated partial ORF sequence [Spicer 1997] - 99% conservation between human (partial) and mouse amino

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HAS2	3	Spicer AP, Olson JS, McDonald JA	Molecular cloning and characterization of a cDNA encoding the third putative mammalian hyaluronan synthase	J Biol Chem	1997	9083017	from [Varki 1999]: - GlcNAc and GlcA are copolymerized from UDP-GlcNAC and UDP-GlcA - synthesis occurs at plasma membrane; assembles from reducing end, causing its extrusion from cell surface - HA synthesizes can polymerize ~100 monosaccharides/sec in vitro from [Itano 2002]: - each HAS protein can independently synthesize HA - HAS2 synthesizes very large HA molecules; smaller molecules synthesized by HAS1, HAS3 - recombinant HAS1 has higher Km for UDP-GlcNAc and UDP-GlcA than HAS2 and HAS3 3036: - clone isolated from human fetal cDNA library [Itano 1996] - 84.4% and 96.0% identity with murine nucleotide sequence and amino acid sequences [Itano 1996]; 22%, 54%, and 92% identity with S. pyogenes, X. laevis, and murine amino acid sequences [Shyjan 1996] - ubiquitous [Itano 1996]; high in ovary; moderate in spleen, thymus, prostate, testes, large intestine, and heart; weak in small intestine [Shyjan 1996] - isolated & expressed in CHO cells [Shyjan 1996] 3037: - cloned and expressed in human 293 and CHO cells [Watanabe 1996] - 55% amino acid identity with Xenopus DG42 and 52% identi 3038: - isolated partial ORF sequence [Spicer 1997] - 99% conservation between human (partial) and mouse amino
HAS2	3	Itano N, Kimata K	Mammalian hyaluronan synthases	IUBMB Life	2002	12512858	from [Varki 1999]: - GlcNAc and GlcA are copolymerized from UDP-GlcNAC and UDP-GlcA - synthesis occurs at plasma membrane; assembles from reducing end, causing its extrusion from cell surface - HA synthesizes can polymerize ~100 monosaccharides/sec in vitro from [Itano 2002]: - each HAS protein can independently synthesize HA - HAS2 synthesizes very large HA molecules; smaller molecules synthesized by HAS1, HAS3 - recombinant HAS1 has higher Km for UDP-GlcNAc and UDP-GlcA than HAS2 and HAS3 3036: - clone isolated from human fetal cDNA library [Itano 1996] - 84.4% and 96.0% identity with murine nucleotide sequence and amino acid sequences [Itano 1996]; 22%, 54%, and 92% identity with S. pyogenes, X. laevis, and murine amino acid sequences [Shyjan 1996] - ubiquitous [Itano 1996]; high in ovary; moderate in spleen, thymus, prostate, testes, large intestine, and heart; weak in small intestine [Shyjan 1996] - isolated & expressed in CHO cells [Shyjan 1996] 3037: - cloned and expressed in human 293 and CHO cells [Watanabe 1996] - 55% amino acid identity with Xenopus DG42 and 52% identi 3038: - isolated partial ORF sequence [Spicer 1997] - 99% conservation between human (partial) and mouse amino
HBZOPT10m	3	Kang DC, Takeshige K, Minakami S.	An intermediate of ubiquinone biosynthesis exists in the microsomal fraction of HepG2 cells.	J Biochem (Tokyo)	1990	1965190	I am not sure about reaction but sequence and physiological evidence for such a reaction it seems that the ubiquinone biosynthesis takes place in mitochondria altough direct evidence is missing but Jonassen and Clarke (2000) found a signal sequence typical for mitochondrial proteins in COQ3 gene sequence. IT
HBZOPT10m	3	Nambudiri AM, Ranganathan S, Rudney H	The role of 3-hydroxy-3-methylglutaryl coenzyme A reductase activity in the regulation of ubiquinone synthesis in human fibroblasts.	J Biol Chem	1980	7380842	I am not sure about reaction but sequence and physiological evidence for such a reaction it seems that the ubiquinone biosynthesis takes place in mitochondria altough direct evidence is missing but Jonassen and Clarke (2000) found a signal sequence typical for mitochondrial proteins in COQ3 gene sequence. IT
HBZOPT10m	3	Forsgren M, Attersand A, Lake S, Grunler J, Swiezewska E, Dallner G, Climent I.	Isolation and functional expression of human COQ2, a gene encoding a polyprenyl transferase involved in the synthesis of CoQ.	Biochem J	2004	15153069	I am not sure about reaction but sequence and physiological evidence for such a reaction it seems that the ubiquinone biosynthesis takes place in mitochondria altough direct evidence is missing but Jonassen and Clarke (2000) found a signal sequence typical for mitochondrial proteins in COQ3 gene sequence. IT

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
HCO3_CLt	3	Parker MD, Ourmozdi EP, Tanner MJ.	Human BTR1, a new bicarbonate transporter superfamily member and human AE4 from kidney.		2001	11302728	Disease: defects in slc4a1 are a cause of hereditary elliptocytosis (he) [mim:109270, 166900, 130600]; also known as hereditary ovalocytosis (HO). It is a genetically heterogeneous, autosomal dominant disorder. It is characterized by variable hemolytic anemia and elliptical or oval red cell shape. Ovalocytosis/elliptocytosis due to SLC4A1 defects is rhesus- unliked (elliptocytosis 2 or EL2). It can also be referred to as elliptocytosis 4 (EL4). Disease: defects in slc4a1 are a cause of hereditary spherocytosis (hs) [mim:109270]. HS is a hematologic disorder leading to chronic hemolytic anemia and characterized by numerous abnormally shaped erythrocytes which are generally spheroidal. Disease: defects in slc4a1 are a cause of familial distal renal tubular acidosis (drta) [mim:179800]. This disease is characterized by reduced ability to acidify urine, variable hyperchloremic hypokalemic metabolic acidosis, nephrocalcinosis, and nephrolithiasis. Inheritance is generally autosomal dominant, but recessive forms have also been reported. MM
HCO3_CLt	3	Alper SL, Darman RB, Chernova MN, Dahl NK.	The AE gene family of Cl/HCO3- exchangers.		2003	12027221	Disease: defects in slc4a1 are a cause of hereditary elliptocytosis (he) [mim:109270, 166900, 130600]; also known as hereditary ovalocytosis (HO). It is a genetically heterogeneous, autosomal dominant disorder. It is characterized by variable hemolytic anemia and elliptical or oval red cell shape. Ovalocytosis/elliptocytosis due to SLC4A1 defects is rhesus- unliked (elliptocytosis 2 or EL2). It can also be referred to as elliptocytosis 4 (EL4). Disease: defects in slc4a1 are a cause of hereditary spherocytosis (hs) [mim:109270]. HS is a hematologic disorder leading to chronic hemolytic anemia and characterized by numerous abnormally shaped erythrocytes which are generally spheroidal. Disease: defects in slc4a1 are a cause of familial distal renal tubular acidosis (drta) [mim:179800]. This disease is characterized by reduced ability to acidify urine, variable hyperchloremic hypokalemic metabolic acidosis, nephrocalcinosis, and nephrolithiasis. Inheritance is generally autosomal dominant, but recessive forms have also been reported. MM
HCO3_CLt	3	Romero MF, Fulton CM, Boron WF.	The SLC4 family of HCO 3 - transporters.		2004	14722772	Disease: defects in slc4a1 are a cause of hereditary elliptocytosis (he) [mim:109270, 166900, 130600]; also known as hereditary ovalocytosis (HO). It is a genetically heterogeneous, autosomal dominant disorder. It is characterized by variable hemolytic anemia and elliptical or oval red cell shape. Ovalocytosis/elliptocytosis due to SLC4A1 defects is rhesus- unliked (elliptocytosis 2 or EL2). It can also be referred to as elliptocytosis 4 (EL4). Disease: defects in slc4a1 are a cause of hereditary spherocytosis (hs) [mim:109270]. HS is a hematologic disorder leading to chronic hemolytic anemia and characterized by numerous abnormally shaped erythrocytes which are generally spheroidal. Disease: defects in slc4a1 are a cause of familial distal renal tubular acidosis (drta) [mim:179800]. This disease is characterized by reduced ability to acidify urine, variable hyperchloremic hypokalemic metabolic acidosis, nephrocalcinosis, and nephrolithiasis. Inheritance is generally autosomal dominant, but recessive forms have also been reported. MM
HCO3_NAt	3	Wang CZ, Yano H, Nagashima K, Seino S.	The Na+-driven Cl-/HCO3- exchanger. Cloning, tissue distribution, and functional characterization.		2000	10993873	0
HDCAtr	2	Schaffer JE.	Fatty acid transport: the roads taken.	Am J Physiol Endocrinol Metab	2002	11788354	General mechanism - diffusional transport Fatty acids are transported as a result of multiple mechanisms - generally accepted that there are 2 main types of transporters: diffusional and protein mediated (e.g. FATP, OCTN, etc). Diffusional transport is concentration dependent (micromolar), wherease protein mediated transport can occur at lower concentrations (nanomolar). For both models transport is proposed to be bidirectional (the direction-determining step is FA activation once inside the cytosol. See Schaffer review (PMID: 11788354) and Pownall manuscript (PMID: 12864740) for further details. NJ

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
HDCAtr	2	Pownall HJ, Hamilton JA.	Energy translocation across cell membranes and membrane models.	Acta Physiol Scand	2003	12864740	General mechanism - diffusional transport Fatty acids are transported as a result of multiple mechanisms - generally accepted that there are 2 main types of transporters: diffusional and protein mediated (e.g. FATP, OCTN, etc). Diffusional transport is concentration dependent (micromolar), wherease protein mediated transport can occur at lower concentrations (nanomolar). For both models transport is proposed to be bidirectional (the direction-determining step is FA activation once inside the cytosol. See Schaffer review (PMID: 11788354) and Pownall manuscript (PMID: 12864740) for further details. NJ
HEX1	2	Orten JM, Neuhaus OW.	Human Biochemistry		1975		- irreversible under physiological conditions [Orten and Neuhaus, Human Biochem 1975] 2645: - outer mitochondrial membrane [RefSeq] - catalyzes initial step in utilization of glucose by the beta-cell and liver [UniProt] 3098: -Protein encoded by transcript 1 (NM_000188) is associated w/ outer mitochondrial membrane. Other transcripts enode cytosolic isoforms. [RefSeq] -Tissue localization from RefSeq, UniProt 3099: - predominant form found in skeletal muscle - outer membrane of mitochondria [RefSeq] 3101: - localized to lung, liver, placenta [Furuta et al, Genomics 1996] - soluble, cytosolic [HInv] 80201: - mito membrane [HInv]
HIBDm	3	Kedishvili NY, Popov KM, Jaskiewicz JA, Harris RA.	Coordinated expression of valine catabolic enzymes during adipogenesis: analysis of activity, mRNA, protein levels, and metabolic consequences.		1994	7527207	0
HIBDm	3	Sweetman, L, Williams, JC	Branched chain organic acidurias	The Metabolic and Molecular Bases of Inherited Disease, 8th ed (Scriver CR, et al, editors)	2001		0
HISD	3	Suchi M, Sano H, Mizuno H, Wada Y.	Molecular cloning and structural characterization of the human histidase gene (HAL).	Genomics	1995	8530107	Histidase (EC 4.3.1.3) is a cytosolic enzyme that catalyzes the nonoxidative deamination of histidine to urocanic acid. Histidinemia, resulting from reduced histidase activity as reported in Cambridge stock his/his mice and in humans, is the most frequent inborn metabolic error in Japan. 8530107
HISDC	3	LOVENBERG W, WEISSBACH H, UDENFRIEND S.	Aromatic L-amino acid decarboxylase.	J Biol Chem	1962	14466899	Textbook reaction.
HIStN1	3	Fei YJ, Sugawara M, Nakanishi T, Huang W, Wang H, Prasad PD, Leibach FH, Ganapathy V	Primary structure, genomic organization, and functional and electrogenic characteristics of human system N 1, a Na+- and H+-coupled glutamine transporter	J Biol Chem	2000	10823827	From first citation: "These data suggest that SN1 mediates the influx of two Na(+) and one amino acid substrate per transport cycle coupled to the efflux of one H(+), rendering the transport process electrogenic." At least somewhat resistant to lithium
HIStN1	3	Mackenzie B, Erickson JD	Sodium-coupled neutral amino acid (System N/A) transporters of the SLC38 gene family	Pflugers Arch	2004	12845534	From first citation: "These data suggest that SN1 mediates the influx of two Na(+) and one amino acid substrate per transport cycle coupled to the efflux of one H(+), rendering the transport process electrogenic." At least somewhat resistant to lithium
HKt	3	Maeda M, Oshiman K, Tamura S, Futai M.	Human gastric (H+ + K+)-ATPase gene. Similarity to (Na+ + K+)-ATPase genes in exon/intron organization but difference in control region.	J Biol Chem	1990	2160952	- Added by RS/TV There are primarily two types of H+/K+ ATPases: (1) Gastric - Gastric H+/K+ ATPase is located in a unique membrane system in parietal cells, is responsible for secretion of acid into the stomach lumen. (Stewart LA, van Driel IR, Toh BH, Gleeson PA. Glycobiology. 1999 Jun;9(6):601-6.) - Also located in cytoplasmic vesicles or apical plasma membranes of the secretory canaliculus (Maeda M, Oshiman K, Tamura S, Futai M. J Biol Chem. 1990 Jun 5;265(16):9027-32.) - Known to be expressed in the kidney as well (Callaghan JM, Tan SS, Khan MA, Curran KA, Campbell WG, Smolka AJ, Toh BH, Gleeson PA, Wingo CS, Cain BD, et al. Am J Physiol. 1995 Mar;268(3 Pt 2):F363-74.) - composed of an alpha and beta subunit [Entrez]

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HKt	3	Callaghan JM, Tan SS, Khan MA, Curran KA, Campbell WG, Smolka AJ, Toh BH, Gleeson PA, Wingo CS, Cain BD, et al.	Renal expression of the gene encoding the gastric H(+)-K(+)-ATPase beta-subunit.	Am J Physiol	1995	7900835	- Added by RS/TV There are primarily two types of H+/K+ ATPases: (1) Gastric - Gastric H+/K+ ATPase is located in a unique membrane system in parietal cells, is responsible for secretion of acid into the stomach lumen. (Stewart LA, van Driel IR, Toh BH, Gleeson PA. Glycobiology. 1999 Jun;9(6):601-6.) - Also located in cytoplasmic vesicles or apical plasma membranes of the secretory canaliculus (Maeda M, Oshiman K, Tamura S, Futai M. J Biol Chem. 1990 Jun 5;265(16):9027-32.) - Known to be expressed in the kidney as well (Callaghan JM, Tan SS, Khan MA, Curran KA, Campbell WG, Smolka AJ, Toh BH, Gleeson PA, Wingo CS, Cain BD, et al. Am J Physiol. 1995 Mar;268(3 Pt 2):F363-74.) - composed of an alpha and beta subunit [Entrez]
HKYNH	3	Toma S, Nakamura M, Tone S, Okuno E, Kido R, Breton J, Avanzi N, Cozzi L, Speciale C, Mostardini M, Gatti S, Benatti L	Cloning and recombinant expression of rat and human kynureninase	FEBS Lett	1997	9180257	Reaction and gene in intro of citation.
HMBS	2	Raich N, Romeo PH, Dubart A, Beaupain D, Cohen-Solal M, Goossens M.	Molecular cloning and complete primary sequence of human erythrocyte porphobilinogen deaminase.	Nucleic Acids Res	1986	2875434	- Added by RS/TV - Porphobilinogen deaminase (Hydroxymethylbilane synthase) (HMBS), catalyzes the head to tail condensation of four molecules of the monopyrrole porphobilinogen, to form the linear tetrapyrrole, hydroxymethylbilane. Catalytic activity also specified by Gene cards. (Raich N, Romeo PH, Dubart A, Beaupain D, Cohen-Solal M, Goossens M. Nucleic Acids Res. 1986 Aug 11;14(15):5955-68) - Although widely distributed in tissues, the enzymes of the heme biosynthesis pathways are particularly active in the liver.
HMGCOARr	3	Luskey KL, Stevens B.	Human 3-hydroxy-3-methylglutaryl coenzyme A reductase. Conserved domains responsible for catalytic activity and sterol-regulated degradation.	J Biol Chem	1985	2991281	ER version - see Olivier and Krisans 2000 ref see also PMID: 2991281 for localization and catalytic activity. NJ
HMGCOASim	3	Mascaro C, Buesa C, Ortiz JA, Haro D, Hegardt FG.	Molecular cloning and tissue expression of human mitochondrial 3-hydroxy-3-methylglutaryl-CoA synthase.	Arch Biochem Biophys	1995	7893153	mit - uniprot pathway for HMG-CoA synthesis for xol specificity: Liver and kidney NJ - Additional information by RS/TV 1) HMG-Coa catalyzes the condensation of acetyl-CoA and acetoacetyl-CoA, yielding Hmg-CoA and CoA. 2) Mitochondrial enzyme 3) Tissue Expression: Expressed highly in liver and colon; low in testis, kidney, heart, and skeletal muscles; very faint in pancreas. 1 through 3 according to Mascaro C, Buesa C, Ortiz JA, Haro D, Hegardt FG. Arch Biochem Biophys. 1995 Mar 10;317(2):385-90.
HMGCOAtm	2	Kovacs WJ, Krisans S.	Cholesterol biosynthesis and regulation: role of peroxisomes.	Adv Exp Med Biol	2003	14713247	Cholesterol biosynthetic pathway requires HMGCOA to be able to move between intracellular compartments (notably peroxisome <-> mitochondria). NJ
HMGCOAtm	2	Biardi L, Krisans K	Compartmentalization of cholesterol biosynthesis	Journal of Biological Chemistry	1996		Cholesterol biosynthetic pathway requires HMGCOA to be able to move between intracellular compartments (notably peroxisome <-> mitochondria). NJ
HPCLx	3	Foulon V, Antonenkov VD, Croes K, Waelkens E, Mannaerts GP, Van Veldhoven PP, Casteels M.	Purification, molecular cloning, and expression of 2-hydroxyphytanoyl-CoA lyase, a peroxisomal thiamine pyrophosphate-dependent enzyme that catalyzes the carbon-carbon bond cleavage during alpha-oxidation of 3-methyl-branched fatty acids.	Proc Natl Acad Sci U S A	1999	10468558	localization: peroxisome (uniprot) specificity: The compound pristanal is the fatty acid analog of pristanic acid. Pristanal is not in PubChem or KEGG, MW and charge inferred from reaction (lyase reaction producing formyl-CoA). Homotetramer catalyzing a carbon-carbon cleavage reaction; cleaves a 2-hydroxy-3-methylacyl-CoA into formyl-CoA and a 2-methyl-branched fatty aldehyde. Reaction specificty see PMID: 10468558 NJ
HPYRDC	2	Rofe AM, James HM, Bais R, Conyers RA	Hepatic oxalate production: the role of hydroxypyruvate	Biochem Med Metab Biol	1986	3778681	- reaction characterized in rat liver hepatocytes [Rofe, Biochem Med Metab Biol 1986] - activity found in mitochondrial and cytosolic fractions [Rofe, Biochem Med Metab Biol 1986]
HPYRR2x	2	Williams HE, Smith LH Jr.	L-glyceric aciduria. A new genetic variant of primary hyperoxaluria	N Eng J Med	1968	5635456	- catalyzed by lactate dehydrogenase [Cregeen, Human Mutat 2003], [Williams, N Eng J Med 1968]
HPYRR2x	2	Cregeen DP, Williams EL, Hulton S, Rumsby G	Molecular analysis of the glyoxylate reductase (GRHPR) gene and description of mutations underlying primary hyperoxaluria type 2	Hum Mutat	2003	14635115	- catalyzed by lactate dehydrogenase [Cregeen, Human Mutat 2003], [Williams, N Eng J Med 1968]

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HPYRtp	2	Johnson SA, Rumsby G, Cregeen D, Hulton SA	Primary hyperoxaluria type 2 in children.	Pediatr Nephrol	2002	12185464	- reaction shown on Mayo Clinic website at: http://mayoresearch.mayo.edu/mayo/research/nephrology/hyper oxaluria.cfm - also shown in Fig 1 of [Johnson 2002]
HS1ly	3	Scott HS, Blanch L, Guo XH, Freeman C, Orsborn A, Baker E, Sutherland GR, Morris CP, Hopwood JJ	Cloning of the sulphamidase gene and identification of mutations in Sanfilippo A syndrome	Nat Genet	1995	7493035	- O-sulfates have to be removed before sulfamidase desulfates amino group of GlcN [Winchester 1996] 6448: - lysosomal [UniProt] - cDNA was isolated and expressed [Scott, Nat Genet 1995] - recombinantly expressed in CHO cells, kinetic properties characterized [Bielicki, Biochem J 1998] - O-sulfates have to be removed before the desulfation of the amino group of glucosamine [Winchester 1996]
HS1ly	3	Bielicki J, Hopwood JJ, Melville EL, Anson DS	Recombinant human sulphamidase: expression, amplification, purification and characterization	Biochem J	1998	9405287	- O-sulfates have to be removed before sulfamidase desulfates amino group of GlcN [Winchester 1996] 6448: - lysosomal [UniProt] - cDNA was isolated and expressed [Scott, Nat Genet 1995] - recombinantly expressed in CHO cells, kinetic properties characterized [Bielicki, Biochem J 1998] - O-sulfates have to be removed before the desulfation of the amino group of glucosamine [Winchester 1996]
HSAT4ly	3	Ausseil J, Loredo-Osti JC, Verner A, Darmond-Zwaig C, Maire I, Poorthuis B, van Diggelen OP, Hudson TJ, Fujiwara TM, Morgan K, Pshezhetsky AV	Localisation of a gene for mucopolysaccharidosis IIIC to the pericentromeric region of chromosome 8	J Med Genet	2004	15591281	- the 2-amino group of GlcN has to be desulfated and reacetylated before hexosaminidic linkage is cleaved [Winchester 1996] - integral lysosomal membrane protein; transfers acetyl group from accoa in cytosol to desulfated 2-amino group of GlcN in the lumen of the lysosome [Winchester 1996] - gene has not been identified, although recent evidence suggests it resides in the pericentromeric region of chromosome 8 [Ausseil 2004] - Mucopolysaccharidosis type IIIC (MPS IIIC, or Sanfilippo syndrome C) is a hereditary disorder caused by deficiency of this enzyme [Ausseil 2004]
HSD11B2r	3	Albiston AL, Obeyesekere VR, Smith RE, Krozowski ZS.	Cloning and tissue distribution of the human 11 beta-hydroxysteroid dehydrogenase type 2 enzyme.	Mol Cell Endocrinol	1994	7859916	ER - uniprot Kidney specific - a/w HTN dz Found in placenta, kidney, pancreas, prostate, ovary, small intestine and colon. Defects in HSD11B2 are the cause of apparent mineralocorticoid excess (AME) [MIM:218030, 207765]. AME is a potentially fatal disease characterized by severe juvenile low-renin hypertension, sodium retention, hypokalemia and low levels of aldosterone. It often leads to nephrocalcinosis. Catalyzes the conversion of cortisol to the inactive metabolite cortisone. Modulates intracellular glucocorticoid levels, thus protecting the nonselective mineralocorticoid receptor from occupation by glucocorticoids. NJ
HSD11B2r	3	Yau JL, Seckl JR.	11beta-hydroxysteroid dehydrogenase type I in the brain; thickening the glucocorticoid soup.	Mol Psychiatry	2001	11673786	ER - uniprot Kidney specific - a/w HTN dz Found in placenta, kidney, pancreas, prostate, ovary, small intestine and colon. Defects in HSD11B2 are the cause of apparent mineralocorticoid excess (AME) [MIM:218030, 207765]. AME is a potentially fatal disease characterized by severe juvenile low-renin hypertension, sodium retention, hypokalemia and low levels of aldosterone. It often leads to nephrocalcinosis. Catalyzes the conversion of cortisol to the inactive metabolite cortisone. Modulates intracellular glucocorticoid levels, thus protecting the nonselective mineralocorticoid receptor from occupation by glucocorticoids. NJ

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HSD11B2r	3	Tomlinson JW, Walker EA, Bujalska IJ, Draper N, Lavery GG, Cooper MS, Hewison M, Stewart PM.	11beta-hydroxysteroid dehydrogenase type 1: a tissue specific regulator of glucocorticoid response.	Endocr Rev	2004	15466942	ER - uniprot Kidney specific - a/w HTN dz Found in placenta, kidney, pancreas, prostate, ovary, small intestine and colon. Defects in HSD11B2 are the cause of apparent mineralocorticoid excess (AME) [MIM:218030, 207765]. AME is a potentially fatal disease characterized by severe juvenile low-renin hypertension, sodium retention, hypokalemia and low levels of aldosterone. It often leads to nephrocalcinosis. Catalyzes the conversion of cortisol to the inactive metabolite cortisone. Modulates intracellular glucocorticoid levels, thus protecting the nonselective mineralocorticoid receptor from occupation by glucocorticoids. NJ
HSD17B1	3	Andersson S, Moghrabi N	Physiology and molecular genetics of 17beta-hydroxysteroid dehydrogenases	Steroids	1997		HSD 17beta dehyd: type I: cytosol type 2,3: microsomes type 4: peroxisomal type 7: inferred from Paynes paper: cytosolic or microsomal (set as microsomal for time being) - return for further searches HSD17B1 specificity: ovary, placenta, mammary glands HSD17B8: reverse direction: estradiol -> estrone. cytosol by default - no detailed localization info. NJ
HSD17B2r	3	Wu L, Einstein M, Geissler WM, Chan HK, Elliston KO, Andersson S.	Expression cloning and characterization of human 17 beta-hydroxysteroid dehydrogenase type 2, a microsomal enzyme possessing 20 alpha-hydroxysteroid dehydrogenase activity.	J Biol Chem	1993	8099587	localization: ER by analogy w/ HSD17B3 specificity: no details Cloning, sequence, biochem: PMID: 8099587 Capable of catalyzing the interconversion of testosterone and androstenedione, as well as estradiol and estrone. Also has 20-alpha-HSD activity. Uses NADH while EDH17B3 uses NADPH. NJ
HSD17B4x	3	Adamski J, Leenders F Carstensen JF, Kaumann M, Markus MM, Husen B, Tesdorpf JG, Seedor U, deLaunoit Y, Jakob F	Steroids, fatty acyl-CoA, and sterols are substrates of 80-kDa multifunctional protein	Steroids	1997		peroxisome: uniprot specificity: Liver and placenta also involved in lanosterol -> cholesterol synthesis pathway NJ
HSD17B4x	3	Leenders F, Dolez V, Begue A, Moller G, Gloeckner JC, deLaunoit Y, Adamski J	Structure of the gene for the human 17-beta-hydroxysteroid dehydrogenase type IV	Mammalian Genome	1998		peroxisome: uniprot specificity: Liver and placenta also involved in lanosterol -> cholesterol synthesis pathway NJ
HSD17B4x	3	Adamski J, Leenders F Carstensen JF, Kaumann M, Markus MM, Husen B, Tesdorpf JG, Seedor U, deLaunoit Y, Jakob F	Steroids, fatty acyl-CoA, and sterols are substrates of 80-kDa multifunctional protein	Steroids	1997		peroxisome: uniprot specificity: Liver and placenta also involved in lanosterol -> cholesterol synthesis pathway NJ
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HSD17B4x	3	Adamski J, Leenders F Carstensen JF, Kaumann M, Markus MM, Husen B, Tesdorpf JG, Seedor U, deLaunoit Y, Jakob F	Steroids, fatty acyl-CoA, and sterols are substrates of 80-kDa multifunctional protein	Steroids	1997		peroxisome: uniprot specificity: Liver and placenta also involved in lanosterol -> cholesterol synthesis pathway NJ
HSD17B4x	3	Marijanovic Z, Laubner D, Moller G, Gege C, Husenn B, Adamski J, Breitling R	Closing the gap: Identification of human 3-ketosteroid reductase, the last unknown enzyme of mammalian cholesterol biosynthesis	Molecular Endocrinology	2005		peroxisome: uniprot specificity: Liver and placenta also involved in lanosterol -> cholesterol synthesis pathway NJ

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HSD17B4x	3	Adamski J, Leenders F Carstensen JF, Kaumann M, Markus MM, Husen B, Tesdorpf JG, Seedor U, deLaunoit Y, Jakob F	Steroids, fatty acyl-CoA, and sterols are substrates of 80-kDa multifunctional protein	Steroids	1997		peroxisome: uniprot specificity: Liver and placenta also involved in lanosterol -> cholesterol synthesis pathway NJ
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HSD17B4x	3	Adamski J, Leenders F Carstensen JF, Kaumann M, Markus MM, Husen B, Tesdorpf JG, Seedor U, deLaunoit Y, Jakob F	Steroids, fatty acyl-CoA, and sterols are substrates of 80-kDa multifunctional protein	Steroids	1997		peroxisome: uniprot specificity: Liver and placenta also involved in lanosterol -> cholesterol synthesis pathway NJ
HSD17B4x	3	Marijanovic Z, Laubner D, Moller G, Gege C, Husenn B, Adamski J, Breitling R	Closing the gap: Identification of human 3-ketosteroid reductase, the last unknown enzyme of mammalian cholesterol biosynthesis	Molecular Endocrinology	2005		peroxisome: uniprot specificity: Liver and placenta also involved in lanosterol -> cholesterol synthesis pathway NJ
HSD3A1r	3	Khanna M, Qin KN, Wang RW, Cheng KC.	Substrate specificity, gene structure, and tissue-specific distribution of multiple human 3 alpha-hydroxysteroid dehydrogenases.	J Biol Chem	1995	7650035	This gene encodes a member of the aldo/keto reductase superfamily, which consists of more than 40 known enzymes and proteins. These enzymes catalyze the conversion of aldehydes and ketones to their corresponding alcohols by utilizing NADH and/or NADPH as cofactors. The enzymes display overlapping but distinct substrate specificity. This enzyme catalyzes the bioreduction of chlordecone, a toxic organochlorine pesticide, to chlordecone alcohol in liver. This gene shares high sequence identity with three other gene members and is clustered with those three genes at chromosome 10p15-p14. see PMID: 7650035 NJ
HSD3B2r	3	Luu-The V.	Analysis and characteristics of multiple types of human 17beta-hydroxysteroid dehydrogenase.	J Steroid Biochem Mol Biol	2001	11384872	ER - uniprot, refs specificity: adrenal glands, testes, ovaries 3beta-HSD is a bifunctional enzyme, that catalyzes the oxidative conversion of delta(5)-ene-3-beta-hydroxy steroid, and the oxidative conversion of ketosteroids. The 3beta-HSD enzymatic system plays a crucial role in the biosynthesis of all classes of hormonal steroids. also PMID: 14643063, 11384872 NJ
HSPASEly	2	Burbach BJ, Friedl A, Mundhenke C, Rapraeger AC	Syndecan-1 accumulates in lysosomes of poorly differentiated breast carcinoma cells	Martix Biol	2003	12782143	- core protein proteolysis and initial GAG chain fragmentation occurs in endosomes, followed by the complete degradation of GAGs in lysosomes [Burbach, Matrix Biol 2003] - single heparan sulfate chains are broken down by a specific endoglucuronidase to oligosaccharides of approcimately 5kDA as they pass thru the endosomal system to lysosomes; NOTE: this functionality is not included in the model as the example heparan sulfate chain is already short - several cell types, including chondrocytes and liver endothelial cells, can bind and endocytose proteoglycans and deliver them to lysosomes for catabolism [Winchester 1996]

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HXPRT	3	Kim SH, Moores JC, David D, Respess JG, Jolly DJ, Friedmann T.	The organization of the human HPRT gene.	Nucleic Acids Res	1986	3008106	IT GeneCards: can act on both hxan and gua. homotetramer purine salvage
HXPRT	3	Wilson JM, Kobayashi R, Fox IH, Kelley WN.	Human hypoxanthine-guanine phosphoribosyltransferase.	J Biol Chem	1983	6853490	IT GeneCards: can act on both hxan and gua. homotetramer purine salvage
HYPOE	3	Jang YM, Kim DW, Kang TC, Won MH, Baek NI, Moon BJ, Choi SY, Kwon OS.	Human pyridoxal phosphatase. Molecular cloning, functional expression, and tissue distribution.	J Biol Chem	2003	14522954	IT homodimer. needs Mg2+ real name: Pyridoxamine-5-phosphate phosphatase
HYXNt	3	Yao SY, Ng AM, Vickers MF, Sundaram M, Cass CE, Baldwin SA, Young JD.	Functional and molecular characterization of nucleobase transport by recombinant human and rat equilibrative nucleoside transporters 1 and 2.	J Biol Chem	2002	12006583	IT
HYXNt	3	Baldwin SA, Beal PR, Yao SY, King AE, Cass CE, Young JD.	The equilibrative nucleoside transporter family, SLC29.	Pflugers Arch	2004	12838422	IT
ICDHyp	3	Geisbrecht BV, Gould SJ	The human PICD gene encodes a cytoplasmic and peroxisomal NADP(+)-dependent isocitrate dehydrogenase	J Biol Chem	1999	10521434	3417: - NADP(+)-dependent isocitrate dehydrogenase found in the cytoplasm and peroxisomes [RefSeq] - identified by homology search; 59% identity to yeast Idp3p [Geisbrecht 1999] - expression in yeast restored partial function to Idp3p knockou [Geisbrecht 1999] - found in peroxisomes and cytoplasm of human and rat liver cells, ~ 27% assoc w/ peroxisome [Geisbrecht 1999] - known gap; the source of intraperoxisomal isocitrate has not been determined [Geisbrecht 1999]
ICDHyrm	3	Sazanov LA, Jackson JB.	Proton-translocating transhydrogenase and NAD- and NADP-linked isocitrate dehydrogenases operate in a substrate cycle which contributes to fine regulation of the tricarboxylic acid cycle activity in mitochondria.	FEBS Lett	1994	8187868	3418: - NADP(+)-dependent isocitrate dehydrogenase found in the mitochondria [RefSeq] - mitochondria [UniProt] - reaction may be reversible [Orten, Human Biochem 1975], [Comte, Am J Physiol Heart Circ Physiol. 2002], [Sazanov, FEBS Lett 1994]
ICDHyrm	3	Comte B, Vincent G, Bouchard B, Benderdour M, Des Rosiers C.	Reverse flux through cardiac NADP(+)-isocitrate dehydrogenase under normoxia and ischemia.	Am J Physiol Heart Circ Physiol	2002	12234803	3418: - NADP(+)-dependent isocitrate dehydrogenase found in the mitochondria [RefSeq] - mitochondria [UniProt] - reaction may be reversible [Orten, Human Biochem 1975], [Comte, Am J Physiol Heart Circ Physiol. 2002], [Sazanov, FEBS Lett 1994]
IDHPOXOX3	3	Nakamura M, Yamazaki I, Kotani T, Ohtaki S	Thyroid peroxidase selects the mechanism of either 1 or 2-electron oxidation of phenols, depending on their substituents	J Biol Chem	1985	2997169	The citations are slightly inspecific, but the reaction mechanism from KEGG seems to be basically consistent, expecially when all four reactions IDHPOXOX(-4) are taken together. - identified [Kimura 1987] and cloned [Magnussen 1987]
IDHPOXOX3	3	Magnusson RP, Chazenbalk GD, Gestautas J, Seto P, Filetti S, DeGroot LJ, Rapoport B.	Molecular cloning of the complementary deoxyribonucleic acid for human thyroid peroxidase.	Mol Endocrinol	1987	3153466	The citations are slightly inspecific, but the reaction mechanism from KEGG seems to be basically consistent, expecially when all four reactions IDHPOXOX(-4) are taken together. - identified [Kimura 1987] and cloned [Magnussen 1987]
IDHPOXOX3	3	Kimura S, Kotani T, McBride OW, Umeki K, Hirai K, Nakayama T, Ohtaki S	Human thyroid peroxidase: complete cDNA and protein sequence, chromosome mapping, and identification of two alternately spliced mRNAs	Proc Natl Acad Sci U S A	1987	3475693	The citations are slightly inspecific, but the reaction mechanism from KEGG seems to be basically consistent, expecially when all four reactions IDHPOXOX(-4) are taken together. - identified [Kimura 1987] and cloned [Magnussen 1987]
IDOAASE1ly	3	Scott HS, Anson DS, Orsborn AM, Nelson PV, Clements PR, Morris CP, Hopwood JJ	Human alpha-L-iduronidase: cDNA isolation and expression	Proc Natl Acad Sci U S A	1991	1946389	3425: - hydrolyzes the teminal alpha-L-iduronic acid residues from heparan sulfate and dermatan sulfate [RefSeq] - isolated from human liver [Clements 1989] - cloned and expressed in CHO cells [Scott 1991]
IDOAASE1ly	3	Clements PR, Brooks DA, McCourt PA, Hopwood JJ	Immunopurification and characterization of human alpha-L-iduronidase with the use of monoclonal antibodies	Biochem J	1989	2470345	3425: - hydrolyzes the teminal alpha-L-iduronic acid residues from heparan sulfate and dermatan sulfate [RefSeq] - isolated from human liver [Clements 1989] - cloned and expressed in CHO cells [Scott 1991]
IDOURtly	3	Havelaar AC, Mancini GM, Beerens CE, Souren RM, Verheijen FW.	Purification of the lysosomal sialic acid transporter. Functional characteristics of a monocarboxylate transporter	J Biol Chem	1998	9852127	H symport with sialic acid (precursors) into lysososome. See PMID: 2768261for biochem characterization and PMID: 10581036 for discussion of particular SNPs with sialic acid storage diseases. Sialic acid storage disorders (due to transporter mutations) require import and export e.g. PMID: 2768266 - hence made reversible. NJ - iduronate was also been shown to be a substrate of purified rat liver enzyme [Havelaar 1998]
ILETA	3	Naylor SL, Shows TB.	Branched-chain aminotransferase deficiency in Chinese hamster cells complemented by two independent genes on human chromosomes 12 and 19.		1980	6933702	reversible reaction, substrate specificities- Somatic Cell Genet. 1980 Sep;6(5):641-52. cytosol - Biochim Biophys Acta. 1997 Apr 25;1339(1):9-13.

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ILETA	3	Bledsoe RK, Dawson PA, Hutson SM.	Cloning of the rat and human mitochondrial branched chain aminotransferases (BCATm).		1997	9165094	reversible reaction, substrate specificities- Somatic Cell Genet. 1980 Sep;6(5):641-52. cytosol - Biochim Biophys Acta. 1997 Apr 25;1339(1):9-13.
IMPD	3	Natsumeda Y, Ohno S, Kawasaki H, Konno Y, Weber G, Suzuki K.	Two distinct cDNAs for human IMP dehydrogenase.	J Biol Chem	1990		IT
IMPD	3	Gu JJ, Kaiser-Rogers K, Rao K, Mitchell BS.	Assignment of the human type I IMP dehydrogenase gene (IMPDH1) to chromosome 7q31.3-q32).	Genomics	1994		IT
IMPD	3	Xiang B, Taylor JC, Markham GD.	Monovalent cation activation and kinetic mechanism of inosine 5'-monophosphate dehydrogenase.	J Biol Chem	1996		IT
INOSTO	3	Arner RJ, Prabhu KS, Reddy CC.	Molecular cloning, expression, and characterization of myo-inositol oxygenase from mouse, rat, and human kidney	Biochem Biophys Res Commun	2004	15504367	- cytoplasmic [UniProt] - myo-inositol oxygenase activity [UniProt] - kidney specific [UniProt] - cloning, expression, and characterization [Arner, Biochem Biophys Res Commun 2004]
INSt	3	Ward JL, Sherali A, Mo ZP, Tse CM.	Kinetic and pharmacological properties of cloned human equilibrative nucleoside transporters, ENT1 and ENT2, stably expressed in nucleoside transporter deficient PK15 cells.	J Biol Chem	2000	10722669	IT
INSTt2r	3	Uldry M, Ibberson M, Horisberger JD, Chatton JY, Riederer BM, Thorens B	Identification of a mammalian H(+)-myo-inositol symporter expressed predominantly in the brain	EMBO J	2001	11500374	114134: - cloned [Uldry, 2001] - transports only myo-inositol, no Glc [Uldry, 2004] - brain, white, brown, amd epididymal adipose, idney [Uldry, 2004]
INSTt4_2	3	Roll P, Massacrier A, Pereira S, Robaglia-Schlupp A, Cau P, Szepetowski P	New human sodium/glucose cotransporter gene (KST1): identification, characterization, and mutation analysis in ICCA (infantile convulsions and choreoathetosis) and BFIC (benign familial infantile convulsions) families	Gene	2002	12039040	- cloned [Roll 2002] and expressed [Coady 2002] - stoichiometry of 2 sodium for 1 MI molecule [Coady 2002] - heart, skeletal muscle, kidney, liver, placenta; weaker expression in brain, spleen, lung, WBC [Roll 2002] - also transports Glc, Xyl at moderate levels and a-methylGlc, Gal, Fuc, 3-O-methylGlc, 2-deoxyGlc at very low levels [Coady 2002]
INSTt4_2	3	Coady MJ, Wallendorff B, Gagnon DG, Lapointe JY	Identification of a novel Na+/myo-inositol cotransporter	J Biol Chem	2002	12133831	- cloned [Roll 2002] and expressed [Coady 2002] - stoichiometry of 2 sodium for 1 MI molecule [Coady 2002] - heart, skeletal muscle, kidney, liver, placenta; weaker expression in brain, spleen, lung, WBC [Roll 2002] - also transports Glc, Xyl at moderate levels and a-methylGlc, Gal, Fuc, 3-O-methylGlc, 2-deoxyGlc at very low levels [Coady 2002]
IPDDIx	3	Breitling R, Laubner D, Clizbe D, Adamski J, Krisans SK	Isopentenyl-diphosphate isomerases in human and mouse: evolutionary analysis of a mammalian gene duplication	J Mol Evol	2003		peroxisomal no tissue specificity IDI1 encodes a peroxisomally-localized enzyme that catalyzes the interconversion of isopentenyl diphosphate (IPP) to its highly electrophilic isomer, dimethylallyl diphosphate (DMAPP), which are the substrates for the successive reaction that results in the synthesis of farnesyl diphosphate and, ultimately, cholesterol. It has been shown in peroxisomal deficiency diseases such as Zellweger syndrome and neonatal adrenoleukodystrophy that there is reduction in IPP isomerase activity. See refs - IDI1 and IDI2 - evolutionarily distinct but appear to catalyze the same reaction! NJ
It	3	Rodriguez AM, Perron B, Lacroix L, Caillou B, Leblanc G, Schlumberger M, Bidart JM, Pourcher T	Identification and characterization of a putative human iodide transporter located at the apical membrane of thyrocytes	J Clin Endocrinol Metab	2002	1217270	160728: - cloned and expressed [Rodriguez 2002] - faciliated diffusion of I-, not cotransport [Rodriguez 2002] - apical pole of the thyroid cells facing the colloid lumen [Rodriguez 2002]
ITCOALm	1	WANG SF, ADLER J, LARDY HA	The pathway of itaconate metabolism by liver mitochondria	J Biol Chem	1961	13783048	- another function of EC 6.2.1.5 according to BRENDA - reaction known to occur w/ GTP as cofactor in rat liver mitochondria [Wang, J Biol Chem 1961] - Itaconate, citraconate, and mesaconate are probably metabolized in the dog, since they could be recovered in the urine to the extent of only 24, 28, and 64 per cent, respectively (see refs in [Adler 1957]) - In guinea pig liver, itaconate is oxidized as rapidly as most members of the tricarboxylic acid cycle, methyl succinate was oxidized 1/6 as fast and mesaconate 1/8 as fast as itaconate [Adler 1957]

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KCCt	3	Gillen CM, Brill S, Payne JA, Forbush B 3rd	Molecular cloning and functional expression of the K Cl cotransporter from rabbit, rat, and human. A new member of the cation-chloride cotransporter family	J Biol Chem	1996	8663127	- 1:1 stoichiometry of K+-Cl- transport [Hebert 2004] - RBC mediate K+-Cl- efflux, neurons mediate both efflux and influx [Hebert 2004] - KCC1, KCC3, KCC4 shown to transport NH4+ in place of K+ [Bergeron 2003] 6560: - cloned [Gillen 1996] - ubiquitous [Gillen 1996] - transport verified in HEK293 cells [Gillen 1996] 57468: - bi-directional transport [Entrez Gene], [Hebert 2004] - cloned [Song 2002] - brain [Song 2002]; also found in rat retina [Hebert 2004] - activity functionally verified in Xenopus laevis oocytes [Song 2002] 9990: - cloned [Hiki 1999], [Mount 1999], [Race 1999] - brain, heart, skeletal muscle, kidney [Hiki 1999]; most abundant in heart, kidney [Mount 1999]; high in kidney, heart, brain, lower in sk muscle, placenta, lung, liver, and pancreas [Race 1999] - 75-76% identical to human, pig, rat, and rabbit KCC1p, 7% identical to rat KCC2p [Race 1999] - activity functionally verified in HEK293 cells [Race 1999] 10723: - cloned [Mount 1999] - muscle, brain, lung, heart, kidney [Mount 1999] - basolateral membraine of type-A intercalated cells and proximal tubule (mouse) [Hebert 2004]
KCCt	3	Hiki K, D'Andrea RJ, Furze J, Crawford J, Woollatt E, Sutherland GR, Vadas MA, Gamble JR	Cloning, characterization, and chromosomal location of a novel human K+-Cl- cotransporter	J Biol Chem	1999	10187864	- 1:1 stoichiometry of K+-Cl- transport [Hebert 2004] - RBC mediate K+-Cl- efflux, neurons mediate both efflux and influx [Hebert 2004] - KCC1, KCC3, KCC4 shown to transport NH4+ in place of K+ [Bergeron 2003] 6560: - cloned [Gillen 1996] - ubiquitous [Gillen 1996] - transport verified in HEK293 cells [Gillen 1996] 57468: - bi-directional transport [Entrez Gene], [Hebert 2004] - cloned [Song 2002] - brain [Song 2002]; also found in rat retina [Hebert 2004] - activity functionally verified in Xenopus laevis oocytes [Song 2002] 9990: - cloned [Hiki 1999], [Mount 1999], [Race 1999] - brain, heart, skeletal muscle, kidney [Hiki 1999]; most abundant in heart, kidney [Mount 1999]; high in kidney, heart, brain, lower in sk muscle, placenta, lung, liver, and pancreas [Race 1999] - 75-76% identical to human, pig, rat, and rabbit KCC1p, 7% identical to rat KCC2p [Race 1999] - activity functionally verified in HEK293 cells [Race 1999] 10723: - cloned [Mount 1999] - muscle, brain, lung, heart, kidney [Mount 1999] - basolateral membraine of type-A intercalated cells and proximal tubule (mouse) [Hebert 2004]

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KCCt	3	Mount DB, Mercado A, Song L, Xu J, George AL Jr, Delpire E, Gamba G	Cloning and characterization of KCC3 and KCC4, new members of the cation-chloride cotransporter gene family	J Biol Chem	1999	10347194	- 1:1 stoichiometry of K+-Cl- transport [Hebert 2004] - RBC mediate K+-Cl- efflux, neurons mediate both efflux and influx [Hebert 2004] - KCC1, KCC3, KCC4 shown to transport NH4+ in place of K+ [Bergeron 2003] 6560: - cloned [Gillen 1996] - ubiquitous [Gillen 1996] - transport verified in HEK293 cells [Gillen 1996] 57468: - bi-directional transport [Entrez Gene], [Hebert 2004] - cloned [Song 2002] - brain [Song 2002]; also found in rat retina [Hebert 2004] - activity functionally verified in Xenopus laevis oocytes [Song 2002] 9990: - cloned [Hiki 1999], [Mount 1999], [Race 1999] - brain, heart, skeletal muscle, kidney [Hiki 1999]; most abundant in heart, kidney [Mount 1999]; high in kidney, heart, brain, lower in sk muscle, placenta, lung, liver, and pancreas [Race 1999] - 75-76% identical to human, pig, rat, and rabbit KCC1p, 7% identical to rat KCC2p [Race 1999] - activity functionally verified in HEK293 cells [Race 1999] 10723: - cloned [Mount 1999] - muscle, brain, lung, heart, kidney [Mount 1999] - basolateral membraine of type-A intercalated cells and proximal tubule (mouse) [Hebert 2004]
KCCt	3	Race JE, Makhlouf FN, Logue PJ, Wilson FH, Dunham PB, Holtzman EJ	Molecular cloning and functional characterization of KCC3, a new K-Cl cotransporter	Am J Physiol	1999	10600773	- 1:1 stoichiometry of K+-Cl- transport [Hebert 2004] - RBC mediate K+-Cl- efflux, neurons mediate both efflux and influx [Hebert 2004] - KCC1, KCC3, KCC4 shown to transport NH4+ in place of K+ [Bergeron 2003] 6560: - cloned [Gillen 1996] - ubiquitous [Gillen 1996] - transport verified in HEK293 cells [Gillen 1996] 57468: - bi-directional transport [Entrez Gene], [Hebert 2004] - cloned [Song 2002] - brain [Song 2002]; also found in rat retina [Hebert 2004] - activity functionally verified in Xenopus laevis oocytes [Song 2002] 9990: - cloned [Hiki 1999], [Mount 1999], [Race 1999] - brain, heart, skeletal muscle, kidney [Hiki 1999]; most abundant in heart, kidney [Mount 1999]; high in kidney, heart, brain, lower in sk muscle, placenta, lung, liver, and pancreas [Race 1999] - 75-76% identical to human, pig, rat, and rabbit KCC1p, 7% identical to rat KCC2p [Race 1999] - activity functionally verified in HEK293 cells [Race 1999] 10723: - cloned [Mount 1999] - muscle, brain, lung, heart, kidney [Mount 1999] - basolateral membraine of type-A intercalated cells and proximal tubule (mouse) [Hebert 2004]

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KCCt	3	Song L, Mercado A, Vazquez N, Xie Q, Desai R, George AL Jr, Gamba G, Mount DB	Molecular, functional, and genomic characterization of human KCC2, the neuronal K-Cl cotransporter	Brain Res Mol Brain Res	2002	121106695	- 1:1 stoichiometry of K+-Cl- transport [Hebert 2004] - RBC mediate K+-Cl- efflux, neurons mediate both efflux and influx [Hebert 2004] - KCC1, KCC3, KCC4 shown to transport NH4+ in place of K+ [Bergeron 2003] 6560: - cloned [Gillen 1996] - ubiquitous [Gillen 1996] - transport verified in HEK293 cells [Gillen 1996] 57468: - bi-directional transport [Entrez Gene], [Hebert 2004] - cloned [Song 2002] - brain [Song 2002]; also found in rat retina [Hebert 2004] - activity functionally verified in Xenopus laevis oocytes [Song 2002] 9990: - cloned [Hiki 1999], [Mount 1999], [Race 1999] - brain, heart, skeletal muscle, kidney [Hiki 1999]; most abundant in heart, kidney [Mount 1999]; high in kidney, heart, brain, lower in sk muscle, placenta, lung, liver, and pancreas [Race 1999] - 75-76% identical to human, pig, rat, and rabbit KCC1p, 7% identical to rat KCC2p [Race 1999] - activity functionally verified in HEK293 cells [Race 1999] 10723: - cloned [Mount 1999] - muscle, brain, lung, heart, kidney [Mount 1999] - basolateral membraine of type-A intercalated cells and proximal tubule (mouse) [Hebert 2004]
KHK2	3	Bais R, James HM, Rofe AM, Conyers RA.	The purification and properties of human liver ketohexokinase. A role for ketohexokinase and fructose-bisphosphate aldolase in the metabolic production of oxalate from xylitol	Biochem J	1985	2996495	- ketohexokinase and fructose-bisphosphate aldolase were purified from human liver [Bais 1985] - ketohexokinase and aldolase could catalyse a reaction sequence which forms glycolaldehyde from D-xylulose [Bais 1985], [Barngrover 1983], [James 1982] - this probably occurs mainly in the liver, to a lesser extent in the kidney, and very little in heart, brain and muscle based on the localization of the enzymes [Bais 1985] - ketohexokinase can phosphorylate D-xylulose as readily as D-fructose, except that higher concentrations of D-xylulose are required [Bais 1985]
KHK2	3	James HM, Bais R, Edwards JB, Rofe AM, Conyers AJ.	Models for the metabolic production of oxalate from xylitol in humans: a role for fructokinase and aldolase.	Aust J Exp Biol Med Sci	1982	6284103	- ketohexokinase and fructose-bisphosphate aldolase were purified from human liver [Bais 1985] - ketohexokinase and aldolase could catalyse a reaction sequence which forms glycolaldehyde from D-xylulose [Bais 1985], [Barngrover 1983], [James 1982] - this probably occurs mainly in the liver, to a lesser extent in the kidney, and very little in heart, brain and muscle based on the localization of the enzymes [Bais 1985] - ketohexokinase can phosphorylate D-xylulose as readily as D-fructose, except that higher concentrations of D-xylulose are required [Bais 1985]
KHK2	3	Barngrover DA, Dills WL Jr.	The involvement of liver fructokinase in the metabolism of D-xylulose and xylitol in isolated rat hepatocytes	J Nutr	1983	6298387	- ketohexokinase and fructose-bisphosphate aldolase were purified from human liver [Bais 1985] - ketohexokinase and aldolase could catalyse a reaction sequence which forms glycolaldehyde from D-xylulose [Bais 1985], [Barngrover 1983], [James 1982] - this probably occurs mainly in the liver, to a lesser extent in the kidney, and very little in heart, brain and muscle based on the localization of the enzymes [Bais 1985] - ketohexokinase can phosphorylate D-xylulose as readily as D-fructose, except that higher concentrations of D-xylulose are required [Bais 1985]
KYN3OX	3	Alberati-Giani D, Cesura AM, Broger C, Warren WD, Rover S, Malherbe P	Cloning and functional expression of human kynurenine 3-monooxygenase	FEBS Lett	1997	9237672	Gene found and enzyme characterized (at least for liver)
KYNAKGAT	3	Cooper AJ	The role of glutamine transaminase K (GTK) in sulfur and alpha-keto acid metabolism in the brain, and in the possible bioactivation of neurotoxicants	Neurochem Int	2004	15016471	First step of reaction described in citation. Also citation describes alternate splicing as the reason for mostly mitochondrial localization in brain and mostly cytosolic in kidney.
KYNATESYN	3	Hartai Z, Klivenyi P, Janaky T, Penke B, Dux L, Vecsei L	Kynurenine metabolism in multiple sclerosis	Acta Neurol Scand	2005	16008534	Second step of a reaction described in the first citation. Second citation (PMID 16008534): "To date, KYNA is the only known endogenous competitive antagonist of all three ionotrophic excitatory amino acid receptors."

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LALDO2	3	Bohren KM, Bullock B, Wermuth B, Gabbay KH	The aldo-keto reductase superfamily. cDNAs and deduced amino acid sequences of human aldehyde and aldose reductases	J Biol Chem	1989	2498333	- D-lactaldehyde is a minor product (5%) of methylglyoxal reduction by NADPH (alsoe reductase) [Vander Jagt 1992] 231: - cytosolic, NADPH [Bohren et al. J Biol Chem 264 (16): 9547, 1989] 10327: - NADP is cofactor [UniProt] 8574: - gene has been cloned, 78% identical with the Rattus norvegicus aflatoxin B1 aldehyde reductase (Afar) [Praml 1998] -rat homolog appears to be Golgi-associated [Kelly 2002] based on N-terminal sequence and immunohistochemistry, however I believe these results more strongly support localization in the outer Golgi membrane (cytosolic in our model) - human AKR7A2 also has Golgi signal sequence and [GO, UniProt] list as Golgi by similarity; however, I've assumed protein is cytosolic due to lack of specific info on location of functional domain and the fact that the only (weak) evidence thus far has come from the rat homolog - NADH or NADPH [UniProt]; specificity is based on mouse homology AFAR2 [Kelly 2002]
LCADi	2	Christopher MM, Eckfeldt JH, Eaton JW.	Propylene glycol ingestion causes D-lactic acidosis	Lab Invest	1990	2296157	- NAD-dependent aldehyde dehydrogenase can convert L or D-lactaldehyde to L or D-lactate, respectively (see Fig 3 of [Ewaschuk 2005]; this pathway is based on original work done in cats [Christopher 1990] suggesting that methylglyoxal metabolism can result in D-lactic acidosis under extreme conditions - aldehyde dehydrogenase from goat liver has been shown to oxidize lactaldehyde to lactic acid; lactaldehyde was found to be primarily oxidized by this enzyme; almost 90% of the total lactaldehyde-oxidizing activity is located in the cytosol; enzyme is also found in mitochondria [Ray 1984]
LCADi	2	Ray S, Ray M.	Oxidation of lactaldehyde by cytosolic aldehyde dehydrogenase and inhibition of cytosolic and mitochondrial aldehyde dehydrogenase by metabolites.	Biochim Biophys Acta	1984	6487654	- NAD-dependent aldehyde dehydrogenase can convert L or D-lactaldehyde to L or D-lactate, respectively (see Fig 3 of [Ewaschuk 2005]; this pathway is based on original work done in cats [Christopher 1990] suggesting that methylglyoxal metabolism can result in D-lactic acidosis under extreme conditions - aldehyde dehydrogenase from goat liver has been shown to oxidize lactaldehyde to lactic acid; lactaldehyde was found to be primarily oxidized by this enzyme; almost 90% of the total lactaldehyde-oxidizing activity is located in the cytosol; enzyme is also found in mitochondria [Ray 1984]
LCADi	2	Ewaschuk JB, Naylor JM, Zello GA	D-lactate in human and ruminant metabolism	J Nutr	2005	15987839	- NAD-dependent aldehyde dehydrogenase can convert L or D-lactaldehyde to L or D-lactate, respectively (see Fig 3 of [Ewaschuk 2005]; this pathway is based on original work done in cats [Christopher 1990] suggesting that methylglyoxal metabolism can result in D-lactic acidosis under extreme conditions - aldehyde dehydrogenase from goat liver has been shown to oxidize lactaldehyde to lactic acid; lactaldehyde was found to be primarily oxidized by this enzyme; almost 90% of the total lactaldehyde-oxidizing activity is located in the cytosol; enzyme is also found in mitochondria [Ray 1984]
LCAT1e	3	Krimbou L, Marcil M, Davignon J, Genest J Jr.	Interaction of lecithin:cholesterol acyltransferase (LCAT).alpha 2-macroglobulin complex with low density lipoprotein receptor-related protein (LRP). Evidence for an alpha 2-macroglobulin/LRP receptor-mediated system participating in LCAT clearance.	J Biol Chem	2001	11435418	localization: extracellular - uniprot This gene encodes the extracellular cholesterol esterifying enzyme, lecithin-cholesterol acyltransferase. The esterification of cholesterol is required for cholesterol transport. Mutations in this gene have been found to cause fish-eye disease as well as LCAT deficiency. NJ
LCAT1e	3	Wang K, Subbaiah PV.	Role of the interfacial binding domain in the oxidative susceptibility of lecithin:cholesterol acyltransferase.	Biochem J	2002	11966470	localization: extracellular - uniprot This gene encodes the extracellular cholesterol esterifying enzyme, lecithin-cholesterol acyltransferase. The esterification of cholesterol is required for cholesterol transport. Mutations in this gene have been found to cause fish-eye disease as well as LCAT deficiency. NJ
LCTStg	2	Alberts B, Johnson A, Lewis J, Raff M, Roberts K, Walter P	Molecular Biology of the Cell, 4th ed.		2002		- reaction would only be found in lactating mammary cells - lactose produced in the Golgi is transported out of the cell via a vesicle [Alberts 2002]
LCTStl	2	Gordon PB, Seglen PO.	Prelysosomal convergence of autophagic and endocytic pathways	Biochem Biophys Res Commun	1988	3126737	- cytosolic lactose can be autophagocytosed and taken into the lysosome (demonstrated in rat hepatocytes) [Gordon 1988]
LDH_D	2	Devlin, TM	Textbook of Biochemistry with Clinical Correlations		2001		- lactate formation is the major fate for pyruvate in red blood cells, lens and cornea of the eye, kidney medulla, testes, and leukocytes [Champe, Biochemistry 2005]

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LDH_D	2	Champe, P.C., Harvey, R.A., Ferrier D.R.	Biochemistry, 3rd edition		2005		- lactate formation is the major fate for pyruvate in red blood cells, lens and cornea of the eye, kidney medulla, testes, and leukocytes [Champe, Biochemistry 2005]
LDH_D	2	Devlin, TM	Textbook of Biochemistry with Clinical Correlations		2001		- lactate formation is the major fate for pyruvate in red blood cells, lens and cornea of the eye, kidney medulla, testes, and leukocytes [Champe, Biochemistry 2005]
LDH_D	2	Champe, P.C., Harvey, R.A., Ferrier D.R.	Biochemistry, 3rd edition		2005		- lactate formation is the major fate for pyruvate in red blood cells, lens and cornea of the eye, kidney medulla, testes, and leukocytes [Champe, Biochemistry 2005]
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LDH_D	2	Champe, P.C., Harvey, R.A., Ferrier D.R.	Biochemistry, 3rd edition		2005		- lactate formation is the major fate for pyruvate in red blood cells, lens and cornea of the eye, kidney medulla, testes, and leukocytes [Champe, Biochemistry 2005]
LDH_D	2	Devlin, TM	Textbook of Biochemistry with Clinical Correlations		2001		- lactate formation is the major fate for pyruvate in red blood cells, lens and cornea of the eye, kidney medulla, testes, and leukocytes [Champe, Biochemistry 2005]
LDH_D	2	Champe, P.C., Harvey, R.A., Ferrier D.R.	Biochemistry, 3rd edition		2005		- lactate formation is the major fate for pyruvate in red blood cells, lens and cornea of the eye, kidney medulla, testes, and leukocytes [Champe, Biochemistry 2005]
LDH_D	2	Devlin, TM	Textbook of Biochemistry with Clinical Correlations		2001		- lactate formation is the major fate for pyruvate in red blood cells, lens and cornea of the eye, kidney medulla, testes, and leukocytes [Champe, Biochemistry 2005]
LDH_D	2	Champe, P.C., Harvey, R.A., Ferrier D.R.	Biochemistry, 3rd edition		2005		- lactate formation is the major fate for pyruvate in red blood cells, lens and cornea of the eye, kidney medulla, testes, and leukocytes [Champe, Biochemistry 2005]
LDH_D	2	Devlin, TM	Textbook of Biochemistry with Clinical Correlations		2001		- lactate formation is the major fate for pyruvate in red blood cells, lens and cornea of the eye, kidney medulla, testes, and leukocytes [Champe, Biochemistry 2005]
LDH_D	2	Champe, P.C., Harvey, R.A., Ferrier D.R.	Biochemistry, 3rd edition		2005		- lactate formation is the major fate for pyruvate in red blood cells, lens and cornea of the eye, kidney medulla, testes, and leukocytes [Champe, Biochemistry 2005]
LDH_D	2	Devlin, TM	Textbook of Biochemistry with Clinical Correlations		2001		- lactate formation is the major fate for pyruvate in red blood cells, lens and cornea of the eye, kidney medulla, testes, and leukocytes [Champe, Biochemistry 2005]
LDH_D	2	Champe, P.C., Harvey, R.A., Ferrier D.R.	Biochemistry, 3rd edition		2005		- lactate formation is the major fate for pyruvate in red blood cells, lens and cornea of the eye, kidney medulla, testes, and leukocytes [Champe, Biochemistry 2005]
LDH_D	2	Devlin, TM	Textbook of Biochemistry with Clinical Correlations		2001		- lactate formation is the major fate for pyruvate in red blood cells, lens and cornea of the eye, kidney medulla, testes, and leukocytes [Champe, Biochemistry 2005]
LDH_L	0	Millan JL, Driscoll CE, LeVan KM, Goldberg E.	Epitopes of human testis-specific lactate dehydrogenase deduced from a cDNA sequence.	Proc Natl Acad Sci U S A	1985	2440048	tissue localization: Ldh1 (HHHH): mycoardium, RBC Ldh2 (HHHM): myocardiam, RBC Ldh3 (HHMM): brain, kidney Ldh4 (HMMM) Ldh5 (MMMM): liver, sk muscle [Devlin, Textbook of Biochem, 2003] [Yu et al, Biochem Pharmacol. 2001 Jul 1;62(1):81-9] 3939: - predominantly expressed in muscle [RefSeq] -cytosolic [RefSeq] 3945: cytosolic [UniProt] 3948: - testis-specific [RefSeq] -cytosolic [UniProt] 92483: - testis specific [UniProt] - Additional information added by RS/TV: Cytosolic according to GeneCards Lactate dehydrogenase (LDH) catalyzes the NAD+-dependent conversion of lactate to pyruvate during anaerobic glycolysis according to Li X. Biochem Biophys Res Commun. 2004 Jul 30;320(3):625-34. LDH has three major isozymes each of which has a specific tissue localization: (1) Ldha.1 predominates in skeletal muscle and the liver (2) Ldhb.1 is highly expressed in the heart (3) Ldhc.1, Ldhc.2 are expressed only in testes and spermatoza. Tissue localization according to

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LDH_L	0	Yu Y, Deck JA, Hunsaker LA, Deck LM, Royer RE, Goldberg E, Vander Jagt DL	Selective active site inhibitors of human lactate dehydrogenases A4, B4, and C4.	Biochem Pharmacol	2001	11377399	tissue localization: Ldh1 (HHHH): mycoardium, RBC Ldh2 (HHHM): myocardiam, RBC Ldh3 (HHMM): brain, kidney Ldh4 (HMMM) Ldh5 (MMMM): liver, sk muscle [Devlin, Textbook of Biochem, 2003] [Yu et al, Biochem Pharmacol. 2001 Jul 1;62(1):81-9] 3939: - predominantly expressed in muscle [RefSeq] -cytosolic [RefSeq] 3945: cytosolic [UniProt] 3948: - testis-specific [RefSeq] -cytosolic [UniProt] 92483: - testis specific [UniProt] - Additional information added by RS/TV: Cytosolic according to GeneCards Lactate dehydrogenase (LDH) catalyzes the NAD+-dependent conversion of lactate to pyruvate during anaerobic glycolysis according to Li X. Biochem Biophys Res Commun. 2004 Jul 30;320(3):625-34. LDH has three major isozymes each of which has a specific tissue localization: (1) Ldha.1 predominates in skeletal muscle and the liver (2) Ldhb.1 is highly expressed in the heart (3) Ldhc.1, Ldhc.2 are expressed only in testes and spermatoza. Tissue localization according to
LDH_L	0	Li X, Qin C, Burghardt R, Safe S.	Hormonal regulation of lactate dehydrogenase-A through activation of protein kinase C pathways in MCF-7 breast cancer cells.	Biochem Biophys Res Commun	2004	15240094	tissue localization: Ldh1 (HHHH): mycoardium, RBC Ldh2 (HHHM): myocardiam, RBC Ldh3 (HHMM): brain, kidney Ldh4 (HMMM) Ldh5 (MMMM): liver, sk muscle [Devlin, Textbook of Biochem, 2003] [Yu et al, Biochem Pharmacol. 2001 Jul 1;62(1):81-9] 3939: - predominantly expressed in muscle [RefSeq] -cytosolic [RefSeq] 3945: cytosolic [UniProt] 3948: - testis-specific [RefSeq] -cytosolic [UniProt] 92483: - testis specific [UniProt] - Additional information added by RS/TV: Cytosolic according to GeneCards Lactate dehydrogenase (LDH) catalyzes the NAD+-dependent conversion of lactate to pyruvate during anaerobic glycolysis according to Li X. Biochem Biophys Res Commun. 2004 Jul 30;320(3):625-34. LDH has three major isozymes each of which has a specific tissue localization: (1) Ldha.1 predominates in skeletal muscle and the liver (2) Ldhb.1 is highly expressed in the heart (3) Ldhc.1, Ldhc.2 are expressed only in testes and spermatoza. Tissue localization according to
LDH_Lm	3	Brooks GA, Dubouchaud H, Brown M, Sicurello JP, Butz CE.	Role of mitochondrial lactate dehydrogenase and lactate oxidation in the intracellular lactate shuttle.	Proc Natl Acad Sci U S A	1999	9927705	- L-lactate is quickly metabolized to pyruvate in the liver [Ewaschuk 2005] - Additional information added by RS/TV: According to the paper listed below Ldh-1 and Ldh-5 are located in the mitochondria as well. According to Entrez gene database Ldh-1 is an alternative name for Ldha.1. Ldh-5 is not listed in Entrez gene database nor does there exist a 'Ldhe' protein. Tissue Localization: Ldh-1 (Ldha.1-m) is located primarily in the heart. All this according to the following paper:Brooks, G; "Role of mitochondrial lactate dehydrogenase and lactate oxidation in the intracellular lactate shuttle"; PNAS 1999.

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LEUKTRC4t	3	Abe T, Kakyo M, Tokui T, Nakagomi R, Nishio T, Nakai D, Nomura H, Unno M, Suzuki M, Naitoh T, Matsuno S, Yawo H.	Identification of a novel gene family encoding human liver-specific organic anion transporter LST-1.	J Biol Chem	1999	10358072	Tissue Specificity: SLCO2A1 - ubiquitous SLCO1A2 - brain, kidney, lung, testis, liver SLCO1B1 - liver SLCO1B3 - liver SLCO2B1 - liver, placenta, spleen, lung, kidney, heart, ovary SLCO3A1 - ubiquitously SLCO4A1 - ubiquitously SLCO1C1 - brain, testis SLCO1B1-Mediates the Na(+)-independent transport of organic anions such as pravastatin, taurocholate, methotrexate, dehydroepiandrosterone sulfate, 17-beta-glucuronosyl estradiol, estrone sulfate, prostaglandin E2, thromboxane B2, leukotriene C3, leukotriene E4, thyroxine and triiodothyronine. May play an important role in the clearance of bile acids and organic anions from the liver. NJ
LEUt4	3	Bertran J, Magagnin S, Werner A, Markovich D, Biber J, Testar X, Zorzano A, Kuhn LC, Palacin M, Murer H	Stimulation of system y(+)-like amino acid transport by the heavy chain of human 4F2 surface antigen in Xenopus laevis oocytes	Proc Natl Acad Sci U S A	1992	1376926	SLC38A4 is found predominantly in liver and transports both cationic and neutral amino acids. The transport of cationic amino acids by SLC38A4 is Na(+) and pH independent, while the transport of neutral amino acids is Na(+) and pH dependent (Hatanaka et al., 2001).[supplied by OMIM] Slc38a1: PMID 10891391 ATA2 mRNA is present in all tissues tested including the liver, kidney, colon, and small intestine as has been reported recently from our laboratory The transport of [14C]MeAIB is inhibited most markedly by alanine, serine, methionine, asparagine and glutamine. Moderate inhibition is observed with glycine, proline, threonine, leucine, and phenylalanine 1:1 Na: aa, no H transport reported SLC7A1 (and presumably 2,3): its role in normal cell metabolism is transport of the cationic amino acids, arginine, lysine, and ornithine across the plasma membrane (PMID 1348489) SLC3A2: PMID 10391915: 4F2hc alone induced, as previously reported (16, 18, 24-27), y+L amino acid transport activity (i.e. sodium-independent L-arginine transport and sodium-dependent L-leucine transport).
LEUt4	3	Pineda M, Fernandez E, Torrents D, Estevez R, Lopez C, Camps M, Lloberas J, Zorzano A, Palacin M	Identification of a membrane protein, LAT-2, that Co-expresses with 4F2 heavy chain, an L-type amino acid transport activity with broad specificity for small and large zwitterionic amino acids	J Biol Chem	1999	10391915	SLC38A4 is found predominantly in liver and transports both cationic and neutral amino acids. The transport of cationic amino acids by SLC38A4 is Na(+) and pH independent, while the transport of neutral amino acids is Na(+) and pH dependent (Hatanaka et al., 2001).[supplied by OMIM] Slc38a1: PMID 10891391 ATA2 mRNA is present in all tissues tested including the liver, kidney, colon, and small intestine as has been reported recently from our laboratory The transport of [14C]MeAIB is inhibited most markedly by alanine, serine, methionine, asparagine and glutamine. Moderate inhibition is observed with glycine, proline, threonine, leucine, and phenylalanine 1:1 Na: aa, no H transport reported SLC7A1 (and presumably 2,3): its role in normal cell metabolism is transport of the cationic amino acids, arginine, lysine, and ornithine across the plasma membrane (PMID 1348489) SLC3A2: PMID 10391915: 4F2hc alone induced, as previously reported (16, 18, 24-27), y+L amino acid transport activity (i.e. sodium-independent L-arginine transport and sodium-dependent L-leucine transport).

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LEUtec	3	Babu E, Kanai Y, Chairoungdua A, Kim do K, Iribe Y, Tangtrongsup S, Jutabha P, Li Y, Ahmed N, Sakamoto S, Anzai N, Nagamori S, Endou H	Identification of a novel system L amino acid transporter structurally distinct from heterodimeric amino acid transporters	J Biol Chem	2003	12930836	From PMID 12930836: Consistent with the results from the inhibition experiments, 14C-labeled L-leucine, L-isoleucine, L-valine, L-phenylalanine, and L-methionine (100 µM) were transported at relatively high rate by LAT3 (Fig. 2b). Among D-amino acids, D-leucine, for which a 14C-labeled compound was available, was confirmed to be transported by LAT3 (Fig. 2b). As observed for L-leucine uptake, the Eadie-Hofstee plots for the uptake of L-isoleucine, L-valine, and L-phenylalanine were curvilinear (data not shown). Kinetic parameters of these amino acid substrates are listed in Table I. From PMID 15659399: We next performed kinetic analysis for the induced transport activity of L-phenylalanine (Fig. 3 and Table I) and L-leucine. Interestingly, and similar to LAT3 (15), the expression of LAT4 in oocytes leads to the presence of a transport activity with two kinetic components. The low affinity component has a Km of 4694 ± 510 µM for L-phenylalanine and 3733 ± 1019 µM for L-leucine, and the high affinity component has a Km of 178 ± 29 µM for L-phenylalanine and 103 ± 62 µM for L-leucin To further characterize the activity induced by LAT4, we meas Other compounds transported by these genes as well.
LEUtec	3	Hediger MA, Romero MF, Peng JB, Rolfs A, Takanaga H, Bruford EA	The ABCs of solute carriers: physiological, pathological and therapeutic implications of human membrane transport proteinsIntroduction	Pflugers Arch	2004	14624363	From PMID 12930836: Consistent with the results from the inhibition experiments, 14C-labeled L-leucine, L-isoleucine, L-valine, L-phenylalanine, and L-methionine (100 µM) were transported at relatively high rate by LAT3 (Fig. 2b). Among D-amino acids, D-leucine, for which a 14C-labeled compound was available, was confirmed to be transported by LAT3 (Fig. 2b). As observed for L-leucine uptake, the Eadie-Hofstee plots for the uptake of L-isoleucine, L-valine, and L-phenylalanine were curvilinear (data not shown). Kinetic parameters of these amino acid substrates are listed in Table I. From PMID 15659399: We next performed kinetic analysis for the induced transport activity of L-phenylalanine (Fig. 3 and Table I) and L-leucine. Interestingly, and similar to LAT3 (15), the expression of LAT4 in oocytes leads to the presence of a transport activity with two kinetic components. The low affinity component has a Km of 4694 ± 510 µM for L-phenylalanine and 3733 ± 1019 µM for L-leucine, and the high affinity component has a Km of 178 ± 29 µM for L-phenylalanine and 103 ± 62 µM for L-leucin To further characterize the activity induced by LAT4, we meas Other compounds transported by these genes as well.
LEUtec	3	Bodoy S, Martin L, Zorzano A, Palacin M, Estevez R, Bertran J	Identification of LAT4, a novel amino acid transporter with system L activity	J Biol Chem	2005	15659399	From PMID 12930836: Consistent with the results from the inhibition experiments, 14C-labeled L-leucine, L-isoleucine, L-valine, L-phenylalanine, and L-methionine (100 µM) were transported at relatively high rate by LAT3 (Fig. 2b). Among D-amino acids, D-leucine, for which a 14C-labeled compound was available, was confirmed to be transported by LAT3 (Fig. 2b). As observed for L-leucine uptake, the Eadie-Hofstee plots for the uptake of L-isoleucine, L-valine, and L-phenylalanine were curvilinear (data not shown). Kinetic parameters of these amino acid substrates are listed in Table I. From PMID 15659399: We next performed kinetic analysis for the induced transport activity of L-phenylalanine (Fig. 3 and Table I) and L-leucine. Interestingly, and similar to LAT3 (15), the expression of LAT4 in oocytes leads to the presence of a transport activity with two kinetic components. The low affinity component has a Km of 4694 ± 510 µM for L-phenylalanine and 3733 ± 1019 µM for L-leucine, and the high affinity component has a Km of 178 ± 29 µM for L-phenylalanine and 103 ± 62 µM for L-leucin To further characterize the activity induced by LAT4, we meas Other compounds transported by these genes as well.
LGTHL	3	Kim NS, Umezawa Y, Ohmura S, Kato S	Human glyoxalase I. cDNA cloning, expression, and sequence similarity to glyoxalase I from Pseudomonas putida	J Biol Chem	1993	7684374	- Catalyzes the conversion of hemimercaptal, formed from methylglyoxal and glutathione, to S-lactoylglutathione [UniProt] - cloned and expressed [Ranganathan 1993], [Kim 1993] - 51% nucleotide homology and 42% amino acid homology with bacterial glyoxalase-I [Ranganathan 1993]; 57% identity with Pseudomonas putida glyoxalase I [Kim 1993]
LGTHL	3	Ranganathan S, Walsh ES, Godwin AK, Tew KD	Cloning and characterization of human colon glyoxalase-I	J Biol Chem	1993	8449929	- Catalyzes the conversion of hemimercaptal, formed from methylglyoxal and glutathione, to S-lactoylglutathione [UniProt] - cloned and expressed [Ranganathan 1993], [Kim 1993] - 51% nucleotide homology and 42% amino acid homology with bacterial glyoxalase-I [Ranganathan 1993]; 57% identity with Pseudomonas putida glyoxalase I [Kim 1993]

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L-LACt2r	3	Garcia CK, Li X, Luna J, Francke U	cDNA cloning of the human monocarboxylate transporter 1 and chromosomal localization of the SLC16A1 locus to 1p13.2-p12	Genomics	1994	7835905	- lactate transported into blood by exercising sk muscle and cells that lack mitochondria, such as red blood cells [Champe, Biochemistry 2005] 6566: - isolated [Garcia 1994] - 86% identtity to hamster protein [Garcia 1994] - expressed [Ritzhaupt, Ellis, J Physiol 1998], [Ritzhaupt, Wood, J Physiol et al 1998] - transports butyrate [Ritzhaupt, Ellis, J Physiol 1998] and lactate [Ritzhaupt, Wood, J Physiol et al 1998] - ubiquitous but predominant in colon [Ritzhaupt, Biochem Soc Trans 1998], [Price 1998], heart, red muscle [Halestrap 1999], [Price 1998] - L-Lactate transport in erythrocytes, cardiac myocytes, and hepatocytes due to proton-linked monocarboxylate transporter (see [Poole 1993] for review) - also transports pyruvate, b-hydroxybutyrate, acetoacetate [Halestrap 2004] - in most tissues MCT1 exports lactate to prevernt fall in cytosolic pH; in sk muscle and heart, MCT1 imports lactate to supply gluconeogenesis and lipogenesis; MCT1 or MCT2 imports lactate in liver, kidney and brain [Halestrap 2004] 9194: - cloned [Lin 1998] - high affinity for pyruvate [Lin 1998] - restricted expression in normal tissues but high in cancer cell l
L-LACt2r	3	Poole RC, Halestrap AP	Transport of lactate and other monocarboxylates across mammalian plasma membranes	Am J Physiol	1993	8476015	- lactate transported into blood by exercising sk muscle and cells that lack mitochondria, such as red blood cells [Champe, Biochemistry 2005] 6566: - isolated [Garcia 1994] - 86% identtity to hamster protein [Garcia 1994] - expressed [Ritzhaupt, Ellis, J Physiol 1998], [Ritzhaupt, Wood, J Physiol et al 1998] - transports butyrate [Ritzhaupt, Ellis, J Physiol 1998] and lactate [Ritzhaupt, Wood, J Physiol et al 1998] - ubiquitous but predominant in colon [Ritzhaupt, Biochem Soc Trans 1998], [Price 1998], heart, red muscle [Halestrap 1999], [Price 1998] - L-Lactate transport in erythrocytes, cardiac myocytes, and hepatocytes due to proton-linked monocarboxylate transporter (see [Poole 1993] for review) - also transports pyruvate, b-hydroxybutyrate, acetoacetate [Halestrap 2004] - in most tissues MCT1 exports lactate to prevernt fall in cytosolic pH; in sk muscle and heart, MCT1 imports lactate to supply gluconeogenesis and lipogenesis; MCT1 or MCT2 imports lactate in liver, kidney and brain [Halestrap 2004] 9194: - cloned [Lin 1998] - high affinity for pyruvate [Lin 1998] - restricted expression in normal tissues but high in cancer cell l
L-LACt2r	3	Price NT, Jackson VN, Halestrap AP	Cloning and sequencing of four new mammalian monocarboxylate transporter (MCT) homologues confirms the existence of a transporter family with an ancient past	Biochem J	1998	9425115	- lactate transported into blood by exercising sk muscle and cells that lack mitochondria, such as red blood cells [Champe, Biochemistry 2005] 6566: - isolated [Garcia 1994] - 86% identtity to hamster protein [Garcia 1994] - expressed [Ritzhaupt, Ellis, J Physiol 1998], [Ritzhaupt, Wood, J Physiol et al 1998] - transports butyrate [Ritzhaupt, Ellis, J Physiol 1998] and lactate [Ritzhaupt, Wood, J Physiol et al 1998] - ubiquitous but predominant in colon [Ritzhaupt, Biochem Soc Trans 1998], [Price 1998], heart, red muscle [Halestrap 1999], [Price 1998] - L-Lactate transport in erythrocytes, cardiac myocytes, and hepatocytes due to proton-linked monocarboxylate transporter (see [Poole 1993] for review) - also transports pyruvate, b-hydroxybutyrate, acetoacetate [Halestrap 2004] - in most tissues MCT1 exports lactate to prevernt fall in cytosolic pH; in sk muscle and heart, MCT1 imports lactate to supply gluconeogenesis and lipogenesis; MCT1 or MCT2 imports lactate in liver, kidney and brain [Halestrap 2004] 9194: - cloned [Lin 1998] - high affinity for pyruvate [Lin 1998] - restricted expression in normal tissues but high in cancer cell l

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L-LACt2r	3	Ritzhaupt A, Ellis A, Hosie KB, Shirazi-Beechey SP	The characterization of butyrate transport across pig and human colonic luminal membrane	J Physiol	1998	9508842	- lactate transported into blood by exercising sk muscle and cells that lack mitochondria, such as red blood cells [Champe, Biochemistry 2005] 6566: - isolated [Garcia 1994] - 86% identtity to hamster protein [Garcia 1994] - expressed [Ritzhaupt, Ellis, J Physiol 1998], [Ritzhaupt, Wood, J Physiol et al 1998] - transports butyrate [Ritzhaupt, Ellis, J Physiol 1998] and lactate [Ritzhaupt, Wood, J Physiol et al 1998] - ubiquitous but predominant in colon [Ritzhaupt, Biochem Soc Trans 1998], [Price 1998], heart, red muscle [Halestrap 1999], [Price 1998] - L-Lactate transport in erythrocytes, cardiac myocytes, and hepatocytes due to proton-linked monocarboxylate transporter (see [Poole 1993] for review) - also transports pyruvate, b-hydroxybutyrate, acetoacetate [Halestrap 2004] - in most tissues MCT1 exports lactate to prevernt fall in cytosolic pH; in sk muscle and heart, MCT1 imports lactate to supply gluconeogenesis and lipogenesis; MCT1 or MCT2 imports lactate in liver, kidney and brain [Halestrap 2004] 9194: - cloned [Lin 1998] - high affinity for pyruvate [Lin 1998] - restricted expression in normal tissues but high in cancer cell l
L-LACt2r	3	Ritzhaupt A, Wood IS, Ellis A, Hosie KB, Shirazi-Beechey SP	Identification of a monocarboxylate transporter isoform type 1 (MCT1) on the luminal membrane of human and pig colon	Biochem Soc Trans	1998	9649795	- lactate transported into blood by exercising sk muscle and cells that lack mitochondria, such as red blood cells [Champe, Biochemistry 2005] 6566: - isolated [Garcia 1994] - 86% identtity to hamster protein [Garcia 1994] - expressed [Ritzhaupt, Ellis, J Physiol 1998], [Ritzhaupt, Wood, J Physiol et al 1998] - transports butyrate [Ritzhaupt, Ellis, J Physiol 1998] and lactate [Ritzhaupt, Wood, J Physiol et al 1998] - ubiquitous but predominant in colon [Ritzhaupt, Biochem Soc Trans 1998], [Price 1998], heart, red muscle [Halestrap 1999], [Price 1998] - L-Lactate transport in erythrocytes, cardiac myocytes, and hepatocytes due to proton-linked monocarboxylate transporter (see [Poole 1993] for review) - also transports pyruvate, b-hydroxybutyrate, acetoacetate [Halestrap 2004] - in most tissues MCT1 exports lactate to prevernt fall in cytosolic pH; in sk muscle and heart, MCT1 imports lactate to supply gluconeogenesis and lipogenesis; MCT1 or MCT2 imports lactate in liver, kidney and brain [Halestrap 2004] 9194: - cloned [Lin 1998] - high affinity for pyruvate [Lin 1998] - restricted expression in normal tissues but high in cancer cell l
L-LACt2r	3	Lin RY, Vera JC, Chaganti RS, Golde DW	Human monocarboxylate transporter 2 (MCT2) is a high affinity pyruvate transporter	J Biol Chem	1998	9786900	- lactate transported into blood by exercising sk muscle and cells that lack mitochondria, such as red blood cells [Champe, Biochemistry 2005] 6566: - isolated [Garcia 1994] - 86% identtity to hamster protein [Garcia 1994] - expressed [Ritzhaupt, Ellis, J Physiol 1998], [Ritzhaupt, Wood, J Physiol et al 1998] - transports butyrate [Ritzhaupt, Ellis, J Physiol 1998] and lactate [Ritzhaupt, Wood, J Physiol et al 1998] - ubiquitous but predominant in colon [Ritzhaupt, Biochem Soc Trans 1998], [Price 1998], heart, red muscle [Halestrap 1999], [Price 1998] - L-Lactate transport in erythrocytes, cardiac myocytes, and hepatocytes due to proton-linked monocarboxylate transporter (see [Poole 1993] for review) - also transports pyruvate, b-hydroxybutyrate, acetoacetate [Halestrap 2004] - in most tissues MCT1 exports lactate to prevernt fall in cytosolic pH; in sk muscle and heart, MCT1 imports lactate to supply gluconeogenesis and lipogenesis; MCT1 or MCT2 imports lactate in liver, kidney and brain [Halestrap 2004] 9194: - cloned [Lin 1998] - high affinity for pyruvate [Lin 1998] - restricted expression in normal tissues but high in cancer cell l

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L-LACt2r	3	Ritzhaupt A, Wood IS, Ellis A, Hosie KB, Shirazi-Beechey SP	Identification and characterization of a monocarboxylate transporter (MCT1) in pig and human colon: its potential to transport L-lactate as well as butyrate	J Physiol	1998	9824713	- lactate transported into blood by exercising sk muscle and cells that lack mitochondria, such as red blood cells [Champe, Biochemistry 2005] 6566: - isolated [Garcia 1994] - 86% identtity to hamster protein [Garcia 1994] - expressed [Ritzhaupt, Ellis, J Physiol 1998], [Ritzhaupt, Wood, J Physiol et al 1998] - transports butyrate [Ritzhaupt, Ellis, J Physiol 1998] and lactate [Ritzhaupt, Wood, J Physiol et al 1998] - ubiquitous but predominant in colon [Ritzhaupt, Biochem Soc Trans 1998], [Price 1998], heart, red muscle [Halestrap 1999], [Price 1998] - L-Lactate transport in erythrocytes, cardiac myocytes, and hepatocytes due to proton-linked monocarboxylate transporter (see [Poole 1993] for review) - also transports pyruvate, b-hydroxybutyrate, acetoacetate [Halestrap 2004] - in most tissues MCT1 exports lactate to prevernt fall in cytosolic pH; in sk muscle and heart, MCT1 imports lactate to supply gluconeogenesis and lipogenesis; MCT1 or MCT2 imports lactate in liver, kidney and brain [Halestrap 2004] 9194: - cloned [Lin 1998] - high affinity for pyruvate [Lin 1998] - restricted expression in normal tissues but high in cancer cell
L-LACt2r	3	Yoon H, Donoso LA, Philp NJ	Cloning of the human monocarboxylate transporter MCT3 gene: localization to chromosome 22q12.3-q13.2.	Genomics	1999	10493836	- lactate transported into blood by exercising sk muscle and cells that lack mitochondria, such as red blood cells [Champe, Biochemistry 2005] 6566: - isolated [Garcia 1994] - 86% identtity to hamster protein [Garcia 1994] - expressed [Ritzhaupt, Ellis, J Physiol 1998], [Ritzhaupt, Wood, J Physiol et al 1998] - transports butyrate [Ritzhaupt, Ellis, J Physiol 1998] and lactate [Ritzhaupt, Wood, J Physiol et al 1998] - ubiquitous but predominant in colon [Ritzhaupt, Biochem Soc Trans 1998], [Price 1998], heart, red muscle [Halestrap 1999], [Price 1998] - L-Lactate transport in erythrocytes, cardiac myocytes, and hepatocytes due to proton-linked monocarboxylate transporter (see [Poole 1993] for review) - also transports pyruvate, b-hydroxybutyrate, acetoacetate [Halestrap 2004] - in most tissues MCT1 exports lactate to prevernt fall in cytosolic pH; in sk muscle and heart, MCT1 imports lactate to supply gluconeogenesis and lipogenesis; MCT1 or MCT2 imports lactate in liver, kidney and brain [Halestrap 2004] 9194: - cloned [Lin 1998] - high affinity for pyruvate [Lin 1998] - restricted expression in normal tissues but high in cancer cell
L-LACt2r	3	Halestrap AP, Price NT	The proton-linked monocarboxylate transporter (MCT) family: structure, function and regulation	Biochem J	1999	10510291	- lactate transported into blood by exercising sk muscle and cells that lack mitochondria, such as red blood cells [Champe, Biochemistry 2005] 6566: - isolated [Garcia 1994] - 86% identtity to hamster protein [Garcia 1994] - expressed [Ritzhaupt, Ellis, J Physiol 1998], [Ritzhaupt, Wood, J Physiol et al 1998] - transports butyrate [Ritzhaupt, Ellis, J Physiol 1998] and lactate [Ritzhaupt, Wood, J Physiol et al 1998] - ubiquitous but predominant in colon [Ritzhaupt, Biochem Soc Trans 1998], [Price 1998], heart, red muscle [Halestrap 1999], [Price 1998] - L-Lactate transport in erythrocytes, cardiac myocytes, and hepatocytes due to proton-linked monocarboxylate transporter (see [Poole 1993] for review) - also transports pyruvate, b-hydroxybutyrate, acetoacetate [Halestrap 2004] - in most tissues MCT1 exports lactate to prevernt fall in cytosolic pH; in sk muscle and heart, MCT1 imports lactate to supply gluconeogenesis and lipogenesis; MCT1 or MCT2 imports lactate in liver, kidney and brain [Halestrap 2004] 9194: - cloned [Lin 1998] - high affinity for pyruvate [Lin 1998] - restricted expression in normal tissues but high in cancer cell

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L-LACt2r	3	Manning Fox JE, Meredith D, Halestrap AP	Characterisation of human monocarboxylate transporter 4 substantiates its role in lactic acid efflux from skeletal muscle	J Physiol	2000	11101640	- lactate transported into blood by exercising sk muscle and cells that lack mitochondria, such as red blood cells [Champe, Biochemistry 2005] 6566: - isolated [Garcia 1994] - 86% identtity to hamster protein [Garcia 1994] - expressed [Ritzhaupt, Ellis, J Physiol 1998], [Ritzhaupt, Wood, J Physiol et al 1998] - transports butyrate [Ritzhaupt, Ellis, J Physiol 1998] and lactate [Ritzhaupt, Wood, J Physiol et al 1998] - ubiquitous but predominant in colon [Ritzhaupt, Biochem Soc Trans 1998], [Price 1998], heart, red muscle [Halestrap 1999], [Price 1998] - L-Lactate transport in erythrocytes, cardiac myocytes, and hepatocytes due to proton-linked monocarboxylate transporter (see [Poole 1993] for review) - also transports pyruvate, b-hydroxybutyrate, acetoacetate [Halestrap 2004] - in most tissues MCT1 exports lactate to prevernt fall in cytosolic pH; in sk muscle and heart, MCT1 imports lactate to supply gluconeogenesis and lipogenesis; MCT1 or MCT2 imports lactate in liver, kidney and brain [Halestrap 2004] 9194: - cloned [Lin 1998] - high affinity for pyruvate [Lin 1998] - restricted expression in normal tissues but high in cancer cell l
L-LACt2r	3	Kim do K, Kanai Y, Matsuo H, Kim JY, Chairoungdua A, Kobayashi Y, Enomoto A, Cha SH, Goya T, Endou H	The human T-type amino acid transporter-1: characterization, gene organization, and chromosomal location	Genomics	2002	11827462	- lactate transported into blood by exercising sk muscle and cells that lack mitochondria, such as red blood cells [Champe, Biochemistry 2005] 6566: - isolated [Garcia 1994] - 86% identtity to hamster protein [Garcia 1994] - expressed [Ritzhaupt, Ellis, J Physiol 1998], [Ritzhaupt, Wood, J Physiol et al 1998] - transports butyrate [Ritzhaupt, Ellis, J Physiol 1998] and lactate [Ritzhaupt, Wood, J Physiol et al 1998] - ubiquitous but predominant in colon [Ritzhaupt, Biochem Soc Trans 1998], [Price 1998], heart, red muscle [Halestrap 1999], [Price 1998] - L-Lactate transport in erythrocytes, cardiac myocytes, and hepatocytes due to proton-linked monocarboxylate transporter (see [Poole 1993] for review) - also transports pyruvate, b-hydroxybutyrate, acetoacetate [Halestrap 2004] - in most tissues MCT1 exports lactate to prevernt fall in cytosolic pH; in sk muscle and heart, MCT1 imports lactate to supply gluconeogenesis and lipogenesis; MCT1 or MCT2 imports lactate in liver, kidney and brain [Halestrap 2004] 9194: - cloned [Lin 1998] - high affinity for pyruvate [Lin 1998] - restricted expression in normal tissues but high in cancer cell l
L-LACt2r	3	Halestrap AP, Meredith D	The SLC16 gene family-from monocarboxylate transporters (MCTs) to aromatic amino acid transporters and beyond	Pflugers Arch	2004	12739169	- lactate transported into blood by exercising sk muscle and cells that lack mitochondria, such as red blood cells [Champe, Biochemistry 2005] 6566: - isolated [Garcia 1994] - 86% identtity to hamster protein [Garcia 1994] - expressed [Ritzhaupt, Ellis, J Physiol 1998], [Ritzhaupt, Wood, J Physiol et al 1998] - transports butyrate [Ritzhaupt, Ellis, J Physiol 1998] and lactate [Ritzhaupt, Wood, J Physiol et al 1998] - ubiquitous but predominant in colon [Ritzhaupt, Biochem Soc Trans 1998], [Price 1998], heart, red muscle [Halestrap 1999], [Price 1998] - L-Lactate transport in erythrocytes, cardiac myocytes, and hepatocytes due to proton-linked monocarboxylate transporter (see [Poole 1993] for review) - also transports pyruvate, b-hydroxybutyrate, acetoacetate [Halestrap 2004] - in most tissues MCT1 exports lactate to prevernt fall in cytosolic pH; in sk muscle and heart, MCT1 imports lactate to supply gluconeogenesis and lipogenesis; MCT1 or MCT2 imports lactate in liver, kidney and brain [Halestrap 2004] 9194: - cloned [Lin 1998] - high affinity for pyruvate [Lin 1998] - restricted expression in normal tissues but high in cancer cell l
LNS14DM	3	Bylund J, Finnstrom N, Oliw EH.	Gene expression of a novel cytochrome P450 of the CYP4F subfamily in human seminal vesicles.	Biochem Biophys Res Commun	1999	10405341	Need to resolve ER vs cytosol - membrane bound ER in uniprot (however some membrane bound enzymes catalyze reactions from the outer side --> substrates and products are cytosolic. NJ
LNS14DMr	3	Lepesheva GI, Waterman MR	CYP51 - the omnipotent P450	Molecular and Cell Endocrinology	2004		ER - see refs specificity: Ubiquitously expressed with highest levels in testis, ovary, adrenal, prostrate, liver, kidney, and lung. Catalyzes C14-demethylation of lanosterol; it transforms lanosterol into 4,4'-dimethyl cholesta-8,14,24-triene-3-beta-ol. NJ
LPASE	3	Perisic O, Fong S, Lynch DE, Bycroft M, Williams RL.	Crystal structure of a calcium-phospholipid binding domain from cytosolic phospholipase A2.	J Biol Chem	1998	9430701	cytoplasm - uniprot NJ

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LPCOXp	3	Ijlst L, de Kromme I, Oostheim W, Wanders RJ.	Molecular cloning and expression of human L-pipecolate oxidase.		2000	10772957	0
LPS2	3	Emi M, Wilson DE, Iverius PH, Wu L, Hata A, Hegele R, Williams RR, Lalouel JM.	Missense mutation (Gly----Glu188) of human lipoprotein lipase imparting functional deficiency.	J Biol Chem	1990	1969408	cytosolic - uniprot See PMID: 1969408 for evidence of biochem, result of SNPs and associated dz. - actually degradation of tag, not synthesis NJ
LPS2e	2	Ben-Zeev O, Doolittle MH.	Maturation of hepatic lipase. Formation of functional enzyme in the endoplasmic reticulum is the rate-limiting step in its secretion.	J Biol Chem	2004	14630921	LIPC: location: secreted. specificity: liver (hepatic lipase). LIPC has the dual functions of triglyceride hydrolase and ligand/bridging factor for receptor-mediated lipoprotein uptake. Hepatic lipase has the capacity to catalyze hydrolysis of phospholipids, mono-, di-, and triglycerides, and acyl-CoA thioesters. It is an important enzyme in HDL metabolism. Hepatic lipase binds heparin. see PMID: 14630921 NJ
LPS3	3	Wall EM, Cao J, Chen N, Buller RM, Upton C.	A novel poxvirus gene and its human homolog are similar to an E. coli lysophospholipase.	Virus Res	1997	9495531	localization: cytosol (by default - no specificity) TISSUE SPECIFICITY: Detected in adipose tissue, lung, liver, kidney, brain and heart. Converts monoacylglycerides to free fatty acids and glycerol. Hydrolyzes 2-arachidonoylglycerol, a putative endocannabinoid By seq homology and needed functionality. See PMID: 9495531 NJ
LPS4e	3	Valentin E, Ghomashchi F, Gelb MH, Lazdunski M, Lambeau G.	Novel human secreted phospholipase A(2) with homology to the group III bee venom enzyme.	J Biol Chem	2000	10713052	location: secreted (uniprot) specificity: Expressed in kidney, heart, liver, and skeletal muscle. Also present in placenta and peripheral blood leukocytes. Not detected in brain, colon, thymus, spleen, small intestine and lung. PA2 catalyzes the calcium-dependent hydrolysis of the 2- acyl groups in 3-sn-phosphoglycerides. Shows an 11-fold preference for phosphatidylglycerol over phosphatidylcholine. NJ
LPSe	3	Giller T, Buchwald P, Blum-Kaelin D, Hunziker W.	Two novel human pancreatic lipase related proteins, hPLRP1 and hPLRP2. Differences in colipase dependence and in lipase activity.	J Biol Chem	1992	1379598	secreted - uniprot actually degradation of tag, not synthesis This gene is a member of the lipase gene family. It encodes a carboxyl esterase that hydrolyzes insoluble, emulsified triglycerides, and is essential for the efficient digestion of dietary fats. This gene is expressed specifically in the pancreas. LIPC: location: secreted. specificity: liver (hepatic lipase). LIPC has the dual functions of triglyceride hydrolase and ligand/bridging factor for receptor-mediated lipoprotein uptake. Hepatic lipase has the capacity to catalyze hydrolysis of phospholipids, mono-, di-, and triglycerides, and acyl-CoA thioesters. It is an important enzyme in HDL metabolism. Hepatic lipase binds heparin. see PMID: 14630921 PNLIPRP1 and PNLIPRP2: PMID: 1379598. Extracellular - secreted enzyme (uniport). TISSUE SPECIFICITY: Pancreas. LIPF: PMID: 3304425 and 2753032. SUBCELLULAR LOCATION: Secreted. Specificity: stomach (gastric lipase) LIPG: PMID: 10318835. Extracellular - secreted. TISSUE SPECIFICITY: High level of expression in the liver, placenta, lung, thyroid, kidney, testis and in the corpus luteum of the ova It is termed endothelial lipase due to the fact that it is synthesize NJ

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
LPSe	3	Davis RC, Diep A, Hunziker W, Klisak I, Mohandas T, Schotz MC, Sparkes RS, Lusis AJ.	Assignment of human pancreatic lipase gene (PNLIP) to chromosome 10q24-q26.	Genomics	1991	1783385	secreted - uniprot actually degradation of tag, not synthesis This gene is a member of the lipase gene family. It encodes a carboxyl esterase that hydrolyzes insoluble, emulsified triglycerides, and is essential for the efficient digestion of dietary fats. This gene is expressed specifically in the pancreas. LIPC: location: secreted. specificity: liver (hepatic lipase). LIPC has the dual functions of triglyceride hydrolase and ligand/bridging factor for receptor-mediated lipoprotein uptake. Hepatic lipase has the capacity to catalyze hydrolysis of phospholipids, mono-, di-, and triglycerides, and acyl-CoA thioesters. It is an important enzyme in HDL metabolism. Hepatic lipase binds heparin. see PMID: 14630921 PNLIPRP1 and PNLIPRP2: PMID: 1379598. Extracellular - secreted enzyme (uniport). TISSUE SPECIFICITY: Pancreas. LIPF: PMID: 3304425 and 2753032. SUBCELLULAR LOCATION: Secreted. Specificity: stomach (gastric lipase) LIPG: PMID: 10318835. Extracellular - secreted. TISSUE SPECIFICITY: High level of expression in the liver, placenta, lung, thyroid, kidney, testis and in the corpus luteum of the ova It is termed endothelial lipase due to the fact that it is synthesize NJ
LPSe	3	Bernback S, Blackberg L.	Human gastric lipase. The N-terminal tetrapeptide is essential for lipid binding and lipase activity.	Eur J Biochem	1989	2753032	secreted - uniprot actually degradation of tag, not synthesis This gene is a member of the lipase gene family. It encodes a carboxyl esterase that hydrolyzes insoluble, emulsified triglycerides, and is essential for the efficient digestion of dietary fats. This gene is expressed specifically in the pancreas. LIPC: location: secreted. specificity: liver (hepatic lipase). LIPC has the dual functions of triglyceride hydrolase and ligand/bridging factor for receptor-mediated lipoprotein uptake. Hepatic lipase has the capacity to catalyze hydrolysis of phospholipids, mono-, di-, and triglycerides, and acyl-CoA thioesters. It is an important enzyme in HDL metabolism. Hepatic lipase binds heparin. see PMID: 14630921 PNLIPRP1 and PNLIPRP2: PMID: 1379598. Extracellular - secreted enzyme (uniport). TISSUE SPECIFICITY: Pancreas. LIPF: PMID: 3304425 and 2753032. SUBCELLULAR LOCATION: Secreted. Specificity: stomach (gastric lipase) LIPG: PMID: 10318835. Extracellular - secreted. TISSUE SPECIFICITY: High level of expression in the liver, placenta, lung, thyroid, kidney, testis and in the corpus luteum of the ova It is termed endothelial lipase due to the fact that it is synthesize NJ
LPSe	3	Bodmer MW, Angal S, Yarranton GT, Harris TJ, Lyons A, King DJ, Pieroni G, Riviere C, Verger R, Lowe PA.	Molecular cloning of a human gastric lipase and expression of the enzyme in yeast.	Biochim Biophys Acta	1987	3304425	secreted - uniprot actually degradation of tag, not synthesis This gene is a member of the lipase gene family. It encodes a carboxyl esterase that hydrolyzes insoluble, emulsified triglycerides, and is essential for the efficient digestion of dietary fats. This gene is expressed specifically in the pancreas. LIPC: location: secreted. specificity: liver (hepatic lipase). LIPC has the dual functions of triglyceride hydrolase and ligand/bridging factor for receptor-mediated lipoprotein uptake. Hepatic lipase has the capacity to catalyze hydrolysis of phospholipids, mono-, di-, and triglycerides, and acyl-CoA thioesters. It is an important enzyme in HDL metabolism. Hepatic lipase binds heparin. see PMID: 14630921 PNLIPRP1 and PNLIPRP2: PMID: 1379598. Extracellular - secreted enzyme (uniport). TISSUE SPECIFICITY: Pancreas. LIPF: PMID: 3304425 and 2753032. SUBCELLULAR LOCATION: Secreted. Specificity: stomach (gastric lipase) LIPG: PMID: 10318835. Extracellular - secreted. TISSUE SPECIFICITY: High level of expression in the liver, placenta, lung, thyroid, kidney, testis and in the corpus luteum of the ova It is termed endothelial lipase due to the fact that it is synthesize NJ

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LPSe	3	Hirata K, Dichek HL, Cioffi JA, Choi SY, Leeper NJ, Quintana L, Kronmal GS, Cooper AD, Quertermous T.	Cloning of a unique lipase from endothelial cells extends the lipase gene family.	J Biol Chem	1999	10318835	secreted - uniprot actually degradation of tag, not synthesis This gene is a member of the lipase gene family. It encodes a carboxyl esterase that hydrolyzes insoluble, emulsified triglycerides, and is essential for the efficient digestion of dietary fats. This gene is expressed specifically in the pancreas. LIPC: location: secreted. specificity: liver (hepatic lipase). LIPC has the dual functions of triglyceride hydrolase and ligand/bridging factor for receptor-mediated lipoprotein uptake. Hepatic lipase has the capacity to catalyze hydrolysis of phospholipids, mono-, di-, and triglycerides, and acyl-CoA thioesters. It is an important enzyme in HDL metabolism. Hepatic lipase binds heparin. see PMID: 14630921 PNLIPRP1 and PNLIPRP2: PMID: 1379598. Extracellular - secreted enzyme (uniport). TISSUE SPECIFICITY: Pancreas. LIPF: PMID: 3304425 and 2753032. SUBCELLULAR LOCATION: Secreted. Specificity: stomach (gastric lipase) LIPG: PMID: 10318835. Extracellular - secreted. TISSUE SPECIFICITY: High level of expression in the liver, placenta, lung, thyroid, kidney, testis and in the corpus luteum of the ova It is termed endothelial lipase due to the fact that it is synthesize NJ
LRAT	3	Jahng WJ, Xue L, Rando RR.	Lecithin retinol acyltransferase is a founder member of a novel family of enzymes.	Biochemistry	2003	14596594	IT
LRAT	3	Zolfaghari R, Ross AC.	Cloning, gene organization and identification of an alternative splicing process in lecithin:retinol acyltransferase cDNA from human liver.	Gene	2004	15474300	IT
LSTO1r	3	Taton M, Husselstein T, Benveniste P, Rahier A	Role of highly conserved residues in the reaction catalyzed by recombinant delta-sterol-C5(6)-desaturase studied by site-directed mutagensis	Biochemistry	2000		ER - see refs no tissue specificity Catalyzes a dehydrogenation to introduce C5-6 double bond into lathosterol. NJ
LTC4CP	2	Reddanna P, Prabhu KS, Whelan J, Reddy CC.	Carboxypeptidase A-catalyzed direct conversion of leukotriene C4 to leukotriene F4.	Arch Biochem Biophys	2003	12729612	Converts LTC4 directly to LTF4 cytoplasmic by default (no other specific information). Conversion performed by carboxypeptidase A (GPR not found yet). PMID: 12729612 NJ
LTD4DP	3	Hammarstrom S, Orning L, Bernstrom K.	Metabolism of leukotrienes.	Mol Cell Biochem	1985	3001504	Unknown GPR, known to occur biochemically. cytosolic by default NJ
LTDCL	3	Kitahama K, Ikemoto K, Jouvet A, Nagatsu I, Sakamoto N, Pearson J	Aromatic L-amino acid decarboxylase- and tyrosine hydroxylase-immunohistochemistry in the adult human hypothalamus	J Chem Neuroanat	1998	9924972	Citation suggests that this reaction produces tryptamine in minute quantities. The biochemical characterization is specific to the brain.
LYSOXp	2	Yung-Feng Chang	Lysine metabolism in the human and the monkey: Demonstration of pipecolic acid formation in the brain and other organs		1982	6811962	PMID 10772957: In higher eukaryotes L-lysine can be degraded via two distinct routes including the saccharopine pathway and the L-pipecolate pathway. since pipecolate oxidase (LPCOXp) occurs in the peroxisome, the three reactions (LYSOXp, PPD2CSPp, 1PPDCRp) preceding it are assumed to be peroxisomal as well MM
LYSOXp	2	Murthy SN, Janardanasarma MK.	Identification of L-amino acid/L-lysine alpha-amino oxidase in mouse brain.		1999	10485319	PMID 10772957: In higher eukaryotes L-lysine can be degraded via two distinct routes including the saccharopine pathway and the L-pipecolate pathway. since pipecolate oxidase (LPCOXp) occurs in the peroxisome, the three reactions (LYSOXp, PPD2CSPp, 1PPDCRp) preceding it are assumed to be peroxisomal as well MM
M1316Mg	0	Misago M, Liao YF, Kudo S, Eto S, Mattei MG, Moremen KW, Fukuda MN.	Molecular cloning and expression of cDNAs encoding human alpha-mannosidase II and a previously unrecognized alpha-mannosidase IIx isozyme.	Proc Natl Acad Sci U S A	1995	8524845	Man2a1p and Man2a2p ubiquitously expressed [Misago et al, PNAS 1995]
M13N2Tg	0	Yen CL, Farese RV Jr.	MGAT2, a monoacylglycerol acyltransferase expressed in the small intestine	J Biol Chem	2003	12621063	There are believed to be over 100 different glycosyltransferases involved in the synthesis of protein-bound and lipid-bound oligosaccharides. UDP-N-acetylglucosamine:alpha-3-D-mannoside beta-1,2-N-acetylglucosaminyltransferase I is a medial-Golgi enzyme essential for the synthesis of hybrid and complex N-glycans. The protein, encoded by a single exon, shows typical features of a type II transmembrane protein. The protein is believed to be essential for normal embryogenesis. [RefSeq] Mgat1p expressed in liver, kidney [Yen and Farese Jr, J Biol Chem 2003]

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
M13N4Tg	0	Yoshida A, Minowa MT, Takamatsu S, Hara T, Oguri S, Ikenaga H, Takeuchi M.	Tissue specific expression and chromosomal mapping of a human UDP-N-acetylglucosamine: alpha1,3-d-mannoside beta1, 4-N-acetylglucosaminyltransferase.	Glycobiology	1999	10024668	Branching structures in complex N-glycans are synthesized on a commom core structure of Man3GlcNAc2Asn in the Golgi apparatus by the N-acetylglucosaminyltransferases. The mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferases, which include isoenzyme A (MGAT4A) and isoenzyme B (MGAT4B), are key N-acetylglucosaminyltransferases regulating formation of tri- and other multiantennary structures. MGAT4A and MGAT4B share 62% amino acid sequence identity. The huamn MGAT4A and bovine GnT-IV share 96% amino acid sequence identity. The expression levels of the MGAT4A mRNA are significantly different in various tissues and cell lines. Alternative splicing of MGAT4B results in two transcript variants encoding different isoforms. [RefSeq] Mgat4ap ubiquitously expressed [Yoshida et al, Glycobiology 1999] [Yoshida et al, Glycoconj J 1998] Mgat4b ubiquitously expressed [Yoshida et al, Glycoconj J 1998]
M13N4Tg	0	Yoshida A, Minowa MT, Takamatsu S, Hara T, Ikenaga H, Takeuchi M.	A novel second isoenzyme of the human UDP-N-acetylglucosamine:alpha1,3-D-mannoside beta1,4-N-acetylglucosaminyltransferase family: cDNA cloning, expression, and chromosomal assignment.	Glycoconj J	1998	10372966	Branching structures in complex N-glycans are synthesized on a commom core structure of Man3GlcNAc2Asn in the Golgi apparatus by the N-acetylglucosaminyltransferases. The mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferases, which include isoenzyme A (MGAT4A) and isoenzyme B (MGAT4B), are key N-acetylglucosaminyltransferases regulating formation of tri- and other multiantennary structures. MGAT4A and MGAT4B share 62% amino acid sequence identity. The huamn MGAT4A and bovine GnT-IV share 96% amino acid sequence identity. The expression levels of the MGAT4A mRNA are significantly different in various tissues and cell lines. Alternative splicing of MGAT4B results in two transcript variants encoding different isoforms. [RefSeq] Mgat4ap ubiquitously expressed [Yoshida et al, Glycobiology 1999] [Yoshida et al, Glycoconj J 1998] Mgat4b ubiquitously expressed [Yoshida et al, Glycoconj J 1998]
M4CET3er	3	Taron BW, Colussi PA, Wiedman JM, Orlean P, Taron CH	Human Smp3p adds a fourth mannose to yeast and human glycosylphosphatidylinositol precursors in vivo	J Biol Chem	2004	15208306	- M4A is more likely to be produced by the adding phosphoethanolamines to M4C rather than mannose addition to H8 [Taron, J Biol Chem 2004] 54872: - gene was cloned, function inferred from knockout [Shishioh, J Biol Chem 2005]
M8MASNterg	0	Spiro RG	Glucose residues as key determinants in the biosynthesis and quality control of glycoproteins with N-linked oligosaccharides.	J Biol Chem	2000	11007802	see Figure 2 in Spiro, J Biol Chem 275(46): 35657-35660 (2000).
MACACI	3	Fernandez-Canon JM, Hejna J, Reifsteck C, Olson S, Grompe M	Gene structure, chromosomal location, and expression pattern of maleylacetoacetate isomerase	Genomics	1999	10373324	This reaction appears to require glutathione as a cofactor, although it doesn't seem to appear in the reaction itself.
MACOXO	3	Zimatkin SM, Anichtchik OV	Alcohol-histamine interactions	Alcohol Alcohol	1999	10344773	Citation gives enzymes that catalyze reaction.
MALT	3	Martiniuk F, Hirschhorn R	Characterization of neutral isozymes of human alpha-glucosidase: differences in substrate specificity, molecular weight and electrophoretic mobility	Biochim Biophys Acta	1981	7018580	- alpha-glucosidase activity [UniProt], [Hirschorn, PNAS 2002] - maltose, maltotriose, and glycogen are substrates of Ganc (neutral alpha-glucosidase C); has similar catalytic properties as GAA [Martiniuk 1981]
MALT	3	Hirschhorn R, Huie ML, Kasper JS	Computer assisted cloning of human neutral alpha-glucosidase C (GANC): a new paralog in the glycosyl hydrolase gene family 31	Proc Natl Acad Sci U S A	2002	12370436	- alpha-glucosidase activity [UniProt], [Hirschorn, PNAS 2002] - maltose, maltotriose, and glycogen are substrates of Ganc (neutral alpha-glucosidase C); has similar catalytic properties as GAA [Martiniuk 1981]
MALTly	3	Hoefsloot LH, Hoogeveen-Westerveld M, Kroos MA, van Beeumen J, Reuser AJ, Oostra BA	Primary structure and processing of lysosomal alpha-glucosidase; homology with the intestinal sucrase-isomaltase complex	EMBO J	1988	3049072	- Essential for the degradation of glygogen to glucose in lysosomes [UniProt], [ReSeq] - lysosomal [RefSeq], [UniProt], [Hoefsloot, EMBO J, 1988] - alpha-glycosidase activity [Hoefsloot, EMBO J, 1988] Note: this rxn currently results in a modeling gap. This rxn is valid in vivo, malt usually arises from glycogen deg, but does not appear in our network for modeling reasons (only made representative structure for glycogen and malt doesn't happen to be one of its degradation products)

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MAN1_7Ber	0	Roth J, Zuber C, Guhl B, Fan JY, Ziak M.	The importance of trimming reactions on asparagine-linked oligosaccharides for protein quality control.	Histochem Cell Biol	2002	11935292	catalyzed by ER mannosidase I [Spiro, J Biol Chem (2000)] [Roth et al, Histochem Cell Biol 117: pp. 159-169 (2002)] Man1b1p ubiquitously expressed [Gonzalez et al, J Biol Chem 1999]
MAOX	2	Yu PH, Lai CT, Zuo DM	Formation of formaldehyde from adrenaline in vivo; a potential risk factor for stress-related angiopathy	Neurochem Res	1997	9131641	References state that when adrenaline is degraded, formaldehyde can be formed, and the amine oxidases are involved.
MAOX	2	Buffoni F, Ignesti G	The copper-containing amine oxidases: biochemical aspects and functional role	Mol Genet Metab	2000	11136547	References state that when adrenaline is degraded, formaldehyde can be formed, and the amine oxidases are involved.
MAOX	2	Conklin DJ, Cowley HR, Wiechmann RJ, Johnson GH, Trent MB, Boor PJ	Vasoactive effects of methylamine in isolated human blood vessels: role of semicarbazide-sensitive amine oxidase, formaldehyde, and hydrogen peroxide	Am J Physiol Heart Circ Physiol	2004	14715500	References state that when adrenaline is degraded, formaldehyde can be formed, and the amine oxidases are involved.
MCCCrm	3	Baumgartner MR, Almashanu S, Suormala T, Obie C, Cole RN, Packman S, Baumgartner ER, Valle D.	The molecular basis of human 3-methylcrotonyl-CoA carboxylase deficiency.		2001	11181649	see citation for all confidence evidence, reversibility, localization tissue - predominantly in kidney and liver MM
MCCCrm	3	Holzinger A, Roschinger W, Lagler F, Mayerhofer PU, Lichtner P, Kattenfeld T, Thuy LP, Nyhan WL, Koch HG, Muntau AC, Roscher AA.	Cloning of the human MCCA and MCCB genes and mutations therein reveal the molecular cause of 3-methylcrotonyl-CoA: carboxylase deficiency.		2001	11406611	see citation for all confidence evidence, reversibility, localization tissue - predominantly in kidney and liver MM
MCITS	2	Weidman SW, Drysdale GR.	he biosynthesis of methylcitrate.	Biochem J	1979	426765	- methylcitrate is known to be synthesized in humans [Weidman, Biochem J 1979] - methylcitrate was found to be a major product of proprionate metabolism in patients with proprionic acidemia and methylmalonic acidemia [Ando, PNAS 1972]
MCITS	2	Ando T, Rasmussen K, Nyhan WL, Hull D.	3-hydroxypropionate: significance of -oxidation of propionate in patients with propionic acidemia and methylmalonic acidemia	Proc Natl Acad Sci U S A	1972	4507604	- methylcitrate is known to be synthesized in humans [Weidman, Biochem J 1979] - methylcitrate was found to be a major product of proprionate metabolism in patients with proprionic acidemia and methylmalonic acidemia [Ando, PNAS 1972]
MCLACCYSR	2	Hannestad U, Martensson J, Sjodahl R, Sorbo B.	3-mercaptolactate cysteine disulfiduria: biochemical studies on affected and unaffected members of a family.		1981	6945862	-this is an inferred reaction based on below information: overproduction of mercaptolactate-cysteine disulfide is called 3 mercaptolactate cysteine disulfiduria, which is thought to occur when excess mercaptolactate, in the presence of cysteine, is converted to the mixed disulfide by oxidation (PMID:6945862) MM
MCLOR	3	Cooper AJ, Haber MT, Meister A.	On the chemistry and biochemistry of 3-mercaptopyruvic acid, the alpha-keto acid analog of cysteine		1982	7054184	lactate dehydrogenase biochemically shown to also use mercaptolactate/mercaptopyruvate as substrate - Cooper et. al. J Biol Chem. 1982 Jan 25;257(2):816-26.
MCOATAm	3	Zhang L, Joshi AK, Smith S.	Cloning, expression, characterization, and interaction of two components of a human mitochondrial fatty acid synthase. Malonyltransferase and acyl carrier protein.	J Biol Chem	2003	12882974	Mitochondrial by swiss prot See also: PMID: 12882974 The protein encoded by this gene is found exclusively in the mitochondrion, where it catalyzes the transfer of a malonyl group from malonyl-CoA to the mitochondrial acyl carrier protein. The encoded protein may be part of a fatty acid synthase complex that is more like the type II prokaryotic and plastid complexes rather than the type I human cytosolic complex. Two transcript variants encoding different isoforms have been found for this gene. Catalyzes the transfer of a malonyl moiety from malonyl- CoA to the free thiol group of the phosphopantetheine arm of the mitochondrial ACP protein (NDUFAB1). This suggests the existence of the biosynthesis of fatty acids in mitochondrias. NJ

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ME2	0	Loeber G, Infante AA, Maurer-Fogy I, Krystek E, Dworkin MB.	Human NAD(+)-dependent mitochondrial malic enzyme. cDNA cloning, primary structure, and expression in Escherichia coli.	J Biol Chem	1991	1993674	- cytosolic [RefSeq], [UniProt] - NADP is cofactor [RefSeq], [UniProt] - Additional information added by RS/TV: Malic enzyme catalyzes the oxidative decarboxylation of malate to pyruvate. Three different isoforms of malic enzyme have been found in mammalian tissues: (1) Me1.1: Cytosolic NADP+ dependent enzyme (2) Me3.1.-m: NADP+ dependent mitochondrial enzyme (3) Me2.1-m: NAD+/NADP+ dependent mitochondrial enzyme Each isoform has different tissue localizations: (1) Me1.1: Liver and adipose tissue (2) Me3.1-m: Brain, heart, skeletal muscle, and adrenals (3)Me2.1-m: Spleen, thymus, and the basal cells of the small intestinal mucosaAll of this according to Loeber G, Infante AA, Maurer-Fogy I, Krystek E, Dworkin MB. J Biol Chem. 1991 Feb 15;266(5):3016-21.
MELATN23DOX	2	Hirata F, Hayaishi O, Tokuyama T, Seno S	In vitro and in vivo formation of two new metabolites of melatonin	J Biol Chem	1974	4814344	Methods are old and not necessarily human experiments, so physiological evidence.
MELATNOX	3	Ma X, Idle JR, Krausz KW, Gonzalez FJ.	METABOLISM OF MELATONIN BY HUMAN CYTOCHROMES P450.	Drug Metab Dispos	2004	15616152	0
METAT	3	Horikawa,S., Tsukada,K.,	Molecular cloning and developmental expression of a human kidney S- adenosylmethionine synthetase.		1992	1426236	Entrez gene - catalyzes the formation of S-adenosylmethionine from methionine and ATP. Methionine adenosyltransferase deficiency is known to be caused by recessive as well as dominant mutations, the latter identified in autosomal dominant persistant hypermethioninemia. -in mammalian tissues, there are three distinct forms of adomet synthases designated as alpha, beta, and gamma. alpha and beta are expressed only in adult liver, while gamma is widely distributed in extrahepatic tissues. MM
METAT	3	Ubagai,T. , Lei,K.J. , Huang,S. , Mudd,S.H. , Levy,H.L. , Chou,J.Y.	Molecular mechanisms of an inborn error of methionine pathway. Methionine adenosyltransferase deficiency.		1995	7560086	Entrez gene - catalyzes the formation of S-adenosylmethionine from methionine and ATP. Methionine adenosyltransferase deficiency is known to be caused by recessive as well as dominant mutations, the latter identified in autosomal dominant persistant hypermethioninemia. -in mammalian tissues, there are three distinct forms of adomet synthases designated as alpha, beta, and gamma. alpha and beta are expressed only in adult liver, while gamma is widely distributed in extrahepatic tissues. MM
METAT	3	Alvarez,L., Corrales,F., Mato,J.M.,	Characterization of a full-length cDNA encoding human liver S- adenosylmethionine synthetase: tissue specific gene expression and mRNA levels in hepatopathies.		1993	8393662	Entrez gene - catalyzes the formation of S-adenosylmethionine from methionine and ATP. Methionine adenosyltransferase deficiency is known to be caused by recessive as well as dominant mutations, the latter identified in autosomal dominant persistant hypermethioninemia. -in mammalian tissues, there are three distinct forms of adomet synthases designated as alpha, beta, and gamma. alpha and beta are expressed only in adult liver, while gamma is widely distributed in extrahepatic tissues. MM
MGCHrm	3	Narisawa K, Gibson KM, Sweetman L, Nyhan WL, Duran M, Wadman SK.	Deficiency of 3-methylglutaconyl-coenzyme A hydratase in two siblings with 3-methylglutaconic aciduria.		1986	3082934	mitochondrial by similarity - UniProt AU-specific RNA-binding enoyl-CoA hydratase (AUH) protein binds to the AU-rich element (ARE), a common element found in the 3' UTR of rapidly decaying mRNA such as c-fos, c-myc and granulocyte/ macrophage colony stimulating factor. ARE elements are involved in directing RNA to rapid degradation and deadenylation. AUH is also homologous to enol-CoA hydratase, an enzyme involved in fatty acid degradation, and has been shown to have intrinsic hydratase enzymatic activity. AUH is thus a bifunctional chimera between RNA binding and metabolic enzyme activity. A possible subcellular localization in the mitochondria has been demonstrated for the mouse homolog of this protein which shares 92% identity with the human protein. It has been suggested that AUH may have a novel role as a mitochondrial located AU-binding protein. reversibility according to citations and Reactome

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MGCHrm	3	IJlst L, Loupatty FJ, Ruiter JP, Duran M, Lehnert W, Wanders RJ.	3-Methylglutaconic aciduria type I is caused by mutations in AUH.		2003	12434311	mitochondrial by similarity - UniProt AU-specific RNA-binding enoyl-CoA hydratase (AUH) protein binds to the AU-rich element (ARE), a common element found in the 3' UTR of rapidly decaying mRNA such as c-fos, c-myc and granulocyte/ macrophage colony stimulating factor. ARE elements are involved in directing RNA to rapid degradation and deadenylation. AUH is also homologous to enol-CoA hydratase, an enzyme involved in fatty acid degradation, and has been shown to have intrinsic hydratase enzymatic activity. AUH is thus a bifunctional chimera between RNA binding and metabolic enzyme activity. A possible subcellular localization in the mitochondria has been demonstrated for the mouse homolog of this protein which shares 92% identity with the human protein. It has been suggested that AUH may have a novel role as a mitochondrial located AU-binding protein. reversibility according to citations and Reactome
MGSA	3	Vander Jagt DL, Robinson B, Taylor KK, Hunsaker LA.	Reduction of trioses by NADPH-dependent aldo-keto reductases. Aldose reductase, methylglyoxal, and diabetic complications	J Biol Chem	1992	1537826	- methylglyoxylate can be produced from the nonenzymatic fragmentation of triose-phosphates [Vander Jagt 1992],[Thornalley 1996] - dhap and g3p are the primary triose-phosphates converted to methylglyoxylate [Beisswenger 2005] - this was the major pathway of methylglyoxalte formation in human red blood cells in vitro under normoglycaemic conditions [Thornalley 1996]
MGSA	3	Thornalley PJ	Pharmacology of methylglyoxal: formation, modification of proteins and nucleic acids, and enzymatic detoxification--a role in pathogenesis and antiproliferative chemotherapy.	Gen Pharmacol	1996	8853285	- methylglyoxylate can be produced from the nonenzymatic fragmentation of triose-phosphates [Vander Jagt 1992],[Thornalley 1996] - dhap and g3p are the primary triose-phosphates converted to methylglyoxylate [Beisswenger 2005] - this was the major pathway of methylglyoxalte formation in human red blood cells in vitro under normoglycaemic conditions [Thornalley 1996]
MGSA	3	Beisswenger BG, Delucia EM, Lapoint N, Sanford RJ, Beisswenger PJ.	Ketosis leads to increased methylglyoxal production on the atkins diet	Ann N Y Acad Sci	2005	16037240	- methylglyoxylate can be produced from the nonenzymatic fragmentation of triose-phosphates [Vander Jagt 1992],[Thornalley 1996] - dhap and g3p are the primary triose-phosphates converted to methylglyoxylate [Beisswenger 2005] - this was the major pathway of methylglyoxalte formation in human red blood cells in vitro under normoglycaemic conditions [Thornalley 1996]
MHISOR	3	Elmore BO, Bollinger JA, Dooley DM	Human kidney diamine oxidase: heterologous expression, purification, and characterization	J Biol Inorg Chem	2002	12072962	Fourth citation is specific for this reaction and gives some help regarding gene associations. MAO is not associated with this reaction because these other genes appeared more accurate.
MI1346PKn	3	Nalaskowski MM, Deschermeier C, Fanick W, Mayr GW	The human homologue of yeast ArgRIII protein is an inositol phosphate multikinase with predominantly nuclear localization	Biochem J	2002	12027805	- reaction described in [Irvine, Philos Trans R Soc Lond B Biol Sci 1988] - gene was cloned and has following activity [Nalaskowski, Biochem J 2002]: Ins(1,4,5)P3 -> Ins(1,4,5,6)P4 Ins(1,4,5)P3 -> Ins(1,3,4,5)P4 Ins(1,3,4,5)P4 -> Ins(1,3,4,5,6)P5 Ins(1,4,5,6(P4 -> Ins(1,3,4,5,6)P5 - protein is 83% identical to rat homolog and has following activity [Chang, J Biol Chem 2002]: Ins(1,3,4,6)P4 -> Ins(1,3,4,5,6)P5 - nucelar localization [Nalaskowski, Biochem J 2002]
MI1346PKn	3	Chang SC, Miller AL, Feng Y, Wente SR, Majerus PW.	The human homolog of the rat inositol phosphate multikinase is an inositol 1,3,4,6-tetrakisphosphate 5-kinase	J Biol Chem	2002	12223481	- reaction described in [Irvine, Philos Trans R Soc Lond B Biol Sci 1988] - gene was cloned and has following activity [Nalaskowski, Biochem J 2002]: Ins(1,4,5)P3 -> Ins(1,4,5,6)P4 Ins(1,4,5)P3 -> Ins(1,3,4,5)P4 Ins(1,3,4,5)P4 -> Ins(1,3,4,5,6)P5 Ins(1,4,5,6(P4 -> Ins(1,3,4,5,6)P5 - protein is 83% identical to rat homolog and has following activity [Chang, J Biol Chem 2002]: Ins(1,3,4,6)P4 -> Ins(1,3,4,5,6)P5 - nucelar localization [Nalaskowski, Biochem J 2002]
MI145PK	3	Takazawa K, Perret J, Dumont JE, Erneux C	Molecular cloning and expression of a new putative inositol 1,4,5-trisphosphate 3-kinase isoenzyme	Biochem J	1991	1654894	- reaction described in [Irvine, Philos Trans R Soc Lond B Biol Sci 1988] 3706, 3707: - inositol 1,4,5-trisphosphate 3-kinase activity [RefSeq] - gene was cloned and expressed [Takazawa, Biochem J 1991] 80271: - inositol 1,4,5-trisphosphate 3-kinase activity [RefSeq] - gene was cloned and expressed [Dewaste, Biochem J 2000]

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MI145PK	3	Dewaste V, Pouillon V, Moreau C, Shears S, Takazawa K, Erneux C	Cloning and expression of a cDNA encoding human inositol 1,4,5-trisphosphate 3-kinase C	Biochem J	2000	11085927	- reaction described in [Irvine, Philos Trans R Soc Lond B Biol Sci 1988] 3706, 3707: - inositol 1,4,5-trisphosphate 3-kinase activity [RefSeq] - gene was cloned and expressed [Takazawa, Biochem J 1991] 80271: - inositol 1,4,5-trisphosphate 3-kinase activity [RefSeq] - gene was cloned and expressed [Dewaste, Biochem J 2000]
MI145PP	3	Laxminarayan KM, Chan BK, Tetaz T, Bird PI, Mitchell CA	Characterization of a cDNA encoding the 43-kDa membrane-associated inositol-polyphosphate 5-phosphatase	J Biol Chem	1994	8006039	- reaction described in [Irvine, Philos Trans R Soc Lond B Biol Sci 1988] 3633: - Ins(1,3,4,5)P3 5-phosphatase activity [UniProt], [Jefferson, J Biol Chem 1995] - found in platelets [UniProt] 8867: - localizes to clathrin-coated invaginations of synaptic nerve terminals [Haffner, FEBS Lett 1997], [UniProt] - Isoform 1 is more enriched than isoform 2 in developing brain as well as non-neuronal cells. Isoform 2 is very abundant in nerve terminals [UniProt] - Inositol polyphosphate 5-phosphatase activity [UniProt], [Stopkova, Psychiatry Res 2004], [Haffner, FEBS Lett 1997] 56623: - Inositol polyphophate 5-phosphatase activity [UniProt], [Kisseleva, J Biol Chem 200] - Cytoplasmic; peripheral membrane protein associated with Golgi stacks [UniProt] - brain, heart, pancreas, testis and spleen [UniProt], [Kisseleva, J Biol Chem 2000 3632: - inositol 1,4,5-trisphosphate 5-phosphatase [RefSeq] - membrane-associated [RefSeq], [UniProt] - Brain; high level in Purkinje cells [UniProt], [De Smedt, FEBS Lett 1994], [Laxminarayan, J Biol Chem 1994] - gene was cloned and expressed; 91% homology to dog homol 3635: - gene was cloned and expressed [Drayer, Biochem Biophys R 3636:
MI145PP	3	De Smedt F, Verjans B, Mailleux P, Erneux C	Cloning and expression of human brain type I inositol 1,4,5-trisphosphate 5-phosphatase. High levels of mRNA in cerebellar Purkinje cells	FEBS Lett	1994	8013665	- reaction described in [Irvine, Philos Trans R Soc Lond B Biol Sci 1988] 3633: - Ins(1,3,4,5)P3 5-phosphatase activity [UniProt], [Jefferson, J Biol Chem 1995] - found in platelets [UniProt] 8867: - localizes to clathrin-coated invaginations of synaptic nerve terminals [Haffner, FEBS Lett 1997], [UniProt] - Isoform 1 is more enriched than isoform 2 in developing brain as well as non-neuronal cells. Isoform 2 is very abundant in nerve terminals [UniProt] - Inositol polyphosphate 5-phosphatase activity [UniProt], [Stopkova, Psychiatry Res 2004], [Haffner, FEBS Lett 1997] 56623: - Inositol polyphophate 5-phosphatase activity [UniProt], [Kisseleva, J Biol Chem 200] - Cytoplasmic; peripheral membrane protein associated with Golgi stacks [UniProt] - brain, heart, pancreas, testis and spleen [UniProt], [Kisseleva, J Biol Chem 2000 3632: - inositol 1,4,5-trisphosphate 5-phosphatase [RefSeq] - membrane-associated [RefSeq], [UniProt] - Brain; high level in Purkinje cells [UniProt], [De Smedt, FEBS Lett 1994], [Laxminarayan, J Biol Chem 1994] - gene was cloned and expressed; 91% homology to dog homol 3635: - gene was cloned and expressed [Drayer, Biochem Biophys R 3636:

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MI145PP	3	Hejna JA, Saito H, Merkens LS, Tittle TV, Jakobs PM, Whitney MA, Grompe M, Friedberg AS, Moses RE	Cloning and characterization of a human cDNA (INPPL1) sharing homology with inositol polyphosphate phosphatases	Genomics	1995	8530088	- reaction described in [Irvine, Philos Trans R Soc Lond B Biol Sci 1988] 3633: - Ins(1,3,4,5)P3 5-phosphatase activity [UniProt], [Jefferson, J Biol Chem 1995] - found in platelets [UniProt] 8867: - localizes to clathrin-coated invaginations of synaptic nerve terminals [Haffner, FEBS Lett 1997], [UniProt] - Isoform 1 is more enriched than isoform 2 in developing brain as well as non-neuronal cells. Isoform 2 is very abundant in nerve terminals [UniProt] - Inositol polyphosphate 5-phosphatase activity [UniProt], [Stopkova, Psychiatry Res 2004], [Haffner, FEBS Lett 1997] 56623: - Inositol polyphophate 5-phosphatase activity [UniProt], [Kisseleva, J Biol Chem 200] - Cytoplasmic; peripheral membrane protein associated with Golgi stacks [UniProt] - brain, heart, pancreas, testis and spleen [UniProt], [Kisseleva, J Biol Chem 2000 3632: - inositol 1,4,5-trisphosphate 5-phosphatase [RefSeq] - membrane-associated [RefSeq], [UniProt] - Brain; high level in Purkinje cells [UniProt], [De Smedt, FEBS Lett 1994], [Laxminarayan, J Biol Chem 1994] - gene was cloned and expressed; 91% homology to dog homol 3635: - gene was cloned and expressed [Drayer, Biochem Biophys R 3636:
MI145PP	3	Drayer AL, Pesesse X, De Smedt F, Woscholski R, Parker P, Erneux C	Cloning and expression of a human placenta inositol 1,3,4,5-tetrakisphosphate and phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase	Biochem Biophys Res Commun	1996	8769125	- reaction described in [Irvine, Philos Trans R Soc Lond B Biol Sci 1988] 3633: - Ins(1,3,4,5)P3 5-phosphatase activity [UniProt], [Jefferson, J Biol Chem 1995] - found in platelets [UniProt] 8867: - localizes to clathrin-coated invaginations of synaptic nerve terminals [Haffner, FEBS Lett 1997], [UniProt] - Isoform 1 is more enriched than isoform 2 in developing brain as well as non-neuronal cells. Isoform 2 is very abundant in nerve terminals [UniProt] - Inositol polyphosphate 5-phosphatase activity [UniProt], [Stopkova, Psychiatry Res 2004], [Haffner, FEBS Lett 1997] 56623: - Inositol polyphophate 5-phosphatase activity [UniProt], [Kisseleva, J Biol Chem 200] - Cytoplasmic; peripheral membrane protein associated with Golgi stacks [UniProt] - brain, heart, pancreas, testis and spleen [UniProt], [Kisseleva, J Biol Chem 2000 3632: - inositol 1,4,5-trisphosphate 5-phosphatase [RefSeq] - membrane-associated [RefSeq], [UniProt] - Brain; high level in Purkinje cells [UniProt], [De Smedt, FEBS Lett 1994], [Laxminarayan, J Biol Chem 1994] - gene was cloned and expressed; 91% homology to dog homol 3635: - gene was cloned and expressed [Drayer, Biochem Biophys R 3636:

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MI145PP	3	Haffner C, Takei K, Chen H, Ringstad N, Hudson A, Butler MH, Salcini AE, Di Fiore PP, De Camilli P	Synaptojanin 1: localization on coated endocytic intermediates in nerve terminals and interaction of its 170 kDa isoform with Eps15	FEBS Lett	1997	9428629	- reaction described in [Irvine, Philos Trans R Soc Lond B Biol Sci 1988] 3633: - Ins(1,3,4,5)P3 5-phosphatase activity [UniProt], [Jefferson, J Biol Chem 1995] - found in platelets [UniProt] 8867: - localizes to clathrin-coated invaginations of synaptic nerve terminals [Haffner, FEBS Lett 1997], [UniProt] - Isoform 1 is more enriched than isoform 2 in developing brain as well as non-neuronal cells. Isoform 2 is very abundant in nerve terminals [UniProt] - Inositol polyphosphate 5-phosphatase activity [UniProt], [Stopkova, Psychiatry Res 2004], [Haffner, FEBS Lett 1997] 56623: - Inositol polyphophate 5-phosphatase activity [UniProt], [Kisseleva, J Biol Chem 200] - Cytoplasmic; peripheral membrane protein associated with Golgi stacks [UniProt] - brain, heart, pancreas, testis and spleen [UniProt], [Kisseleva, J Biol Chem 2000 3632: - inositol 1,4,5-trisphosphate 5-phosphatase [RefSeq] - membrane-associated [RefSeq], [UniProt] - Brain; high level in Purkinje cells [UniProt], [De Smedt, FEBS Lett 1994], [Laxminarayan, J Biol Chem 1994] - gene was cloned and expressed; 91% homology to dog homol 3635: - gene was cloned and expressed [Drayer, Biochem Biophys R 3636:
MI145PP	3	Pesesse X, Moreau C, Drayer AL, Woscholski R, Parker P, Erneux C	The SH2 domain containing inositol 5-phosphatase SHIP2 displays phosphatidylinositol 3,4,5-trisphosphate and inositol 1,3,4,5-tetrakisphosphate 5-phosphatase activity	FEBS Lett	1998	9824312	- reaction described in [Irvine, Philos Trans R Soc Lond B Biol Sci 1988] 3633: - Ins(1,3,4,5)P3 5-phosphatase activity [UniProt], [Jefferson, J Biol Chem 1995] - found in platelets [UniProt] 8867: - localizes to clathrin-coated invaginations of synaptic nerve terminals [Haffner, FEBS Lett 1997], [UniProt] - Isoform 1 is more enriched than isoform 2 in developing brain as well as non-neuronal cells. Isoform 2 is very abundant in nerve terminals [UniProt] - Inositol polyphosphate 5-phosphatase activity [UniProt], [Stopkova, Psychiatry Res 2004], [Haffner, FEBS Lett 1997] 56623: - Inositol polyphophate 5-phosphatase activity [UniProt], [Kisseleva, J Biol Chem 200] - Cytoplasmic; peripheral membrane protein associated with Golgi stacks [UniProt] - brain, heart, pancreas, testis and spleen [UniProt], [Kisseleva, J Biol Chem 2000 3632: - inositol 1,4,5-trisphosphate 5-phosphatase [RefSeq] - membrane-associated [RefSeq], [UniProt] - Brain; high level in Purkinje cells [UniProt], [De Smedt, FEBS Lett 1994], [Laxminarayan, J Biol Chem 1994] - gene was cloned and expressed; 91% homology to dog homol 3635: - gene was cloned and expressed [Drayer, Biochem Biophys R 3636:

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MI145PP	3	Mochizuki Y, Takenawa T	Novel inositol polyphosphate 5-phosphatase localizes at membrane ruffles	J Biol Chem	1999	10593988	- reaction described in [Irvine, Philos Trans R Soc Lond B Biol Sci 1988] 3633: - Ins(1,3,4,5)P3 5-phosphatase activity [UniProt], [Jefferson, J Biol Chem 1995] - found in platelets [UniProt] 8867: - localizes to clathrin-coated invaginations of synaptic nerve terminals [Haffner, FEBS Lett 1997], [UniProt] - Isoform 1 is more enriched than isoform 2 in developing brain as well as non-neuronal cells. Isoform 2 is very abundant in nerve terminals [UniProt] - Inositol polyphosphate 5-phosphatase activity [UniProt], [Stopkova, Psychiatry Res 2004], [Haffner, FEBS Lett 1997] 56623: - Inositol polyphophate 5-phosphatase activity [UniProt], [Kisseleva, J Biol Chem 200] - Cytoplasmic; peripheral membrane protein associated with Golgi stacks [UniProt] - brain, heart, pancreas, testis and spleen [UniProt], [Kisseleva, J Biol Chem 2000 3632: - inositol 1,4,5-trisphosphate 5-phosphatase [RefSeq] - membrane-associated [RefSeq], [UniProt] - Brain; high level in Purkinje cells [UniProt], [De Smedt, FEBS Lett 1994], [Laxminarayan, J Biol Chem 1994] - gene was cloned and expressed; 91% homology to dog homol 3635: - gene was cloned and expressed [Drayer, Biochem Biophys R 3636:
MI145PP	3	Stopkova P, Vevera J, Paclt I, Zukov I, Lachman HM	Analysis of SYNJ1, a candidate gene for 21q22 linked bipolar disorder: a replication study	Psychiatry Res	2004	15261714	- reaction described in [Irvine, Philos Trans R Soc Lond B Biol Sci 1988] 3633: - Ins(1,3,4,5)P3 5-phosphatase activity [UniProt], [Jefferson, J Biol Chem 1995] - found in platelets [UniProt] 8867: - localizes to clathrin-coated invaginations of synaptic nerve terminals [Haffner, FEBS Lett 1997], [UniProt] - Isoform 1 is more enriched than isoform 2 in developing brain as well as non-neuronal cells. Isoform 2 is very abundant in nerve terminals [UniProt] - Inositol polyphosphate 5-phosphatase activity [UniProt], [Stopkova, Psychiatry Res 2004], [Haffner, FEBS Lett 1997] 56623: - Inositol polyphophate 5-phosphatase activity [UniProt], [Kisseleva, J Biol Chem 200] - Cytoplasmic; peripheral membrane protein associated with Golgi stacks [UniProt] - brain, heart, pancreas, testis and spleen [UniProt], [Kisseleva, J Biol Chem 2000 3632: - inositol 1,4,5-trisphosphate 5-phosphatase [RefSeq] - membrane-associated [RefSeq], [UniProt] - Brain; high level in Purkinje cells [UniProt], [De Smedt, FEBS Lett 1994], [Laxminarayan, J Biol Chem 1994] - gene was cloned and expressed; 91% homology to dog homol 3635: - gene was cloned and expressed [Drayer, Biochem Biophys R 3636:
MI14PP	3	York JD, Veile RA, Donis-Keller H, Majerus PW	Cloning, heterologous expression, and chromosomal localization of human inositol polyphosphate 1-phosphatase	Proc Natl Acad Sci U S A	1993	8390685	- reaction described in [Irvine, Philos Trans R Soc Lond B Biol Sci 1988] - inositol polyphosphate-1-phosphatase activity [RefSeq] - Ubiquitously expressed, with highest levels in pancreas and kidney. [UniProt], [York, PNAS 1993] - gene was cloned and expressed; 84% identical to bovine homolog [York, PNAS 1993]
MI1PP	3	McAllister G, Whiting P, Hammond EA, Knowles MR, Atack JR, Bailey FJ, Maigetter R, Ragan CI.	cDNA cloning of human and rat brain myo-inositol monophosphatase. Expression and characterization of the human recombinant enzyme	Biochem J	1992	1377913	- reaction described in [Irvine, Philos Trans R Soc Lond B Biol Sci 1988] 3612: - cytosolic [UniProt] - gene was cloned and expressed; protein has 97% homology to rat, bovine homologs [McAllister, Biochem J 1992] 3613: - gene has been cloned and has homology to IMPA1 [Yoshikawa, Mol Psychiatry 1997]
MI1PP	3	Irvine RF, Moor RM, Pollock WK, Smith PM, Wreggett KA	Inositol phosphates: proliferation, metabolism and function	Philos Trans R Soc Lond B Biol Sci	1988	2906139	- reaction described in [Irvine, Philos Trans R Soc Lond B Biol Sci 1988] 3612: - cytosolic [UniProt] - gene was cloned and expressed; protein has 97% homology to rat, bovine homologs [McAllister, Biochem J 1992] 3613: - gene has been cloned and has homology to IMPA1 [Yoshikawa, Mol Psychiatry 1997]

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MI1PP	3	Yoshikawa T, Turner G, Esterling LE, Sanders AR, Detera-Wadleigh SD	A novel human myo-inositol monophosphatase gene, IMP.18p, maps to a susceptibility region for bipolar disorder	Mol Psychiatry	1997	9322233	- reaction described in [Irvine, Philos Trans R Soc Lond B Biol Sci 1988] 3612: - cytosolic [UniProt] - gene was cloned and expressed; protein has 97% homology to rat, bovine homologs [McAllister, Biochem J 1992] 3613: - gene has been cloned and has homology to IMPA1 [Yoshikawa, Mol Psychiatry 1997]
MI1PS	3	Guan G, Dai P, Shechter I.	cDNA cloning and gene expression analysis of human myo-inositol 1-phosphate synthase	Arch Biochem Biophys	2003	12941308	- gene has been cloned and expressed [Guan, Arch Biochem Biophys 2003] - highly expressed in human testis, ovary, heart, placenta, and pancreas; low expression in blood leukocyte, thymus, skeletal muscle, and colon [Guan, Arch Biochem Biophys 2003]
MI34PP	3	Norris FA, Auethavekiat V, Majerus PW	The isolation and characterization of cDNA encoding human and rat brain inositol polyphosphate 4-phosphatase	J Biol Chem	1995	7608176	- reaction described in [Irvine, Philos Trans R Soc Lond B Biol Sci 1988] 3631: - inositol polyphosphate 4-phosphatase activity [RefSeq] - gene was cloned; 97% identical to rat homolog [Norris, J Biol Chem 1995] - rat protein was highly expressed in brain, heart, and skeletal muscle [Norris, J Biol Chem 1995] 8821: - inositol polyphosphate 4-phosphatase activity [RefSeq] - gene has been cloned and its sequence has 37% similarity to INPP4A and 90% similarity to rat homolog [Norris, J Biol Chem 1997]
MI34PP	3	Norris FA, Atkins RC, Majerus PW	The cDNA cloning and characterization of inositol polyphosphate 4-phosphatase type II. Evidence for conserved alternative splicing in the 4-phosphatase family	J Biol Chem	1997	9295334	- reaction described in [Irvine, Philos Trans R Soc Lond B Biol Sci 1988] 3631: - inositol polyphosphate 4-phosphatase activity [RefSeq] - gene was cloned; 97% identical to rat homolog [Norris, J Biol Chem 1995] - rat protein was highly expressed in brain, heart, and skeletal muscle [Norris, J Biol Chem 1995] 8821: - inositol polyphosphate 4-phosphatase activity [RefSeq] - gene has been cloned and its sequence has 37% similarity to INPP4A and 90% similarity to rat homolog [Norris, J Biol Chem 1997]
MICITDr	2	Beach RL, Aogaichi T, Plaut GW.	Identification of D-threo-alpha-methylisocitrate as stereochemically specific substrate for bovine heart aconitase and inhibitor of TPN-linked isocitrate dehydrogenase.	J Biol Chem	1977	856801	-evidence from mitochondrial bovine heart aconitase suggests that it converts alpha-methyl-cis-aconitate to alpha-methylisocitrate but not alpha-methylcitrate; see [Lauble 1995] for structural modeling and [Beach 1977] for biochemical studies
MICITDr	2	Lauble H, Stout CD	Steric and conformational features of the aconitase mechanism.	Proteins	1995	7675781	-evidence from mitochondrial bovine heart aconitase suggests that it converts alpha-methyl-cis-aconitate to alpha-methylisocitrate but not alpha-methylcitrate; see [Lauble 1995] for structural modeling and [Beach 1977] for biochemical studies
MM8Ag	0	Tremblay LO, Herscovics A.	Characterization of a cDNA encoding a novel human Golgi alpha 1, 2-mannosidase (IC) involved in N-glycan biosynthesis	J Biol Chem	2000	10915796	pathway taken from Trembey and Hersovics. J Biol Chem 275(41):31655-60 (2000). MAN1A1 encodes a class I mammalian Golgi 1,2-mannosidase which is a type II transmembrane protein. This protein catalyzes the removal of 3 distinct mannose residues from peptide-bound Man(9)-GlcNAc(2) oligosaccharides and belongs to family 47 of glycosyl hydrolases. [RefSeq] Man1a1p and Man1a2p ubiquitously expressed [Tremblay et al, Glycobiology 1998] Man1c1p expressed in all tissue tested except lung, muscle, pancreas [Tremblay and Herscovic, J Biol Chem 2000]
MM8Ber	0	Tremblay LO, Campbell Dyke N, Herscovics A.	Molecular cloning, chromosomal mapping and tissue-specific expression of a novel human alpha1,2-mannosidase gene involved in N-glycan maturation.	Glycobiology	1998	9592125	cloning and expression of 11253 cleaves Man9GlcNAc2 to Man8GlcNAc2 isomer B localized to ER [Tremblay and Herscovics, Glycobiology 9(10): 1073-78 (1999)] Man1b1p ubiquitously expressed [Gonzalez et al, J Biol Chem 1999]
MM8Ber	0	Gonzalez DS, Karaveg K, Vandersall-Nairn AS, Lal A, Moremen KW.	Identification, expression, and characterization of a cDNA encoding human endoplasmic reticulum mannosidase I, the enzyme that catalyzes the first mannose trimming step in mammalian Asn-linked oligosaccharide biosynthesis.	J Biol Chem	1999	10409699	cloning and expression of 11253 cleaves Man9GlcNAc2 to Man8GlcNAc2 isomer B localized to ER [Tremblay and Herscovics, Glycobiology 9(10): 1073-78 (1999)] Man1b1p ubiquitously expressed [Gonzalez et al, J Biol Chem 1999]

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MMCD	1	Kerner J, Hoppel CL.	Radiochemical malonyl-CoA decarboxylase assay: activity and subcellular distribution in heart and skeletal muscle.	Anal Biochem	2002	12123667	- methylmalonate reaction added based on GO annotation - Additional information added by RS/TV: - Malonyl-CoA decarboxylase is the main route for the disposal of malonyl-CoA - MCD is reported to be predominantly localized in the heart, as well as skeletal muscle. - MCD has been found in the cytoplasm, mitochondria, and peroxisome. All this according to Kerner J, Hoppel CL. Anal Biochem. 2002 Jul 15;306(2):283-9 Radiochemical malonyl-CoA decarboxylase assay: activity and subcellular distribution in heart and skeletal muscle. summary of localization data (see refs in Wightman 2003]): - enzymatic activity: mito, cyto - Western blot: perox, cyto - seq analysis: mito, perox
MMCD	1	Wightman PJ, Santer R, Ribes A, Dougherty F, McGill N, Thorburn DR, FitzPatrick DR	MLYCD mutation analysis: evidence for protein mistargeting as a cause of MLYCD deficiency	Hum Mutat	2003	12955715	- methylmalonate reaction added based on GO annotation - Additional information added by RS/TV: - Malonyl-CoA decarboxylase is the main route for the disposal of malonyl-CoA - MCD is reported to be predominantly localized in the heart, as well as skeletal muscle. - MCD has been found in the cytoplasm, mitochondria, and peroxisome. All this according to Kerner J, Hoppel CL. Anal Biochem. 2002 Jul 15;306(2):283-9 Radiochemical malonyl-CoA decarboxylase assay: activity and subcellular distribution in heart and skeletal muscle. summary of localization data (see refs in Wightman 2003]): - enzymatic activity: mito, cyto - Western blot: perox, cyto - seq analysis: mito, perox
MMEm	3	Bobik TA, Rasche ME.	Identification of the human methylmalonyl-CoA racemase gene based on the analysis of prokaryotic gene arrangements. Implications for decoding the human genome.	J Biol Chem	2001	11481338	- mitochondrial (probable) [UniProt] - identification of gene by homology search and biochemical characterization of protein [Bobik, J Biol Chem 2001] - reaction described in Devlin p. 637, Orten p. 262
MMMm	3	Ledley FD, Rosenblatt DS.	Mutations in mut methylmalonic acidemia: clinical and enzymatic correlations.		1997	8990001	- reaction described in Devlin p. 637, Orten p. 262 MM
MMSAD1m	3	Kedishvili NY, Popov KM, Rougraff PM, Zhao Y, Crabb DW, Harris RA.	CoA-dependent methylmalonate-semialdehyde dehydrogenase, a unique member of the aldehyde dehydrogenase superfamily. cDNA cloning, evolutionary relationships, and tissue distribution.		1992	1527093	- reaction described in Devlin p. 812 - mitochondrial [RefSeq] - catalyzes the irreversible oxidative decarboxylation of methylmalonate semialdehydes to propionyl-CoA [RefSeq]
MMSAD1m	3	Chambliss,K.L. , Gray,R.G. , Rylance,G. , Pollitt,R.J. , Gibson,K.M.	Molecular characterization of methylmalonate semialdehyde dehydrogenase deficiency.		2000	10947204	- reaction described in Devlin p. 812 - mitochondrial [RefSeq] - catalyzes the irreversible oxidative decarboxylation of methylmalonate semialdehydes to propionyl-CoA [RefSeq]
MMSAD3m	3	Scholem RD, Brown GK	Metabolism of malonic semialdehyde in man	Biochem J	1983	6418146	- another function of EC 1.2.1.18, which was assumed to be present based on physiological data - malonic semialdehyde is directly converted into acetyl-CoA in man [Scholem, Biochem J 1983] - mitochondrial [RefSeq] - catalyzes the irreversible oxidative decarboxylation of malonate semialdehydes to acetyl-CoA [RefSeq]
MTAP	3	Della Ragione F, Carteni-Farina M, Gragnaniello V, Schettino MI, Zappia V	Purification and characterization of 5'-deoxy-5'-methylthioadenosine phosphorylase from human placenta	J Biol Chem	1986	3091600	This reaction is well characterized and degrades 5mta, a byproduct of sprm and spmd synthesis. The enzyme is deactivated in many cancers. It is possible that this reaction is reversible, depending on conditions of course. However, it is unlikely due to rapid removal of ade (see second citation).
MTAP	3	Evans GB, Furneaux RH, Lenz DH, Painter GF, Schramm VL, Singh V, Tyler PC	Second generation transition state analogue inhibitors of human 5'-methylthioadenosine phosphorylase	J Med Chem	2005	16000004	This reaction is well characterized and degrades 5mta, a byproduct of sprm and spmd synthesis. The enzyme is deactivated in many cancers. It is possible that this reaction is reversible, depending on conditions of course. However, it is unlikely due to rapid removal of ade (see second citation).

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MTHFDm	3	Yang XM, MacKenzie RE	NAD-dependent methylenetetrahydrofolate dehydrogenase-methenyltetrahydrofolate cyclohydrolase is the mammalian homolog of the mitochondrial enzyme encoded by the yeast MIS1 gene	Biochemistry	1993	8218174	25902: - encodes the mitochondrial isozyme of C1-tetrahydrofolate (THF) synthase, a trifunctional enzyme containing formyl-THF synthetase, methenyl-THF cyclohydrolase, and methylene-THF dehydrogenase activities [Prasannan, J Biol Chem 2003] 10797: - NAD is preferred cofactor, but can also use NADP at a lower Vmax, higher Km [Yang, Biochemistry 1993]
MTRI	2	Myers RW, Abeles RH	Conversion of 5-S-ethyl-5-thio-D-ribose to ethionine in Klebsiella pneumoniae. Basis for the selective toxicity of 5-S-ethyl-5-thio-D-ribose	J Biol Chem	1989	2543672	This reaction follows the scheme in the reference, checked for bacteria and given physiological data since the end product, met-L, is known for humans. A candidate gene has been determined based on homology with yeast: MGC3207 (84245). This association has not been included in the resonstruction because it is far from certain.
N3Tg	0	Ju T, Brewer K, D'Souza A, Cummings RD, Canfield WM.	Cloning and expression of human core 1 beta1,3-galactosyltransferase.	J Biol Chem	2002	11677243	C1galt1p expressed in kidney, heart, placenta, liver, brain, sk muscle [Ju et al, J Biol Chem 2002]
NACASPAH	3	Kaul R, Gao GP, Balamurugan K, Matalon R	Cloning of the human aspartoacylase cDNA and a common missense mutation in Canavan disease	Nat Genet	1993	8252036	This reaction, perhaps more correctly characterized under aspartate metabolism, is related to Canavan disease. KEGG also suggests an alternate form of this reaction involving N-Formyl-L-aspartate, but there is no particular evidence for that reaction and it doesn't not close a gap on its own.
NACHEX27ly	3	Franke I, Resch A, Dassler T, Maier T, Bock A.	YfiK from Escherichia coli promotes export of O-acetylserine and cysteine.	J Bacteriol	2003	12562784	- beta-N-acetylhexosaminidase needed for hyaluronan degradation [Varki, pg 275] 3073, 3074: -The subunits encoded by the genes HEXA and HEXB are synthesized as precursor proteins; processing and subunit assembly in the endoplasmatic reticulum yields three isoforms; beta-hexosaminidase A (alpha, beta), beta-hexosaminidase B (beta, beta) and beta-hexosaminidase S (alpha, alpha). The proteins are targeted to the lysosomes, where final processing produces the mature enzymes. [Maier et al, J Mol Biol. 328(3):669-81 (2003)] - lysosomal [Liu, Glycobiology 1999] - occurs in degradation of Asn-linked glycoproteins [Liu, Glycobiology 1999] - the active site of the beta -subunit hydrolyzes uncharged substrates, whereas the alpha -subunit, in addition, cleaves negatively charged substrate [Hepbildikler 2002] - Hexb -/- mice (expressing only HexS) showed no increased accumulation of glycosaminoglycans, indicating that Hex S involved in their catabolism [Hepbildikler 2002] - acts on N-acetylglucosides and N-acetylgalactosides [BRENDA]
NADK	3	Williams MB, Jones HP.	Calmodulin-dependent NAD kinase of human neutrophils.	Arch Biochem Biophys	1985	2982330	IT expressed in most tissues but not in skeletal muscle cells
NADK	3	Lerner F, Niere M, Ludwig A, Ziegler M.	Structural and functional characterization of human NAD kinase.	Biochem Biophys Res Commun	2001	11594753	IT expressed in most tissues but not in skeletal muscle cells
NADPN	2	Boyer CS, Moore GA, Moldeus P.	Submitochondrial localization of the NAD+ glycohydrolase. Implications for the role of pyridine nucleotide hydrolysis in mitochondrial calcium fluxes.	J Biol Chem	1993	8382685	IT Boyer et al reported NAD glycohydrolase location on outer membrane of rat mitochondria. In addition, Bender (book) mentioned degradation of NAD(P) in cell ADPribose moiety is normally transfered to protein which profoundly affect the target protein effector function. protein modification is reversed by hydrolases leading to liberation of ADPrib. the free ADPrib pool is tightly regulated in cell since it is a highly reactive molecule which causes non-enzymatic mom-ADP-ribosylation of proteins (from Rongvaux et alm BioEsssays 25, 683-690,2003; Yang et al, JBC, 275(12),8844-8853,2000;and Di Lisa, Ziegler, FEBS lett, 492, 2001,4-8)
NADPN	2	Bender DA	Nutritional Biochemistry of the Vitamins		2003		IT Boyer et al reported NAD glycohydrolase location on outer membrane of rat mitochondria. In addition, Bender (book) mentioned degradation of NAD(P) in cell ADPribose moiety is normally transfered to protein which profoundly affect the target protein effector function. protein modification is reversed by hydrolases leading to liberation of ADPrib. the free ADPrib pool is tightly regulated in cell since it is a highly reactive molecule which causes non-enzymatic mom-ADP-ribosylation of proteins (from Rongvaux et alm BioEsssays 25, 683-690,2003; Yang et al, JBC, 275(12),8844-8853,2000;and Di Lisa, Ziegler, FEBS lett, 492, 2001,4-8)
NADPNe	3	Kim UH, Han MK, Park BH, Kim HR, An NH.	Function of NAD glycohydrolase in ADP-ribose uptake from NAD by human erythrocytes.	Biochim Biophys Acta	1993	8394137	IT

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NADPNe	3	Kontani K, Nishina H, Ohoka Y, Takahashi K, Katada T.	NAD glycohydrolase specifically induced by retinoic acid in human leukemic HL-60 cells. Identification of the NAD glycohydrolase as leukocyte cell surface antigen CD38.	J Biol Chem	1993		IT
NADS2	3	Hara N, Yamada K, Terashima M, Osago H, Shimoyama M, Tsuchiya M.	Molecular identification of human glutamine- and ammonia-dependent NAD synthetases. Carbon-nitrogen hydrolase domain confers glutamine dependency.	J Biol Chem	2003	12547821	IT
NAGAly	3	Wang AM, Bishop DF, Desnick RJ.	Human alpha-N-acetylgalactosaminidase-molecular cloning, nucleotide sequence, and expression of a full length cDNA. Homology with human alpha-galactosidase A suggests evolution from a common ancestral gene.	J Biol Chem	1990	2174888	lysosomal - uniprot, wang ref NAGA encodes the lysosomal enzyme alpha-N-acetylgalactosaminidase, which cleaves alpha-N-acetylgalactosaminyl moieties from glycoconjugates. Mutations in NAGA have been identified as the cause of Schindler disease types I and II (type II also known as Kanzaki disease). NJ 4668: - protein isolated from human placenta [Tsuji 1989] - purified from human lung, expressed in COS-1 cells [Wang 1990] - has "striking" homology to human alpha-galactosidase A and yeast alpha-galactosidase [Tsuji 1989]; 46.9-64.7% amino acid identity w/ alpha-Gal A exons 1 through 6, but exon 7 had only 15.8% homology with numerous gaps [Wang 1990]
NAGAly	3	Tsuji S, Yamauchi T, Hiraiwa M, Isobe T, Okuyama T, Sakimura K, Takahashi Y, Nishizawa M, Uda Y, Miyatake T.	Molecular cloning of a full-length cDNA for human alpha-N-acetylgalactosaminidase (alpha-galactosidase B)	Biochem Biophys Res Commun	1989	2551294	lysosomal - uniprot, wang ref NAGA encodes the lysosomal enzyme alpha-N-acetylgalactosaminidase, which cleaves alpha-N-acetylgalactosaminyl moieties from glycoconjugates. Mutations in NAGA have been identified as the cause of Schindler disease types I and II (type II also known as Kanzaki disease). NJ 4668: - protein isolated from human placenta [Tsuji 1989] - purified from human lung, expressed in COS-1 cells [Wang 1990] - has "striking" homology to human alpha-galactosidase A and yeast alpha-galactosidase [Tsuji 1989]; 46.9-64.7% amino acid identity w/ alpha-Gal A exons 1 through 6, but exon 7 had only 15.8% homology with numerous gaps [Wang 1990]
NaKt	3	Wang J, Schwinger RH, Frank K, Muller-Ehmsen J, Martin-Vasallo P, Pressley TA, Xiang A, Erdmann E, McDonough AA.	Regional expression of sodium pump subunits isoforms and Na+-Ca++ exchanger in the human heart.	J Clin Invest	1996	8833915	- Added by KS/TV - The Na-K ATPase functions to maintain sodium and potassium gradients across membranes that subserve cellular activities such as volume regulation, action potentials, and secondary active transport. - This enzyme is composed of two subunits, a large catalytic subunit (alpha) and a smaller glycoprotein subunit (beta) [Entrez] - Expression for each subunit is as follows: 1) alpha1: ubiquitously 2) alpha2: brain, heart skeletal muscle 3) alpha3: brain and heart 4) alpha4: testis and skeletal muscle 5) beta1: ubiquitously 6) beta2: neural, heart 7) beta3: human placenta 8) beta4: skeletal muscle - Based on this expression data 11 different combinations of the two subunits were created: 1) Following combinations assumed to be expressed ubiquitously: alpha1/beta1, alpha1/beta2, alpha1/beta3, alpha1/beta4, alpha2/beta1, alpha3/beta1, alpha4/beta1 2) Following combination expresed in heart: alpha1/beta1, alpha2/beta1, alpha3/beta1 (according to Wang J, et al. J Clin Invest. 1996 Oct 1;98(7):1650-8.) 3) Following combinatons expressed in brain/neural tissues: alp 4) Following combination expressed in skeletal muscle: alpha4/ - Note: Protein name Atp1a3b4 indicates combination of alpha3

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NaKt	3	Stengelin MK, Hoffman JF.	Na,K-ATPase subunit isoforms in human reticulocytes: evidence from reverse transcription-PCR for the presence of alpha1, alpha3, beta2, beta3, and gamma.	Proc Natl Acad Sci U S A	1997	9159180	- Added by KS/TV - The Na-K ATPase functions to maintain sodium and potassium gradients across membranes that subserve cellular activities such as volume regulation, action potentials, and secondary active transport. - This enzyme is composed of two subunits, a large catalytic subunit (alpha) and a smaller glycoprotein subunit (beta) [Entrez] - Expression for each subunit is as follows: 1) alpha1: ubiquitously 2) alpha2: brain, heart skeletal muscle 3) alpha3: brain and heart 4) alpha4: testis and skeletal muscle 5) beta1: ubiquitously 6) beta2: neural, heart 7) beta3: human placenta 8) beta4: skeletal muscle - Based on this expression data 11 different combinations of the two subunits were created: 1) Following combinations assumed to be expressed ubiquitously: alpha1/beta1, alpha1/beta2, alpha1/beta3, alpha1/beta4, alpha2/beta1, alpha3/beta1, alpha4/beta1 2) Following combination expresed in heart: alpha1/beta1, alpha2/beta1, alpha3/beta1 (according to Wang J, et al. J Clin Invest. 1996 Oct 1;98(7):1650-8.) 3) Following combinatons expressed in brain/neural tissues: alp 4) Following combination expressed in skeletal muscle: alpha4/ - Note: Protein name Atp1a3b4 indicates combination of alpha3
NaKt	3	Pestov NB, Adams G, Shakhparonov MI, Modyanov NN.	Identification of a novel gene of the X,K-ATPase beta-subunit family that is predominantly expressed in skeletal and heart muscles	FEBS Lett	1999	10456317	- Added by KS/TV - The Na-K ATPase functions to maintain sodium and potassium gradients across membranes that subserve cellular activities such as volume regulation, action potentials, and secondary active transport. - This enzyme is composed of two subunits, a large catalytic subunit (alpha) and a smaller glycoprotein subunit (beta) [Entrez] - Expression for each subunit is as follows: 1) alpha1: ubiquitously 2) alpha2: brain, heart skeletal muscle 3) alpha3: brain and heart 4) alpha4: testis and skeletal muscle 5) beta1: ubiquitously 6) beta2: neural, heart 7) beta3: human placenta 8) beta4: skeletal muscle - Based on this expression data 11 different combinations of the two subunits were created: 1) Following combinations assumed to be expressed ubiquitously: alpha1/beta1, alpha1/beta2, alpha1/beta3, alpha1/beta4, alpha2/beta1, alpha3/beta1, alpha4/beta1 2) Following combination expresed in heart: alpha1/beta1, alpha2/beta1, alpha3/beta1 (according to Wang J, et al. J Clin Invest. 1996 Oct 1;98(7):1650-8.) 3) Following combinatons expressed in brain/neural tissues: alp 4) Following combination expressed in skeletal muscle: alpha4/ - Note: Protein name Atp1a3b4 indicates combination of alpha3
NAt	3	Kwon HM, Yamauchi A, Uchida S, Preston AS, Garcia-Perez A, Burg MB, Handler JS	Cloning of the cDNa for a Na+/myo-inositol cotransporter, a hypertonicity stress protein	J Biol Chem	1992	1372904	6523: -cloned [Hediger 1989] - cotransports Glc/2 Na+, Gal/2 Na+ [Quick 2001] - H+ can replace Na+ in sugar cotransport [Hirayama 1994] - behaves as urea channel in the absence of substrates; cotransports urea under substrate-transporting conditions [Leung 2000] - Na+ transport occurs by a saturable uniport mechanism; water permeation is through a low conductance water channel [Loo 1999] - brush border membrane [Wright 1994] - plasma membrane; see [Wright 2004] for refs 6526: - cloned [Kwon 1992], [Berry 1995] - kidney, brain, placenta, pancreas, heart, skeletal muscle, lung [Berry 1995] - Na+/myo-inositol cotransport; also transports other sugars (incl glc) with low affinity [Hager 1995], [Kwon 1992] - plasma membrane; see [Wright 2004] for refs - transports Na+ in the absence of sugar [Wright, Physiology 2004] 6528: - cloned [Dai 1996] - gene has 84% identity to the rat homolog [Smanik 1996] - sodium iodide cotransport [Dai 1996]; 2 Na+ per I- [Eskandari, 1997] - primarily in thyroid gland [De La Vieja 2000], also expressed in breast, bladder, colon, endometrium, kidney, prostate, and pa - also transports ClO3-, SCN-, SeCN-, NO3-, Br-, BF4-, IO4-, I - basolateral plasma membrane; see [Wright 2004] for refs - transports Na+ in the absence of sugar [Wright, Physiology 20

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NAt	3	Hager K, Hazama A, Kwon HM, Loo DD, Handler JS, Wright EM	Kinetics and specificity of the renal Na+/myo-inositol cotransporter expressed in Xenopus oocytes	J Membr Biol	1995	7537337	6523: -cloned [Hediger 1989] - cotransports Glc/2 Na+, Gal/2 Na+ [Quick 2001] - H+ can replace Na+ in sugar cotransport [Hirayama 1994] - behaves as urea channel in the absence of substrates; cotransports urea under substrate-transporting conditions [Leung 2000] - Na+ transport occurs by a saturable uniport mechanism; water permeation is through a low conductance water channel [Loo 1999] - brush border membrane [Wright 1994] - plasma membrane; see [Wright 2004] for refs 6526: - cloned [Kwon 1992], [Berry 1995] - kidney, brain, placenta, pancreas, heart, skeletal muscle, lung [Berry 1995] - Na+/myo-inositol cotransport; also transports other sugars (incl glc) with low affinity [Hager 1995], [Kwon 1992] - plasma membrane; see [Wright 2004] for refs - transports Na+ in the absence of sugar [Wright, Physiology 2004] 6528: - cloned [Dai 1996] - gene has 84% identity to the rat homolog [Smanik 1996] - sodium iodide cotransport [Dai 1996]; 2 Na+ per I- [Eskandari, 1997] - primarily in thyroid gland [De La Vieja 2000], also expressed in breast, bladder, colon, endometrium, kidney, prostate, and pa - also transports ClO3-, SCN-, SeCN-, NO3-, Br-, BF4-, IO4-, I - basolateral plasma membrane; see [Wright 2004] for refs - transports Na+ in the absence of sugar [Wright, Physiology 20
NAt	3	Berry GT, Mallee JJ, Kwon HM, Rim JS, Mulla WR, Muenke M, Spinner NB	The human osmoregulatory Na+/myo-inositol cotransporter gene (SLC5A3): molecular cloning and localization to chromosome 21	Genomics	1995	7789985	6523: -cloned [Hediger 1989] - cotransports Glc/2 Na+, Gal/2 Na+ [Quick 2001] - H+ can replace Na+ in sugar cotransport [Hirayama 1994] - behaves as urea channel in the absence of substrates; cotransports urea under substrate-transporting conditions [Leung 2000] - Na+ transport occurs by a saturable uniport mechanism; water permeation is through a low conductance water channel [Loo 1999] - brush border membrane [Wright 1994] - plasma membrane; see [Wright 2004] for refs 6526: - cloned [Kwon 1992], [Berry 1995] - kidney, brain, placenta, pancreas, heart, skeletal muscle, lung [Berry 1995] - Na+/myo-inositol cotransport; also transports other sugars (incl glc) with low affinity [Hager 1995], [Kwon 1992] - plasma membrane; see [Wright 2004] for refs - transports Na+ in the absence of sugar [Wright, Physiology 2004] 6528: - cloned [Dai 1996] - gene has 84% identity to the rat homolog [Smanik 1996] - sodium iodide cotransport [Dai 1996]; 2 Na+ per I- [Eskandari, 1997] - primarily in thyroid gland [De La Vieja 2000], also expressed in breast, bladder, colon, endometrium, kidney, prostate, and pa - also transports ClO3-, SCN-, SeCN-, NO3-, Br-, BF4-, IO4-, I - basolateral plasma membrane; see [Wright 2004] for refs - transports Na+ in the absence of sugar [Wright, Physiology 20
NAt	3	Wright EM, Loo DD, Hirayama BA, Turk E	Surprising versatility of Na+-glucose cotransporters: SLC5	Physiology (Bethesda)	2004	15546855	6523: -cloned [Hediger 1989] - cotransports Glc/2 Na+, Gal/2 Na+ [Quick 2001] - H+ can replace Na+ in sugar cotransport [Hirayama 1994] - behaves as urea channel in the absence of substrates; cotransports urea under substrate-transporting conditions [Leung 2000] - Na+ transport occurs by a saturable uniport mechanism; water permeation is through a low conductance water channel [Loo 1999] - brush border membrane [Wright 1994] - plasma membrane; see [Wright 2004] for refs 6526: - cloned [Kwon 1992], [Berry 1995] - kidney, brain, placenta, pancreas, heart, skeletal muscle, lung [Berry 1995] - Na+/myo-inositol cotransport; also transports other sugars (incl glc) with low affinity [Hager 1995], [Kwon 1992] - plasma membrane; see [Wright 2004] for refs - transports Na+ in the absence of sugar [Wright, Physiology 2004] 6528: - cloned [Dai 1996] - gene has 84% identity to the rat homolog [Smanik 1996] - sodium iodide cotransport [Dai 1996]; 2 Na+ per I- [Eskandari, 1997] - primarily in thyroid gland [De La Vieja 2000], also expressed in breast, bladder, colon, endometrium, kidney, prostate, and pa - also transports ClO3-, SCN-, SeCN-, NO3-, Br-, BF4-, IO4-, I - basolateral plasma membrane; see [Wright 2004] for refs - transports Na+ in the absence of sugar [Wright, Physiology 20

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NAt3_1	3	Sardet C, Franchi A, Pouyssegur J	Molecular cloning, primary structure, and expression of the human growth factor-activatable Na+/H+ antiporter.	Cell	1989	2536298	6548: - cloned [Sardet 1989] - restored H+-activated Na+ influx in kockout [Sardet 1989] - ubiquitous [Orlowski 2004] - rabbit homolog localized to basolateral surface of plasma membrane (see ref in [Malakooti 1999]) - evidence for 1:1 stoichiometry reviewed in [Aronson 1985] - Na+/NH4+ exchange suggested in [Aronson 1985] for plasmalemmal NHE proteins [Orlowski 2004] - also exchanges Li+/H+ (not included in model) [Aronson 1985] 6549: - cloned [Ghishan 1995]*, [Malakooti 1999] * Ghishan cloned truncated sequence, Malakooti cloned full sequence - high in sk muscle, colon, and kidney and lower in testis, prostate, ovary, sm intestine [Malakooti 1999] - rabbit homolog localized in apical membrane (see refs in [Malakooti 1999]) - catalyzes Na+/H+ exchange activity in LAP1 cells lacking endogenous NHE activity [Malakooti 1999] - Na+/NH4+ exchange suggested in [Aronson 1985] for plasmalemmal NHE proteins [Orlowski 2004] - also exchanges Li+/H+ (not included in model) [Aronson 1985] 6550: - cloned [Brant 1995] - 89 and 88% amino acid identity with rat and rabbit NHE3 [Br - established Na+/H+ exchange in deficient PS120 cells [Brant kidney >> small intestine >> testes > ovary > colon = prostate >> - rabbit homolog localized in apical membrane (see ref in [Bran - Na+/NH4+ exchange suggested in [Aronson 1985] for plasma - also exchanges Li+/H+ (not included in model) [Aronson 198
NAt3_1	3	Aronson PS	Kinetic properties of the plasma membrane Na+-H+ exchanger	Annu Rev Physiol	1985	2581505	6548: - cloned [Sardet 1989] - restored H+-activated Na+ influx in kockout [Sardet 1989] - ubiquitous [Orlowski 2004] - rabbit homolog localized to basolateral surface of plasma membrane (see ref in [Malakooti 1999]) - evidence for 1:1 stoichiometry reviewed in [Aronson 1985] - Na+/NH4+ exchange suggested in [Aronson 1985] for plasmalemmal NHE proteins [Orlowski 2004] - also exchanges Li+/H+ (not included in model) [Aronson 1985] 6549: - cloned [Ghishan 1995]*, [Malakooti 1999] * Ghishan cloned truncated sequence, Malakooti cloned full sequence - high in sk muscle, colon, and kidney and lower in testis, prostate, ovary, sm intestine [Malakooti 1999] - rabbit homolog localized in apical membrane (see refs in [Malakooti 1999]) - catalyzes Na+/H+ exchange activity in LAP1 cells lacking endogenous NHE activity [Malakooti 1999] - Na+/NH4+ exchange suggested in [Aronson 1985] for plasmalemmal NHE proteins [Orlowski 2004] - also exchanges Li+/H+ (not included in model) [Aronson 1985] 6550: - cloned [Brant 1995] - 89 and 88% amino acid identity with rat and rabbit NHE3 [Br - established Na+/H+ exchange in deficient PS120 cells [Brant kidney >> small intestine >> testes > ovary > colon = prostate >> - rabbit homolog localized in apical membrane (see ref in [Bran - Na+/NH4+ exchange suggested in [Aronson 1985] for plasma - also exchanges Li+/H+ (not included in model) [Aronson 198
NAt3_1	3	Brant SR, Yun CH, Donowitz M, Tse CM	Cloning, tissue distribution, and functional analysis of the human Na+/N+ exchanger isoform, NHE3	Am J Physiol	1995	7631746	6548: - cloned [Sardet 1989] - restored H+-activated Na+ influx in kockout [Sardet 1989] - ubiquitous [Orlowski 2004] - rabbit homolog localized to basolateral surface of plasma membrane (see ref in [Malakooti 1999]) - evidence for 1:1 stoichiometry reviewed in [Aronson 1985] - Na+/NH4+ exchange suggested in [Aronson 1985] for plasmalemmal NHE proteins [Orlowski 2004] - also exchanges Li+/H+ (not included in model) [Aronson 1985] 6549: - cloned [Ghishan 1995]*, [Malakooti 1999] * Ghishan cloned truncated sequence, Malakooti cloned full sequence - high in sk muscle, colon, and kidney and lower in testis, prostate, ovary, sm intestine [Malakooti 1999] - rabbit homolog localized in apical membrane (see refs in [Malakooti 1999]) - catalyzes Na+/H+ exchange activity in LAP1 cells lacking endogenous NHE activity [Malakooti 1999] - Na+/NH4+ exchange suggested in [Aronson 1985] for plasmalemmal NHE proteins [Orlowski 2004] - also exchanges Li+/H+ (not included in model) [Aronson 1985] 6550: - cloned [Brant 1995] - 89 and 88% amino acid identity with rat and rabbit NHE3 [Br - established Na+/H+ exchange in deficient PS120 cells [Brant kidney >> small intestine >> testes > ovary > colon = prostate >> - rabbit homolog localized in apical membrane (see ref in [Bran - Na+/NH4+ exchange suggested in [Aronson 1985] for plasma - also exchanges Li+/H+ (not included in model) [Aronson 198

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NAt3_1	3	Klanke CA, Su YR, Callen DF, Wang Z, Meneton P, Baird N, Kandasamy RA, Orlowski J, Otterud BE, Leppert M, et al	Molecular cloning and physical and genetic mapping of a novel human Na+/H+ exchanger (NHE5/SLC9A5) to chromosome 16q22.1	Genomics	1995	7759094	6548: - cloned [Sardet 1989] - restored H+-activated Na+ influx in kockout [Sardet 1989] - ubiquitous [Orlowski 2004] - rabbit homolog localized to basolateral surface of plasma membrane (see ref in [Malakooti 1999]) - evidence for 1:1 stoichiometry reviewed in [Aronson 1985] - Na+/NH4+ exchange suggested in [Aronson 1985] for plasmalemmal NHE proteins [Orlowski 2004] - also exchanges Li+/H+ (not included in model) [Aronson 1985] 6549: - cloned [Ghishan 1995]*, [Malakooti 1999] * Ghishan cloned truncated sequence, Malakooti cloned full sequence - high in sk muscle, colon, and kidney and lower in testis, prostate, ovary, sm intestine [Malakooti 1999] - rabbit homolog localized in apical membrane (see refs in [Malakooti 1999]) - catalyzes Na+/H+ exchange activity in LAP1 cells lacking endogenous NHE activity [Malakooti 1999] - Na+/NH4+ exchange suggested in [Aronson 1985] for plasmalemmal NHE proteins [Orlowski 2004] - also exchanges Li+/H+ (not included in model) [Aronson 1985] 6550: - cloned [Brant 1995] - 89 and 88% amino acid identity with rat and rabbit NHE3 [Br - established Na+/H+ exchange in deficient PS120 cells [Brant kidney >> small intestine >> testes > ovary > colon = prostate >> - rabbit homolog localized in apical membrane (see ref in [Bran - Na+/NH4+ exchange suggested in [Aronson 1985] for plasma - also exchanges Li+/H+ (not included in model) [Aronson 198
NAt3_1	3	Szpirer C, Szpirer J, Riviere M, Levan G, Orlowski J	Chromosomal assignment of four genes encoding Na/H exchanger isoforms in human and rat.	Mamm Genome	1994	8199403	6548: - cloned [Sardet 1989] - restored H+-activated Na+ influx in kockout [Sardet 1989] - ubiquitous [Orlowski 2004] - rabbit homolog localized to basolateral surface of plasma membrane (see ref in [Malakooti 1999]) - evidence for 1:1 stoichiometry reviewed in [Aronson 1985] - Na+/NH4+ exchange suggested in [Aronson 1985] for plasmalemmal NHE proteins [Orlowski 2004] - also exchanges Li+/H+ (not included in model) [Aronson 1985] 6549: - cloned [Ghishan 1995]*, [Malakooti 1999] * Ghishan cloned truncated sequence, Malakooti cloned full sequence - high in sk muscle, colon, and kidney and lower in testis, prostate, ovary, sm intestine [Malakooti 1999] - rabbit homolog localized in apical membrane (see refs in [Malakooti 1999]) - catalyzes Na+/H+ exchange activity in LAP1 cells lacking endogenous NHE activity [Malakooti 1999] - Na+/NH4+ exchange suggested in [Aronson 1985] for plasmalemmal NHE proteins [Orlowski 2004] - also exchanges Li+/H+ (not included in model) [Aronson 1985] 6550: - cloned [Brant 1995] - 89 and 88% amino acid identity with rat and rabbit NHE3 [Br - established Na+/H+ exchange in deficient PS120 cells [Brant kidney >> small intestine >> testes > ovary > colon = prostate >> - rabbit homolog localized in apical membrane (see ref in [Bran - Na+/NH4+ exchange suggested in [Aronson 1985] for plasma - also exchanges Li+/H+ (not included in model) [Aronson 198
NAt3_1	3	Ghishan FK, Knobel SM, Summar M	Molecular cloning, sequencing, chromosomal localization, and tissue distribution of the human Na+/H+ exchanger (SLC9A2)	Genomics	1995	8595899	6548: - cloned [Sardet 1989] - restored H+-activated Na+ influx in kockout [Sardet 1989] - ubiquitous [Orlowski 2004] - rabbit homolog localized to basolateral surface of plasma membrane (see ref in [Malakooti 1999]) - evidence for 1:1 stoichiometry reviewed in [Aronson 1985] - Na+/NH4+ exchange suggested in [Aronson 1985] for plasmalemmal NHE proteins [Orlowski 2004] - also exchanges Li+/H+ (not included in model) [Aronson 1985] 6549: - cloned [Ghishan 1995]*, [Malakooti 1999] * Ghishan cloned truncated sequence, Malakooti cloned full sequence - high in sk muscle, colon, and kidney and lower in testis, prostate, ovary, sm intestine [Malakooti 1999] - rabbit homolog localized in apical membrane (see refs in [Malakooti 1999]) - catalyzes Na+/H+ exchange activity in LAP1 cells lacking endogenous NHE activity [Malakooti 1999] - Na+/NH4+ exchange suggested in [Aronson 1985] for plasmalemmal NHE proteins [Orlowski 2004] - also exchanges Li+/H+ (not included in model) [Aronson 1985] 6550: - cloned [Brant 1995] - 89 and 88% amino acid identity with rat and rabbit NHE3 [Br - established Na+/H+ exchange in deficient PS120 cells [Brant kidney >> small intestine >> testes > ovary > colon = prostate >> - rabbit homolog localized in apical membrane (see ref in [Bran - Na+/NH4+ exchange suggested in [Aronson 1985] for plasma - also exchanges Li+/H+ (not included in model) [Aronson 198

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NAt3_1	3	Baird NR, Orlowski J, Szabo EZ, Zaun HC, Schultheis PJ, Menon AG, Shull GE	Molecular cloning, genomic organization, and functional expression of Na+/H+ exchanger isoform 5 (NHE5) from human brain	J Biol Chem	1999	9933641	6548: - cloned [Sardet 1989] - restored H+-activated Na+ influx in kockout [Sardet 1989] - ubiquitous [Orlowski 2004] - rabbit homolog localized to basolateral surface of plasma membrane (see ref in [Malakooti 1999]) - evidence for 1:1 stoichiometry reviewed in [Aronson 1985] - Na+/NH4+ exchange suggested in [Aronson 1985] for plasmalemmal NHE proteins [Orlowski 2004] - also exchanges Li+/H+ (not included in model) [Aronson 1985] 6549: - cloned [Ghishan 1995]*, [Malakooti 1999] * Ghishan cloned truncated sequence, Malakooti cloned full sequence - high in sk muscle, colon, and kidney and lower in testis, prostate, ovary, sm intestine [Malakooti 1999] - rabbit homolog localized in apical membrane (see refs in [Malakooti 1999]) - catalyzes Na+/H+ exchange activity in LAP1 cells lacking endogenous NHE activity [Malakooti 1999] - Na+/NH4+ exchange suggested in [Aronson 1985] for plasmalemmal NHE proteins [Orlowski 2004] - also exchanges Li+/H+ (not included in model) [Aronson 1985] 6550: - cloned [Brant 1995] - 89 and 88% amino acid identity with rat and rabbit NHE3 [Br - established Na+/H+ exchange in deficient PS120 cells [Brant kidney >> small intestine >> testes > ovary > colon = prostate >> - rabbit homolog localized in apical membrane (see ref in [Bran - Na+/NH4+ exchange suggested in [Aronson 1985] for plasma - also exchanges Li+/H+ (not included in model) [Aronson 198
NAt3_1	3	Malakooti J, Dahdal RY, Schmidt L, Layden TJ, Dudeja PK, Ramaswamy K	Molecular cloning, tissue distribution, and functional expression of the human Na(+)/H(+) exchanger NHE2	Am J Physiol	1999	10444453	6548: - cloned [Sardet 1989] - restored H+-activated Na+ influx in kockout [Sardet 1989] - ubiquitous [Orlowski 2004] - rabbit homolog localized to basolateral surface of plasma membrane (see ref in [Malakooti 1999]) - evidence for 1:1 stoichiometry reviewed in [Aronson 1985] - Na+/NH4+ exchange suggested in [Aronson 1985] for plasmalemmal NHE proteins [Orlowski 2004] - also exchanges Li+/H+ (not included in model) [Aronson 1985] 6549: - cloned [Ghishan 1995]*, [Malakooti 1999] * Ghishan cloned truncated sequence, Malakooti cloned full sequence - high in sk muscle, colon, and kidney and lower in testis, prostate, ovary, sm intestine [Malakooti 1999] - rabbit homolog localized in apical membrane (see refs in [Malakooti 1999]) - catalyzes Na+/H+ exchange activity in LAP1 cells lacking endogenous NHE activity [Malakooti 1999] - Na+/NH4+ exchange suggested in [Aronson 1985] for plasmalemmal NHE proteins [Orlowski 2004] - also exchanges Li+/H+ (not included in model) [Aronson 1985] 6550: - cloned [Brant 1995] - 89 and 88% amino acid identity with rat and rabbit NHE3 [Br - established Na+/H+ exchange in deficient PS120 cells [Brant kidney >> small intestine >> testes > ovary > colon = prostate >> - rabbit homolog localized in apical membrane (see ref in [Bran - Na+/NH4+ exchange suggested in [Aronson 1985] for plasma - also exchanges Li+/H+ (not included in model) [Aronson 198
NAt3_1	3	Orlowski J, Grinstein S	Diversity of the mammalian sodium/proton exchange SLC9 gene family	Pflugers Arch	2004	12845533	6548: - cloned [Sardet 1989] - restored H+-activated Na+ influx in kockout [Sardet 1989] - ubiquitous [Orlowski 2004] - rabbit homolog localized to basolateral surface of plasma membrane (see ref in [Malakooti 1999]) - evidence for 1:1 stoichiometry reviewed in [Aronson 1985] - Na+/NH4+ exchange suggested in [Aronson 1985] for plasmalemmal NHE proteins [Orlowski 2004] - also exchanges Li+/H+ (not included in model) [Aronson 1985] 6549: - cloned [Ghishan 1995]*, [Malakooti 1999] * Ghishan cloned truncated sequence, Malakooti cloned full sequence - high in sk muscle, colon, and kidney and lower in testis, prostate, ovary, sm intestine [Malakooti 1999] - rabbit homolog localized in apical membrane (see refs in [Malakooti 1999]) - catalyzes Na+/H+ exchange activity in LAP1 cells lacking endogenous NHE activity [Malakooti 1999] - Na+/NH4+ exchange suggested in [Aronson 1985] for plasmalemmal NHE proteins [Orlowski 2004] - also exchanges Li+/H+ (not included in model) [Aronson 1985] 6550: - cloned [Brant 1995] - 89 and 88% amino acid identity with rat and rabbit NHE3 [Br - established Na+/H+ exchange in deficient PS120 cells [Brant kidney >> small intestine >> testes > ovary > colon = prostate >> - rabbit homolog localized in apical membrane (see ref in [Bran - Na+/NH4+ exchange suggested in [Aronson 1985] for plasma - also exchanges Li+/H+ (not included in model) [Aronson 198

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NAt3_1g	3	Numata M, Orlowski J	Molecular cloning and characterization of a novel (Na+,K+)/H+ exchanger localized to the trans-Golgi network	J Biol Chem	2001	11279194	84679: - cloned [Numata 2001] - ubiquitous [Numata 2001] - localizes predominantly to trans-Golgi network [Numata 2001], [Nakamura 2005] - catalyzes Na+/H+ and K+/H+ exchange [Numata 2001] 23315: - cloned [Nakamura 2005] - localizes to mid-to trans-Golgi [Nakamura 2005] - ubiquitous; most highly expressed in sk muscle, kidney [Nakamura 2005] - catalyzes Na+/H+ and K+/H+ exchange [Nakamura 2005]
NAt3_1g	3	Nakamura N, Tanaka S, Teko Y, Mitsui K, Kanazawa H.	Four Na+/H+ exchanger isoforms are distributed to Golgi and post-Golgi compartments and are involved in organelle pH regulation.	J Biol Chem	2005	15522866	84679: - cloned [Numata 2001] - ubiquitous [Numata 2001] - localizes predominantly to trans-Golgi network [Numata 2001], [Nakamura 2005] - catalyzes Na+/H+ and K+/H+ exchange [Numata 2001] 23315: - cloned [Nakamura 2005] - localizes to mid-to trans-Golgi [Nakamura 2005] - ubiquitous; most highly expressed in sk muscle, kidney [Nakamura 2005] - catalyzes Na+/H+ and K+/H+ exchange [Nakamura 2005]
NCAMUP	2	Sofue M, Yoshimura Y, Nishida M, Kawada J.	Possible multifunction of glucose transporter. Transport of nicotinamide by reconstituted liposomes.	Biochem J	1992	1463467	IT it is taken up from blood in one way or another - it does not seem to be GLUT1 as reported formerly Ball (book) mentioned that it is thought that ncam anf nac can diffuse through membrane
NCAMUP	2	Reyes AM, Bustamante F, Rivas CI, Ortega M, Donnet C, Rossi JP, Fischbarg J, Vera JC.	Nicotinamide is not a substrate of the facilitative hexose transporter GLUT1.	Biochemistry	2002	12069599	IT it is taken up from blood in one way or another - it does not seem to be GLUT1 as reported formerly Ball (book) mentioned that it is thought that ncam anf nac can diffuse through membrane
NCCt	3	Simon DB, Nelson-Williams C, Bia MJ, Ellison D, Karet FE, Molina AM, Vaara I, Iwata F, Cushner HM, Koolen M, Gainza FJ, Gitleman HJ, Lifton RP	Gitelman's variant of Bartter's syndrome, inherited hypokalaemic alkalosis, is caused by mutations in the thiazide-sensitive Na-Cl cotransporter	Nat Genet	1996	8528245	6559: - major salt reabsorption pathway in apical membrane of distal convoluted tubule [Hebert 2004] - kidney [Mastroianni 1996], [Chang 1996], lower in sm intestine, placenta, prostate, colon, spleen [Chang 1996] - cloned [Simon 1996], [Mastroianni 1996], [Chang 1996] - predominantly expressed in kidney [Hebert 2004] - 1:1 stoiciometry of Na+-Cl- transport [Hebert 2001]
NCCt	3	Chang H, Tashiro K, Hirai M, Ikeda K, Kurokawa K, Fujita T	Identification of a cDNA encoding a thiazide-sensitive sodium-chloride cotransporter from the human and its mRNA expression in various tissues	Biochem Biophys Res Commun	1996	8670281	6559: - major salt reabsorption pathway in apical membrane of distal convoluted tubule [Hebert 2004] - kidney [Mastroianni 1996], [Chang 1996], lower in sm intestine, placenta, prostate, colon, spleen [Chang 1996] - cloned [Simon 1996], [Mastroianni 1996], [Chang 1996] - predominantly expressed in kidney [Hebert 2004] - 1:1 stoiciometry of Na+-Cl- transport [Hebert 2001]
NCCt	3	Mastroianni N, De Fusco M, Zollo M, Arrigo G, Zuffardi O, Bettinelli A, Ballabio A, Casari G	Molecular cloning, expression pattern, and chromosomal localization of the human Na-Cl thiazide-sensitive cotransporter (SLC12A3).	Genomics	1996	8812482	6559: - major salt reabsorption pathway in apical membrane of distal convoluted tubule [Hebert 2004] - kidney [Mastroianni 1996], [Chang 1996], lower in sm intestine, placenta, prostate, colon, spleen [Chang 1996] - cloned [Simon 1996], [Mastroianni 1996], [Chang 1996] - predominantly expressed in kidney [Hebert 2004] - 1:1 stoiciometry of Na+-Cl- transport [Hebert 2001]

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NCKt	3	Tucker JE, Winkfein RJ, Cooper CB, Schnetkamp PP	cDNA cloning of the human retinal rod Na-Ca + K exchanger: comparison with a revised bovine sequence	Invest Ophthalmol Vis Sci	1998	9478004	9187: - cloned [Tucker 1998] - 64.3% identity with bovine protein [Tucker 1998] - only found in retinal rod photoreceptors and platelets [Kimura 1999] NCKX1, NCKX2 have following characterisitics: - exchanges in 4Na+:1Ca2+:1K+ ratio* - bidirectional transporter* - selectivity for Na+ is absolute; Ca2+ can be replaced by Sr2+; K+ can be replaced by Rb+, Nh4+* * see refs in [Schnetkamp 2004] for refs 25769: - cloned [Prinsen 2000] - detected K-dependent Na-Ca exchange activity when recombinantly expressed in insect cells [Prinsen 2000] - only found in brain, retinal ganglion cels, cone photoreceptors (chicken transcript Northern blot) [Prinsen 2000] - see notes for 9187 about function 57419: - cloned [Kraev 2001] - displayed K+-dependent Na+/Ca2+ exchanger activity [Kraev 2001] but stoichiometry has not been established (assumed the same as NCKX1 & NCKX2) - most abundant in brain, lower levels in aorta, uterus, and intestine [Kraev 2001] 123041: - cloned [Li 2002] - demonstrated K+-dependent Na+/Ca2+ exchanger activity [Li 2002] but stoichiometry has not been established (assumed t - abundantly expressed in brain , aorta, lung, and thymus, lower
NCKt	3	Kimura M, Jeanclos EM, Donnelly RJ, Lytton J, Reeves JP, Aviv A.	Physiological and molecular characterization of the Na+/Ca2+ exchanger in human platelets	Am J Physiol	1999	10484410	9187: - cloned [Tucker 1998] - 64.3% identity with bovine protein [Tucker 1998] - only found in retinal rod photoreceptors and platelets [Kimura 1999] NCKX1, NCKX2 have following characterisitics: - exchanges in 4Na+:1Ca2+:1K+ ratio* - bidirectional transporter* - selectivity for Na+ is absolute; Ca2+ can be replaced by Sr2+; K+ can be replaced by Rb+, Nh4+* * see refs in [Schnetkamp 2004] for refs 25769: - cloned [Prinsen 2000] - detected K-dependent Na-Ca exchange activity when recombinantly expressed in insect cells [Prinsen 2000] - only found in brain, retinal ganglion cels, cone photoreceptors (chicken transcript Northern blot) [Prinsen 2000] - see notes for 9187 about function 57419: - cloned [Kraev 2001] - displayed K+-dependent Na+/Ca2+ exchanger activity [Kraev 2001] but stoichiometry has not been established (assumed the same as NCKX1 & NCKX2) - most abundant in brain, lower levels in aorta, uterus, and intestine [Kraev 2001] 123041: - cloned [Li 2002] - demonstrated K+-dependent Na+/Ca2+ exchanger activity [Li 2002] but stoichiometry has not been established (assumed t - abundantly expressed in brain , aorta, lung, and thymus, lower

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NCKt	3	Prinsen CF, Szerencsei RT, Schnetkamp PP	Molecular cloning and functional expression of the potassium-dependent sodium-calcium exchanger from human and chicken retinal cone photoreceptors	J Neurosci	2000	10662833	9187: - cloned [Tucker 1998] - 64.3% identity with bovine protein [Tucker 1998] - only found in retinal rod photoreceptors and platelets [Kimura 1999] NCKX1, NCKX2 have following characterisitics: - exchanges in 4Na+:1Ca2+:1K+ ratio* - bidirectional transporter* - selectivity for Na+ is absolute; Ca2+ can be replaced by Sr2+; K+ can be replaced by Rb+, Nh4+* * see refs in [Schnetkamp 2004] for refs 25769: - cloned [Prinsen 2000] - detected K-dependent Na-Ca exchange activity when recombinantly expressed in insect cells [Prinsen 2000] - only found in brain, retinal ganglion cels, cone photoreceptors (chicken transcript Northern blot) [Prinsen 2000] - see notes for 9187 about function 57419: - cloned [Kraev 2001] - displayed K+-dependent Na+/Ca2+ exchanger activity [Kraev 2001] but stoichiometry has not been established (assumed the same as NCKX1 & NCKX2) - most abundant in brain, lower levels in aorta, uterus, and intestine [Kraev 2001] 123041: - cloned [Li 2002] - demonstrated K+-dependent Na+/Ca2+ exchanger activity [Li 2002] but stoichiometry has not been established (assumed t - abundantly expressed in brain , aorta, lung, and thymus, lower
NCKt	3	Kraev A, Quednau BD, Leach S, Li XF, Dong H, Winkfein R, Perizzolo M, Cai X, Yang R, Philipson KD, Lytton J	Molecular cloning of a third member of the potassium-dependent sodium-calcium exchanger gene family, NCKX3	J Biol Chem	2001	11294880	9187: - cloned [Tucker 1998] - 64.3% identity with bovine protein [Tucker 1998] - only found in retinal rod photoreceptors and platelets [Kimura 1999] NCKX1, NCKX2 have following characterisitics: - exchanges in 4Na+:1Ca2+:1K+ ratio* - bidirectional transporter* - selectivity for Na+ is absolute; Ca2+ can be replaced by Sr2+; K+ can be replaced by Rb+, Nh4+* * see refs in [Schnetkamp 2004] for refs 25769: - cloned [Prinsen 2000] - detected K-dependent Na-Ca exchange activity when recombinantly expressed in insect cells [Prinsen 2000] - only found in brain, retinal ganglion cels, cone photoreceptors (chicken transcript Northern blot) [Prinsen 2000] - see notes for 9187 about function 57419: - cloned [Kraev 2001] - displayed K+-dependent Na+/Ca2+ exchanger activity [Kraev 2001] but stoichiometry has not been established (assumed the same as NCKX1 & NCKX2) - most abundant in brain, lower levels in aorta, uterus, and intestine [Kraev 2001] 123041: - cloned [Li 2002] - demonstrated K+-dependent Na+/Ca2+ exchanger activity [Li 2002] but stoichiometry has not been established (assumed t - abundantly expressed in brain , aorta, lung, and thymus, lower

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NCKt	3	Li XF, Kraev AS, Lytton J	Molecular cloning of a fourth member of the potassium-dependent sodium-calcium exchanger gene family, NCKX4	J Biol Chem	2002	12379639	9187: - cloned [Tucker 1998] - 64.3% identity with bovine protein [Tucker 1998] - only found in retinal rod photoreceptors and platelets [Kimura 1999] NCKX1, NCKX2 have following characterisitics: - exchanges in 4Na+:1Ca2+:1K+ ratio* - bidirectional transporter* - selectivity for Na+ is absolute; Ca2+ can be replaced by Sr2+; K+ can be replaced by Rb+, Nh4+* * see refs in [Schnetkamp 2004] for refs 25769: - cloned [Prinsen 2000] - detected K-dependent Na-Ca exchange activity when recombinantly expressed in insect cells [Prinsen 2000] - only found in brain, retinal ganglion cels, cone photoreceptors (chicken transcript Northern blot) [Prinsen 2000] - see notes for 9187 about function 57419: - cloned [Kraev 2001] - displayed K+-dependent Na+/Ca2+ exchanger activity [Kraev 2001] but stoichiometry has not been established (assumed the same as NCKX1 & NCKX2) - most abundant in brain, lower levels in aorta, uterus, and intestine [Kraev 2001] 123041: - cloned [Li 2002] - demonstrated K+-dependent Na+/Ca2+ exchanger activity [Li 2002] but stoichiometry has not been established (assumed t - abundantly expressed in brain , aorta, lung, and thymus, lower
NCKt	3	Schnetkamp PP	The SLC24 Na+/Ca2+-K+ exchanger family: vision and beyond.	Pflugers Arch	2004	14770312	9187: - cloned [Tucker 1998] - 64.3% identity with bovine protein [Tucker 1998] - only found in retinal rod photoreceptors and platelets [Kimura 1999] NCKX1, NCKX2 have following characterisitics: - exchanges in 4Na+:1Ca2+:1K+ ratio* - bidirectional transporter* - selectivity for Na+ is absolute; Ca2+ can be replaced by Sr2+; K+ can be replaced by Rb+, Nh4+* * see refs in [Schnetkamp 2004] for refs 25769: - cloned [Prinsen 2000] - detected K-dependent Na-Ca exchange activity when recombinantly expressed in insect cells [Prinsen 2000] - only found in brain, retinal ganglion cels, cone photoreceptors (chicken transcript Northern blot) [Prinsen 2000] - see notes for 9187 about function 57419: - cloned [Kraev 2001] - displayed K+-dependent Na+/Ca2+ exchanger activity [Kraev 2001] but stoichiometry has not been established (assumed the same as NCKX1 & NCKX2) - most abundant in brain, lower levels in aorta, uterus, and intestine [Kraev 2001] 123041: - cloned [Li 2002] - demonstrated K+-dependent Na+/Ca2+ exchanger activity [Li 2002] but stoichiometry has not been established (assumed t - abundantly expressed in brain , aorta, lung, and thymus, lower
NDP7g	3	Wang TF, Guidotti G	Golgi localization and functional expression of human uridine diphosphatase	J Biol Chem	1998	9556635	9583: - gene is alternatively spliced into 2 transcripts which have different localizations and enzymatic activities: LALP70 is identical to the human Golgi UDPase with the exception of additional 24 bp in the central region of the LALP70 cDNA [Biederbick 2000] - UDPase cleaves CTP most efficiently followed by CDP, UDP, and GTP; LALP70 has highest enzyme activity on UTP and TTP [Biederbick 2000] UDPase (from [Wang 1998]): - identified by homology search & cloned - heart, brain, placenta, lung, liver, skeletal muscle, kidney, pancreas; - increased disphosphatase activity detected in transfected COS-7 cells; highest w/ UDP as substrate, lower activity w/ GDP, CDP, TDP - immunofluorescence staining suggests Golgi lumen localization LALP70 (from [Biederbick 1999]): - cloned and expressed - ubiquitous - lysosomal/autophagic vacuole membrane protein NOTE: only included reaction for UDP

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NDP7g	3	Biederbick A, Rose S, Elsasser HP	A human intracellular apyrase-like protein, LALP70, localizes to lysosomal/autophagic vacuoles	J Cell Sci	1999	10393803	9583: - gene is alternatively spliced into 2 transcripts which have different localizations and enzymatic activities: LALP70 is identical to the human Golgi UDPase with the exception of additional 24 bp in the central region of the LALP70 cDNA [Biederbick 2000] - UDPase cleaves CTP most efficiently followed by CDP, UDP, and GTP; LALP70 has highest enzyme activity on UTP and TTP [Biederbick 2000] UDPase (from [Wang 1998]): - identified by homology search & cloned - heart, brain, placenta, lung, liver, skeletal muscle, kidney, pancreas; - increased disphosphatase activity detected in transfected COS-7 cells; highest w/ UDP as substrate, lower activity w/ GDP, CDP, TDP - immunofluorescence staining suggests Golgi lumen localization LALP70 (from [Biederbick 1999]): - cloned and expressed - ubiquitous - lysosomal/autophagic vacuole membrane protein NOTE: only included reaction for UDP
NDP7g	3	Biederbick A, Kosan C, Kunz J, Elsasser HP	First apyrase splice variants have different enzymatic properties.	J Biol Chem	2000	10858452	9583: - gene is alternatively spliced into 2 transcripts which have different localizations and enzymatic activities: LALP70 is identical to the human Golgi UDPase with the exception of additional 24 bp in the central region of the LALP70 cDNA [Biederbick 2000] - UDPase cleaves CTP most efficiently followed by CDP, UDP, and GTP; LALP70 has highest enzyme activity on UTP and TTP [Biederbick 2000] UDPase (from [Wang 1998]): - identified by homology search & cloned - heart, brain, placenta, lung, liver, skeletal muscle, kidney, pancreas; - increased disphosphatase activity detected in transfected COS-7 cells; highest w/ UDP as substrate, lower activity w/ GDP, CDP, TDP - immunofluorescence staining suggests Golgi lumen localization LALP70 (from [Biederbick 1999]): - cloned and expressed - ubiquitous - lysosomal/autophagic vacuole membrane protein NOTE: only included reaction for UDP
NDPK2m	2	Milon L, Rousseau-Merck MF, Munier A, Erent M, Lascu I, Capeau J, Lacombe ML.	nm23-H4, a new member of the family of human nm23/nucleoside diphosphate kinase genes localised on chromosome 16p13.	Hum Genet	1997	9099850	0
NH4t3r	3	Ridgwell K, Spurr NK, Laguda B, MacGeoch C, Avent ND, Tanner MJ	Isolation of cDNA clones for a 50 kDa glycoprotein of the human erythrocyte membrane associated with Rh (rhesus) blood-group antigen expression	Biochem J	1992	1417776	6005: - cloned [Ridgwell 1992] - NH4+/H+ antiport [Westhoff 2002] - found in RBC as part of a multi-subunit complex with the Rh polypeptides [Nakhoul 2004] 57127: - cloned [Liu 2001] - liver, kidney, and skin [Liu 2001] - NH4+/H+ electroneutral exchange [Ludewig 2004]
NH4t3r	3	Liu Z, Peng J, Mo R, Hui C, Huang CH	Rh type B glycoprotein is a new member of the Rh superfamily and a putative ammonia transporter in mammals	J Biol Chem	2001	11024028	6005: - cloned [Ridgwell 1992] - NH4+/H+ antiport [Westhoff 2002] - found in RBC as part of a multi-subunit complex with the Rh polypeptides [Nakhoul 2004] 57127: - cloned [Liu 2001] - liver, kidney, and skin [Liu 2001] - NH4+/H+ electroneutral exchange [Ludewig 2004]
NH4t3r	3	Nakhoul NL, Hamm LL	Non-erythroid Rh glycoproteins: a putative new family of mammalian ammonium transporters	Pflugers Arch	2004	12920597	6005: - cloned [Ridgwell 1992] - NH4+/H+ antiport [Westhoff 2002] - found in RBC as part of a multi-subunit complex with the Rh polypeptides [Nakhoul 2004] 57127: - cloned [Liu 2001] - liver, kidney, and skin [Liu 2001] - NH4+/H+ electroneutral exchange [Ludewig 2004]
NH4t3r	3	Westhoff CM, Siegel DL, Burd CG, Foskett JK	Mechanism of genetic complementation of ammonium transport in yeast by human erythrocyte Rh-associated glycoprotein	J Biol Chem	2004	14966114	6005: - cloned [Ridgwell 1992] - NH4+/H+ antiport [Westhoff 2002] - found in RBC as part of a multi-subunit complex with the Rh polypeptides [Nakhoul 2004] 57127: - cloned [Liu 2001] - liver, kidney, and skin [Liu 2001] - NH4+/H+ electroneutral exchange [Ludewig 2004]

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NH4t3r	3	Ludewig U	Electroneutral ammonium transport by basolateral rhesus B glycoprotein	J Physiol	2004	15284342	6005: - cloned [Ridgwell 1992] - NH4+/H+ antiport [Westhoff 2002] - found in RBC as part of a multi-subunit complex with the Rh polypeptides [Nakhoul 2004] 57127: - cloned [Liu 2001] - liver, kidney, and skin [Liu 2001] - NH4+/H+ electroneutral exchange [Ludewig 2004]
NKCCt	3	Payne JA, Xu JC, Haas M, Lytle CY, Ward D, Forbush B 3rd	Primary structure, functional expression, and chromosomal localization of the bumetanide-sensitive Na-K-Cl cotransporter in human colon	J Biol Chem	1995	7629105	- NKCC1, NKCC2, KCC1, KCC3, KCC4 shown to transport NH4+ in place of K+ [Bergeron 2003] 6557: - kidney-specific; apical membrane of the thick ascending limb of Henle's loop and the macula densa [Entrez Gene], [Hebert 2004] - accounts for most of the NaCl resorption [Entrez Gene], [Hebert 2004] - stoichiometry of 1Na:1K:2Cl [Entrez Gene], [Hebert 2004] - cloned [Simon 1996] 6558: - ubiquitous; basolateral membrane of epithelial cells, also found in non-epithelial cells [Hebert 2004] - stoichiometry of 1Na:1K:2Cl [Russell 2000] - cloned [Payne 1995]
NKCCt	3	Simon DB, Karet FE, Hamdan JM, DiPietro A, Sanjad SA, Lifton RP	Bartter's syndrome, hypokalaemic alkalosis with hypercalciuria, is caused by mutations in the Na-K-2Cl cotransporter NKCC2	Nat Genet	1996	8640224	- NKCC1, NKCC2, KCC1, KCC3, KCC4 shown to transport NH4+ in place of K+ [Bergeron 2003] 6557: - kidney-specific; apical membrane of the thick ascending limb of Henle's loop and the macula densa [Entrez Gene], [Hebert 2004] - accounts for most of the NaCl resorption [Entrez Gene], [Hebert 2004] - stoichiometry of 1Na:1K:2Cl [Entrez Gene], [Hebert 2004] - cloned [Simon 1996] 6558: - ubiquitous; basolateral membrane of epithelial cells, also found in non-epithelial cells [Hebert 2004] - stoichiometry of 1Na:1K:2Cl [Russell 2000] - cloned [Payne 1995]
NKCCt	3	Russell JM	Sodium-potassium-chloride cotransport	Physiol Rev	2000	10617769	- NKCC1, NKCC2, KCC1, KCC3, KCC4 shown to transport NH4+ in place of K+ [Bergeron 2003] 6557: - kidney-specific; apical membrane of the thick ascending limb of Henle's loop and the macula densa [Entrez Gene], [Hebert 2004] - accounts for most of the NaCl resorption [Entrez Gene], [Hebert 2004] - stoichiometry of 1Na:1K:2Cl [Entrez Gene], [Hebert 2004] - cloned [Simon 1996] 6558: - ubiquitous; basolateral membrane of epithelial cells, also found in non-epithelial cells [Hebert 2004] - stoichiometry of 1Na:1K:2Cl [Russell 2000] - cloned [Payne 1995]
NKCCt	3	Bergeron MJ, Gagnon E, Wallendorff B, Lapointe JY, Isenring P.	Ammonium transport and pH regulation by K(+)-Cl(-) cotransporters	Am J Physiol Renal Physiol	2003	12657561	- NKCC1, NKCC2, KCC1, KCC3, KCC4 shown to transport NH4+ in place of K+ [Bergeron 2003] 6557: - kidney-specific; apical membrane of the thick ascending limb of Henle's loop and the macula densa [Entrez Gene], [Hebert 2004] - accounts for most of the NaCl resorption [Entrez Gene], [Hebert 2004] - stoichiometry of 1Na:1K:2Cl [Entrez Gene], [Hebert 2004] - cloned [Simon 1996] 6558: - ubiquitous; basolateral membrane of epithelial cells, also found in non-epithelial cells [Hebert 2004] - stoichiometry of 1Na:1K:2Cl [Russell 2000] - cloned [Payne 1995]

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NKCCt	3	Hebert SC, Mount DB, Gamba G	Molecular physiology of cation-coupled Cl- cotransport: the SLC12 family	Pflugers Arch	2004	12739168	- NKCC1, NKCC2, KCC1, KCC3, KCC4 shown to transport NH4+ in place of K+ [Bergeron 2003] 6557: - kidney-specific; apical membrane of the thick ascending limb of Henle's loop and the macula densa [Entrez Gene], [Hebert 2004] - accounts for most of the NaCl resorption [Entrez Gene], [Hebert 2004] - stoichiometry of 1Na:1K:2Cl [Entrez Gene], [Hebert 2004] - cloned [Simon 1996] 6558: - ubiquitous; basolateral membrane of epithelial cells, also found in non-epithelial cells [Hebert 2004] - stoichiometry of 1Na:1K:2Cl [Russell 2000] - cloned [Payne 1995]
NMNATn	3	Schweiger M, Hennig K, Lerner F, Niere M, Hirsch-Kauffmann M, Specht T, Weise C, Oei SL, Ziegler M.	Characterization of recombinant human nicotinamide mononucleotide adenylyl transferase (NMNAT), a nuclear enzyme essential for NAD synthesis.	FEBS Lett	2001	11248244	IT
NMNATr	3	Raffaelli N, Sorci L, Amici A, Emanuelli M, Mazzola F, Magni G.	Identification of a novel human nicotinamide mononucleotide adenylyltransferase.	Biochem Biophys Res Commun	2003	12359228	IT
NMPTRCOX	2	Frydman J, Ruiz O, Robetto E, Dellacha JM, Frydman RB	Modulation of insulin induced ornithine decarboxylase by putrescine and methylputrescines in H-35 hepatoma cells	Mol Cell Biochem	1991	2051998	these compounds are found in mamallian cells according to the reference--so physiological evidence diamine oxidase from pig apparantly does NOT do this reaction, but may do others (PMID 3111885)
NMPTRCOX	2	Frydman RB, Ruiz O, Kreisel M, Bachrach U	Oxidation of N-alkyl and C-alkylputrescines by diamine oxidases	FEBS Lett	1987	3111885	these compounds are found in mamallian cells according to the reference--so physiological evidence diamine oxidase from pig apparantly does NOT do this reaction, but may do others (PMID 3111885)
NNAT	3	Yalowitz JA, Xiao S, Biju MP, Antony AC, Cummings OW, Deeg MA, Jayaram HN.	Characterization of human brain nicotinamide 5'-mononucleotide adenylyltransferase-2 and expression in human pancreas.	Biochem J	2004	14516279	IT
NNAT	3	Zhou T, Kurnasov O, Tomchick DR, Binns DD, Grishin NV, Marquez VE, Osterman AL, Zhang H.	Structure of human nicotinamide/nicotinic acid mononucleotide adenylyltransferase. Basis for the dual substrate specificity and activation of the oncolytic agent tiazofurin	J Biol Chem	2002		IT
NNATm	3	Zhang X, Kurnasov OV, Karthikeyan S, Grishin NV, Osterman AL, Zhang H.	Structural characterization of a human cytosolic NMN/NaMN adenylyltransferase and implication in human NAD biosynthesis.	J Biol Chem	2003	12574164	IT
NNATn	3	Emanuelli M, Carnevali F, Saccucci F, Pierella F, Amici A, Raffaelli N, Magni G.	Molecular cloning, chromosomal localization, tissue mRNA levels, bacterial expression, and enzymatic properties of human NMN adenylyltransferase.	J Biol Chem	2001	11027696	IT
NNDPR	2	Okuno E, White RJ, Schwarcz R.	Quinolinic acid phosphoribosyltransferase: purification and partial characterization from human liver and brain.	J Biochem (Tokyo)	1988	3139649	IT
NNDPR	2	Fukuoka SI, Nyaruhucha CM, Shibata K.	Characterization and functional expression of the cDNA encoding human brain quinolinate phosphoribosyltransferase.	Biochim Biophys Acta	1998	9473669	IT
NNMT	3	Aksoy S, Szumlanski CL, Weinshilboum RM.	Human liver nicotinamide N-methyltransferase. cDNA cloning, expression, and biochemical characterization.	J Biol Chem	1994	8182091	IT can be further oxidzied to n-methyl-pyridone-2-carbamide and n-methyl-pyridone-4-carbamide (but rxn in kegg seems to be wrong --> not included yet)
NOS1	3	Brenman JE, Chao DS, Xia H, Aldape K, Bredt DS	Nitric oxide synthase complexed with dystrophin and absent from skeletal muscle sarcolemma in Duchenne muscular dystrophy	Cell	1995	7545544	split form based on references
NOS1	3	Bloch KD, Wolfram JR, Brown DM, Roberts JD Jr, Zapol DG, Lepore JJ, Filippov G, Thomas JE, Jacob HJ, Bloch DB.	Three members of the nitric oxide synthase II gene family (NOS2A, NOS2B, and NOS2C) colocalize to human chromosome 17.	Genomics	1995	7558036	split form based on references
NOS1	3	Geoffrey M. Cooper	The Cell A Molecular Approach		2000		split form based on references
NS26T2g	0	Ikehara Y, Kojima N, Kurosawa N, Kudo T, Kono M, Nishihara S, Issiki S, Morozumi K, Itzkowitz S, Tsuda T, Nishimura SI, Tsuji S, Narimatsu H	Cloning and expression of a human gene encoding an N-acetylgalactosamine-alpha2,6-sialyltransferase (ST6GalNAc I): a candidate for synthesis of cancer-associated sialyl-Tn antigens	Glycobiology	1999	10536037	Siat7ap expressed in intestine [Ikehara et al, Glycobiology 1999]
NTD1	3	Rampazzo C, Gallinaro L, Milanesi E, Frigimelica E, Reichard P, Bianchi V	A deoxyribonucleotidase in mitochondria: involvement in regulation of dNTP pools and possible link to genetic disease.	Proc Natl Acad Sci U S A	2000	10899995	IT 30833.1: highest activity on 5'dUMP (100%), follwoed by 5'dIMP (96%): rampazzo et al, 2000; acts also on 3'dTMP
NTD1	3	Oka J, Matsumoto A, Hosokawa Y, Inoue S.	Molecular cloning of human cytosolic purine 5'-nucleotidase.	Biochem Biophys Res Commun	1994		IT 30833.1: highest activity on 5'dUMP (100%), follwoed by 5'dIMP (96%): rampazzo et al, 2000; acts also on 3'dTMP
NTD2	3	Amici A, Magni G.	Human erythrocyte pyrimidine 5'-nucleotidase, PN-I.	Arch Biochem Biophys	2002	11795870	IT
NTD3	3	Hunsucker SA, Spychala J, Mitchell BS.	Human cytosolic 5'-nucleotidase I: characterization and role in nucleoside analog resistance.	J Biol Chem	2001	11133996	IT 93034: highest affinity with dCMP, but acts also on AMP and IMP. ADP was necessary for max activity: Hunsucker et al 2001

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NTD7e	3	Hashikawa T, Takedachi M, Terakura M, Saho T, Yamada S, Thompson LF, Shimabukuro Y, Murakami S.	Involvement of CD73 (ecto-5'-nucleotidase) in adenosine generation by human gingival fibroblasts.	J Dent Res	2003	14578500	IT
NTP3e	3	Smith TM, Hicks-Berger CA, Kim S, Kirley TL.	Cloning, expression, and characterization of a soluble calcium-activated nucleotidase, a human enzyme belonging to a new family of extracellular nucleotidases.	Arch Biochem Biophys	2002	12234496	IT preferred substrates depends on publication: (Smith, 2002): UDP>GDP> UTP>GTP>ADP>ATP (since activity with ADP and ATP were really weak I did not included these reactions) (Murphy , 2003): GDP>UDP>IDP calcium dependent activation
NTP3e	3	Murphy DM, Ivanenkov VV, Kirley TL.	Bacterial expression and characterization of a novel, soluble, calcium-binding, and calcium-activated human nucleotidase.	Biochemistry	2003	12600208	IT preferred substrates depends on publication: (Smith, 2002): UDP>GDP> UTP>GTP>ADP>ATP (since activity with ADP and ATP were really weak I did not included these reactions) (Murphy , 2003): GDP>UDP>IDP calcium dependent activation
NTPP9	3	Lin S, McLennan AG, Ying K, Wang Z, Gu S, Jin H, Wu C, Liu W, Yuan Y, Tang R, Xie Y, Mao Y.	Cloning, expression, and characterization of a human inosine triphosphate pyrophosphatase encoded by the itpa gene.	J Biol Chem	2001	11278832	enzyme can also act on ATP, dATp, CTP, dCTP,UTP, dTTP, GTP, dGTP. However, the activity for those compounds were almost 100 time smaller than for XTP, ITP, dITP. I would only consider these compounds for hte enzyme if there is no other enzyme that uses these compounds better. IT
O2Stx	2	Archibald F.	Oxygen toxicity and the health and survival of eukaryote cells: a new piece is added to the puzzle.	Proc Natl Acad Sci U S A	2003	12939409	- inferred that superoxide can diffuse across cell membranes; according to [Archibald 2003], superoxide dismutase can "catalyze the dismutation of two superoxide anions to O2 + H2O2 at superoxide diffusion-limited rates, making them the fastest enzymes known"
O2tm	1	Koyama T, Kinjo M, Araiso T.	Oxygen diffusion through mitochondrial membranes.	Adv Exp Med Biol	1989	2551143	- Additional info by RS/TV - No genes found. - Some data found for the existence of a diffusion mechanism for oxygen across the mitochondrial membrane. Oxygen gradients were recorded in the following paper: Koyama T, Kinjo M, Araiso T. Adv Exp Med Biol. 1989;248:763-7. - oxygen assumed to be transported freely into all compartments
OCBTm	3	Horwich AL, Fenton WA, Williams KR, Kalousek F, Kraus JP, Doolittle RF, Konigsberg W, Rosenberg LE	Structure and expression of a complementary DNA for the nuclear coded precursor of human mitochondrial ornithine transcarbamylase	Science	1984	6372096	SAB reviewed - Additional information added by RS/TV: - Mitochondrial according to Entrez Gene database - Expressed solely in the liver and small intestine (Dekaney CM, Wu G, Jaeger LA. Pediatr Res. 2003 Feb;53(2):274-80.)
OCBTm	3	Dekaney CM, Wu G, Jaeger LA.	Gene expression and activity of enzymes in the arginine biosynthetic pathway in porcine fetal small intestine.	Pediatr Res	2003	12538786	SAB reviewed - Additional information added by RS/TV: - Mitochondrial according to Entrez Gene database - Expressed solely in the liver and small intestine (Dekaney CM, Wu G, Jaeger LA. Pediatr Res. 2003 Feb;53(2):274-80.)
OCOAT1m	3	Fukao T, Mitchell GA, Song XQ, Nakamura H, Kassovska-Bratinova S, Orii KE, Wraith JE, Besley G, Wanders RJ, Niezen-Koning KE, Berry GT, Palmieri M, Kondo N.	Succinyl-CoA:3-ketoacid CoA transferase (SCOT): cloning of the human SCOT gene, tertiary structural modeling of the human SCOT monomer, and characterization of three pathogenic mutations.		2000	10964512	tissue - 5019 (abundant in heart, followed in order by kidney, brain, and muscle, whereas in liver it is undetectable; also detectable in leukocytes and fibroblasts.); 64064 (testis specific) mitochondrial - Harvester, UniProt, GeneCards MM - Checked over by RS/TV
OCOAT1m	3	Tanaka H, Kohroki J, Iguchi N, Onishi M, Nishimune Y.	Cloning and characterization of a human orthologue of testis-specific succinyl CoA: 3-oxo acid CoA transferase (Scot-t) cDNA.		2002	11756565	tissue - 5019 (abundant in heart, followed in order by kidney, brain, and muscle, whereas in liver it is undetectable; also detectable in leukocytes and fibroblasts.); 64064 (testis specific) mitochondrial - Harvester, UniProt, GeneCards MM - Checked over by RS/TV

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OIVD1m	3	Lau KS, Herring WJ, Chuang JL, McKean M, Danner DJ, Cox RP, Chuang DT.	Structure of the gene encoding dihydrolipoyl transacylase (E2) component of human branched chain alpha-keto acid dehydrogenase complex and characterization of an E2 pseudogene.		1992	1429740	This process, carried out by the mitochondrial branched-chain alpha-ketoacid dehydrogenase complex, consists of five distinct reactions. First, alpha-ketoisocaproate is oxidatively decarboxylated, catalyzed by the E1 component of the complex. Lipoamide associated with E1 is reduced at the same time. Next, the isovaleryl group derived from alpha-ketoisocaproate is transferred to coenzyme A in two steps catalyzed by the E2 component of the complex (dihydrolipoyl transacetylase). Finally, the oxidized form of lipoamide is regenerated and electrons are transferred to NAD+ in two steps catalyzed by the E3 component of the complex (dihydrolipoyl dehydrogenase). [Reactome]
OIVD1m	3	Fisher CW, Chuang JL, Griffin TA, Lau KS, Cox RP, Chuang DT.	Molecular phenotypes in cultured maple syrup urine disease cells. Complete E1 alpha cDNA sequence and mRNA and subunit contents of the human branched chain alpha-keto acid dehydrogenase complex.		1989	2914958	This process, carried out by the mitochondrial branched-chain alpha-ketoacid dehydrogenase complex, consists of five distinct reactions. First, alpha-ketoisocaproate is oxidatively decarboxylated, catalyzed by the E1 component of the complex. Lipoamide associated with E1 is reduced at the same time. Next, the isovaleryl group derived from alpha-ketoisocaproate is transferred to coenzyme A in two steps catalyzed by the E2 component of the complex (dihydrolipoyl transacetylase). Finally, the oxidized form of lipoamide is regenerated and electrons are transferred to NAD+ in two steps catalyzed by the E3 component of the complex (dihydrolipoyl dehydrogenase). [Reactome]
OMPDC	3	Suttle DP, Bugg BY, Winkler JK, Kanalas JJ.	Molecular cloning and nucleotide sequence for the complete coding region of human UMP synthase.	Proc Natl Acad Sci U S A	1988	3279416	IT no infos about localization in cell
OMPDC	3	Patterson D, Jones C, Morse H, Rumsby P, Miller Y, Davis R.	Structural gene coding for multifunctional protein carrying orotate phosphoribosyltransferase and OMP decarboxylase activity is located on long arm of human chromosome 3.	Somatic Cell Genet	1983	6574608	IT no infos about localization in cell
OMPDC	3	McClard RW, Black MJ, Livingstone LR, Jones ME.	Isolation and initial characterization of the single polypeptide that synthesizes uridine 5'-monophosphate from orotate in Ehrlich ascites carcinoma. Purification by tandem affinity chromatography of uridine-5'-monophosphate synthase.	Biochemistry	1980	6893554	IT no infos about localization in cell
OMPDC	3	Suchi M, Mizuno H, Kawai Y, Tsuboi T, Sumi S, Okajima K, Hodgson ME, Ogawa H, Wada Y.	Molecular cloning of the human UMP synthase gene and characterization of point mutations in two hereditary orotic aciduria families.	Am J Hum Genet	1997	9042911	IT no infos about localization in cell
ORNDC	3	Hsieh JT, Denning MF, Heidel SM, Verma AK.	Expression of human chromosome 2 ornithine decarboxylase gene in ornithine decarboxylase-deficient Chinese hamster ovary cells	Cancer Res	1990	2317811	Gene and enzyme characterized
ORNDC	3	Zhu MY, Iyo A, Piletz JE, Regunathan S	Expression of human arginine decarboxylase, the biosynthetic enzyme for agmatine	Biochim Biophys Acta	2004		Gene and enzyme characterized
ORNTArm	3	Shen BW, Hennig M, Hohenester E, Jansonius JN, Schirmer T	Crystal structure of human recombinant ornithine aminotransferase	J Mol Biol	1998	9514741	Enzyme and reaction characterized
P45011A1m	3	Sakaki T, Inouye K.	Practical application of mammalian cytochrome P450.	J Biosci Bioeng	2000	16232916	mit- see refs specificity: adrenal cortex, ovary, testis, placenta, giant trophoblast Catalyzes the side-chain cleavage reaction of cholesterol to pregnenolone Further details of 4mptnl not known - degraded to isocaproic acid and isocapryl alcohol (see PMID: 8645003) - details and downstream metabolism not known. NJ
P45017A2r	3	Payne AH, Hales DB	Overview of steroidogenic enzymes in the pathway from cholesterol to active steroid hormones	Endocrine Reviews	2004		ER - by refs - also noted to be microsomal, need to return and review lit again specificity: leydig cells (testis), adrenal cortex, thecal cells (ovary) Conversion of pregnenolone and progesterone to their 17- alpha hydroxylated products and subsequently to dehydroepiandrosterone (DHEA) and androstenedione. Catalyzes both the 17-alpha-hydroxylation and the 17,20-lyase reaction. Involved in sexual development during fetal life and a puberty. NJ
P45017A2r	3	Korzekwa KR, Trager WF, Mancewicz J, Osawa Y	Studies on the mechanism of aromatase and other cytochrome P450 mediated deformylation reactions	J Steroid Biochem Mol Biol	1993		ER - by refs - also noted to be microsomal, need to return and review lit again specificity: leydig cells (testis), adrenal cortex, thecal cells (ovary) Conversion of pregnenolone and progesterone to their 17- alpha hydroxylated products and subsequently to dehydroepiandrosterone (DHEA) and androstenedione. Catalyzes both the 17-alpha-hydroxylation and the 17,20-lyase reaction. Involved in sexual development during fetal life and a puberty. NJ

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P45017A2r	3	Korzekwa KR, Trager WF, Mancewicz J, Osawa Y	Studies on the mechanism of aromatase and other cytochrome P450 mediated deformylation reactions	J Steroid Biochem Mol Biol	1993		ER - by refs - also noted to be microsomal, need to return and review lit again specificity: leydig cells (testis), adrenal cortex, thecal cells (ovary) Conversion of pregnenolone and progesterone to their 17- alpha hydroxylated products and subsequently to dehydroepiandrosterone (DHEA) and androstenedione. Catalyzes both the 17-alpha-hydroxylation and the 17,20-lyase reaction. Involved in sexual development during fetal life and a puberty. NJ
P4501B1r	3	Tang YM, Wo YY, Stewart J, Hawkins AL, Griffin CA, Sutter TR, Greenlee WF.	Isolation and characterization of the human cytochrome P450 CYP1B1 gene.	J Biol Chem	1996	8910454	ER - uniprot The enzyme encoded by this gene localizes to the endoplasmic reticulum and metabolizes procarcinogens such as polycyclic aromatic hydrocarbons and 17beta-estradiol. Mutations in this gene have been associated with primary congenital glaucoma; therefore it is thought that the enzyme also metabolizes a signaling molecule involved in eye development, possibly a steroid. biochem and gene exp - Tang ref NJ
P4502A6	3	Oscarson M, Gullsten H, Rautio A, Bernal ML, Sinues B, Dahl ML, Stengard JH, Pelkonen O, Raunio H, Ingelman-Sundberg M.	Genotyping of human cytochrome P450 2A6 (CYP2A6), a nicotine C-oxidase.	FEBS Let	1998	9827545	ER - placed on cytsolic side because of xenobiotic rxn. CYP2A6, encodes a member of the cytochrome P450 superfamily of enzymes. The cytochrome P450 proteins are monooxygenases which catalyze many reactions involved in drug metabolism and synthesis of cholesterol, steroids and other lipids. This protein localizes to the endoplasmic reticulum and its expression is induced by phenobarbital. The enzyme is known to hydroxylate coumarin, and also metabolizes nicotine, aflatoxin B1, nitrosamines, and some pharmaceuticals. Individuals with certain allelic variants are said to have a poor metabolizer phenotype, meaning they do not efficiently metabolize coumarin or nicotine. This gene is part of a large cluster of cytochrome P450 genes from the CYP2A, CYP2B and CYP2F subfamilies on chromosome 19q. The gene was formerly referred to as CYP2A3; however, it has been renamed CYP2A6. Oscarson - 2A6 NJ NJ
P4502C18	2	Goldstein JA, Faletto MB, Romkes-Sparks M, Sullivan T, Kitareewan S, Raucy JL, Lasker JM, Ghanayem BI.	Evidence that CYP2C19 is the major (S)-mephenytoin 4'-hydroxylase in humans.	Biochemistry	1994	8110777	ER - placed on cytsolic side because of xenobiotic rxn. NJ
P4502C19	3	Meier UT, Meyer UA.	Genetic polymorphism of human cytochrome P-450 (S)-mephenytoin 4-hydroxylase. Studies with human autoantibodies suggest a functionally altered cytochrome P-450 isozyme as cause of the genetic deficiency.	Biochemistry	1987	3442670	ER - placed on cytsolic side because of xenobiotic rxn. This protein localizes to the endoplasmic reticulum and is known to metabolize many xenobiotics, including the anticonvulsive drug mephenytoin, omeprazole, diazepam and some barbiturates. Polymorphism within this gene is associated with variable ability to metabolize mephenytoin, known as the poor metabolizer and extensive metabolizer phenotypes. NJ

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
P4502C9	3	Umbenhauer DR, Martin MV, Lloyd RS, Guengerich FP.	Cloning and sequence determination of a complementary DNA related to human liver microsomal cytochrome P-450 S-mephenytoin 4-hydroxylase.	Biochemistry	1987		ER - placed on cytsolic side because of xenobiotic rxn. This protein localizes to the endoplasmic reticulum and its expression is induced by rifampin. The enzyme is known to metabolize many xenobiotics, including phenytoin, tolbutamide, ibuprofen and S-warfarin. Studies identifying individuals who are poor metabolizers of phenytoin and tolbutamide suggest that this gene is polymorphic. NJ
P4502C9	3	Meehan RR, Gosden JR, Rout D, Hastie ND, Friedberg T, Adesnik M, Buckland R, van Heyningen V, Fletcher J, Spurr NK, et al.	Human cytochrome P-450 PB-1: a multigene family involved in mephenytoin and steroid oxidations that maps to chromosome 10.	Am J Hum Genet	1988	2827463	ER - placed on cytsolic side because of xenobiotic rxn. This protein localizes to the endoplasmic reticulum and its expression is induced by rifampin. The enzyme is known to metabolize many xenobiotics, including phenytoin, tolbutamide, ibuprofen and S-warfarin. Studies identifying individuals who are poor metabolizers of phenytoin and tolbutamide suggest that this gene is polymorphic. NJ
P4502C92	3	Miyazawa M, Shindo M, Shimada T.	Metabolism of (+)- and (-)-limonenes to respective carveols and perillyl alcohols by CYP2C9 and CYP2C19 in human liver microsomes.	Drug Metab Dispos	2002	11950794	ER bound enzyme - assumed to take place on outer membrane (no evidence to support 1 direction vs another). specificity: liver (possibly intestines) see Miyazawa ref PMID 11950794 for rxn specificity NJ
P4502E1	3	Umeno M, McBride OW, Yang CS, Gelboin HV, Gonzalez FJ.	Human ethanol-inducible P450IIE1: complete gene sequence, promoter characterization, chromosome mapping, and cDNA-directed expression.	Biochemistry	1988	3233219	ER - placed on cytsolic side because of xenobiotic rxn. This protein localizes to the endoplasmic reticulum and is induced by ethanol, the diabetic state, and starvation. The enzyme metabolizes both endogenous substrates, such as ethanol, acetone, and acetal, as well as exogenous substrates including benzene, carbon tetrachloride, ethylene glycol, and nitrosamines which are premutagens found in cigarette smoke. Due to its many substrates, this enzyme may be involved in such varied processes as gluconeogenesis, hepatic cirrhosis, diabetes, and cancer. NJ
P4502F1	3	Nhamburo PT, Kimura S, McBride OW, Kozak CA, Gelboin HV, Gonzalez FJ.	The human CYP2F gene subfamily: identification of a cDNA encoding a new cytochrome P450, cDNA-directed expression, and chromosome mapping.	Biochemistry	1990	1974816	ER - placed on cytsolic side because of xenobiotic rxn. This protein localizes to the endoplasmic reticulum and is known to dehydrogenate 3-methylindole, an endogenous toxin derived from the fermentation of tryptophan, as well as xenobiotic substrates such as naphthalene and ethoxycoumarin. This gene is part of a large cluster of cytochrome P450 genes from the CYP2A, CYP2B and CYP2F subfamilies on chromosome 19q. NJ
P4503A4	3	Molowa DT, Schuetz EG, Wrighton SA, Watkins PB, Kremers P, Mendez-Picon G, Parker GA, Guzelian PS.	Complete cDNA sequence of a cytochrome P-450 inducible by glucocorticoids in human liver.	Proc Natl Acad Sci U S A	1986	3460094	ER -does not specifiy inner vs outer - assumed outer membrane since aflatoxin is an exogenous metabolite This protein localizes to the endoplasmic reticulum and its expression is induced by glucocorticoids and some pharmacological agents. This enzyme is involved in the metabolism of approximately half the drugs which are are used today, including acetaminophen, codeine, cyclosporin A, diazepam and erythromycin. The enzyme also metabolizes some steroids and carcinogens. This gene is part of a cluster of cytochrome P450 genes on chromosome 7q21.1. Previously another CYP3A gene, CYP3A3, was thought to exist; however, it is now thought that this sequence represents a transcript variant of CYP3A4. NJ
P4503A4	3	Finta C, Zaphiropoulos PG.	Intergenic mRNA molecules resulting from trans-splicing.	J Biol Chem	2002	11726664	ER -does not specifiy inner vs outer - assumed outer membrane since aflatoxin is an exogenous metabolite This protein localizes to the endoplasmic reticulum and its expression is induced by glucocorticoids and some pharmacological agents. This enzyme is involved in the metabolism of approximately half the drugs which are are used today, including acetaminophen, codeine, cyclosporin A, diazepam and erythromycin. The enzyme also metabolizes some steroids and carcinogens. This gene is part of a cluster of cytochrome P450 genes on chromosome 7q21.1. Previously another CYP3A gene, CYP3A3, was thought to exist; however, it is now thought that this sequence represents a transcript variant of CYP3A4. NJ

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P4503A7r	3	Komori M, Nishio K, Ohi H, Kitada M, Kamataki T.	Molecular cloning and sequence analysis of cDNA containing the entire coding region for human fetal liver cytochrome P-450.	J Biochem (Tokyo)	1989	2722762	ER - uniprot biochem act, seq see Komori ref This enzyme hydroxylates testosterone and dehydroepiandrosterone 3-sulphate, which is involved in the formation of estriol during pregnancy. The enzyme also metabolizes some drugs such as aflatoxin B1. This gene is part of a cluster of cytochrome P450 genes on chromosome 7q21.1. Transcript variants have been described, but it is not known whether these transcripts are normally produced. NJ
P4504B1r	3	Nhamburo PT, Gonzalez FJ, McBride OW, Gelboin HV, Kimura S.	Identification of a new P450 expressed in human lung: complete cDNA sequence, cDNA-directed expression, and chromosome mapping.	Biochemistry	1989		Membrane-bound. Endoplasmic reticulum. - uniprot P450 can be induced to high levels in liver and other tissues by various foreign compounds, including drugs, pesticides, and carcinogens. Rxn specificity - from Lewis ref (which refers to rendic ref). NJ
P4504B1r	3	Rendic S.	Summary of information on human CYP enzymes: human P450 metabolism data.	Drug Metab Rev	2002	11996015	Membrane-bound. Endoplasmic reticulum. - uniprot P450 can be induced to high levels in liver and other tissues by various foreign compounds, including drugs, pesticides, and carcinogens. Rxn specificity - from Lewis ref (which refers to rendic ref). NJ
P4504F121r	3	Lewis DF.	57 varieties: the human cytochromes P450.	Pharmacogenomics	2004	15579107	ER - uniprot - inner vs outer membrane not specified, assumed inner specific hydroxylation product not defined, general omega hydroxy arachidonic acid used When expressed in yeast the enzyme is capable of oxdizing arachidonic acid; however, its physiological function has not been determined. This gene is part of a cluster of cytochrome P450 genes on chromosome 19.
P4504F122r	3	Kikuta Y, Kusunose E, Kondo T, Yamamoto S, Kinoshita H, Kusunose M.	Cloning and expression of a novel form of leukotriene B4 omega-hydroxylase from human liver.	FEBS Lett	1994	8026587	ER - uniprot - inner vs outer membrane not specified, assumed inner kikuta (1993) ref for exp evidence leukotriene B4 specificty not as good as cyp4f2 - see lewis ref Cyp4f2 see Kikuta 1994 ref For possible additional, alternative substrates see PMID: 15145985. This protein localizes to the endoplasmic reticulum. The enzyme starts the process of inactivating and degrading leukotriene B4, a potent mediator of inflammation. This gene is part of a cluster of cytochrome P450 genes on chromosome 19. NJ
P4504F122r	3	Kikuta Y, Kusunose E, Endo K, Yamamoto S, Sogawa K, Fujii-Kuriyama Y, Kusunose M.	A novel form of cytochrome P-450 family 4 in human polymorphonuclear leukocytes. cDNA cloning and expression of leukotriene B4 omega-hydroxylase.	J Biol Chem	1993	8486631	ER - uniprot - inner vs outer membrane not specified, assumed inner kikuta (1993) ref for exp evidence leukotriene B4 specificty not as good as cyp4f2 - see lewis ref Cyp4f2 see Kikuta 1994 ref For possible additional, alternative substrates see PMID: 15145985. This protein localizes to the endoplasmic reticulum. The enzyme starts the process of inactivating and degrading leukotriene B4, a potent mediator of inflammation. This gene is part of a cluster of cytochrome P450 genes on chromosome 19. NJ

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P4504F122r	3	Le Quere V, Plee-Gautier E, Potin P, Madec S, Salaun JP.	Human CYP4F3s are the main catalysts in the oxidation of fatty acid epoxides.	J Lipid Res	2004	15145985	ER - uniprot - inner vs outer membrane not specified, assumed inner kikuta (1993) ref for exp evidence leukotriene B4 specificty not as good as cyp4f2 - see lewis ref Cyp4f2 see Kikuta 1994 ref For possible additional, alternative substrates see PMID: 15145985. This protein localizes to the endoplasmic reticulum. The enzyme starts the process of inactivating and degrading leukotriene B4, a potent mediator of inflammation. This gene is part of a cluster of cytochrome P450 genes on chromosome 19. NJ
P4507A1r	3	Russell DW	The enzymes, regulation, and genetics of bile acid synthesis	Annu Rev Biochem	2003		ER: uniprot NJ
P4508B11r	3	Gafvels M, Olin M, Chowdhary BP, Raudsepp T, Andersson U, Persson B, Jansson M, Bjorkhem I, Eggertsen G	Structure and chromosomal assignment of the sterol 12-alpha-hydroxylase gene (cyp8b1) in human and mouse	Genomics	1999		ER - uniprot NADH/NADPH can be used as cofactors specificity: liver (also kidney to a smaller degree) Involved in bile acid synthesis and is responsible for the conversion of 7 alpha-hydroxy-4-cholesten-3-one into 7 alpha, 12 alpha-dihydroxy-4-cholesten-3-one. Responsible for the balance between formation of cholic acid and chenodeoxycholic acid. Has a rather broad substrate specificity including a number of 7-alpha- hydroxylated C27 steroids. NJ
P450LTB4r	2	Soberman RJ.	Cytochrome P-450LTB and inactivation of leukotriene B4.	Methods Enzymol	1990	2172735	ER localization inferred by similarity w/ preceding rxn (P450F122r). See refs for supporting physiological data (PMID: 2172735, etc). No GPR identified yet. NJ
P5CDm	3	Hu CA, Lin WW, Valle D.	Cloning, characterization, and expression of cDNAs encoding human delta 1-pyrroline-5-carboxylate dehydrogenase.		1996	8621661	Mitochondrial matrix; preferred cofactor NAD - Hu et al. J Biol Chem. 1996 Apr 19;271(16):9795-800. Genetic data - Geraghty et. al. Hum Mol Genet. 1998 Sep;7(9):1411-5. Reversible according to Reactome database predominantly in liver
P5CDm	3	Geraghty MT, Vaughn D, Nicholson AJ, Lin WW, Jimenez-Sanchez G, Obie C, Flynn MP, Valle D, Hu CA.	Mutations in the Delta1-pyrroline 5-carboxylate dehydrogenase gene cause type II hyperprolinemia.		1998	9700195	Mitochondrial matrix; preferred cofactor NAD - Hu et al. J Biol Chem. 1996 Apr 19;271(16):9795-800. Genetic data - Geraghty et. al. Hum Mol Genet. 1998 Sep;7(9):1411-5. Reversible according to Reactome database predominantly in liver
P5CR	3	Merrill MJ, Yeh GC, Phang JM.	Purified human erythrocyte pyrroline-5-carboxylate reductase. Preferential oxidation of NADPH.	J Biol Chem	1989	2722838	prefers NADPH according to ref
PAFH	3	Hattori M, Adachi H, Tsujimoto M, Arai H, Inoue K.	Miller-Dieker lissencephaly gene encodes a subunit of brain platelet-activating factor acetylhydrolase [corrected]	Nature	1994		cytoplasmic - uniprot and refs TISSUE SPECIFICITY: In the adult, expressed in brain, skeletal muscle, kidney, thymus, spleen, colon, testis, ovary and peripheral blood leukocytes. In the fetus, highest expression occurs in brain. Specificity for isoform 2: high in B and T lymphocytes. In brain, expression is restricted to amygdala and frontal cortex. Isoform 2: cloning and expression ref: Hattori (1996) Cytosolic PAF-AH IB is formed of three subunits of 45 kDa (alpha), 30 kDa (beta) and 29 kDa (gamma). The catalytic activity of the enzyme resides in the beta and gamma subunits, whereas the alpha subunit has regulatory activity. Trimer formation is not essential for the catalytic activity. PAFAH1B1 was identified as encoding a gene that when mutated or lost caused the lissencephaly associated with Miller-Dieker lissencephaly syndrome. PAFAH1B1 encodes the non-catalytic alpha subunit of the intracellular Ib isoform of platelet-activating factor acteylhydrolase, a heterotrimeric enzyme that specifically catalyzes the removal of the acetyl group at the SN-2 position of platelet-activating factor (identified as 1-O-alkyl-2- NJ

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PAFH	3	Adachi H, Tsujimoto M, Hattori M, Arai H, Inoue K.	cDNA cloning of human cytosolic platelet-activating factor acetylhydrolase gamma-subunit and its mRNA expression in human tissues.	Biochem Biophys Res Commun	1995	7669037	cytoplasmic - uniprot and refs TISSUE SPECIFICITY: In the adult, expressed in brain, skeletal muscle, kidney, thymus, spleen, colon, testis, ovary and peripheral blood leukocytes. In the fetus, highest expression occurs in brain. Specificity for isoform 2: high in B and T lymphocytes. In brain, expression is restricted to amygdala and frontal cortex. Isoform 2: cloning and expression ref: Hattori (1996) Cytosolic PAF-AH IB is formed of three subunits of 45 kDa (alpha), 30 kDa (beta) and 29 kDa (gamma). The catalytic activity of the enzyme resides in the beta and gamma subunits, whereas the alpha subunit has regulatory activity. Trimer formation is not essential for the catalytic activity. PAFAH1B1 was identified as encoding a gene that when mutated or lost caused the lissencephaly associated with Miller-Dieker lissencephaly syndrome. PAFAH1B1 encodes the non-catalytic alpha subunit of the intracellular Ib isoform of platelet-activating factor acteylhydrolase, a heterotrimeric enzyme that specifically catalyzes the removal of the acetyl group at the SN-2 position of platelet-activating factor (identified as 1-O-alkyl-2 NJ
PAFH	3	Hattori K, Adachi H, Matsuzawa A, Yamamoto K, Tsujimoto M, Aoki J, Hattori M, Arai H, Inoue K.	cDNA cloning and expression of intracellular platelet activating factor (PAF) acetylhydrolase II. Its homology with plasma PAF acetylhydrolase.	J Biol Chem	1996	8955149	cytoplasmic - uniprot and refs TISSUE SPECIFICITY: In the adult, expressed in brain, skeletal muscle, kidney, thymus, spleen, colon, testis, ovary and peripheral blood leukocytes. In the fetus, highest expression occurs in brain. Specificity for isoform 2: high in B and T lymphocytes. In brain, expression is restricted to amygdala and frontal cortex. Isoform 2: cloning and expression ref: Hattori (1996) Cytosolic PAF-AH IB is formed of three subunits of 45 kDa (alpha), 30 kDa (beta) and 29 kDa (gamma). The catalytic activity of the enzyme resides in the beta and gamma subunits, whereas the alpha subunit has regulatory activity. Trimer formation is not essential for the catalytic activity. PAFAH1B1 was identified as encoding a gene that when mutated or lost caused the lissencephaly associated with Miller-Dieker lissencephaly syndrome. PAFAH1B1 encodes the non-catalytic alpha subunit of the intracellular Ib isoform of platelet-activating factor acteylhydrolase, a heterotrimeric enzyme that specifically catalyzes the removal of the acetyl group at the SN-2 position of platelet-activating factor (identified as 1-O-alkyl-2 NJ
PAFHe	3	Stafforini DM, Satoh K, Atkinson DL, Tjoelker LW, Eberhardt C, Yoshida H, Imaizumi T, Takamatsu S, Zimmerman GA, McIntyre TM, Gray PW, Prescott SM.	Platelet-activating factor acetylhydrolase deficiency. A missense mutation near the active site of an anti-inflammatory phospholipase.	J Clin Invest	2005	8675689	localization: plasma/extracellular (uniprot) specificity: plasma Modulates the action of platelet-activating factor (PAF) by hydrolyzing the sn-2 ester bond to yield the biologically inactive lyso-PAF. Has a specificity for substrates with a short residue at the sn-2 position. It is inactive against long-chain phospholipids. See PMID: 8675689 NJ
PAPStg	3	Kamiyama S, Suda T, Ueda R, Suzuki M, Okubo R, Kikuchi N, Chiba Y, Goto S, Toyoda H, Saigo K, Watanabe M, Narimatsu H, Jigami Y, Nishihara S	Molecular cloning and identification of 3'-phosphoadenosine 5'-phosphosulfate transporter	J Biol Chem	2003	12716889	- 48.1% identity w/ Drosophila protein [Kamiyama 2003] - Golgi [Kamiyama 2003] - PAPS transport [Kamiyama 2003] - high in placenta and pancreas, low in colon and heart [Kamiyama 2003]
PCHOLP_hs	3	Colley WC, Sung TC, Roll R, Jenco J, Hammond SM, Altshuller Y, Bar-Sagi D, Morris AJ, Frohman MA.	Phospholipase D2, a distinct phospholipase D isoform with novel regulatory properties that provokes cytoskeletal reorganization.	Curr Biol	1997	9395408	cytosol - uniprot - Colley ref - PMID 9395408 NJ
PCHOLP_hs	3	Lopez I, Arnold RS, Lambeth JD.	Cloning and initial characterization of a human phospholipase D2 (hPLD2). ADP-ribosylation factor regulates hPLD2.	J Biol Chem	1998	9582313	cytosol - uniprot - Colley ref - PMID 9395408 NJ
PCHOLPm_hs	3	Hammond SM, Altshuller YM, Sung TC, Rudge SA, Rose K, Engebrecht J, Morris AJ, Frohman MA.	Human ADP-ribosylation factor-activated phosphatidylcholine-specific phospholipase D defines a new and highly conserved gene family.	J Biol Chem	1995	8530346	perinuclear regions for PLD1 - need to doublecheck for mit specificity - localization: Colley PMID 9395408 Tissue specificity: Expressed abundantly in the pancreas and heart and at high levels in brain, placenta, spleen, uterus and small intestine. Implicated as a critical step in numerous cellular pathways, including signal transduction, membrane trafficking, and the regulation of mitosis. May be involved in the regulation of perinuclear intravesicular membrane traffic (By similarity). NJ

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PCHOLPm_hs	3	Cases S, Stone SJ, Zhou P, Yen E, Tow B, Lardizabal KD, Voelker T, Farese RV Jr.	Cloning of DGAT2, a second mammalian diacylglycerol acyltransferase, and related family members.	J Biol Chem	2001	11481335	perinuclear regions for PLD1 - need to doublecheck for mit specificity - localization: Colley PMID 9395408 Tissue specificity: Expressed abundantly in the pancreas and heart and at high levels in brain, placenta, spleen, uterus and small intestine. Implicated as a critical step in numerous cellular pathways, including signal transduction, membrane trafficking, and the regulation of mitosis. May be involved in the regulation of perinuclear intravesicular membrane traffic (By similarity). NJ
PCLAD	3	Fukuoka S, Ishiguro K, Yanagihara K, Tanabe A, Egashira Y, Sanada H, Shibata K	Identification and expression of a cDNA encoding human alpha-amino-beta-carboxymuconate-epsilon-semialdehyde decarboxylase (ACMSD). A key enzyme for the tryptophan-niacine pathway and "quinolinate hypothesis"	J Biol Chem	2002	12140278	Only known conversion of cmusa to avoid quln formation.
PCm	3	Freytag SO, Collier KJ.	Molecular cloning of a cDNA for human pyruvate carboxylase. Structural relationship to other biotin-containing carboxylases and regulation of mRNA content in differentiating preadipocytes.	J Biol Chem	1984	6548474	mitochondrial matrix [RefSeq], [UniProt] - found in liver, kidney, and intestine, NOT sk muscle, heart, or brain [Orten, Human Biochem 1975] - Additional information added by RS/TV: Two transcriptional variants according to Entrez Gene database Pyruvate carboxylase catalyzes the formation of oxaloacetate from pyruvate and HCO3-. Pyruvate carboxylase is located solely in the mitochondrial matrix. Pyruvate carboxylate is present in a variety of tissues for various reasons: (1) Gluconeogenic tissues such as the liver and kideny (2) Lipogenic tissues such as the liver, adipose, lactating mammary gland, and adrenal gland. (3) Other tissues where it has an anapleurotic role. All this according to Freytag SO, Collier KJ. J Biol Chem. 1984 Oct 25;259(20):12831-7.
PCRNtc	3	Jakobs BS, Wanders RJ.	Fatty acid beta-oxidation in peroxisomes and mitochondria: the first, unequivocal evidence for the involvement of carnitine in shuttling propionyl-CoA from peroxisomes to mitochondria.	Biochem Biophys Res Commun	1995	7654220	Peroxisomes don't have general carnitine transport shuttles, an exception is ppcoa/pcrn. PMID: 7654220 NJ
PCt	3	Ruetz S, Gros P.	Phosphatidylcholine translocase: a physiological role for the mdr2 gene.	Cell	1994	7912658	ABC transporter for phosphatidyl choline transport into bile. Localized on basolateral membrane of hepatocytes and cholangiocytes (liver and bile ducts). Alternative splicing of this gene results in several products of undetermined function. See PMID: 7912658 for characterization and function. Also Meier and Steiger review. PMID: 7893760 for promoter characterization PMID: 7912658 - PC translocase NJ
PCt	3	Meier PJ, Stieger B.	Bile salt transporters.	Annu Rev Physiol	2002	11826283	ABC transporter for phosphatidyl choline transport into bile. Localized on basolateral membrane of hepatocytes and cholangiocytes (liver and bile ducts). Alternative splicing of this gene results in several products of undetermined function. See PMID: 7912658 for characterization and function. Also Meier and Steiger review. PMID: 7893760 for promoter characterization PMID: 7912658 - PC translocase NJ

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PDE1	3	Miki T, Taira M, Hockman S, Shimada F, Lieman J, Napolitano M, Ward D, Taira M, Makino H, Manganiello VC.	Characterization of the cDNA and gene encoding human PDE3B, the cGIP1 isoform of the human cyclic GMP-inhibited cyclic nucleotide phosphodiesterase family.	Genomics	1996	8884271	IMPORTANT: IT is thought that the PDE's contribute to a compartimentalization of cell signaling. Although I found ER-membrane associated PDE's, there is no experimental evidence that they act in ER but in cytoplasm (by inhibition) PDH4: White et al, fund activity in Y79 retinoblastoma cells; PDHa: are stored in granules of neutrophiles and eosinophiles PDH4: Lefievre et al, Spermatozoa. PDE3A: is ER-membrane associated. However, if inhibited, intracellular cAMP concentration increase. expressed in cardiomycytes, paletes, spermatozoa, vascular smooth muscle cells. Wechsler et al, found 3 isoforms of PDE3A, produced by 2 transcripts -- > in LocusLink & SimPheny only 1 transcript -- > keep in mind;can used cGMP and cAMP as substrate but they compete for binding site PDE3B: adipocytes and hepatocytes PDE2A: is expressed in brain and to a lesser extent in heart, placenta, lung, skeletal muscle, kidney and pancreas PDE1A: has a higher affinitiy to cGMP than to cAMP; calmodulin-dependent; in spermatozoa, in Y79 retinoblastoma cells PDE1B: has preference for cGMP, calmodulin-dependent PDE7B: specific for cAMP, expressed in brain, heart, liver PDE7A:Messenger RNA transcripts were detected by RT-PCR PDE11A: no infos where located. Different groups identified in IT
PDE1	3	Rosman GJ, Martins TJ, Sonnenburg WK, Beavo JA, Ferguson K, Loughney K.	Isolation and characterization of human cDNAs encoding a cGMP-stimulated 3',5'-cyclic nucleotide phosphodiesterase.	Gene	1997	9210593	IMPORTANT: IT is thought that the PDE's contribute to a compartimentalization of cell signaling. Although I found ER-membrane associated PDE's, there is no experimental evidence that they act in ER but in cytoplasm (by inhibition) PDH4: White et al, fund activity in Y79 retinoblastoma cells; PDHa: are stored in granules of neutrophiles and eosinophiles PDH4: Lefievre et al, Spermatozoa. PDE3A: is ER-membrane associated. However, if inhibited, intracellular cAMP concentration increase. expressed in cardiomycytes, paletes, spermatozoa, vascular smooth muscle cells. Wechsler et al, found 3 isoforms of PDE3A, produced by 2 transcripts -- > in LocusLink & SimPheny only 1 transcript -- > keep in mind;can used cGMP and cAMP as substrate but they compete for binding site PDE3B: adipocytes and hepatocytes PDE2A: is expressed in brain and to a lesser extent in heart, placenta, lung, skeletal muscle, kidney and pancreas PDE1A: has a higher affinitiy to cGMP than to cAMP; calmodulin-dependent; in spermatozoa, in Y79 retinoblastoma cells PDE1B: has preference for cGMP, calmodulin-dependent PDE7B: specific for cAMP, expressed in brain, heart, liver PDE7A:Messenger RNA transcripts were detected by RT-PCR PDE11A: no infos where located. Different groups identified in IT
PDE1	3	Yu J, Wolda SL, Frazier AL, Florio VA, Martins TJ, Snyder PB, Harris EA, McCaw KN, Farrell CA, Steiner B, Bentley JK, Beavo JA, Ferguson K, Gelinas R.	Identification and characterisation of a human calmodulin-stimulated phosphodiesterase PDE1B1.	Cell Signal	1997	9419816	IMPORTANT: IT is thought that the PDE's contribute to a compartimentalization of cell signaling. Although I found ER-membrane associated PDE's, there is no experimental evidence that they act in ER but in cytoplasm (by inhibition) PDH4: White et al, fund activity in Y79 retinoblastoma cells; PDHa: are stored in granules of neutrophiles and eosinophiles PDH4: Lefievre et al, Spermatozoa. PDE3A: is ER-membrane associated. However, if inhibited, intracellular cAMP concentration increase. expressed in cardiomycytes, paletes, spermatozoa, vascular smooth muscle cells. Wechsler et al, found 3 isoforms of PDE3A, produced by 2 transcripts -- > in LocusLink & SimPheny only 1 transcript -- > keep in mind;can used cGMP and cAMP as substrate but they compete for binding site PDE3B: adipocytes and hepatocytes PDE2A: is expressed in brain and to a lesser extent in heart, placenta, lung, skeletal muscle, kidney and pancreas PDE1A: has a higher affinitiy to cGMP than to cAMP; calmodulin-dependent; in spermatozoa, in Y79 retinoblastoma cells PDE1B: has preference for cGMP, calmodulin-dependent PDE7B: specific for cAMP, expressed in brain, heart, liver PDE7A:Messenger RNA transcripts were detected by RT-PCR PDE11A: no infos where located. Different groups identified in IT

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PDE1	3	Fawcett L, Baxendale R, Stacey P, McGrouther C, Harrow I, Soderling S, Hetman J, Beavo JA, Phillips SC.	Molecular cloning and characterization of a distinct human phosphodiesterase gene family: PDE11A.	Proc Natl Acad Sci U S A	2000	10725373	IMPORTANT: IT is thought that the PDE's contribute to a compartimentalization of cell signaling. Although I found ER-membrane associated PDE's, there is no experimental evidence that they act in ER but in cytoplasm (by inhibition) PDH4: White et al, fund activity in Y79 retinoblastoma cells; PDHa: are stored in granules of neutrophiles and eosinophiles PDH4: Lefievre et al, Spermatozoa. PDE3A: is ER-membrane associated. However, if inhibited, intracellular cAMP concentration increase. expressed in cardiomycytes, paletes, spermatozoa, vascular smooth muscle cells. Wechsler et al, found 3 isoforms of PDE3A, produced by 2 transcripts -- > in LocusLink & SimPheny only 1 transcript -- > keep in mind;can used cGMP and cAMP as substrate but they compete for binding site PDE3B: adipocytes and hepatocytes PDE2A: is expressed in brain and to a lesser extent in heart, placenta, lung, skeletal muscle, kidney and pancreas PDE1A: has a higher affinitiy to cGMP than to cAMP; calmodulin-dependent; in spermatozoa, in Y79 retinoblastoma cells PDE1B: has preference for cGMP, calmodulin-dependent PDE7B: specific for cAMP, expressed in brain, heart, liver PDE7A:Messenger RNA transcripts were detected by RT-PCR PDE11A: no infos where located. Different groups identified in IT
PDE1	3	Gardner C, Robas N, Cawkill D, Fidock M.	Cloning and characterization of the human and mouse PDE7B, a novel cAMP-specific cyclic nucleotide phosphodiesterase.	Biochem Biophys Res Commun	2000	10872825	IMPORTANT: IT is thought that the PDE's contribute to a compartimentalization of cell signaling. Although I found ER-membrane associated PDE's, there is no experimental evidence that they act in ER but in cytoplasm (by inhibition) PDH4: White et al, fund activity in Y79 retinoblastoma cells; PDHa: are stored in granules of neutrophiles and eosinophiles PDH4: Lefievre et al, Spermatozoa. PDE3A: is ER-membrane associated. However, if inhibited, intracellular cAMP concentration increase. expressed in cardiomycytes, paletes, spermatozoa, vascular smooth muscle cells. Wechsler et al, found 3 isoforms of PDE3A, produced by 2 transcripts -- > in LocusLink & SimPheny only 1 transcript -- > keep in mind;can used cGMP and cAMP as substrate but they compete for binding site PDE3B: adipocytes and hepatocytes PDE2A: is expressed in brain and to a lesser extent in heart, placenta, lung, skeletal muscle, kidney and pancreas PDE1A: has a higher affinitiy to cGMP than to cAMP; calmodulin-dependent; in spermatozoa, in Y79 retinoblastoma cells PDE1B: has preference for cGMP, calmodulin-dependent PDE7B: specific for cAMP, expressed in brain, heart, liver PDE7A:Messenger RNA transcripts were detected by RT-PCR PDE11A: no infos where located. Different groups identified in IT
PDE1	3	Yuasa K, Kotera J, Fujishige K, Michibata H, Sasaki T, Omori K.	Isolation and characterization of two novel phosphodiesterase PDE11A variants showing unique structure and tissue-specific expression.	J Biol Chem	2000	10906126	IMPORTANT: IT is thought that the PDE's contribute to a compartimentalization of cell signaling. Although I found ER-membrane associated PDE's, there is no experimental evidence that they act in ER but in cytoplasm (by inhibition) PDH4: White et al, fund activity in Y79 retinoblastoma cells; PDHa: are stored in granules of neutrophiles and eosinophiles PDH4: Lefievre et al, Spermatozoa. PDE3A: is ER-membrane associated. However, if inhibited, intracellular cAMP concentration increase. expressed in cardiomycytes, paletes, spermatozoa, vascular smooth muscle cells. Wechsler et al, found 3 isoforms of PDE3A, produced by 2 transcripts -- > in LocusLink & SimPheny only 1 transcript -- > keep in mind;can used cGMP and cAMP as substrate but they compete for binding site PDE3B: adipocytes and hepatocytes PDE2A: is expressed in brain and to a lesser extent in heart, placenta, lung, skeletal muscle, kidney and pancreas PDE1A: has a higher affinitiy to cGMP than to cAMP; calmodulin-dependent; in spermatozoa, in Y79 retinoblastoma cells PDE1B: has preference for cGMP, calmodulin-dependent PDE7B: specific for cAMP, expressed in brain, heart, liver PDE7A:Messenger RNA transcripts were detected by RT-PCR PDE11A: no infos where located. Different groups identified in IT

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PDE1	3	Shakur Y, Takeda K, Kenan Y, Yu ZX, Rena G, Brandt D, Houslay MD, Degerman E, Ferrans VJ, Manganiello VC.	Membrane localization of cyclic nucleotide phosphodiesterase 3 (PDE3). Two N-terminal domains are required for the efficient targeting to, and association of, PDE3 with endoplasmic reticulum.	J Biol Chem	2000	10952971	IMPORTANT: IT is thought that the PDE's contribute to a compartimentalization of cell signaling. Although I found ER-membrane associated PDE's, there is no experimental evidence that they act in ER but in cytoplasm (by inhibition) PDH4: White et al, fund activity in Y79 retinoblastoma cells; PDHa: are stored in granules of neutrophiles and eosinophiles PDH4: Lefievre et al, Spermatozoa. PDE3A: is ER-membrane associated. However, if inhibited, intracellular cAMP concentration increase. expressed in cardiomycytes, paletes, spermatozoa, vascular smooth muscle cells. Wechsler et al, found 3 isoforms of PDE3A, produced by 2 transcripts -- > in LocusLink & SimPheny only 1 transcript -- > keep in mind;can used cGMP and cAMP as substrate but they compete for binding site PDE3B: adipocytes and hepatocytes PDE2A: is expressed in brain and to a lesser extent in heart, placenta, lung, skeletal muscle, kidney and pancreas PDE1A: has a higher affinitiy to cGMP than to cAMP; calmodulin-dependent; in spermatozoa, in Y79 retinoblastoma cells PDE1B: has preference for cGMP, calmodulin-dependent PDE7B: specific for cAMP, expressed in brain, heart, liver PDE7A:Messenger RNA transcripts were detected by RT-PCR PDE11A: no infos where located. Different groups identified in IT
PDE1	3	Hetman JM, Robas N, Baxendale R, Fidock M, Phillips SC, Soderling SH, Beavo JA.	Cloning and characterization of two splice variants of human phosphodiesterase 11A.	Proc Natl Acad Sci U S A	2000	11050148	IMPORTANT: IT is thought that the PDE's contribute to a compartimentalization of cell signaling. Although I found ER-membrane associated PDE's, there is no experimental evidence that they act in ER but in cytoplasm (by inhibition) PDH4: White et al, fund activity in Y79 retinoblastoma cells; PDHa: are stored in granules of neutrophiles and eosinophiles PDH4: Lefievre et al, Spermatozoa. PDE3A: is ER-membrane associated. However, if inhibited, intracellular cAMP concentration increase. expressed in cardiomycytes, paletes, spermatozoa, vascular smooth muscle cells. Wechsler et al, found 3 isoforms of PDE3A, produced by 2 transcripts -- > in LocusLink & SimPheny only 1 transcript -- > keep in mind;can used cGMP and cAMP as substrate but they compete for binding site PDE3B: adipocytes and hepatocytes PDE2A: is expressed in brain and to a lesser extent in heart, placenta, lung, skeletal muscle, kidney and pancreas PDE1A: has a higher affinitiy to cGMP than to cAMP; calmodulin-dependent; in spermatozoa, in Y79 retinoblastoma cells PDE1B: has preference for cGMP, calmodulin-dependent PDE7B: specific for cAMP, expressed in brain, heart, liver PDE7A:Messenger RNA transcripts were detected by RT-PCR PDE11A: no infos where located. Different groups identified in IT
PDE1	3	Secchiero P, Zella D, Curreli S, Mirandola P, Capitani S, Gallo RC, Zauli G.	Pivotal role of cyclic nucleoside phosphodiesterase 4 in Tat-mediated CD4+ T cell hyperactivation and HIV type 1 replication.	Proc Natl Acad Sci U S A	2000	11114167	IMPORTANT: IT is thought that the PDE's contribute to a compartimentalization of cell signaling. Although I found ER-membrane associated PDE's, there is no experimental evidence that they act in ER but in cytoplasm (by inhibition) PDH4: White et al, fund activity in Y79 retinoblastoma cells; PDHa: are stored in granules of neutrophiles and eosinophiles PDH4: Lefievre et al, Spermatozoa. PDE3A: is ER-membrane associated. However, if inhibited, intracellular cAMP concentration increase. expressed in cardiomycytes, paletes, spermatozoa, vascular smooth muscle cells. Wechsler et al, found 3 isoforms of PDE3A, produced by 2 transcripts -- > in LocusLink & SimPheny only 1 transcript -- > keep in mind;can used cGMP and cAMP as substrate but they compete for binding site PDE3B: adipocytes and hepatocytes PDE2A: is expressed in brain and to a lesser extent in heart, placenta, lung, skeletal muscle, kidney and pancreas PDE1A: has a higher affinitiy to cGMP than to cAMP; calmodulin-dependent; in spermatozoa, in Y79 retinoblastoma cells PDE1B: has preference for cGMP, calmodulin-dependent PDE7B: specific for cAMP, expressed in brain, heart, liver PDE7A:Messenger RNA transcripts were detected by RT-PCR PDE11A: no infos where located. Different groups identified in IT

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PDE1	3	Manns JM, Brenna KJ, Colman RW, Sheth SB.	Differential regulation of human platelet responses by cGMP inhibited and stimulated cAMP phosphodiesterases.	Thromb Haemost	2002	12038792	IMPORTANT: IT is thought that the PDE's contribute to a compartimentalization of cell signaling. Although I found ER-membrane associated PDE's, there is no experimental evidence that they act in ER but in cytoplasm (by inhibition) PDH4: White et al, fund activity in Y79 retinoblastoma cells; PDHa: are stored in granules of neutrophiles and eosinophiles PDH4: Lefievre et al, Spermatozoa. PDE3A: is ER-membrane associated. However, if inhibited, intracellular cAMP concentration increase. expressed in cardiomycytes, paletes, spermatozoa, vascular smooth muscle cells. Wechsler et al, found 3 isoforms of PDE3A, produced by 2 transcripts -- > in LocusLink & SimPheny only 1 transcript -- > keep in mind;can used cGMP and cAMP as substrate but they compete for binding site PDE3B: adipocytes and hepatocytes PDE2A: is expressed in brain and to a lesser extent in heart, placenta, lung, skeletal muscle, kidney and pancreas PDE1A: has a higher affinitiy to cGMP than to cAMP; calmodulin-dependent; in spermatozoa, in Y79 retinoblastoma cells PDE1B: has preference for cGMP, calmodulin-dependent PDE7B: specific for cAMP, expressed in brain, heart, liver PDE7A:Messenger RNA transcripts were detected by RT-PCR PDE11A: no infos where located. Different groups identified in IT
PDE1	3	Lefievre L, de Lamirande E, Gagnon C.	Presence of cyclic nucleotide phosphodiesterases PDE1A, existing as a stable complex with calmodulin, and PDE3A in human spermatozoa.	Biol Reprod	2002	12135876	IMPORTANT: IT is thought that the PDE's contribute to a compartimentalization of cell signaling. Although I found ER-membrane associated PDE's, there is no experimental evidence that they act in ER but in cytoplasm (by inhibition) PDH4: White et al, fund activity in Y79 retinoblastoma cells; PDHa: are stored in granules of neutrophiles and eosinophiles PDH4: Lefievre et al, Spermatozoa. PDE3A: is ER-membrane associated. However, if inhibited, intracellular cAMP concentration increase. expressed in cardiomycytes, paletes, spermatozoa, vascular smooth muscle cells. Wechsler et al, found 3 isoforms of PDE3A, produced by 2 transcripts -- > in LocusLink & SimPheny only 1 transcript -- > keep in mind;can used cGMP and cAMP as substrate but they compete for binding site PDE3B: adipocytes and hepatocytes PDE2A: is expressed in brain and to a lesser extent in heart, placenta, lung, skeletal muscle, kidney and pancreas PDE1A: has a higher affinitiy to cGMP than to cAMP; calmodulin-dependent; in spermatozoa, in Y79 retinoblastoma cells PDE1B: has preference for cGMP, calmodulin-dependent PDE7B: specific for cAMP, expressed in brain, heart, liver PDE7A:Messenger RNA transcripts were detected by RT-PCR PDE11A: no infos where located. Different groups identified in IT
PDE1	3	Wechsler J, Choi YH, Krall J, Ahmad F, Manganiello VC, Movsesian MA.	Isoforms of cyclic nucleotide phosphodiesterase PDE3A in cardiac myocytes.	J Biol Chem	2002	12154085	IMPORTANT: IT is thought that the PDE's contribute to a compartimentalization of cell signaling. Although I found ER-membrane associated PDE's, there is no experimental evidence that they act in ER but in cytoplasm (by inhibition) PDH4: White et al, fund activity in Y79 retinoblastoma cells; PDHa: are stored in granules of neutrophiles and eosinophiles PDH4: Lefievre et al, Spermatozoa. PDE3A: is ER-membrane associated. However, if inhibited, intracellular cAMP concentration increase. expressed in cardiomycytes, paletes, spermatozoa, vascular smooth muscle cells. Wechsler et al, found 3 isoforms of PDE3A, produced by 2 transcripts -- > in LocusLink & SimPheny only 1 transcript -- > keep in mind;can used cGMP and cAMP as substrate but they compete for binding site PDE3B: adipocytes and hepatocytes PDE2A: is expressed in brain and to a lesser extent in heart, placenta, lung, skeletal muscle, kidney and pancreas PDE1A: has a higher affinitiy to cGMP than to cAMP; calmodulin-dependent; in spermatozoa, in Y79 retinoblastoma cells PDE1B: has preference for cGMP, calmodulin-dependent PDE7B: specific for cAMP, expressed in brain, heart, liver PDE7A:Messenger RNA transcripts were detected by RT-PCR PDE11A: no infos where located. Different groups identified in IT

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PDE1	3	Smith SJ, Brookes-Fazakerley S, Donnelly LE, Barnes PJ, Barnette MS, Giembycz MA.	Ubiquitous expression of phosphodiesterase 7A in human proinflammatory and immune cells	Am J Physiol Lung Cell Mol Physiol	2003	12388353	IMPORTANT: IT is thought that the PDE's contribute to a compartimentalization of cell signaling. Although I found ER-membrane associated PDE's, there is no experimental evidence that they act in ER but in cytoplasm (by inhibition) PDH4: White et al, fund activity in Y79 retinoblastoma cells; PDHa: are stored in granules of neutrophiles and eosinophiles PDH4: Lefievre et al, Spermatozoa. PDE3A: is ER-membrane associated. However, if inhibited, intracellular cAMP concentration increase. expressed in cardiomycytes, paletes, spermatozoa, vascular smooth muscle cells. Wechsler et al, found 3 isoforms of PDE3A, produced by 2 transcripts -- > in LocusLink & SimPheny only 1 transcript -- > keep in mind;can used cGMP and cAMP as substrate but they compete for binding site PDE3B: adipocytes and hepatocytes PDE2A: is expressed in brain and to a lesser extent in heart, placenta, lung, skeletal muscle, kidney and pancreas PDE1A: has a higher affinitiy to cGMP than to cAMP; calmodulin-dependent; in spermatozoa, in Y79 retinoblastoma cells PDE1B: has preference for cGMP, calmodulin-dependent PDE7B: specific for cAMP, expressed in brain, heart, liver PDE7A:Messenger RNA transcripts were detected by RT-PCR PDE11A: no infos where located. Different groups identified in IT
PDE1	3	Gamanuma M, Yuasa K, Sasaki T, Sakurai N, Kotera J, Omori K.	Comparison of enzymatic characterization and gene organization of cyclic nucleotide phosphodiesterase 8 family in humans.	Cell Signal	2003	12681444	IMPORTANT: IT is thought that the PDE's contribute to a compartimentalization of cell signaling. Although I found ER-membrane associated PDE's, there is no experimental evidence that they act in ER but in cytoplasm (by inhibition) PDH4: White et al, fund activity in Y79 retinoblastoma cells; PDHa: are stored in granules of neutrophiles and eosinophiles PDH4: Lefievre et al, Spermatozoa. PDE3A: is ER-membrane associated. However, if inhibited, intracellular cAMP concentration increase. expressed in cardiomycytes, paletes, spermatozoa, vascular smooth muscle cells. Wechsler et al, found 3 isoforms of PDE3A, produced by 2 transcripts -- > in LocusLink & SimPheny only 1 transcript -- > keep in mind;can used cGMP and cAMP as substrate but they compete for binding site PDE3B: adipocytes and hepatocytes PDE2A: is expressed in brain and to a lesser extent in heart, placenta, lung, skeletal muscle, kidney and pancreas PDE1A: has a higher affinitiy to cGMP than to cAMP; calmodulin-dependent; in spermatozoa, in Y79 retinoblastoma cells PDE1B: has preference for cGMP, calmodulin-dependent PDE7B: specific for cAMP, expressed in brain, heart, liver PDE7A:Messenger RNA transcripts were detected by RT-PCR PDE11A: no infos where located. Different groups identified in IT
PDE1	3	Pryzwansky KB, Madden VJ	Type 4A cAMP-specific phosphodiesterase is stored in granules of human neutrophils and eosinophils.	Cell Tissue Res	2003	12764607	IMPORTANT: IT is thought that the PDE's contribute to a compartimentalization of cell signaling. Although I found ER-membrane associated PDE's, there is no experimental evidence that they act in ER but in cytoplasm (by inhibition) PDH4: White et al, fund activity in Y79 retinoblastoma cells; PDHa: are stored in granules of neutrophiles and eosinophiles PDH4: Lefievre et al, Spermatozoa. PDE3A: is ER-membrane associated. However, if inhibited, intracellular cAMP concentration increase. expressed in cardiomycytes, paletes, spermatozoa, vascular smooth muscle cells. Wechsler et al, found 3 isoforms of PDE3A, produced by 2 transcripts -- > in LocusLink & SimPheny only 1 transcript -- > keep in mind;can used cGMP and cAMP as substrate but they compete for binding site PDE3B: adipocytes and hepatocytes PDE2A: is expressed in brain and to a lesser extent in heart, placenta, lung, skeletal muscle, kidney and pancreas PDE1A: has a higher affinitiy to cGMP than to cAMP; calmodulin-dependent; in spermatozoa, in Y79 retinoblastoma cells PDE1B: has preference for cGMP, calmodulin-dependent PDE7B: specific for cAMP, expressed in brain, heart, liver PDE7A:Messenger RNA transcripts were detected by RT-PCR PDE11A: no infos where located. Different groups identified in IT

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PDE1	3	Kotera J, Sasaki T, Kobayashi T, Fujishige K, Yamashita Y, Omori K.	Subcellular localization of cyclic nucleotide phosphodiesterase type 10A variants, and alteration of the localization by cAMP-dependent protein kinase-dependent phosphorylation.	J Biol Chem	2004	14604994	IMPORTANT: IT is thought that the PDE's contribute to a compartimentalization of cell signaling. Although I found ER-membrane associated PDE's, there is no experimental evidence that they act in ER but in cytoplasm (by inhibition) PDH4: White et al, fund activity in Y79 retinoblastoma cells; PDHa: are stored in granules of neutrophiles and eosinophiles PDH4: Lefievre et al, Spermatozoa. PDE3A: is ER-membrane associated. However, if inhibited, intracellular cAMP concentration increase. expressed in cardiomycytes, paletes, spermatozoa, vascular smooth muscle cells. Wechsler et al, found 3 isoforms of PDE3A, produced by 2 transcripts -- > in LocusLink & SimPheny only 1 transcript -- > keep in mind;can used cGMP and cAMP as substrate but they compete for binding site PDE3B: adipocytes and hepatocytes PDE2A: is expressed in brain and to a lesser extent in heart, placenta, lung, skeletal muscle, kidney and pancreas PDE1A: has a higher affinitiy to cGMP than to cAMP; calmodulin-dependent; in spermatozoa, in Y79 retinoblastoma cells PDE1B: has preference for cGMP, calmodulin-dependent PDE7B: specific for cAMP, expressed in brain, heart, liver PDE7A:Messenger RNA transcripts were detected by RT-PCR PDE11A: no infos where located. Different groups identified in IT
PDE1	3	Scapin G, Patel SB, Chung C, Varnerin JP, Edmondson SD, Mastracchio A, Parmee ER, Singh SB, Becker JW, Van der Ploeg LH, Tota MR.	Crystal structure of human phosphodiesterase 3B: atomic basis for substrate and inhibitor specificity.	Biochemistry	2004	15147193	IMPORTANT: IT is thought that the PDE's contribute to a compartimentalization of cell signaling. Although I found ER-membrane associated PDE's, there is no experimental evidence that they act in ER but in cytoplasm (by inhibition) PDH4: White et al, fund activity in Y79 retinoblastoma cells; PDHa: are stored in granules of neutrophiles and eosinophiles PDH4: Lefievre et al, Spermatozoa. PDE3A: is ER-membrane associated. However, if inhibited, intracellular cAMP concentration increase. expressed in cardiomycytes, paletes, spermatozoa, vascular smooth muscle cells. Wechsler et al, found 3 isoforms of PDE3A, produced by 2 transcripts -- > in LocusLink & SimPheny only 1 transcript -- > keep in mind;can used cGMP and cAMP as substrate but they compete for binding site PDE3B: adipocytes and hepatocytes PDE2A: is expressed in brain and to a lesser extent in heart, placenta, lung, skeletal muscle, kidney and pancreas PDE1A: has a higher affinitiy to cGMP than to cAMP; calmodulin-dependent; in spermatozoa, in Y79 retinoblastoma cells PDE1B: has preference for cGMP, calmodulin-dependent PDE7B: specific for cAMP, expressed in brain, heart, liver PDE7A:Messenger RNA transcripts were detected by RT-PCR PDE11A: no infos where located. Different groups identified in IT
PDE1	3	Goraya TA, Masada N, Ciruela A, Cooper DM.	Sustained entry of Ca2+ is required to activate Ca2+-calmodulin-dependent phosphodiesterase 1A.	J Biol Chem	2004	15272012	IMPORTANT: IT is thought that the PDE's contribute to a compartimentalization of cell signaling. Although I found ER-membrane associated PDE's, there is no experimental evidence that they act in ER but in cytoplasm (by inhibition) PDH4: White et al, fund activity in Y79 retinoblastoma cells; PDHa: are stored in granules of neutrophiles and eosinophiles PDH4: Lefievre et al, Spermatozoa. PDE3A: is ER-membrane associated. However, if inhibited, intracellular cAMP concentration increase. expressed in cardiomycytes, paletes, spermatozoa, vascular smooth muscle cells. Wechsler et al, found 3 isoforms of PDE3A, produced by 2 transcripts -- > in LocusLink & SimPheny only 1 transcript -- > keep in mind;can used cGMP and cAMP as substrate but they compete for binding site PDE3B: adipocytes and hepatocytes PDE2A: is expressed in brain and to a lesser extent in heart, placenta, lung, skeletal muscle, kidney and pancreas PDE1A: has a higher affinitiy to cGMP than to cAMP; calmodulin-dependent; in spermatozoa, in Y79 retinoblastoma cells PDE1B: has preference for cGMP, calmodulin-dependent PDE7B: specific for cAMP, expressed in brain, heart, liver PDE7A:Messenger RNA transcripts were detected by RT-PCR PDE11A: no infos where located. Different groups identified in IT

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PDE1	3	White JB, Thompson WJ, Pittler SJ.	Characterization of 3',5' cyclic nucleotide phosphodiesterase activity in Y79 retinoblastoma cells: absence of functional PDE6.	Mol Vis	2004	15480303	IMPORTANT: IT is thought that the PDE's contribute to a compartimentalization of cell signaling. Although I found ER-membrane associated PDE's, there is no experimental evidence that they act in ER but in cytoplasm (by inhibition) PDH4: White et al, fund activity in Y79 retinoblastoma cells; PDHa: are stored in granules of neutrophiles and eosinophiles PDH4: Lefievre et al, Spermatozoa. PDE3A: is ER-membrane associated. However, if inhibited, intracellular cAMP concentration increase. expressed in cardiomycytes, paletes, spermatozoa, vascular smooth muscle cells. Wechsler et al, found 3 isoforms of PDE3A, produced by 2 transcripts -- > in LocusLink & SimPheny only 1 transcript -- > keep in mind;can used cGMP and cAMP as substrate but they compete for binding site PDE3B: adipocytes and hepatocytes PDE2A: is expressed in brain and to a lesser extent in heart, placenta, lung, skeletal muscle, kidney and pancreas PDE1A: has a higher affinitiy to cGMP than to cAMP; calmodulin-dependent; in spermatozoa, in Y79 retinoblastoma cells PDE1B: has preference for cGMP, calmodulin-dependent PDE7B: specific for cAMP, expressed in brain, heart, liver PDE7A:Messenger RNA transcripts were detected by RT-PCR PDE11A: no infos where located. Different groups identified in IT
PDE4	3	Shimizu-Matsumoto A, Itoh K, Inazawa J, Nishida K, Matsumoto Y, Kinoshita S, Matsubara K, Okubo K.	Isolation and chromosomal localization of the human cone cGMP phosphodiesterase gamma cDNA (PDE6H).	Genomics	1996	8786098	IMPORTANT: IT is thought that the PDE's contribute to a compartimentalization of cell signaling. Although I found ER-membrane associated PDE's, there is no experimental evidence that they act in ER but in cytoplasm (by inhibition) PDE6: I am not sure if I understood the GPR in GeneCards right. --> therefore Conf level 0 PDE6 mRNA expression is very high in retina, and some groups found it only there expressed, however, White et al, 2004, Mol. Vis., 10,738-749, measured no PDE6 activity in Y70 retinoblastoma cells but the mRNA expression. There might be postranslational modification for a active stable PDE6 that do not occurs in retinoblasoma cells ... PDE1, PDE4: White et al, 2004, Mol. Vis., 10,738-749, measured activity in Y70 retinoblastoma cells b PDE3A: is ER-membrane associated. However, if inhibited, intracellular cAMP concentration increase. expressed in cardiomycytes, paletes, spermatozoa, vascular smooth muscle cells. Wechsler et al, found 3 isoforms of PDE3A, produced by 2 transcripts -- > in LocusLink & SimPheny only 1 transcript -- > keep in mind; can used cGMP and cAMP as substrate but the PDE3B: adipocytes and hepatocytes PDE2A: is expressed in brain and to a lesser extent in heart, pla PDE1A: has a higher affinitiy to cGMP than to cAMP; calmodu PDE1B: has preference for cGMP, calmodulin-dependent, high
PDE4	3	Fisher DA, Smith JF, Pillar JS, St Denis SH, Cheng JB.	Isolation and characterization of PDE9A, a novel human cGMP-specific phosphodiesterase.	J Biol Chem	1998	9624146	IMPORTANT: IT is thought that the PDE's contribute to a compartimentalization of cell signaling. Although I found ER-membrane associated PDE's, there is no experimental evidence that they act in ER but in cytoplasm (by inhibition) PDE6: I am not sure if I understood the GPR in GeneCards right. --> therefore Conf level 0 PDE6 mRNA expression is very high in retina, and some groups found it only there expressed, however, White et al, 2004, Mol. Vis., 10,738-749, measured no PDE6 activity in Y70 retinoblastoma cells but the mRNA expression. There might be postranslational modification for a active stable PDE6 that do not occurs in retinoblasoma cells ... PDE1, PDE4: White et al, 2004, Mol. Vis., 10,738-749, measured activity in Y70 retinoblastoma cells b PDE3A: is ER-membrane associated. However, if inhibited, intracellular cAMP concentration increase. expressed in cardiomycytes, paletes, spermatozoa, vascular smooth muscle cells. Wechsler et al, found 3 isoforms of PDE3A, produced by 2 transcripts -- > in LocusLink & SimPheny only 1 transcript -- > keep in mind; can used cGMP and cAMP as substrate but the PDE3B: adipocytes and hepatocytes PDE2A: is expressed in brain and to a lesser extent in heart, pla PDE1A: has a higher affinitiy to cGMP than to cAMP; calmodu PDE1B: has preference for cGMP, calmodulin-dependent, high

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PDE4	3	Yanaka N, Kotera J, Ohtsuka A, Akatsuka H, Imai Y, Michibata H, Fujishige K, Kawai E, Takebayashi S, Okumura K, Omori K.	Expression, structure and chromosomal localization of the human cGMP-binding cGMP-specific phosphodiesterase PDE5A gene.	Eur J Biochem	1998	9716380	compartimentalization of cell signaling. Although I found ER-membrane associated PDE's, there is no experimental evidence that they act in ER but in cytoplasm (by inhibition) PDE6: I am not sure if I understood the GPR in GeneCards right. --> therefore Conf level 0 PDE6 mRNA expression is very high in retina, and some groups found it only there expressed, however, White et al, 2004, Mol. Vis., 10,738-749, measured no PDE6 activity in Y70 retinoblastoma cells but the mRNA expression. There might be postranslational modification for a active stable PDE6 that do not occurs in retinoblasoma cells ... PDE1, PDE4: White et al, 2004, Mol. Vis., 10,738-749, measured activity in Y70 retinoblastoma cells b PDE3A: is ER-membrane associated. However, if inhibited, intracellular cAMP concentration increase. expressed in cardiomycytes, paletes, spermatozoa, vascular smooth muscle cells. Wechsler et al, found 3 isoforms of PDE3A, produced by 2 transcripts -- > in LocusLink & SimPheny only 1 transcript --> keep in mind; can used cGMP and cAMP as substrate but the PDE3B: adipocytes and hepatocytes PDE2A: is expressed in brain and to a lesser extent in heart, pla PDE1A: has a higher affinitiy to cGMP than to cAMP; calmodu PDE1B: has preference for cGMP, calmodulin-dependent, high
PDE4	3	Identification and distribution of different mRNA variants produced by differential splicing in the human phosphodiesterase 9A gene.	Identification and distribution of different mRNA variants produced by differential splicing in the human phosphodiesterase 9A gene.	Biochem Biophys Res Commun	2003	12565835	compartimentalization of cell signaling. Although I found ER-membrane associated PDE's, there is no experimental evidence that they act in ER but in cytoplasm (by inhibition) PDE6: I am not sure if I understood the GPR in GeneCards right. --> therefore Conf level 0 PDE6 mRNA expression is very high in retina, and some groups found it only there expressed, however, White et al, 2004, Mol. Vis., 10,738-749, measured no PDE6 activity in Y70 retinoblastoma cells but the mRNA expression. There might be postranslational modification for a active stable PDE6 that do not occurs in retinoblasoma cells ... PDE1, PDE4: White et al, 2004, Mol. Vis., 10,738-749, measured activity in Y70 retinoblastoma cells b PDE3A: is ER-membrane associated. However, if inhibited, intracellular cAMP concentration increase. expressed in cardiomycytes, paletes, spermatozoa, vascular smooth muscle cells. Wechsler et al, found 3 isoforms of PDE3A, produced by 2 transcripts -- > in LocusLink & SimPheny only 1 transcript --> keep in mind; can used cGMP and cAMP as substrate but the PDE3B: adipocytes and hepatocytes PDE2A: is expressed in brain and to a lesser extent in heart, pla PDE1A: has a higher affinitiy to cGMP than to cAMP; calmodu PDE1B: has preference for cGMP, calmodulin-dependent, high
PDE4	3	Wang P, Wu P, Egan RW, Billah MM.	Identification and characterization of a new human type 9 cGMP-specific phosphodiesterase splice variant (PDE9A5). Differential tissue distribution and subcellular localization of PDE9A variants.	Gene	2003	14527714	compartimentalization of cell signaling. Although I found ER-membrane associated PDE's, there is no experimental evidence that they act in ER but in cytoplasm (by inhibition) PDE6: I am not sure if I understood the GPR in GeneCards right. --> therefore Conf level 0 PDE6 mRNA expression is very high in retina, and some groups found it only there expressed, however, White et al, 2004, Mol. Vis., 10,738-749, measured no PDE6 activity in Y70 retinoblastoma cells but the mRNA expression. There might be postranslational modification for a active stable PDE6 that do not occurs in retinoblasoma cells ... PDE1, PDE4: White et al, 2004, Mol. Vis., 10,738-749, measured activity in Y70 retinoblastoma cells b PDE3A: is ER-membrane associated. However, if inhibited, intracellular cAMP concentration increase. expressed in cardiomycytes, paletes, spermatozoa, vascular smooth muscle cells. Wechsler et al, found 3 isoforms of PDE3A, produced by 2 transcripts -- > in LocusLink & SimPheny only 1 transcript --> keep in mind; can used cGMP and cAMP as substrate but the PDE3B: adipocytes and hepatocytes PDE2A: is expressed in brain and to a lesser extent in heart, pla PDE1A: has a higher affinitiy to cGMP than to cAMP; calmodu PDE1B: has preference for cGMP, calmodulin-dependent, high
PDX5PO	3	Kang JH, Hong ML, Kim DW, Park J, Kang TC, Won MH, Baek NI, Moon BJ, Choi SY, Kwon OS.	Genomic organization, tissue distribution and deletion mutation of human pyridoxine 5'-phosphate oxidase.	Eur J Biochem	2004	15182361	mainly expressed in liver, skeletal muscle and kidney. Erys also have PDX5PO activity (see Review) IT
PDX5PO	3	Mehansho H, Henderson LM.	Transport and accumulation of pyridoxine and pyridoxal by erythrocytes.	J Biol Chem	1980	J Biol Chem.	mainly expressed in liver, skeletal muscle and kidney. Erys also have PDX5PO activity (see Review) IT
PE_HSter	2	Daleke DL, Lyles JV.	Identification and purification of aminophospholipid flippases.	Biochim Biophys Acta	2000	10856717	- evidence for scramblase that translocates phosphatidylethanolamine, phosphatidylcholine, and phosphatidylserine in rat liver ER membranes [Chang 2004] NJ: additional comments: Energy independent, so rev, scramblase activity.

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PE_HSter	2	Chang QL, Gummadi SN, Menon AK	Chemical modification identifies two populations of glycerophospholipid flippase in rat liver ER	Biochemistry	2004	15311932	- evidence for scramblase that translocates phosphatidylethanolamine, phosphatidylcholine, and phosphatidylserine in rat liver ER membranes [Chang 2004] NJ: additional comments: Energy independent, so rev, scramblase activity.
PEAMNO	2	Lyles GA	Mammalian plasma and tissue-bound semicarbazide-sensitive amine oxidases: biochemical, pharmacological and toxicological aspects	Int J Biochem Cell Biol	1996	8920635	4th citation gives evidence that MAOB does this more than MAOA, but the journal is slightly suspect and the data may be from rats, so physiological evidence.
PEAMNO	2	Smith DJ, Salmi M, Bono P, Hellman J, Leu T, Jalkanen S.	Cloning of vascular adhesion protein 1 reveals a novel multifunctional adhesion molecule	J Exp Med	1998	9653080	4th citation gives evidence that MAOB does this more than MAOA, but the journal is slightly suspect and the data may be from rats, so physiological evidence.
PEAMNO	2	Shih JC, Chen K, Ridd MJ	Role of MAO A and B in neurotransmitter metabolism and behavior	Pol J Pharmacol	1999	10389141	4th citation gives evidence that MAOB does this more than MAOA, but the journal is slightly suspect and the data may be from rats, so physiological evidence.
PEAMNO	2	Buffoni F, Ignesti G	Biochemical aspects and functional role of the copper containing amine oxidases	Inflammopharmacology	2003	15035803	4th citation gives evidence that MAOB does this more than MAOA, but the journal is slightly suspect and the data may be from rats, so physiological evidence.
PEFLIP	3	Mouro I, Halleck MS, Schlegel RA, Mattei MG, Williamson P, Zachowski A, Devaux P, Cartron JP, Colin Y.	Cloning, expression, and chromosomal mapping of a human ATPase II gene, member of the third subfamily of P-type ATPases and orthologous to the presumed bovine and murine aminophospholipid translocase.	Biochem Biophys Res Commun	1999	10198212	transport out of mitochondria - flip and flip (not to be confused w/ flip-flop) mechanisms are ATP dependent, wherease scramblase transport of lipids is not - PMID: 10856717 Largely inferred transport at this time (sequence homology characterizes it as a phosphlipid, ATP dependent transporter). ATP10A: PMID: 11353404 - The protein encoded by this gene belongs to the family of P-type cation transport ATPases, and to the subfamily of aminophospholipid-transporting ATPases. The aminophospholipid translocases transport phosphatidylserine and phosphatidylethanolamine from one side of a bilayer to another. This gene is maternally expressed. It maps within the most common interval of deletion responsible for Angelman syndrome, also known as 'happy puppet syndrome'. ATP8A1: PMID: 10198212 for cloning and expression. The P-type adenosinetriphosphatases (P-type ATPases) are a family of proteins which use the free energy of ATP hydrolysis to drive uphill transport of ions across membranes. Several subfamilies of P-type ATPases have been identified. One subfamily catalyzes transport of heavy metal ions. Another subfamily tran NJ
PEFLIP	3	Herzing LB, Kim SJ, Cook EH Jr, Ledbetter DH.	The human aminophospholipid-transporting ATPase gene ATP10C maps adjacent to UBE3A and exhibits similar imprinted expression.	Am J Hum Genet	2001	11353404	transport out of mitochondria - flip and flip (not to be confused w/ flip-flop) mechanisms are ATP dependent, wherease scramblase transport of lipids is not - PMID: 10856717 Largely inferred transport at this time (sequence homology characterizes it as a phosphlipid, ATP dependent transporter). ATP10A: PMID: 11353404 - The protein encoded by this gene belongs to the family of P-type cation transport ATPases, and to the subfamily of aminophospholipid-transporting ATPases. The aminophospholipid translocases transport phosphatidylserine and phosphatidylethanolamine from one side of a bilayer to another. This gene is maternally expressed. It maps within the most common interval of deletion responsible for Angelman syndrome, also known as 'happy puppet syndrome'. ATP8A1: PMID: 10198212 for cloning and expression. The P-type adenosinetriphosphatases (P-type ATPases) are a family of proteins which use the free energy of ATP hydrolysis to drive uphill transport of ions across membranes. Several subfamilies of P-type ATPases have been identified. One subfamily catalyzes transport of heavy metal ions. Another subfamily tran NJ
PEPCKm	0	Modaressi S, Christ B, Bratke J, Zahn S, Heise T, Jungermann K.	Molecular cloning, sequencing and expression of the cDNA of the mitochondrial form of phosphoenolpyruvate carboxykinase from human liver.	Biochem J	1996	8645161	mitochondrial [UniProt] - found in liver, kidney, and intestine, NOT sk muscle, heart, or brain [Orten, Human Biochem 1975] - Additional information by RS/TV: Phosphoenolpyruvate carboykinase (PCK) (EC 4.1.1.32) catalyses the GTP-driven conversion of oxaloacetate to phosphoenolpyruvate. Tissue localization: Mainly in the liver and the kidney Subcellular Localization: Exists as two isozymes, Pck1.1 is in the cytosol. Pck2.1-m is in the mitochondria. All according to Modaressi S, Christ B, Bratke J, Zahn S, Heise T, Jungermann K. Biochem J. 1996 May 1;315 (Pt 3):807-14.

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PEROXx	3	Adamski J, Normand T, Leenders F, Monte D, Begue A, Stehelin D, Jungblut PW, de Launoit Y.	Molecular cloning of a novel widely expressed human 80 kDa 17 beta-hydroxysteroid dehydrogenase IV.	Biochem J	1995	7487879	to dmnoncoa which is transported out of the peroxisome, into the mitochondria and degraded 1x -> a heptanoyl-CoA - however "the metabolic fate of 2,6 dimethylheptanoyl-CoA IS NOT KNOWN" see PMID: 11591435 (Verhoeven review article). See also Mukherji (PMID:12814641) ACOX3: PMID: 15599942, Zha et al ACOX3, which is expressed at extremely low level in other human organs studied including the liver, might contribute significantly to peroxisomal branched chain fatty acid beta-oxidation in human prostate tissue and some prostate cancer cell lines. Acyl-Coenzyme A oxidase 3 also know as pristanoyl CoA oxidase (ACOX3)is involved in the desaturation of 2-methyl branched fatty acids in peroxisomes. Unlike the rat homolog, the human gene is expressed in very low amounts in liver such that its mRNA was undetectable by routine Northern-blot analysis or its product by immunoblotting or by enzyme activity measurements. However the human cDNA encoding a 700 amino acid protein with a peroxisomal targeting C-terminal tripeptide S-K-L was isolated and is thought to be expressed un HSD17B4: PMID: 7487879 ACAA1: PMID: 1679347, Bout Acetyl-Coenzyme A acyltransferase (ACAA1) is an enzyme op
PEROXx	3	Zha S, Ferdinandusse S, Hicks JL, Denis S, Dunn TA, Wanders RJ, Luo J, De Marzo AM, Isaacs WB.	Peroxisomal branched chain fatty acid beta-oxidation pathway is upregulated in prostate cancer.	Prostate	2005	15599942	to dmnoncoa which is transported out of the peroxisome, into the mitochondria and degraded 1x -> a heptanoyl-CoA - however "the metabolic fate of 2,6 dimethylheptanoyl-CoA IS NOT KNOWN" see PMID: 11591435 (Verhoeven review article). See also Mukherji (PMID:12814641) ACOX3: PMID: 15599942, Zha et al ACOX3, which is expressed at extremely low level in other human organs studied including the liver, might contribute significantly to peroxisomal branched chain fatty acid beta-oxidation in human prostate tissue and some prostate cancer cell lines. Acyl-Coenzyme A oxidase 3 also know as pristanoyl CoA oxidase (ACOX3)is involved in the desaturation of 2-methyl branched fatty acids in peroxisomes. Unlike the rat homolog, the human gene is expressed in very low amounts in liver such that its mRNA was undetectable by routine Northern-blot analysis or its product by immunoblotting or by enzyme activity measurements. However the human cDNA encoding a 700 amino acid protein with a peroxisomal targeting C-terminal tripeptide S-K-L was isolated and is thought to be expressed un HSD17B4: PMID: 7487879 ACAA1: PMID: 1679347, Bout Acetyl-Coenzyme A acyltransferase (ACAA1) is an enzyme op
PETHCT	3	Nakashima A, Hosaka K, Nikawa J	Cloning of a human cDNA for CTP-Phosphoethanolamine cytidylyltransferase by complementation in vivo of a yeast mutant	Journal of Biological Chemistry	1997		cytoplasmic - unitprot NJ
PETOHMm_hs	2	Walkey CJ, Shields DJ, Vance DE.	Identification of three novel cDNAs for human phosphatidylethanolamine N-methyltransferase and localization of the human gene on chromosome 17p11.2.	Biochim Biophys Acta	1999	9989271	Original version added to subset of amino acid metabolism and created an unknown compound. Literature appears to support the conversion of pe-> pchol in humans. localization: ER and mit according to Swiss-Prot * Function: Catalyzes three sequential methylation of phosphatidylethanolamine (PE) by AdoMet, thus producing phosphatidylcholine (PC). * Catalytic activity: S-adenosyl-L-methionine + phosphatidylethanolamine = S-adenosyl-L-homocysteine + phosphatidyl-N-methylethanolamine. * Enzyme regulation: The first methylation is rate-limiting. NJ
PFK	2	Eto K, Sakura H, Yasuda K, Hayakawa T, Kawasaki E, Moriuchi R, Nagataki S, Yazaki Y, Kadowaki T	Cloning of a complete protein-coding sequence of human platelet-type phosphofructokinase isozyme from pancreatic islet	Biochem Biophys Res Commun	1994	8117307	-muscle only contains homotetratmer of M subunits - liver only contains homotetramer of L subunits - platelets, white blood cells contain all 5 L,M heterotetramer combinations (4L, 3LM, 2L2M, LM3, M4) [Eto et al, Biochem Biophys Res Comm 1994] -tetramer of randomly associated isozymes available in individual tissues [Eto et al, Biochem Biophys Res Comm 1994] - higher proportion of P subunits found in brain, platelet, fibroids [UniProt] - physiologically irreversible [Orten, Human Biochm 1975]
PGCD	3	Cho HM, Jun DY, Bae MA, Ahn JD, Kim YH.	Nucleotide sequence and differential expression of the human 3-phosphoglycerate dehydrogenase gene.		2000	10713460	irreversible according to Lehninger (pg. 844, 4th ed.) cytosolic based on mouse localisation (Kazuyuki et. al, 2004 PMID:14645240)

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PGDIr	3	Yamashima T, Sakuda K, Tohma Y, Yamashita J, Oda H, Irikura D, Eguchi N, Beuckmann CT, Kanaoka Y, Urade Y, Hayaishi O	Prostaglandin D synthase (beta-trace) in human arachnoid and meningioma cells: roles as a cell marker or in cerebrospinal fluid absorption, tumorigenesis, and calcification process.	J Neurosci	1997		location: found in cytosol + ER membrane specificity: different transcripts have different specificities - see refs, e.g. PTGDS has brain (oligodendrocyte specificity) and PGDS has hematopoietic cell specificity. The protein encoded by this gene is a glutathione-independent prostaglandin D synthase that catalyzes the conversion of prostaglandin H2 (PGH2) to postaglandin D2 (PGD2). PGD2 functions as a neuromodulator as well as a trophic factor in the central nervous system. PGD2 is also involved in smooth muscle contraction/relaxation and is a potent inhibitor of platelet aggregation. This gene is preferentially expressed in brain. Studies with transgenic mice overexpressing this gene suggest that this gene may be also involved in the regulation of non-rapid eye movement sleep. NJ
PGDIr	3	Mahmud I, Ueda N, Yamaguchi H, Yamashita R, Yamamoto S, Kanaoka Y, Urade Y, Hayaishi O.	Prostaglandin D synthase in human megakaryoblastic cells.	J Biol Chem	1997	9353279	location: found in cytosol + ER membrane specificity: different transcripts have different specificities - see refs, e.g. PTGDS has brain (oligodendrocyte specificity) and PGDS has hematopoietic cell specificity. The protein encoded by this gene is a glutathione-independent prostaglandin D synthase that catalyzes the conversion of prostaglandin H2 (PGH2) to postaglandin D2 (PGD2). PGD2 functions as a neuromodulator as well as a trophic factor in the central nervous system. PGD2 is also involved in smooth muscle contraction/relaxation and is a potent inhibitor of platelet aggregation. This gene is preferentially expressed in brain. Studies with transgenic mice overexpressing this gene suggest that this gene may be also involved in the regulation of non-rapid eye movement sleep. NJ
PGDIr	3		Goodman & Gilman's the pharmacological basis of therapeutics		2001		location: found in cytosol + ER membrane specificity: different transcripts have different specificities - see refs, e.g. PTGDS has brain (oligodendrocyte specificity) and PGDS has hematopoietic cell specificity. The protein encoded by this gene is a glutathione-independent prostaglandin D synthase that catalyzes the conversion of prostaglandin H2 (PGH2) to postaglandin D2 (PGD2). PGD2 functions as a neuromodulator as well as a trophic factor in the central nervous system. PGD2 is also involved in smooth muscle contraction/relaxation and is a potent inhibitor of platelet aggregation. This gene is preferentially expressed in brain. Studies with transgenic mice overexpressing this gene suggest that this gene may be also involved in the regulation of non-rapid eye movement sleep. NJ
PGESr	3	Han R, Tsui S, Smith TJ.	Up-regulation of prostaglandin E2 synthesis by interleukin-1beta in human orbital fibroblasts involves coordinate induction of prostaglandin-endoperoxide H synthase-2 and glutathione-dependent prostaglandin E2 synthase expression.	J Biol Chem	2002	11847219	ER: uniprot specificity: none The protein encoded by this gene is a glutathione-dependent prostaglandin E synthase. The expression of this gene has been shown to be induced by proinflammatory cytokine interleukin 1 beta (IL1B). Its expression can also be induced by tumor suppressor protein TP53, and may be involved in TP53 induced apoptosis. Knockout studies in mice suggest that this gene may contribute to the pathogenesis of collagen-induced arthritis and mediate acute pain during inflammatory responses. Alternatively spliced transcript variants encoding distinct isoforms have been observed. For PTGES2: The protein encoded by this gene is a membrane-associated prostaglandin E synthase, which catalyzes the conversion of prostaglandin H2 to prostaglandin E2. This protein also has been shown to activate the transcription regulated by a gamma-interferon-activated transcription element (GATE). Four alternatively spliced transcript variants encoding three distinct isoforms have been observed. NJ
PGLYCP	3	Mulley JC, Barton N, Callen DF	Localisation of human PGP and HAGH genes to 16p13.3	Cytogenet Cell Genet	1990	2164460	- existence of PGP in human RBC is well established; has been purified and biochemically characterized [Zecher 1982] - has been detected in all human tissues [- chr location of gene has been identified [Mulley 1990]
PGLYCP	3	Zecher R, Schwulera U, Wolf HU.	Purification, isolation and characterization of a phosphoglycolate phosphatase isoenzyme from human erythrocytes.	Int J Biochem	1982	6290284	- existence of PGP in human RBC is well established; has been purified and biochemically characterized [Zecher 1982] - has been detected in all human tissues [- chr location of gene has been identified [Mulley 1990]

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PGPPT	2	Schlame M, Rua D, Greenberg ML.	The biosynthesis and functional role of cardiolipin.	Prog Lipid Res	2000	10799718	cytoplasm - uniprot NJ
PGS	3	Funk CD, Funk LB, Kennedy ME, Pong AS, Fitzgerald GA.	Human platelet/erythroleukemia cell prostaglandin G/H synthase: cDNA cloning, expression, and gene chromosomal assignment.	FASEB J	1991	1907252	ER membrane - uniprot, cytoplasmic: see ref by Maihofner Cloned version came from platelets - PMID: 1907252 Specific cofactor determined based on consistency w/ other parts of pathway (biosynthetic, O2 dependent). HemeB is a cofactor, but no evidence that it is a metabolized cofactor. aka COX1 and COX2 Prostaglandin-endoperoxide synthase (PTGS), also known as cyclooxygenase, is the key enzyme in prostaglandin biosynthesis, and acts both as a dioxygenase and as a peroxidase. There are two isozymes of PTGS: a constitutive PTGS1 and an inducible PTGS2, which differ in their regulation of expression and tissue distribution. This gene encodes PTGS2, which shows 86% - 89% amino acid sequence identity with mouse, rat, sheep, bovine, horse and rabit PTGS2 proteins, respectively. Human PTGS2 is expressed in a limited number of cell types and regulated by specific stimulatory events, suggesting that it is responsible for the prostanoid biosynthesis involved in inflammation and mitogenesis. The expression of this gene is deregulated in epithelial tumors. NJ
PGS	3	Maihofner C, Probst-Cousin S, Bergmann M, Neuhuber W, Neundorfer B, Heuss D.	Expression and localization of cyclooxygenase-1 and 2 in human sporadic amyotrophic lateral sclerosis.	Eur J Neurosci	2003	14511332	ER membrane - uniprot, cytoplasmic: see ref by Maihofner Cloned version came from platelets - PMID: 1907252 Specific cofactor determined based on consistency w/ other parts of pathway (biosynthetic, O2 dependent). HemeB is a cofactor, but no evidence that it is a metabolized cofactor. aka COX1 and COX2 Prostaglandin-endoperoxide synthase (PTGS), also known as cyclooxygenase, is the key enzyme in prostaglandin biosynthesis, and acts both as a dioxygenase and as a peroxidase. There are two isozymes of PTGS: a constitutive PTGS1 and an inducible PTGS2, which differ in their regulation of expression and tissue distribution. This gene encodes PTGS2, which shows 86% - 89% amino acid sequence identity with mouse, rat, sheep, bovine, horse and rabit PTGS2 proteins, respectively. Human PTGS2 is expressed in a limited number of cell types and regulated by specific stimulatory events, suggesting that it is responsible for the prostanoid biosynthesis involved in inflammation and mitogenesis. The expression of this gene is deregulated in epithelial tumors. NJ
PHCDm	2	Valle D, Goodman SI, Harris SC, Phang JM.	Genetic evidence for a common enzyme catalyzing the second step in the degradation of proline and hydroxyproline.	J Clin Invest	1979	500817	based on KEGG and citation - ALDH4A1 catalyzes the oxidation of both delta 1-pyrroline-5-carboxylate and delta 1-pyrroline-3-hydroxy-5-carboxylate (the second steps in the degradation of proline and hydroxyproline, respectively) [Valle 1979] - isolated mouse liver mitochondria produced glyoxylate from hydroxyproline [Knight 2005]
PHCDm	2	Takayama T, Fujita K, Suzuki K, Sakaguchi M, Fujie M, Nagai E, Watanabe S, Ichiyama A, Ogawa Y	Control of oxalate formation from L-hydroxyproline in liver mitochondria	J Am Soc Nephrol	2003	12660328	based on KEGG and citation - ALDH4A1 catalyzes the oxidation of both delta 1-pyrroline-5-carboxylate and delta 1-pyrroline-3-hydroxy-5-carboxylate (the second steps in the degradation of proline and hydroxyproline, respectively) [Valle 1979] - isolated mouse liver mitochondria produced glyoxylate from hydroxyproline [Knight 2005]
PHEACGLNt	0	Vanholder RC, Glorieux G, De Smet R, De Deyn PP	Low water-soluble uremic toxins	Adv Ren Replace Ther	2003	14681857	Compound (or one with a very similar name) is said to be present in the urine, so some transport is necessary. Gene and mechanism unknown. SAB
PHEMEt	3	Shayeghi M, Latunde-Dada GO, Oakhill JS, Laftah AH, Takeuchi K, Halliday N, Khan Y, Warley A, McCann FE, Hider RC, Frazer DM, Anderson GJ, Vulpe CD, Simpson RJ, McKie AT	Identification of an intestinal heme transporter	Cell	2005	16143108	- mouse protein was isolated from duodenum; shown to mediate heme transport in a temperature-dependent and saturable manner [Shayeghi 2005] - sequence of mouse gene was aligned with human, rabbit, rat, and zebrafish orthologs [Shayeghi 2005] - organic heme is known to be absorbed from the diet (breakdown of hemoglobin and myoglobin contained in red meat) [Shayeghi 2005] - in mammals, duodenal enterocytes and hepatocytes are major sites of heme transport [Shayeghi 2005] - heme has been shown to diffuse across model lipid membranes; also, studies in isolated hepatocytes and intestine-like cell line Caco-2 have demonstrated that heme uiptake takes place by a staurable carrier mediated process [Shayeghi 2005]
PHETA1	2	Jeremy M. Berg, John L. Tymoczko, Lubert Stryer, Neil D. Clarke	Biochemistry		2002		Well-established that this reaction, or one with alternate cofactors, takes place excessively in individuals with phenylketonuria.

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PHETHPTOX2	3	Waters PJ, Parniak MA, Nowacki P, Scriver CR	In vitro expression analysis of mutations in phenylalanine hydroxylase: linking genotype to phenotype and structure to function	Hum Mutat	1998	9450897	Gene and reaction characterized. A cause of PKU.
PHYHx	3	Jansen GA, Mihalik SJ, Watkins PA, Moser HW, Jakobs C, Denis S, Wanders RJ.	Phytanoyl-CoA hydroxylase is present in human liver, located in peroxisomes, and deficient in Zellweger syndrome: direct, unequivocal evidence for the new, revised pathway of phytanic acid alpha-oxidation in humans.	Biochem Biophys Res Commun	1996	8954107	localization: peroxisome (uniprot) specificity: Expressed in liver, kidney, and T-cells, but not in spleen, brain, heart, lung and skeletal muscle. The protein encoded by this gene is a peroxisomal enzyme. It catalyzes the initial alpha-oxidation step in the degradation of phytanic acid and converts phytanoyl-CoA to 2-hydroxyphytanoyl-CoA. It interacts specifically with the immunophilin FKBP52. Refsum disease, an autosomal recessive neurologic disorder, is caused by the deficiency of this encoded protein.
PHYHx	3	Jansen GA, Ofman R, Ferdinandusse S, Ijlst L, Muijsers AO, Skjeldal OH, Stokke O, Jakobs C, Besley GT, Wraith JE, Wanders RJ.	Refsum disease is caused by mutations in the phytanoyl-CoA hydroxylase gene.	Nat Genet	1997	9326940	localization: peroxisome (uniprot) specificity: Expressed in liver, kidney, and T-cells, but not in spleen, brain, heart, lung and skeletal muscle. The protein encoded by this gene is a peroxisomal enzyme. It catalyzes the initial alpha-oxidation step in the degradation of phytanic acid and converts phytanoyl-CoA to 2-hydroxyphytanoyl-CoA. It interacts specifically with the immunophilin FKBP52. Refsum disease, an autosomal recessive neurologic disorder, is caused by the deficiency of this encoded protein.
PHYQt	3	David A. Bender	Vitamin K		2003		uptake in proximal small intestin and incorporation in chylomicrons extrahepatic tissues take up phyQ from chylomicrons and synthesize menaquinone-4 which is hte principal vitamer in tissues other than the liver. some menaquinone-4 is also absorbed into the portal system from the colon - vitamin K1, comes from plants - estrogens increase PhyQ absorption - menaquinones (vit k2) are mainly absorbed from terminal ileum (where bile salts are present) into hepatic portal vein - about 90% of total liver content of vit K is menaquinone 7 to 13 and the hepatic pool of phyQ turns over considerably faster than that of menaquinone --> little storage of vit k liver makes catabolism of Vit k - however I could not find out how! IT
PI345P3P	3	Ono H, Katagiri H, Funaki M, Anai M, Inukai K, Fukushima Y, Sakoda H, Ogihara T, Onishi Y, Fujishiro M, Kikuchi M, Oka Y, Asano T	Regulation of phosphoinositide metabolism, Akt phosphorylation, and glucose transport by PTEN (phosphatase and tensin homolog deleted on chromosome 10) in 3T3-L1 adipocytes	Mol Endocrinol	2001	11463863	- has PtdIns(3,4,5)P3 phosphatase activity [RefSeq], [UniProt], [Ono, Mol Endocrinol 2001]
PI34P5K	3	Cunningham TW, Majerus PW	Pathway for the formation of D-3 phosphate containing inositol phospholipids in PDGF stimulated NIH 3T3 fibroblasts	Biochem Biophys Res Commun	1991	1850246	- reaction described in [Tolias, Chem Phys Lipids 1999] - whether this rxn occurs significantly in vivo is contraversial [Cunningham, J Biol Chem 1990], [Cunningham, Biophys Biochem Res Commun 1991], [Stephens, Nature 1991], [Carter, Biochem J 1994]
PI34P5K	3	Stephens LR, Hughes KT, Irvine RF	Pathway of phosphatidylinositol(3,4,5)-trisphosphate synthesis in activated neutrophils	Nature	1991	1851250	- reaction described in [Tolias, Chem Phys Lipids 1999] - whether this rxn occurs significantly in vivo is contraversial [Cunningham, J Biol Chem 1990], [Cunningham, Biophys Biochem Res Commun 1991], [Stephens, Nature 1991], [Carter, Biochem J 1994]
PI34P5K	3	Cunningham TW, Lips DL, Bansal VS, Caldwell KK, Mitchell CA, Majerus PW	Pathway for the formation of D-3 phosphate containing inositol phospholipids in intact human platelets	J Biol Chem	1990	2174884	- reaction described in [Tolias, Chem Phys Lipids 1999] - whether this rxn occurs significantly in vivo is contraversial [Cunningham, J Biol Chem 1990], [Cunningham, Biophys Biochem Res Commun 1991], [Stephens, Nature 1991], [Carter, Biochem J 1994]
PI34P5K	3	Carter AN, Huang R, Sorisky A, Downes CP, Rittenhouse SE	Phosphatidylinositol 3,4,5-trisphosphate is formed from phosphatidylinositol 4,5-bisphosphate in thrombin-stimulated platelets	Biochem J	1994	8042983	- reaction described in [Tolias, Chem Phys Lipids 1999] - whether this rxn occurs significantly in vivo is contraversial [Cunningham, J Biol Chem 1990], [Cunningham, Biophys Biochem Res Commun 1991], [Stephens, Nature 1991], [Carter, Biochem J 1994]
PI35P3P	3	Walker DM, Urbe S, Dove SK, Tenza D, Raposo G, Clague MJ	Characterization of MTMR3. an inositol lipid 3-phosphatase with novel substrate specificity	Curr Biol	2001	11676921	- isolated from HeLa cells; was shown to hydrolyze PtdIns3P and PtdIns(3,5)P2 to PtdIns and PtdIns5P, respeectively, in vitro and when heterologously expressed in S. cerevisiae [Walker 2001]

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PI45P3K	3	Carpenter CL, Duckworth BC, Auger KR, Cohen B, Schaffhausen BS, Cantley LC	Purification and characterization of phosphoinositide 3-kinase from rat liver	J Biol Chem	1990	2174051	- rat protein is heterodimer of an 85 kd regulatory subunit that mediates binding to phosphorylated proteins and a 110 kd catalytic subunit [Carpenter, J Biol Chem 1990] - 3 known class IA catalytic subunits: PIK3CA (p110a), PIK3CB (p110b), PIK3CD (p110c) which form complexes with 85 kDa regulatory subunits: PIK3R1 (p85a, p55a, p50a), PIK3R2 (p85b), PIK3R3 (p55c) [Wymann, Curr Opin Cell Biol 2005] - PIK3CG is class IB member; interacts with PIK3R5 (p101) and PIK adapter protein (p87). [Wymann, Curr Opin Cell Biol 2005] 5290: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, PtdIns(4,5)P2 [RefSeq], [UniProt] - gene has been cloned; 99% identical to bovine protein [Volinia, Genomics 1994] 5291: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, PtdIns(4,5)P2 [UniProt], [Hu, Mol Cell Biol 1993] - expressed ubiquitously [UniProt], [Hu, Mol Cell Biol 1993] - 42% identical to bovine PI 3-kinase and 28% identical to S. cerevisiae Vps34 [Hu, Mol Cell Biol 1993] 5293: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, PtdIns(4,5)P2 [UniProt], [Vanhaesebroeck, PNAS 19997] - leukocytes [UniProt], [Vanhaesebroeck, PNAS 19997] - gene has been cloned, characterized [Vanhaesebroeck, PNAS 5294: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, Pt - Pancreas, skeletal muscle, liver and heart [UniProt]
PI45P3K	3	Stoyanov B, Volinia S, Hanck T, Rubio I, Loubtchenkov M, Malek D, Stoyanova S, Vanhaesebroeck B, Dhand R, Nurnberg B, et al	Cloning and characterization of a G protein-activated human phosphoinositide-3 kinase	Science	1995	7624799	- rat protein is heterodimer of an 85 kd regulatory subunit that mediates binding to phosphorylated proteins and a 110 kd catalytic subunit [Carpenter, J Biol Chem 1990] - 3 known class IA catalytic subunits: PIK3CA (p110a), PIK3CB (p110b), PIK3CD (p110c) which form complexes with 85 kDa regulatory subunits: PIK3R1 (p85a, p55a, p50a), PIK3R2 (p85b), PIK3R3 (p55c) [Wymann, Curr Opin Cell Biol 2005] - PIK3CG is class IB member; interacts with PIK3R5 (p101) and PIK adapter protein (p87). [Wymann, Curr Opin Cell Biol 2005] 5290: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, PtdIns(4,5)P2 [RefSeq], [UniProt] - gene has been cloned; 99% identical to bovine protein [Volinia, Genomics 1994] 5291: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, PtdIns(4,5)P2 [UniProt], [Hu, Mol Cell Biol 1993] - expressed ubiquitously [UniProt], [Hu, Mol Cell Biol 1993] - 42% identical to bovine PI 3-kinase and 28% identical to S. cerevisiae Vps34 [Hu, Mol Cell Biol 1993] 5293: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, PtdIns(4,5)P2 [UniProt], [Vanhaesebroeck, PNAS 19997] - leukocytes [UniProt], [Vanhaesebroeck, PNAS 19997] - gene has been cloned, characterized [Vanhaesebroeck, PNAS 5294: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, Pt - Pancreas, skeletal muscle, liver and heart [UniProt]
PI45P3K	3	Volinia S, Hiles I, Ormondroyd E, Nizetic D, Antonacci R, Rocchi M, Waterfield MD	Molecular cloning, cDNA sequence, and chromosomal localization of the human phosphatidylinositol 3-kinase p110 alpha (PIK3CA) gene	Genomics	1994	7713498	- rat protein is heterodimer of an 85 kd regulatory subunit that mediates binding to phosphorylated proteins and a 110 kd catalytic subunit [Carpenter, J Biol Chem 1990] - 3 known class IA catalytic subunits: PIK3CA (p110a), PIK3CB (p110b), PIK3CD (p110c) which form complexes with 85 kDa regulatory subunits: PIK3R1 (p85a, p55a, p50a), PIK3R2 (p85b), PIK3R3 (p55c) [Wymann, Curr Opin Cell Biol 2005] - PIK3CG is class IB member; interacts with PIK3R5 (p101) and PIK adapter protein (p87). [Wymann, Curr Opin Cell Biol 2005] 5290: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, PtdIns(4,5)P2 [RefSeq], [UniProt] - gene has been cloned; 99% identical to bovine protein [Volinia, Genomics 1994] 5291: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, PtdIns(4,5)P2 [UniProt], [Hu, Mol Cell Biol 1993] - expressed ubiquitously [UniProt], [Hu, Mol Cell Biol 1993] - 42% identical to bovine PI 3-kinase and 28% identical to S. cerevisiae Vps34 [Hu, Mol Cell Biol 1993] 5293: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, PtdIns(4,5)P2 [UniProt], [Vanhaesebroeck, PNAS 19997] - leukocytes [UniProt], [Vanhaesebroeck, PNAS 19997] - gene has been cloned, characterized [Vanhaesebroeck, PNAS 5294: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, Pt - Pancreas, skeletal muscle, liver and heart [UniProt]

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PI45P3K	3	Hu P, Mondino A, Skolnik EY, Schlessinger J	Cloning of a novel, ubiquitously expressed human phosphatidylinositol 3-kinase and identification of its binding site on p85	Mol Cell Biol	1993	8246984	- fat protein is heterodimer of an 85 kd regulatory subunit that mediates binding to phosphorylated proteins and a 110 kd catalytic subunit [Carpenter, J Biol Chem 1990] - 3 known class IA catalytic subunits: PIK3CA (p110a), PIK3CB (p110b), PIK3CD (p110c) which form complexes with 85 kDa regulatory subunits: PIK3R1 (p85a, p55a, p50a), PIK3R2 (p85b), PIK3R3 (p55c) [Wymann, Curr Opin Cell Biol 2005] - PIK3CG is class IB member; interacts with PIK3R5 (p101) and PIK adapter protein (p87). [Wymann, Curr Opin Cell Biol 2005] 5290: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, PtdIns(4,5)P2 [RefSeq], [UniProt] - gene has been cloned; 99% identical to bovine protein [Volinia, Genomics 1994] 5291: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, PtdIns(4,5)P2 [UniProt], [Hu, Mol Cell Biol 1993] - expressed ubiquitously [UniProt], [Hu, Mol Cell Biol 1993] - 42% identical to bovine PI 3-kinase and 28% identical to S. cerevisiae Vps34 [Hu, Mol Cell Biol 1993] 5293: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, PtdIns(4,5)P2 [UniProt], [Vanhaesebroeck, PNAS 19997] - leukocytes [UniProt], [Vanhaesebroeck, PNAS 19997] - gene has been cloned, characterized [Vanhaesebroeck, PNAS 5294: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, Pt - Pancreas, skeletal muscle, liver and heart [UniProt]
PI45P3K	3	Vanhaesebroeck B, Welham MJ, Kotani K, Stein R, Warne PH, Zvelebil MJ, Higashi K, Volinia S, Downward J, Waterfield MD	P110delta, a novel phosphoinositide 3-kinase in leukocytes	Proc Natl Acad Sci U S A	1997	9113989	- fat protein is heterodimer of an 85 kd regulatory subunit that mediates binding to phosphorylated proteins and a 110 kd catalytic subunit [Carpenter, J Biol Chem 1990] - 3 known class IA catalytic subunits: PIK3CA (p110a), PIK3CB (p110b), PIK3CD (p110c) which form complexes with 85 kDa regulatory subunits: PIK3R1 (p85a, p55a, p50a), PIK3R2 (p85b), PIK3R3 (p55c) [Wymann, Curr Opin Cell Biol 2005] - PIK3CG is class IB member; interacts with PIK3R5 (p101) and PIK adapter protein (p87). [Wymann, Curr Opin Cell Biol 2005] 5290: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, PtdIns(4,5)P2 [RefSeq], [UniProt] - gene has been cloned; 99% identical to bovine protein [Volinia, Genomics 1994] 5291: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, PtdIns(4,5)P2 [UniProt], [Hu, Mol Cell Biol 1993] - expressed ubiquitously [UniProt], [Hu, Mol Cell Biol 1993] - 42% identical to bovine PI 3-kinase and 28% identical to S. cerevisiae Vps34 [Hu, Mol Cell Biol 1993] 5293: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, PtdIns(4,5)P2 [UniProt], [Vanhaesebroeck, PNAS 19997] - leukocytes [UniProt], [Vanhaesebroeck, PNAS 19997] - gene has been cloned, characterized [Vanhaesebroeck, PNAS 5294: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, Pt - Pancreas, skeletal muscle, liver and heart [UniProt]
PI45P3K	3	Brock C, Schaefer M, Reusch HP, Czupalla C, Michalke M, Spicher K, Schultz G, Nurnberg B	Roles of G beta gamma in membrane recruitment and activation of p110 gamma/p101 phosphoinositide 3-kinase gamma.	J Cell Biol	2003	12507995	- fat protein is heterodimer of an 85 kd regulatory subunit that mediates binding to phosphorylated proteins and a 110 kd catalytic subunit [Carpenter, J Biol Chem 1990] - 3 known class IA catalytic subunits: PIK3CA (p110a), PIK3CB (p110b), PIK3CD (p110c) which form complexes with 85 kDa regulatory subunits: PIK3R1 (p85a, p55a, p50a), PIK3R2 (p85b), PIK3R3 (p55c) [Wymann, Curr Opin Cell Biol 2005] - PIK3CG is class IB member; interacts with PIK3R5 (p101) and PIK adapter protein (p87). [Wymann, Curr Opin Cell Biol 2005] 5290: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, PtdIns(4,5)P2 [RefSeq], [UniProt] - gene has been cloned; 99% identical to bovine protein [Volinia, Genomics 1994] 5291: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, PtdIns(4,5)P2 [UniProt], [Hu, Mol Cell Biol 1993] - expressed ubiquitously [UniProt], [Hu, Mol Cell Biol 1993] - 42% identical to bovine PI 3-kinase and 28% identical to S. cerevisiae Vps34 [Hu, Mol Cell Biol 1993] 5293: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, PtdIns(4,5)P2 [UniProt], [Vanhaesebroeck, PNAS 19997] - leukocytes [UniProt], [Vanhaesebroeck, PNAS 19997] - gene has been cloned, characterized [Vanhaesebroeck, PNAS 5294: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, Pt - Pancreas, skeletal muscle, liver and heart [UniProt]

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PI45P3K	3	Wymann MP, Marone R	Phosphoinositide 3-kinase in disease: timing, location, and scaffolding	Curr Opin Cell Biol	2005	15780590	- 1at protein is heterodimer of an 85 kd regulatory subunit that mediates binding to phosphorylated proteins and a 110 kd catalytic subunit [Carpenter, J Biol Chem 1990] - 3 known class IA catalytic subunits: PIK3CA (p110a), PIK3CB (p110b), PIK3CD (p110c) which form complexes with 85 kDa regulatory subunits: PIK3R1 (p85a, p55a, p50a), PIK3R2 (p85b), PIK3R3 (p55c) [Wymann, Curr Opin Cell Biol 2005] - PIK3CG is class IB member; interacts with PIK3R5 (p101) and PIK adapter protein (p87). [Wymann, Curr Opin Cell Biol 2005] 5290: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, PtdIns(4,5)P2 [RefSeq], [UniProt] - gene has been cloned; 99% identical to bovine protein [Volinia, Genomics 1994] 5291: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, PtdIns(4,5)P2 [UniProt], [Hu, Mol Cell Biol 1993] - expressed ubiquitously [UniProt], [Hu, Mol Cell Biol 1993] - 42% identical to bovine PI 3-kinase and 28% identical to S. cerevisiae Vps34 [Hu, Mol Cell Biol 1993] 5293: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, PtdIns(4,5)P2 [UniProt], [Vanhaesebroeck, PNAS 19997] - leukocytes [UniProt], [Vanhaesebroeck, PNAS 19997] - gene has been cloned, characterized [Vanhaesebroeck, PNAS 5294: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, Pt - Pancreas, skeletal muscle, liver and heart [UniProt]
PI45P5P	3	Jefferson AB, Majerus PW	Properties of type II inositol polyphosphate 5-phosphatase	J Biol Chem	1995	7721860	8867: - localizes to clathrin-coated invaginations of synaptic nerve terminals [Haffner, FEBS Lett 1997], [UniProt] - Isoform 1 is more enriched than isoform 2 in developing brain as well as non-neuronal cells. Isoform 2 is very abundant in nerve terminals [UniProt] - PtdIns4P 5-phosphatase activity [UniProt], [Stopkova, Psychiatry Res 2004] 4952: - phospatidylinositol polyphosphate 5-phosphatase activity [RefSeq], [UniProt], [Zhang, PNAS 1995] - golgi cisternae [RefSeq] - Brain, skeletal muscle, heart, kidney, lung, placenta, and fibroblasts [UniProt] - associates w/ Rac GTPase in trans-Golgi (assume this occurs at cytosolic surface of outer membrane) [Faucherre, Hum Mol Genet 2003] 8871: - PtdIns4P 5-phosphatase activity [UniProt], [Spaenij-Dekking, Leukemia 2003] - cytosolic and synaptic nerve termini [Malecz, Curr Biol 2000] 3633: - PtdIns4P 5-phosphatase activity [UniProt], [Jefferson, J Biol Chem 1995] - found in platelets [UniProt] 56623: - PtdIns4P 5-phosphatase activity [UniProt], [Kisseleva, J Biol Chem 200] - Cytoplasmic; peripheral membrane protein associated with Gc - brain, heart, pancreas, testis and spleen [UniProt], [Kisseleva,

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PI45P5P	3	Zhang X, Jefferson AB, Auethavekiat V, Majerus PW	The protein deficient in Lowe syndrome is a phosphatidylinositol-4,5-bisphosphate 5-phosphatase	Proc Natl Acad Sci U S A	1995	7761412	8867: - localizes to clathrin-coated invaginations of synaptic nerve terminals [Haffner, FEBS Lett 1997], [UniProt] - Isoform 1 is more enriched than isoform 2 in developing brain as well as non-neuronal cells. Isoform 2 is very abundant in nerve terminals [UniProt] - PtdIns4P 5-phosphatase activity [UniProt], [Stopkova, Psychiatry Res 2004] 4952: - phospatidylinositol polyphosphate 5-phosphatase activity [RefSeq], [UniProt], [Zhang, PNAS 1995] - golgi cisternae [RefSeq] - Brain, skeletal muscle, heart, kidney, lung, placenta, and fibroblasts [UniProt] - associates w/ Rac GTPase in trans-Golgi (assume this occurs at cytosolic surface of outer membrane) [Faucherre, Hum Mol Genet 2003] 8871: - PtdIns4P 5-phosphatase activity [UniProt], [Spaenij-Dekking, Leukemia 2003] - cytosolic and synaptic nerve termini [Malecz, Curr Biol 2000] 3633: - PtdIns4P 5-phosphatase activity [UniProt], [Jefferson, J Biol Chem 1995] - found in platelets [UniProt] 56623: - PtdIns4P 5-phosphatase activity [UniProt], [Kisseleva, J Biol Chem 200] - Cytoplasmic; peripheral membrane protein associated with Go - brain, heart, pancreas, testis and spleen [UniProt], [Kisseleva,
PI45P5P	3	Kisseleva MV, Wilson MP, Majerus PW	The isolation and characterization of a cDNA encoding phospholipid-specific inositol polyphosphate 5-phosphatase	J Biol Chem	2000	10764818	8867: - localizes to clathrin-coated invaginations of synaptic nerve terminals [Haffner, FEBS Lett 1997], [UniProt] - Isoform 1 is more enriched than isoform 2 in developing brain as well as non-neuronal cells. Isoform 2 is very abundant in nerve terminals [UniProt] - PtdIns4P 5-phosphatase activity [UniProt], [Stopkova, Psychiatry Res 2004] 4952: - phospatidylinositol polyphosphate 5-phosphatase activity [RefSeq], [UniProt], [Zhang, PNAS 1995] - golgi cisternae [RefSeq] - Brain, skeletal muscle, heart, kidney, lung, placenta, and fibroblasts [UniProt] - associates w/ Rac GTPase in trans-Golgi (assume this occurs at cytosolic surface of outer membrane) [Faucherre, Hum Mol Genet 2003] 8871: - PtdIns4P 5-phosphatase activity [UniProt], [Spaenij-Dekking, Leukemia 2003] - cytosolic and synaptic nerve termini [Malecz, Curr Biol 2000] 3633: - PtdIns4P 5-phosphatase activity [UniProt], [Jefferson, J Biol Chem 1995] - found in platelets [UniProt] 56623: - PtdIns4P 5-phosphatase activity [UniProt], [Kisseleva, J Biol Chem 200] - Cytoplasmic; peripheral membrane protein associated with Go - brain, heart, pancreas, testis and spleen [UniProt], [Kisseleva,

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PI45P5P	3	Faucherre A, Desbois P, Satre V, Lunardi J, Dorseuil O, Gacon G	Lowe syndrome protein OCRL1 interacts with Rac GTPase in the trans-Golgi network.	Hum Mol Genet	2003	12915445	8867: - localizes to clathrin-coated invaginations of synaptic nerve terminals [Haffner, FEBS Lett 1997], [UniProt] - Isoform 1 is more enriched than isoform 2 in developing brain as well as non-neuronal cells. Isoform 2 is very abundant in nerve terminals [UniProt] - PtdIns4P 5-phosphatase activity [UniProt], [Stopkova, Psychiatry Res 2004] 4952: - phospatidylinositol polyphosphate 5-phosphatase activity [RefSeq], [UniProt], [Zhang, PNAS 1995] - golgi cisternae [RefSeq] - Brain, skeletal muscle, heart, kidney, lung, placenta, and fibroblasts [UniProt] - associates w/ Rac GTPase in trans-Golgi (assume this occurs at cytosolic surface of outer membrane) [Faucherre, Hum Mol Genet 2003] 8871: - PtdIns4P 5-phosphatase activity [UniProt], [Spaenij-Dekking, Leukemia 2003] - cytosolic and synaptic nerve termini [Malecz, Curr Biol 2000] 3633: - PtdIns4P 5-phosphatase activity [UniProt], [Jefferson, J Biol Chem 1995] - found in platelets [UniProt] 56623: - PtdIns4P 5-phosphatase activity [UniProt], [Kisseleva, J Biol Chem 200] - Cytoplasmic; peripheral membrane protein associated with Gc - brain, heart, pancreas, testis and spleen [UniProt], [Kisseleva,
PI45PLC	3	Park D, Jhon DY, Kriz R, Knopf J, Rhee SG	Cloning, sequencing, expression, and Gq-independent activation of phospholipase C-beta 2	J Biol Chem	1992	1644792	substrates [Leung, Mol Cancer 2004] - PLC family is composed of 11 subtypes: ß1, 2, 3 and 4, ¿ 1 and 2, d1, 3 and 4, e, and ¿ [Leung, Mol Cancer 2004] 84812: - gene was cloned [Kim, Cytogenet Cell Genet 1999] 5333: - gene was cloned [Ishikawa, Cytogenet Cell Genet 1997] - expression and biochemical characterization [Cheng, J Biol Chem 1995] 23007: - function inferred from electronic annotation [GO] 51196: - gene was cloned and characterized [Song, J Biol Chem 2001], [Lopez, J Biol Chem 2001] 5336: - gene was mapped [Hernandez, Genomics 1994] 5332: - predominantly expressed in retina [UniProt], [Alvarez, Genomics 1995] - gene was cloned and compared to mammalian homologs [Alvarez, Genomics 1995] 26236: - gene was identified, cloned and expressed [Peruzzi, Biochim Biophys Acta 2002], [Caricasole, Biochim Biophys Acta 2000], [Peruzzi, Biochim Biophys Acta 2000] - nuclear [Peruzzi, Biochim Biophys Acta 2000] and cytosolic [Caricasole, Biochim Biophys Acta 2000] 89869: - gene was cloned and expressed [Saunders, Development 2002 - sperm-specific [Saunders, Development 2002]

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PI45PLC	3	Burgess WH, Dionne CA, Kaplow J, Mudd R, Friesel R, Zilberstein A, Schlessinger J, Jaye M	Characterization and cDNA cloning of phospholipase C-gamma, a major substrate for heparin-binding growth factor 1 (acidic fibroblast growth factor)-activated tyrosine kinase	Mol Cell Biol	1990	2167438	substrates [Leung, Mol Cancer 2004] - PLC family is composed of 11 subtypes: ß1, 2, 3 and 4, ¿ 1 and 2, d1, 3 and 4, e, and ¿ [Leung, Mol Cancer 2004] 84812: - gene was cloned [Kim, Cytogenet Cell Genet 1999] 5333: - gene was cloned [Ishikawa, Cytogenet Cell Genet 1997] - expression and biochemical characterization [Cheng, J Biol Chem 1995] 23007: - function inferred from electronic annotation [GO] 51196: - gene was cloned and characterized [Song, J Biol Chem 2001], [Lopez, J Biol Chem 2001] 5336: - gene was mapped [Hernandez, Genomics 1994] 5332: - predominantly expressed in retina [UniProt], [Alvarez, Genomics 1995] - gene was cloned and compared to mammalian homologs [Alvarez, Genomics 1995] 26236: - gene was identified, cloned and expressed [Peruzzi, Biochim Biophys Acta 2002], [Caricasole, Biochim Biophys Acta 2000], [Peruzzi, Biochim Biophys Acta 2000] - nuclear [Peruzzi, Biochim Biophys Acta 2000] and cytosolic [Caricasole, Biochim Biophys Acta 2000] 89869: - gene was cloned and expressed [Saunders, Development 2002 - sperm-specific [Saunders, Development 2002]
PI45PLC	3	Lagercrantz J, Carson E, Phelan C, Grimmond S, Rosen A, Dare E, Nordenskjold M, Hayward NK, Larsson C, Weber G	Genomic organization and complete cDNA sequence of the human phosphoinositide-specific phospholipase C beta 3 gene (PLCB3)	Genomics	1995	7607669	substrates [Leung, Mol Cancer 2004] - PLC family is composed of 11 subtypes: ß1, 2, 3 and 4, ¿ 1 and 2, d1, 3 and 4, e, and ¿ [Leung, Mol Cancer 2004] 84812: - gene was cloned [Kim, Cytogenet Cell Genet 1999] 5333: - gene was cloned [Ishikawa, Cytogenet Cell Genet 1997] - expression and biochemical characterization [Cheng, J Biol Chem 1995] 23007: - function inferred from electronic annotation [GO] 51196: - gene was cloned and characterized [Song, J Biol Chem 2001], [Lopez, J Biol Chem 2001] 5336: - gene was mapped [Hernandez, Genomics 1994] 5332: - predominantly expressed in retina [UniProt], [Alvarez, Genomics 1995] - gene was cloned and compared to mammalian homologs [Alvarez, Genomics 1995] 26236: - gene was identified, cloned and expressed [Peruzzi, Biochim Biophys Acta 2002], [Caricasole, Biochim Biophys Acta 2000], [Peruzzi, Biochim Biophys Acta 2000] - nuclear [Peruzzi, Biochim Biophys Acta 2000] and cytosolic [Caricasole, Biochim Biophys Acta 2000] 89869: - gene was cloned and expressed [Saunders, Development 2002 - sperm-specific [Saunders, Development 2002]

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PI45PLC	3	Mazuruk K, Schoen TJ, Chader GJ, Rodriguez IR	Structural organization and expression of the human phosphatidylinositol-specific phospholipase C beta-3 gene	Biochem Biophys Res Commun	1995	7612006	substrates [Leung, Mol Cancer 2004] - PLC family is composed of 11 subtypes: ß1, 2, 3 and 4, ¿ 1 and 2, d1, 3 and 4, e, and ¿ [Leung, Mol Cancer 2004] 84812: - gene was cloned [Kim, Cytogenet Cell Genet 1999] 5333: - gene was cloned [Ishikawa, Cytogenet Cell Genet 1997] - expression and biochemical characterization [Cheng, J Biol Chem 1995] 23007: - function inferred from electronic annotation [GO] 51196: - gene was cloned and characterized [Song, J Biol Chem 2001], [Lopez, J Biol Chem 2001] 5336: - gene was mapped [Hernandez, Genomics 1994] 5332: - predominantly expressed in retina [UniProt], [Alvarez, Genomics 1995] - gene was cloned and compared to mammalian homologs [Alvarez, Genomics 1995] 26236: - gene was identified, cloned and expressed [Peruzzi, Biochim Biophys Acta 2002], [Caricasole, Biochim Biophys Acta 2000], [Peruzzi, Biochim Biophys Acta 2000] - nuclear [Peruzzi, Biochim Biophys Acta 2000] and cytosolic [Caricasole, Biochim Biophys Acta 2000] 89869: - gene was cloned and expressed [Saunders, Development 2002 - sperm-specific [Saunders, Development 2002]
PI45PLC	3	Kohno T, Otsuka T, Takano H, Yamamoto T, Hamaguchi M, Terada M, Yokota J	Identification of a novel phospholipase C family gene at chromosome 2q33 that is homozygously deleted in human small cell lung carcinoma	Hum Mol Genet	1995	7633416	substrates [Leung, Mol Cancer 2004] - PLC family is composed of 11 subtypes: ß1, 2, 3 and 4, ¿ 1 and 2, d1, 3 and 4, e, and ¿ [Leung, Mol Cancer 2004] 84812: - gene was cloned [Kim, Cytogenet Cell Genet 1999] 5333: - gene was cloned [Ishikawa, Cytogenet Cell Genet 1997] - expression and biochemical characterization [Cheng, J Biol Chem 1995] 23007: - function inferred from electronic annotation [GO] 51196: - gene was cloned and characterized [Song, J Biol Chem 2001], [Lopez, J Biol Chem 2001] 5336: - gene was mapped [Hernandez, Genomics 1994] 5332: - predominantly expressed in retina [UniProt], [Alvarez, Genomics 1995] - gene was cloned and compared to mammalian homologs [Alvarez, Genomics 1995] 26236: - gene was identified, cloned and expressed [Peruzzi, Biochim Biophys Acta 2002], [Caricasole, Biochim Biophys Acta 2000], [Peruzzi, Biochim Biophys Acta 2000] - nuclear [Peruzzi, Biochim Biophys Acta 2000] and cytosolic [Caricasole, Biochim Biophys Acta 2000] 89869: - gene was cloned and expressed [Saunders, Development 2002 - sperm-specific [Saunders, Development 2002]

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PI45PLC	3	Sinke RJ, Geurts van Kessel AG	Localization of the human phosphatidylinositol-specific phospholipase c beta 3 gene (PLCB3) within chromosome band 11q13	Genoics	1995	7789993	substrates [Leung, Mol Cancer 2004] - PLC family is composed of 11 subtypes: ß1, 2, 3 and 4, ¿ 1 and 2, d1, 3 and 4, e, and ¿ [Leung, Mol Cancer 2004] 84812: - gene was cloned [Kim, Cytogenet Cell Genet 1999] 5333: - gene was cloned [Ishikawa, Cytogenet Cell Genet 1997] - expression and biochemical characterization [Cheng, J Biol Chem 1995] 23007: - function inferred from electronic annotation [GO] 51196: - gene was cloned and characterized [Song, J Biol Chem 2001], [Lopez, J Biol Chem 2001] 5336: - gene was mapped [Hernandez, Genomics 1994] 5332: - predominantly expressed in retina [UniProt], [Alvarez, Genomics 1995] - gene was cloned and compared to mammalian homologs [Alvarez, Genomics 1995] 26236: - gene was identified, cloned and expressed [Peruzzi, Biochim Biophys Acta 2002], [Caricasole, Biochim Biophys Acta 2000], [Peruzzi, Biochim Biophys Acta 2000] - nuclear [Peruzzi, Biochim Biophys Acta 2000] and cytosolic [Caricasole, Biochim Biophys Acta 2000] 89869: - gene was cloned and expressed [Saunders, Development 2002 - sperm-specific [Saunders, Development 2002]
PI45PLC	3	Hernandez D, Egan SE, Yulug IG, Fisher EM	Mapping the gene that encodes phosphatidylinositol-specific phospholipase C-gamma 2 in the human and the mouse	Genomics	1994	7835906	substrates [Leung, Mol Cancer 2004] - PLC family is composed of 11 subtypes: ß1, 2, 3 and 4, ¿ 1 and 2, d1, 3 and 4, e, and ¿ [Leung, Mol Cancer 2004] 84812: - gene was cloned [Kim, Cytogenet Cell Genet 1999] 5333: - gene was cloned [Ishikawa, Cytogenet Cell Genet 1997] - expression and biochemical characterization [Cheng, J Biol Chem 1995] 23007: - function inferred from electronic annotation [GO] 51196: - gene was cloned and characterized [Song, J Biol Chem 2001], [Lopez, J Biol Chem 2001] 5336: - gene was mapped [Hernandez, Genomics 1994] 5332: - predominantly expressed in retina [UniProt], [Alvarez, Genomics 1995] - gene was cloned and compared to mammalian homologs [Alvarez, Genomics 1995] 26236: - gene was identified, cloned and expressed [Peruzzi, Biochim Biophys Acta 2002], [Caricasole, Biochim Biophys Acta 2000], [Peruzzi, Biochim Biophys Acta 2000] - nuclear [Peruzzi, Biochim Biophys Acta 2000] and cytosolic [Caricasole, Biochim Biophys Acta 2000] 89869: - gene was cloned and expressed [Saunders, Development 2002 - sperm-specific [Saunders, Development 2002]

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PI45PLC	3	Weber G, Friedman E, Grimmond S, Hayward NK, Phelan C, Skogseid B, Gobl A, Zedenius J, Sandelin K, Teh BT, et al.	The phospholipase C beta 3 gene located in the MEN1 region shows loss of expression in endocrine tumours	Hum Mol Genet	1994	7849701	substrates [Leung, Mol Cancer 2004] - PLC family is composed of 11 subtypes: ß1, 2, 3 and 4, ¿ 1 and 2, d1, 3 and 4, e, and ¿ [Leung, Mol Cancer 2004] 84812: - gene was cloned [Kim, Cytogenet Cell Genet 1999] 5333: - gene was cloned [Ishikawa, Cytogenet Cell Genet 1997] - expression and biochemical characterization [Cheng, J Biol Chem 1995] 23007: - function inferred from electronic annotation [GO] 51196: - gene was cloned and characterized [Song, J Biol Chem 2001], [Lopez, J Biol Chem 2001] 5336: - gene was mapped [Hernandez, Genomics 1994] 5332: - predominantly expressed in retina [UniProt], [Alvarez, Genomics 1995] - gene was cloned and compared to mammalian homologs [Alvarez, Genomics 1995] 26236: - gene was identified, cloned and expressed [Peruzzi, Biochim Biophys Acta 2002], [Caricasole, Biochim Biophys Acta 2000], [Peruzzi, Biochim Biophys Acta 2000] - nuclear [Peruzzi, Biochim Biophys Acta 2000] and cytosolic [Caricasole, Biochim Biophys Acta 2000] 89869: - gene was cloned and expressed [Saunders, Development 2002 - sperm-specific [Saunders, Development 2002]
PI45PLC	3	Cheng HF, Jiang MJ, Chen CL, Liu SM, Wong LP, Lomasney JW, King K	Cloning and identification of amino acid residues of human phospholipase C delta 1 essential for catalysis	J Biol Chem	1995	7890667	substrates [Leung, Mol Cancer 2004] - PLC family is composed of 11 subtypes: ß1, 2, 3 and 4, ¿ 1 and 2, d1, 3 and 4, e, and ¿ [Leung, Mol Cancer 2004] 84812: - gene was cloned [Kim, Cytogenet Cell Genet 1999] 5333: - gene was cloned [Ishikawa, Cytogenet Cell Genet 1997] - expression and biochemical characterization [Cheng, J Biol Chem 1995] 23007: - function inferred from electronic annotation [GO] 51196: - gene was cloned and characterized [Song, J Biol Chem 2001], [Lopez, J Biol Chem 2001] 5336: - gene was mapped [Hernandez, Genomics 1994] 5332: - predominantly expressed in retina [UniProt], [Alvarez, Genomics 1995] - gene was cloned and compared to mammalian homologs [Alvarez, Genomics 1995] 26236: - gene was identified, cloned and expressed [Peruzzi, Biochim Biophys Acta 2002], [Caricasole, Biochim Biophys Acta 2000], [Peruzzi, Biochim Biophys Acta 2000] - nuclear [Peruzzi, Biochim Biophys Acta 2000] and cytosolic [Caricasole, Biochim Biophys Acta 2000] 89869: - gene was cloned and expressed [Saunders, Development 2002 - sperm-specific [Saunders, Development 2002]

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PI45PLC	3	Alvarez RA, Ghalayini AJ, Xu P, Hardcastle A, Bhattacharya S, Rao PN, Pettenati MJ, Anderson RE, Baehr W.	cDNA sequence and gene locus of the human retinal phosphoinositide-specific phospholipase-C beta 4 (PLCB4)	Genomics	1995	8530101	substrates [Leung, Mol Cancer 2004] - PLC family is composed of 11 subtypes: ß1, 2, 3 and 4, ¿ 1 and 2, d1, 3 and 4, e, and ¿ [Leung, Mol Cancer 2004] 84812: - gene was cloned [Kim, Cytogenet Cell Genet 1999] 5333: - gene was cloned [Ishikawa, Cytogenet Cell Genet 1997] - expression and biochemical characterization [Cheng, J Biol Chem 1995] 23007: - function inferred from electronic annotation [GO] 51196: - gene was cloned and characterized [Song, J Biol Chem 2001], [Lopez, J Biol Chem 2001] 5336: - gene was mapped [Hernandez, Genomics 1994] 5332: - predominantly expressed in retina [UniProt], [Alvarez, Genomics 1995] - gene was cloned and compared to mammalian homologs [Alvarez, Genomics 1995] 26236: - gene was identified, cloned and expressed [Peruzzi, Biochim Biophys Acta 2002], [Caricasole, Biochim Biophys Acta 2000], [Peruzzi, Biochim Biophys Acta 2000] - nuclear [Peruzzi, Biochim Biophys Acta 2000] and cytosolic [Caricasole, Biochim Biophys Acta 2000] 89869: - gene was cloned and expressed [Saunders, Development 2002] - sperm-specific [Saunders, Development 2002]
PI45PLC	3	Ishikawa S, Takahashi T, Ogawa M, Nakamura Y	Genomic structure of the human PLCD1 (phospholipase C delta 1) locus on 3p22-->p21.3	Cytogenet Cell Genet	1997	9345909	substrates [Leung, Mol Cancer 2004] - PLC family is composed of 11 subtypes: ß1, 2, 3 and 4, ¿ 1 and 2, d1, 3 and 4, e, and ¿ [Leung, Mol Cancer 2004] 84812: - gene was cloned [Kim, Cytogenet Cell Genet 1999] 5333: - gene was cloned [Ishikawa, Cytogenet Cell Genet 1997] - expression and biochemical characterization [Cheng, J Biol Chem 1995] 23007: - function inferred from electronic annotation [GO] 51196: - gene was cloned and characterized [Song, J Biol Chem 2001], [Lopez, J Biol Chem 2001] 5336: - gene was mapped [Hernandez, Genomics 1994] 5332: - predominantly expressed in retina [UniProt], [Alvarez, Genomics 1995] - gene was cloned and compared to mammalian homologs [Alvarez, Genomics 1995] 26236: - gene was identified, cloned and expressed [Peruzzi, Biochim Biophys Acta 2002], [Caricasole, Biochim Biophys Acta 2000], [Peruzzi, Biochim Biophys Acta 2000] - nuclear [Peruzzi, Biochim Biophys Acta 2000] and cytosolic [Caricasole, Biochim Biophys Acta 2000] 89869: - gene was cloned and expressed [Saunders, Development 2002] - sperm-specific [Saunders, Development 2002]

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
PI45PLC	3	Kim H, Suh PG, Ryu SH, Park SH	Assignment of the human PLC delta3 gene (PLCD3) to human chromosome band 17q21 by fluorescence in situ hybridization	Cytogenet Cell Genet	1999	10702670	substrates [Leung, Mol Cancer 2004] - PLC family is composed of 11 subtypes: ß1, 2, 3 and 4, ¿ 1 and 2, d1, 3 and 4, e, and ¿ [Leung, Mol Cancer 2004] 84812: - gene was cloned [Kim, Cytogenet Cell Genet 1999] 5333: - gene was cloned [Ishikawa, Cytogenet Cell Genet 1997] - expression and biochemical characterization [Cheng, J Biol Chem 1995] 23007: - function inferred from electronic annotation [GO] 51196: - gene was cloned and characterized [Song, J Biol Chem 2001], [Lopez, J Biol Chem 2001] 5336: - gene was mapped [Hernandez, Genomics 1994] 5332: - predominantly expressed in retina [UniProt], [Alvarez, Genomics 1995] - gene was cloned and compared to mammalian homologs [Alvarez, Genomics 1995] 26236: - gene was identified, cloned and expressed [Peruzzi, Biochim Biophys Acta 2002], [Caricasole, Biochim Biophys Acta 2000], [Peruzzi, Biochim Biophys Acta 2000] - nuclear [Peruzzi, Biochim Biophys Acta 2000] and cytosolic [Caricasole, Biochim Biophys Acta 2000] 89869: - gene was cloned and expressed [Saunders, Development 2002] - sperm-specific [Saunders, Development 2002]
PI45PLC	3	Kim H, Suh PG, Ryu SH, Park SH	Assignment of the human PLC delta4 gene (PLCD4) to human chromosome band 2q35 by fluorescence in situ hybridization	Cytogenet Cell Genet	1999	10702683	substrates [Leung, Mol Cancer 2004] - PLC family is composed of 11 subtypes: ß1, 2, 3 and 4, ¿ 1 and 2, d1, 3 and 4, e, and ¿ [Leung, Mol Cancer 2004] 84812: - gene was cloned [Kim, Cytogenet Cell Genet 1999] 5333: - gene was cloned [Ishikawa, Cytogenet Cell Genet 1997] - expression and biochemical characterization [Cheng, J Biol Chem 1995] 23007: - function inferred from electronic annotation [GO] 51196: - gene was cloned and characterized [Song, J Biol Chem 2001], [Lopez, J Biol Chem 2001] 5336: - gene was mapped [Hernandez, Genomics 1994] 5332: - predominantly expressed in retina [UniProt], [Alvarez, Genomics 1995] - gene was cloned and compared to mammalian homologs [Alvarez, Genomics 1995] 26236: - gene was identified, cloned and expressed [Peruzzi, Biochim Biophys Acta 2002], [Caricasole, Biochim Biophys Acta 2000], [Peruzzi, Biochim Biophys Acta 2000] - nuclear [Peruzzi, Biochim Biophys Acta 2000] and cytosolic [Caricasole, Biochim Biophys Acta 2000] 89869: - gene was cloned and expressed [Saunders, Development 2002] - sperm-specific [Saunders, Development 2002]

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PI45PLC	3	Peruzzi D, Calabrese G, Faenza I, Manzoli L, Matteucci A, Gianfrancesco F, Billi AM, Stuppia L, Palka G, Cocco L	Identification and chromosomal localisation by fluorescence in situ hybridisation of human gene of phosphoinositide-specific phospholipase C beta(1)	Biochim Biophy Acta	2000	10760467	substrates [Leung, Mol Cancer 2004] - PLC family is composed of 11 subtypes: ß1, 2, 3 and 4, ¿ 1 and 2, d1, 3 and 4, e, and ¿ [Leung, Mol Cancer 2004] 84812: - gene was cloned [Kim, Cytogenet Cell Genet 1999] 5333: - gene was cloned [Ishikawa, Cytogenet Cell Genet 1997] - expression and biochemical characterization [Cheng, J Biol Chem 1995] 23007: - function inferred from electronic annotation [GO] 51196: - gene was cloned and characterized [Song, J Biol Chem 2001], [Lopez, J Biol Chem 2001] 5336: - gene was mapped [Hernandez, Genomics 1994] 5332: - predominantly expressed in retina [UniProt], [Alvarez, Genomics 1995] - gene was cloned and compared to mammalian homologs [Alvarez, Genomics 1995] 26236: - gene was identified, cloned and expressed [Peruzzi, Biochim Biophys Acta 2002], [Caricasole, Biochim Biophys Acta 2000], [Peruzzi, Biochim Biophys Acta 2000] - nuclear [Peruzzi, Biochim Biophys Acta 2000] and cytosolic [Caricasole, Biochim Biophys Acta 2000] 89869: - gene was cloned and expressed [Saunders, Development 2002 - sperm-specific [Saunders, Development 2002]
PI45PLC	3	Lopez I, Mak EC, Ding J, Hamm HE, Lomasney JW	A novel bifunctional phospholipase c that is regulated by Galpha 12 and stimulates the Ras/mitogen-activated protein kinase pathway	J Biol Chem	2001	11022047	substrates [Leung, Mol Cancer 2004] - PLC family is composed of 11 subtypes: ß1, 2, 3 and 4, ¿ 1 and 2, d1, 3 and 4, e, and ¿ [Leung, Mol Cancer 2004] 84812: - gene was cloned [Kim, Cytogenet Cell Genet 1999] 5333: - gene was cloned [Ishikawa, Cytogenet Cell Genet 1997] - expression and biochemical characterization [Cheng, J Biol Chem 1995] 23007: - function inferred from electronic annotation [GO] 51196: - gene was cloned and characterized [Song, J Biol Chem 2001], [Lopez, J Biol Chem 2001] 5336: - gene was mapped [Hernandez, Genomics 1994] 5332: - predominantly expressed in retina [UniProt], [Alvarez, Genomics 1995] - gene was cloned and compared to mammalian homologs [Alvarez, Genomics 1995] 26236: - gene was identified, cloned and expressed [Peruzzi, Biochim Biophys Acta 2002], [Caricasole, Biochim Biophys Acta 2000], [Peruzzi, Biochim Biophys Acta 2000] - nuclear [Peruzzi, Biochim Biophys Acta 2000] and cytosolic [Caricasole, Biochim Biophys Acta 2000] 89869: - gene was cloned and expressed [Saunders, Development 2002 - sperm-specific [Saunders, Development 2002]

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PI45PLC	3	Song C, Hu CD, Masago M, Kariyai K, Yamawaki-Kataoka Y, Shibatohge M, Wu D, Satoh T, Kataoka T	Regulation of a novel human phospholipase C, PLCepsilon, through membrane targeting by Ras	J Biol Chem	2001	11022048	substrates [Leung, Mol Cancer 2004] - PLC family is composed of 11 subtypes: ß1, 2, 3 and 4, ¿ 1 and 2, d1, 3 and 4, e, and ¿ [Leung, Mol Cancer 2004] 84812: - gene was cloned [Kim, Cytogenet Cell Genet 1999] 5333: - gene was cloned [Ishikawa, Cytogenet Cell Genet 1997] - expression and biochemical characterization [Cheng, J Biol Chem 1995] 23007: - function inferred from electronic annotation [GO] 51196: - gene was cloned and characterized [Song, J Biol Chem 2001], [Lopez, J Biol Chem 2001] 5336: - gene was mapped [Hernandez, Genomics 1994] 5332: - predominantly expressed in retina [UniProt], [Alvarez, Genomics 1995] - gene was cloned and compared to mammalian homologs [Alvarez, Genomics 1995] 26236: - gene was identified, cloned and expressed [Peruzzi, Biochim Biophys Acta 2002], [Caricasole, Biochim Biophys Acta 2000], [Peruzzi, Biochim Biophys Acta 2000] - nuclear [Peruzzi, Biochim Biophys Acta 2000] and cytosolic [Caricasole, Biochim Biophys Acta 2000] 89869: - gene was cloned and expressed [Saunders, Development 2002 - sperm-specific [Saunders, Development 2002]
PI45PLC	3	Caricasole A, Sala C, Roncarati R, Formenti E, Terstappen GC	Cloning and characterization of the human phosphoinositide-specific phospholipase C-beta 1 (PLC beta 1)	Biochim Biophys Acta	2000	11118617	substrates [Leung, Mol Cancer 2004] - PLC family is composed of 11 subtypes: ß1, 2, 3 and 4, ¿ 1 and 2, d1, 3 and 4, e, and ¿ [Leung, Mol Cancer 2004] 84812: - gene was cloned [Kim, Cytogenet Cell Genet 1999] 5333: - gene was cloned [Ishikawa, Cytogenet Cell Genet 1997] - expression and biochemical characterization [Cheng, J Biol Chem 1995] 23007: - function inferred from electronic annotation [GO] 51196: - gene was cloned and characterized [Song, J Biol Chem 2001], [Lopez, J Biol Chem 2001] 5336: - gene was mapped [Hernandez, Genomics 1994] 5332: - predominantly expressed in retina [UniProt], [Alvarez, Genomics 1995] - gene was cloned and compared to mammalian homologs [Alvarez, Genomics 1995] 26236: - gene was identified, cloned and expressed [Peruzzi, Biochim Biophys Acta 2002], [Caricasole, Biochim Biophys Acta 2000], [Peruzzi, Biochim Biophys Acta 2000] - nuclear [Peruzzi, Biochim Biophys Acta 2000] and cytosolic [Caricasole, Biochim Biophys Acta 2000] 89869: - gene was cloned and expressed [Saunders, Development 2002 - sperm-specific [Saunders, Development 2002]

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PI45PLC	3	Saunders CM, Larman MG, Parrington J, Cox LJ, Royse J, Blayney LM, Swann K, Lai FA	PLC zeta: a sperm-specific trigger of Ca(2+) oscillations in eggs and embryo development	Development	2002	12117804	substrates [Leung, Mol Cancer 2004] - PLC family is composed of 11 subtypes: ß1, 2, 3 and 4, ¿ 1 and 2, d1, 3 and 4, e, and ¿ [Leung, Mol Cancer 2004] 84812: - gene was cloned [Kim, Cytogenet Cell Genet 1999] 5333: - gene was cloned [Ishikawa, Cytogenet Cell Genet 1997] - expression and biochemical characterization [Cheng, J Biol Chem 1995] 23007: - function inferred from electronic annotation [GO] 51196: - gene was cloned and characterized [Song, J Biol Chem 2001], [Lopez, J Biol Chem 2001] 5336: - gene was mapped [Hernandez, Genomics 1994] 5332: - predominantly expressed in retina [UniProt], [Alvarez, Genomics 1995] - gene was cloned and compared to mammalian homologs [Alvarez, Genomics 1995] 26236: - gene was identified, cloned and expressed [Peruzzi, Biochim Biophys Acta 2002], [Caricasole, Biochim Biophys Acta 2000], [Peruzzi, Biochim Biophys Acta 2000] - nuclear [Peruzzi, Biochim Biophys Acta 2000] and cytosolic [Caricasole, Biochim Biophys Acta 2000] 89869: - gene was cloned and expressed [Saunders, Development 2002] - sperm-specific [Saunders, Development 2002]
PI45PLC	3	Peruzzi D, Aluigi M, Manzoli L, Billi AM, Di Giorgio FP, Morleo M, Martelli AM, Cocco L	Molecular characterization of the human PLC beta1 gene	Biochim Biophys Acta	2002	12213492	substrates [Leung, Mol Cancer 2004] - PLC family is composed of 11 subtypes: ß1, 2, 3 and 4, ¿ 1 and 2, d1, 3 and 4, e, and ¿ [Leung, Mol Cancer 2004] 84812: - gene was cloned [Kim, Cytogenet Cell Genet 1999] 5333: - gene was cloned [Ishikawa, Cytogenet Cell Genet 1997] - expression and biochemical characterization [Cheng, J Biol Chem 1995] 23007: - function inferred from electronic annotation [GO] 51196: - gene was cloned and characterized [Song, J Biol Chem 2001], [Lopez, J Biol Chem 2001] 5336: - gene was mapped [Hernandez, Genomics 1994] 5332: - predominantly expressed in retina [UniProt], [Alvarez, Genomics 1995] - gene was cloned and compared to mammalian homologs [Alvarez, Genomics 1995] 26236: - gene was identified, cloned and expressed [Peruzzi, Biochim Biophys Acta 2002], [Caricasole, Biochim Biophys Acta 2000], [Peruzzi, Biochim Biophys Acta 2000] - nuclear [Peruzzi, Biochim Biophys Acta 2000] and cytosolic [Caricasole, Biochim Biophys Acta 2000] 89869: - gene was cloned and expressed [Saunders, Development 2002] - sperm-specific [Saunders, Development 2002]

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PI45PLC	3	Cox LJ, Larman MG, Saunders CM, Hashimoto K, Swann K, Lai FA	Sperm phospholipase Czeta from humans and cynomolgus monkeys triggers Ca2+ oscillations, activation and development of mouse oocytes	Reproduction	2002	12416999	substrates [Leung, Mol Cancer 2004] - PLC family is composed of 11 subtypes: ß1, 2, 3 and 4, ¿ 1 and 2, d1, 3 and 4, e, and ¿ [Leung, Mol Cancer 2004] 84812: - gene was cloned [Kim, Cytogenet Cell Genet 1999] 5333: - gene was cloned [Ishikawa, Cytogenet Cell Genet 1997] - expression and biochemical characterization [Cheng, J Biol Chem 1995] 23007: - function inferred from electronic annotation [GO] 51196: - gene was cloned and characterized [Song, J Biol Chem 2001], [Lopez, J Biol Chem 2001] 5336: - gene was mapped [Hernandez, Genomics 1994] 5332: - predominantly expressed in retina [UniProt], [Alvarez, Genomics 1995] - gene was cloned and compared to mammalian homologs [Alvarez, Genomics 1995] 26236: - gene was identified, cloned and expressed [Peruzzi, Biochim Biophys Acta 2002], [Caricasole, Biochim Biophys Acta 2000], [Peruzzi, Biochim Biophys Acta 2000] - nuclear [Peruzzi, Biochim Biophys Acta 2000] and cytosolic [Caricasole, Biochim Biophys Acta 2000] 89869: - gene was cloned and expressed [Saunders, Development 2002] - sperm-specific [Saunders, Development 2002]
PI45PLC	3	Carozzi AJ, Kriz RW, Webster C, Parker PJ	Identification, purification and characterization of a novel phosphatidylinositol-specific phospholipase C, a third member of the beta subfamily	Eur J Biochem	1992	13333955	substrates [Leung, Mol Cancer 2004] - PLC family is composed of 11 subtypes: ß1, 2, 3 and 4, ¿ 1 and 2, d1, 3 and 4, e, and ¿ [Leung, Mol Cancer 2004] 84812: - gene was cloned [Kim, Cytogenet Cell Genet 1999] 5333: - gene was cloned [Ishikawa, Cytogenet Cell Genet 1997] - expression and biochemical characterization [Cheng, J Biol Chem 1995] 23007: - function inferred from electronic annotation [GO] 51196: - gene was cloned and characterized [Song, J Biol Chem 2001], [Lopez, J Biol Chem 2001] 5336: - gene was mapped [Hernandez, Genomics 1994] 5332: - predominantly expressed in retina [UniProt], [Alvarez, Genomics 1995] - gene was cloned and compared to mammalian homologs [Alvarez, Genomics 1995] 26236: - gene was identified, cloned and expressed [Peruzzi, Biochim Biophys Acta 2002], [Caricasole, Biochim Biophys Acta 2000], [Peruzzi, Biochim Biophys Acta 2000] - nuclear [Peruzzi, Biochim Biophys Acta 2000] and cytosolic [Caricasole, Biochim Biophys Acta 2000] 89869: - gene was cloned and expressed [Saunders, Development 2002] - sperm-specific [Saunders, Development 2002]

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
PI45PLC	3	Leung DW, Tompkins C, Brewer J, Ball A, Coon M, Morris V, Waggoner D, Singer JW	Phospholipase C delta-4 overexpression upregulates ErbB1/2 expression, Erk signaling pathway, and proliferation in MCF-7 cells	Mol Cancer	2004	15140260	substrates [Leung, Mol Cancer 2004] - PLC family is composed of 11 subtypes: ß1, 2, 3 and 4, ¿ 1 and 2, d1, 3 and 4, e, and ¿ [Leung, Mol Cancer 2004] 84812: - gene was cloned [Kim, Cytogenet Cell Genet 1999] 5333: - gene was cloned [Ishikawa, Cytogenet Cell Genet 1997] - expression and biochemical characterization [Cheng, J Biol Chem 1995] 23007: - function inferred from electronic annotation [GO] 51196: - gene was cloned and characterized [Song, J Biol Chem 2001], [Lopez, J Biol Chem 2001] 5336: - gene was mapped [Hernandez, Genomics 1994] 5332: - predominantly expressed in retina [UniProt], [Alvarez, Genomics 1995] - gene was cloned and compared to mammalian homologs [Alvarez, Genomics 1995] 26236: - gene was identified, cloned and expressed [Peruzzi, Biochim Biophys Acta 2002], [Caricasole, Biochim Biophys Acta 2000], [Peruzzi, Biochim Biophys Acta 2000] - nuclear [Peruzzi, Biochim Biophys Acta 2000] and cytosolic [Caricasole, Biochim Biophys Acta 2000] 89869: - gene was cloned and expressed [Saunders, Development 2002 - sperm-specific [Saunders, Development 2002]
PI45PLCn	3	Irvine RF	Nuclear lipid signalling	Nat Rev Mol Cell Biol	2003	12728269	26236: - gene was identified, cloned and expressed [Peruzzi, Biochim Biophys Acta 2002], [Caricasole, Biochim Biophys Acta 2000], [Peruzzi, Biochim Biophys Acta 2000] - nuclear [Peruzzi, Biochim Biophys Acta 2000] and cytosolic [Caricasole, Biochim Biophys Acta 2000] - see fig1 of [Irvine 2003]
PI4P5K	3	Burriss Garrett RJ, Redman CM	Localization of enzymes involved in polyphosphoinositids metabolism on the cytoplasmic surface of the human erythrocyte membrane	Biochim Biophys Acta	1975	164238	cytoplasm - by default Particularly abundant in platelets and in brain. Present in most tissues, except notably skeletal muscle and small intestine. Catalyzes the phosphorylation of phosphatidylinositol-4-phosphate on the fifth hydroxyl of the myo-inositol ring, to form phosphatidylinositol-4,5-biphosphate. NJ - present on the cytosolic surface of human erythrocyte membranes [Burriss Garrett, Biochim Biophys Acta 1975] 5305: - catalyzes PtdIns4P 5-kinase rxn [RefSeq], [UniProt] - expressed ubiquitously, with high levels in the brain [UniProt] - homolgy to S. cerevisiae proteins Fab1p and Mss4p [Boronenkov, J Biol Chem 1995] - protein expressed in E. coli [Boronenkov, J Biol Chem 1995] 8394: - gene has been cloned, expressed, and characterized [Loijens, J Biol Chem 1996] 8395: - gene has been cloned and shown to have PtdIns4P 5-kinase activity [Carvajal, Nat Genet 1996] 8396: - catalyzes PtdIns4P 5-kinase rxn [RefSeq], [UniProt] - Cytoplasmic. Peripheral membrane protein associated with the plasma membrane and the endoplasmic reticulum (By similarity). [UniProt] - Highly expressed in brain, heart, pancreas, skeletal muscle and

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
PI4P5K	3	Boronenkov IV, Anderson RA	The sequence of phosphatidylinositol-4-phosphate 5-kinase defines a novel family of lipid kinases	J Biol Chem	1995	7852364	cytoplasm - by default Particularly abundant in platelets and in brain. Present in most tissues, except notably skeletal muscle and small intestine. Catalyzes the phosphorylation of phosphatidylinositol-4-phosphate on the fifth hydroxyl of the myo-inositol ring, to form phosphatidylinositol-4,5-biphosphate. NJ - present on the cytosolic surface of human erythrocyte membranes [Burriss Garrett, Biochim Biophys Acta 1975] 5305: - catalyzes PtdIns4P 5-kinase rxn [RefSeq], [UniProt] - expressed ubiquitously, with high levels in the brain [UniProt] - homolgy to S. cerevisiae proteins Fab1p and Mss4p [Boronenkov, J Biol Chem 1995] - protein expressed in E. coli [Boronenkov, J Biol Chem 1995] 8394: - gene has been cloned, expressed, and characterized [Loijens, J Biol Chem 1996] 8395: - gene has been cloned and shown to have PtdIns4P 5-kinase activity [Carvajal, Nat Genet 1996] 8396: - catalyzes PtdIns4P 5-kinase rxn [RefSeq], [UniProt] - Cytoplasmic. Peripheral membrane protein associated with the plasma membrane and the endoplasmic reticulum (By similarity). [UniProt] - Highly expressed in brain, heart, pancreas, skeletal muscle and
PI4P5K	3	Carvajal JJ, Pook MA, dos Santos M, Doudney K, Hillermann R, Minogue S, Williamson R, Hsuan JJ, Chamberlain S	The Friedreich's ataxia gene encodes a novel phosphatidylinositol-4- phosphate 5-kinase	Nat Genet	1996	8841185	cytoplasm - by default Particularly abundant in platelets and in brain. Present in most tissues, except notably skeletal muscle and small intestine. Catalyzes the phosphorylation of phosphatidylinositol-4-phosphate on the fifth hydroxyl of the myo-inositol ring, to form phosphatidylinositol-4,5-biphosphate. NJ - present on the cytosolic surface of human erythrocyte membranes [Burriss Garrett, Biochim Biophys Acta 1975] 5305: - catalyzes PtdIns4P 5-kinase rxn [RefSeq], [UniProt] - expressed ubiquitously, with high levels in the brain [UniProt] - homolgy to S. cerevisiae proteins Fab1p and Mss4p [Boronenkov, J Biol Chem 1995] - protein expressed in E. coli [Boronenkov, J Biol Chem 1995] 8394: - gene has been cloned, expressed, and characterized [Loijens, J Biol Chem 1996] 8395: - gene has been cloned and shown to have PtdIns4P 5-kinase activity [Carvajal, Nat Genet 1996] 8396: - catalyzes PtdIns4P 5-kinase rxn [RefSeq], [UniProt] - Cytoplasmic. Peripheral membrane protein associated with the plasma membrane and the endoplasmic reticulum (By similarity). [UniProt] - Highly expressed in brain, heart, pancreas, skeletal muscle and

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PI4P5K	3	Loijens JC, Anderson RA	Type I phosphatidylinositol-4-phosphate 5-kinases are distinct members of this novel lipid kinase family	J Biol Chem	1996	8955136	cytoplasm - by default Particularly abundant in platelets and in brain. Present in most tissues, except notably skeletal muscle and small intestine. Catalyzes the phosphorylation of phosphatidylinositol-4-phosphate on the fifth hydroxyl of the myo-inositol ring, to form phosphatidylinositol-4,5-biphosphate. NJ - present on the cytosolic surface of human erythrocyte membranes [Burriss Garrett, Biochim Biophys Acta 1975] 5305: - catalyzes PtdIns4P 5-kinase rxn [RefSeq], [UniProt] - expressed ubiquitously, with high levels in the brain [UniProt] - homolgy to S. cerevisiae proteins Fab1p and Mss4p [Boronenkov, J Biol Chem 1995] - protein expressed in E. coli [Boronenkov, J Biol Chem 1995] 8394: - gene has been cloned, expressed, and characterized [Loijens, J Biol Chem 1996] 8395: - gene has been cloned and shown to have PtdIns4P 5-kinase activity [Carvajal, Nat Genet 1996] 8396: - catalyzes PtdIns4P 5-kinase rxn [RefSeq], [UniProt] - Cytoplasmic. Peripheral membrane protein associated with the plasma membrane and the endoplasmic reticulum (By similarity). [UniProt] - Highly expressed in brain, heart, pancreas, skeletal muscle and
PI4PP	2	Holub BJ	Metabolism and function of myo-inositol and inositol phospholipids	Annu Rev Nutr	1986	2425833	- reaction described in [Holub, Ann Rev Nutr 1986]
PI5P4K	3	Zhang X, Loijens JC, Boronenkov IV, Parker GJ, Norris FA, Chen J, Thum O, Prestwich GD, Majerus PW, Anderson RA	Phosphatidylinositol-4-phosphate 5-kinase isozymes catalyze the synthesis of 3-phosphate-containing phosphatidylinositol signaling molecules	J Biol Chem	1997	9211928	- type II a and b PIP4Ks have much higher 4-kinase activity for or PtdIns5P than PtdIns3P in vitro [Rameh, Nature 1997], [Zhang, J Biol Chem 1997] - reaction described in [Tolias, Chem Phys Lipids 1999]
PI5P4K	3	Rameh LE, Tolias KF, Duckworth BC, Cantley LC	A new pathway for synthesis of phosphatidylinositol-4,5-bisphosphate	Nature	1997	9367159	- type II a and b PIP4Ks have much higher 4-kinase activity for or PtdIns5P than PtdIns3P in vitro [Rameh, Nature 1997], [Zhang, J Biol Chem 1997] - reaction described in [Tolias, Chem Phys Lipids 1999]
PI5P4K	3	Tolias KF, Cantley LC	Pathways for phosphoinositide synthesis	Chem Phys Lipids	1999	10358929	- type II a and b PIP4Ks have much higher 4-kinase activity for or PtdIns5P than PtdIns3P in vitro [Rameh, Nature 1997], [Zhang, J Biol Chem 1997] - reaction described in [Tolias, Chem Phys Lipids 1999]
PIACGT	3	Miyata T, Takeda J, Iida Y, Yamada N, Inoue N, Takahashi M, Maeda K, Kitani T, Kinoshita T	The cloning of PIG-A, a component in the early step of GPI-anchor biosynthesis	Science	1993	7680492	51227 (PIGP): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - ubiquitous [UniProt], [Shibuya, Biochem Biophys Res Commun 2000], [Togashi, DNA Res 2000] - gene was cloned [Shibuya, Biochem Biophys Res Commun 2000], [Togashi, DNA Res 2000] - mouse homolog has been cloned and characterized [Choi, Mamm Genome 2001] 5277 (PIGA): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - gene was cloned [Miyata, Science 1993] and characterized [Iida, Blood 1994] 5279 (PIGC): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - gene has 20% similarity w/ yeast homolog [Inoue, Biochem Biophys Res Commun 1996] - gene was isolated [Hong, Genomics 1997] 5283 (PIGH): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - cloning and expression [Kamitami, J Biol Chem 1993] 9091 (PIGQ):

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PIACGT	3	Iida Y, Takeda J, Miyata T, Inoue N, Nishimura J, Kitani T, Maeda K, Kinoshita T	Characterization of genomic PIG-A gene: a gene for glycosylphosphatidylinositol-anchor biosynthesis and paroxysmal nocturnal hemoglobinuria	Blood	1994	8193350	51227 (PIGP): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - ubiquitous [UniProt], [Shibuya, Biochem Biophys Res Commun 2000], [Togashi, DNA Res 2000] - gene was cloned [Shibuya, Biochem Biophys Res Commun 2000], [Togashi, DNA Res 2000] - mouse homolog has been cloned and characterized [Choi, Mamm Genome 2001] 5277 (PIGA): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - gene was cloned [Miyata, Science 1993] and characterized [Iida, Blood 1994] 5279 (PIGC): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - gene has 20% similarity w/ yeast homolog [Inoue, Biochem Biophys Res Commun 1996] - gene was isolated [Hong, Genomics 1997] 5283 (PIGH): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - cloning and expression [Kamitami, J Biol Chem 1993] 9091 (PIGQ):
PIACGT	3	Kamitani T, Chang HM, Rollins C, Waneck GL, Yeh ET.	Correction of the class H defect in glycosylphosphatidylinositol anchor biosynthesis in Ltk- cells by a human cDNA clone	J Biol Chem	1993	8407896	51227 (PIGP): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - ubiquitous [UniProt], [Shibuya, Biochem Biophys Res Commun 2000], [Togashi, DNA Res 2000] - gene was cloned [Shibuya, Biochem Biophys Res Commun 2000], [Togashi, DNA Res 2000] - mouse homolog has been cloned and characterized [Choi, Mamm Genome 2001] 5277 (PIGA): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - gene was cloned [Miyata, Science 1993] and characterized [Iida, Blood 1994] 5279 (PIGC): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - gene has 20% similarity w/ yeast homolog [Inoue, Biochem Biophys Res Commun 1996] - gene was isolated [Hong, Genomics 1997] 5283 (PIGH): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - cloning and expression [Kamitami, J Biol Chem 1993] 9091 (PIGQ):
PIACGT	3	Inoue N, Watanabe R, Takeda J, Kinoshita T	PIG-C, one of the three human genes involved in the first step of glycosylphosphatidylinositol biosynthesis is a homologue of Saccharomyces cerevisiae GPI2	Biochem Biophys Res Commun	1996	8806613	51227 (PIGP): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - ubiquitous [UniProt], [Shibuya, Biochem Biophys Res Commun 2000], [Togashi, DNA Res 2000] - gene was cloned [Shibuya, Biochem Biophys Res Commun 2000], [Togashi, DNA Res 2000] - mouse homolog has been cloned and characterized [Choi, Mamm Genome 2001] 5277 (PIGA): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - gene was cloned [Miyata, Science 1993] and characterized [Iida, Blood 1994] 5279 (PIGC): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - gene has 20% similarity w/ yeast homolog [Inoue, Biochem Biophys Res Commun 1996] - gene was isolated [Hong, Genomics 1997] 5283 (PIGH): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - cloning and expression [Kamitami, J Biol Chem 1993] 9091 (PIGQ):

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
PIACGT	3	Hong Y, Ohishi K, Inoue N, Endo Y, Fujita T, Takeda J, Kinoshita T	Structures and chromosomal localizations of the glycosylphosphatidylinositol synthesis gene PIGC and its pseudogene PIGCP1	Genomics	1997	9325057	51227 (PIGP): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - ubiquitous [UniProt], [Shibuya, Biochem Biophys Res Commun 2000], [Togashi, DNA Res 2000] - gene was cloned [Shibuya, Biochem Biophys Res Commun 2000], [Togashi, DNA Res 2000] - mouse homolog has been cloned and characterized [Choi, Mamm Genome 2001] 5277 (PIGA): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - gene was cloned [Miyata, Science 1993] and characterized [Iida, Blood 1994] 5279 (PIGC): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - gene has 20% similarity w/ yeast homolog [Inoue, Biochem Biophys Res Commun 1996] - gene was isolated [Hong, Genomics 1997] 5283 (PIGH): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - cloning and expression [Kamitami, J Biol Chem 1993] 9091 (PIGQ):
PIACGT	3	Watanabe R, Inoue N, Westfall B, Taron CH, Orlean P, Takeda J, Kinoshita T	The first step of glycosylphosphatidylinositol biosynthesis is mediated by a complex of PIG-A, PIG-H, PIG-C and GPI1	EMBO J	1998	9463366	51227 (PIGP): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - ubiquitous [UniProt], [Shibuya, Biochem Biophys Res Commun 2000], [Togashi, DNA Res 2000] - gene was cloned [Shibuya, Biochem Biophys Res Commun 2000], [Togashi, DNA Res 2000] - mouse homolog has been cloned and characterized [Choi, Mamm Genome 2001] 5277 (PIGA): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - gene was cloned [Miyata, Science 1993] and characterized [Iida, Blood 1994] 5279 (PIGC): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - gene has 20% similarity w/ yeast homolog [Inoue, Biochem Biophys Res Commun 1996] - gene was isolated [Hong, Genomics 1997] 5283 (PIGH): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - cloning and expression [Kamitami, J Biol Chem 1993] 9091 (PIGQ):
PIACGT	3	Shibuya K, Kudoh J, Minoshima S, Kawasaki K, Asakawa S, Shimizu N	Isolation of two novel genes, DSCR5 and DSCR6, from Down syndrome critical region on human chromosome 21q22.2	Biochem Biophys Res Commun	2000	10814524	51227 (PIGP): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - ubiquitous [UniProt], [Shibuya, Biochem Biophys Res Commun 2000], [Togashi, DNA Res 2000] - gene was cloned [Shibuya, Biochem Biophys Res Commun 2000], [Togashi, DNA Res 2000] - mouse homolog has been cloned and characterized [Choi, Mamm Genome 2001] 5277 (PIGA): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - gene was cloned [Miyata, Science 1993] and characterized [Iida, Blood 1994] 5279 (PIGC): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - gene has 20% similarity w/ yeast homolog [Inoue, Biochem Biophys Res Commun 1996] - gene was isolated [Hong, Genomics 1997] 5283 (PIGH): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - cloning and expression [Kamitami, J Biol Chem 1993] 9091 (PIGQ):

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PIACGT	3	Togashi T, Choi DK, Taylor TD, Suzuki Y, Sugano S, Hattori M, Sakaki Y	A novel gene, DSCR5, from the distal Down syndrome critical region on chromosome 21q22.2	DNA Res	2000	10907851	51227 (PIGF): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - ubiquitous [UniProt], [Shibuya, Biochem Biophys Res Commun 2000], [Togashi, DNA Res 2000] - gene was cloned [Shibuya, Biochem Biophys Res Commun 2000], [Togashi, DNA Res 2000] - mouse homolog has been cloned and characterized [Choi, Mamm Genome 2001] 5277 (PIGA): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - gene was cloned [Miyata, Science 1993] and characterized [Iida, Blood 1994] 5279 (PIGC): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - gene has 20% similarity w/ yeast homolog [Inoue, Biochem Biophys Res Commun 1996] - gene was isolated [Hong, Genomics 1997] 5283 (PIGH): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - cloning and expression [Kamitami, J Biol Chem 1993] 9091 (PIGQ):
PIACGT	3	Choi DK, Suzuki Y, Yoshimura S, Togashi T, Hida M, Taylor TD, Wang Y, Sugano S, Hattori M, Sakaki Y	Molecular cloning and characterization of a gene expressed in mouse developing tongue, mDscr5 gene, a homolog of human DSCR5 (Down syndrome Critical Region gene 5)	Mamm Genome	2001	11331941	51227 (PIGF): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - ubiquitous [UniProt], [Shibuya, Biochem Biophys Res Commun 2000], [Togashi, DNA Res 2000] - gene was cloned [Shibuya, Biochem Biophys Res Commun 2000], [Togashi, DNA Res 2000] - mouse homolog has been cloned and characterized [Choi, Mamm Genome 2001] 5277 (PIGA): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - gene was cloned [Miyata, Science 1993] and characterized [Iida, Blood 1994] 5279 (PIGC): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - gene has 20% similarity w/ yeast homolog [Inoue, Biochem Biophys Res Commun 1996] - gene was isolated [Hong, Genomics 1997] 5283 (PIGH): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - cloning and expression [Kamitami, J Biol Chem 1993] 9091 (PIGQ):
PIACGT	3	Tiede A, Daniels RJ, Higgs DR, Mehrein Y, Schmidt RE, Schubert J	The human GPI1 gene is required for efficient glycosylphosphatidylinositol biosynthesis	Gene	2001	11418246	51227 (PIGF): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - ubiquitous [UniProt], [Shibuya, Biochem Biophys Res Commun 2000], [Togashi, DNA Res 2000] - gene was cloned [Shibuya, Biochem Biophys Res Commun 2000], [Togashi, DNA Res 2000] - mouse homolog has been cloned and characterized [Choi, Mamm Genome 2001] 5277 (PIGA): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - gene was cloned [Miyata, Science 1993] and characterized [Iida, Blood 1994] 5279 (PIGC): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - gene has 20% similarity w/ yeast homolog [Inoue, Biochem Biophys Res Commun 1996] - gene was isolated [Hong, Genomics 1997] 5283 (PIGH): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - cloning and expression [Kamitami, J Biol Chem 1993] 9091 (PIGQ):

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PIACGT	3	Eisenhaber B, Maurer-Stroh S, Novatchkova M, Schneider G, Eisenhaber F	Enzymes and auxiliary factors for GPI lipid anchor biosynthesis and post-translational transfer to proteins	Bioesssays	2003	12655644	5122? (PIGP): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - ubiquitous [UniProt], [Shibuya, Biochem Biophys Res Commun 2000], [Togashi, DNA Res 2000] - gene was cloned [Shibuya, Biochem Biophys Res Commun 2000], [Togashi, DNA Res 2000] - mouse homolog has been cloned and characterized [Choi, Mamm Genome 2001] 5277 (PIGA): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - gene was cloned [Miyata, Science 1993] and characterized [Iida, Blood 1994] 5279 (PIGC): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - gene has 20% similarity w/ yeast homolog [Inoue, Biochem Biophys Res Commun 1996] - gene was isolated [Hong, Genomics 1997] 5283 (PIGH): - component of phosphatidylinositol N-acetylglucosaminyltransferase complex [RefSeq], [UniProt], [Eisenhaber, Bioessays 2003] - cloning and expression [Kamitami, J Biol Chem 1993] 9091 (PIGQ):
PIK3	3	Volinia S, Dhand R, Vanhaesebroeck B, MacDougall LK, Stein R, Zvelebil MJ, Domin J, Panaretou C, Waterfield MD	A human phosphatidylinositol 3-kinase complex related to the yeast Vps34p-Vps15p protein sorting system	EMBO J	1995	7628435	5286: - phosphoinositide 3-kinase activity [RefSeq] - acts on PtdIns and PtdIns4P [Domin, Biochem J 1997] - gene has been cloned [Domin, Biochem J 1997] 5287: - Found mostly in the microsome, but also in the plasma membrane and cytosol [UniProt] - gene was cloned and expressed [Arcaro, J Biol Chem 1998] - acts on PtdIns and PtdIns4P [Arcaro, J Biol Chem 1998] 5288: - acts on PtdIns and PtdIns4P [UniProt], [Rozycka, Genomics 1998] - gene has been cloned [Rozycka, Genomics 1998] - Highly expressed in liver, prostate and testis. Lower levels in small intestine, kidney and pancreas.[UniProt] 5290: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, PtdIns(4,5)P2 [RefSeq], [UniProt] - gene has been cloned; 99% identical to bovine protein [Volinia, Genomics 1994] 5291: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, PtdIns(4,5)P2 [UniProt], [Hu, Mol Cell Biol 1993] - expressed ubiquitously [UniProt], [Hu, Mol Cell Biol 1993] - 42% identical to bovine PI 3-kinase and 28% identical to S. cerevisiae Vps34 [Hu, Mol Cell Biol 1993] 5293: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, Pt - leukocytes [UniProt], [Vanhaesebroeck, PNAS 19997] - gene has been cloned, characterized [Vanhaesebroeck, PNAS 5294: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, Pt

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PIK3	3	Domin J, Pages F, Volinia S, Rittenhouse SE, Zvelebil MJ, Stein RC, Waterfield MD	Cloning of a human phosphoinositide 3-kinase with a C2 domain that displays reduced sensitivity to the inhibitor wortmannin	Biochem J	1997	9337861	5286: - phosphoinositide 3-kinase activity [RefSeq] - acts on PtdIns and PtdIns4P [Domin, Biochem J 1997] - gene has been cloned [Domin, Biochem J 1997] 5287: - Found mostly in the microsome, but also in the plasma membrane and cytosol [UniProt] - gene was cloned and expressed [Arcaro, J Biol Chem 1998] - acts on PtdIns and PtdIns4P [Arcaro, J Biol Chem 1998] 5288: - acts on PtdIns and PtdIns4P [UniProt], [Rozycka, Genomics 1998] - gene has been cloned [Rozycka, Genomics 1998] - Highly expressed in liver, prostate and testis. Lower levels in small intestine, kidney and pancreas.[UniProt] 5290: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, PtdIns(4,5)P2 [RefSeq], [UniProt] - gene has been cloned; 99% identical to bovine protein [Volinia, Genomics 1994] 5291: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, PtdIns(4,5)P2 [UniProt], [Hu, Mol Cell Biol 1993] - expressed ubiquitously [UniProt], [Hu, Mol Cell Biol 1993] - 42% identical to bovine PI 3-kinase and 28% identical to S. cerevisiae Vps34 [Hu, Mol Cell Biol 1993] 5293: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, Pt - leukocytes [UniProt], [Vanhaesebroeck, PNAS 19997] - gene has been cloned, characterized [Vanhaesebroeck, PNAS 5294: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, Pt
PIK3	3	Arcaro A, Volinia S, Zvelebil MJ, Stein R, Watton SJ, Layton MJ, Gout I, Ahmadi K, Downward J, Waterfield MD	Human phosphoinositide 3-kinase C2beta, the role of calcium and the C2 domain in enzyme activity	J Biol Chem	1998	9830063	5286: - phosphoinositide 3-kinase activity [RefSeq] - acts on PtdIns and PtdIns4P [Domin, Biochem J 1997] - gene has been cloned [Domin, Biochem J 1997] 5287: - Found mostly in the microsome, but also in the plasma membrane and cytosol [UniProt] - gene was cloned and expressed [Arcaro, J Biol Chem 1998] - acts on PtdIns and PtdIns4P [Arcaro, J Biol Chem 1998] 5288: - acts on PtdIns and PtdIns4P [UniProt], [Rozycka, Genomics 1998] - gene has been cloned [Rozycka, Genomics 1998] - Highly expressed in liver, prostate and testis. Lower levels in small intestine, kidney and pancreas.[UniProt] 5290: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, PtdIns(4,5)P2 [RefSeq], [UniProt] - gene has been cloned; 99% identical to bovine protein [Volinia, Genomics 1994] 5291: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, PtdIns(4,5)P2 [UniProt], [Hu, Mol Cell Biol 1993] - expressed ubiquitously [UniProt], [Hu, Mol Cell Biol 1993] - 42% identical to bovine PI 3-kinase and 28% identical to S. cerevisiae Vps34 [Hu, Mol Cell Biol 1993] 5293: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, Pt - leukocytes [UniProt], [Vanhaesebroeck, PNAS 19997] - gene has been cloned, characterized [Vanhaesebroeck, PNAS 5294: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, Pt

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PIK3	3	Rozycka M, Lu YJ, Brown RA, Lau MR, Shipley JM, Fry MJ	cDNA cloning of a third human C2-domain-containing class II phosphoinositide 3-kinase, PI3K-C2gamma, and chromosomal assignment of this gene (PIK3C2G) to 12p12	Genomics	1998	9878262	5286: - phosphoinositide 3-kinase activity [RefSeq] - acts on PtdIns and PtdIns4P [Domin, Biochem J 1997] - gene has been cloned [Domin, Biochem J 1997] 5287: - Found mostly in the microsome, but also in the plasma membrane and cytosol [UniProt] - gene was cloned and expressed [Arcaro, J Biol Chem 1998] - acts on PtdIns and PtdIns4P [Arcaro, J Biol Chem 1998] 5288: - acts on PtdIns and PtdIns4P [UniProt], [Rozycka, Genomics 1998] - gene has been cloned [Rozycka, Genomics 1998] - Highly expressed in liver, prostate and testis. Lower levels in small intestine, kidney and pancreas.[UniProt] 5290: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, PtdIns(4,5)P2 [RefSeq], [UniProt] - gene has been cloned; 99% identical to bovine protein [Volinia, Genomics 1994] 5291: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, PtdIns(4,5)P2 [UniProt], [Hu, Mol Cell Biol 1993] - expressed ubiquitously [UniProt], [Hu, Mol Cell Biol 1993] - 42% identical to bovine PI 3-kinase and 28% identical to S. cerevisiae Vps34 [Hu, Mol Cell Biol 1993] 5293: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, Pt - leukocytes [UniProt], [Vanhaesebroeck, PNAS 19997] - gene has been cloned, characterized [Vanhaesebroeck, PNAS 5294: - catalytic subunit of PIK3, phosphorylates PtdIns, PtdIns4P, Pt
PIK4	3	Nakagawa T, Goto K, Kondo H	Cloning, expression, and localization of 230-kDa phosphatidylinositol 4-kinase	J Biol Chem	1996	8662589	cytoplasmic - uniprot Expressed ubiquitously. Highest levels in placenta and brain. Little or no expression in lung, liver, pancreas, testis or leukocytes. PI4KII, PI4K2B: no separte reaction explicitly associated w/ it -> assumed to have same PIK4 NJ 5297: - rat protein was found to be closely assoc w/ Golgi vesicles and vacuoles [Nakagawa, J Biol Chem 1996] - present on the cytosolic surface of human erythrocyte membranes [Burriss Garrett, Biochim Biophys Acta 1975] 5298: - enzyme is primarily cytosolic; associates peripherally with plasma membranes, endoplasmic reticulum, and Golgi [Wei, J Biol Chem 2002]
PIK4	3	Wei YJ, Sun HQ, Yamamoto M, Wlodarski P, Kunii K, Martinez M, Barylko B, Albanesi JP, Yin HL.	ype II phosphatidylinositol 4-kinase beta is a cytosolic and peripheral membrane protein that is recruited to the plasma membrane and activated by Rac-GTP	J Biol Chem	2002	12324459	cytoplasmic - uniprot Expressed ubiquitously. Highest levels in placenta and brain. Little or no expression in lung, liver, pancreas, testis or leukocytes. PI4KII, PI4K2B: no separte reaction explicitly associated w/ it -> assumed to have same PIK4 NJ 5297: - rat protein was found to be closely assoc w/ Golgi vesicles and vacuoles [Nakagawa, J Biol Chem 1996] - present on the cytosolic surface of human erythrocyte membranes [Burriss Garrett, Biochim Biophys Acta 1975] 5298: - enzyme is primarily cytosolic; associates peripherally with plasma membranes, endoplasmic reticulum, and Golgi [Wei, J Biol Chem 2002]

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PIK4	3	Minogue S, Anderson JS, Waugh MG, dosSantos M, Corless S, Cramer R, Hsuan JJ	Cloning of a human type II phosphatidylinositol 4-kinase reveals a novel lipid kinase family	Journal of Biological Chemistry	2001		cytoplasmic - uniprot Expressed ubiquitously. Highest levels in placenta and brain. Little or no expression in lung, liver, pancreas, testis or leukocytes. PI4KII, PI4K2B: no separte reaction explicitly associated w/ it -> assumed to have same PIK4 NJ 5297: - rat protein was found to be closely assoc w/ Golgi vesicles and vacuoles [Nakagawa, J Biol Chem 1996] - present on the cytosolic surface of human erythrocyte membranes [Burriss Garrett, Biochim Biophys Acta 1975] 5298: - enzyme is primarily cytosolic; associates peripherally with plasma membranes, endoplasmic reticulum, and Golgi [Wei, J Biol Chem 2002]
PIK4	3	Wong K, Cantley LC	Cloning and characterization of a human phosphatidylinositol 4-kinase	Journal of Biological Chemsitry	1994		cytoplasmic - uniprot Expressed ubiquitously. Highest levels in placenta and brain. Little or no expression in lung, liver, pancreas, testis or leukocytes. PI4KII, PI4K2B: no separte reaction explicitly associated w/ it -> assumed to have same PIK4 NJ 5297: - rat protein was found to be closely assoc w/ Golgi vesicles and vacuoles [Nakagawa, J Biol Chem 1996] - present on the cytosolic surface of human erythrocyte membranes [Burriss Garrett, Biochim Biophys Acta 1975] 5298: - enzyme is primarily cytosolic; associates peripherally with plasma membranes, endoplasmic reticulum, and Golgi [Wei, J Biol Chem 2002]
PIK5	3	Tolias KF, Rameh LE, Ishihara H, Shibasaki Y, Chen J, Prestwich GD, Cantley LC, Carpenter CL	Type I phosphatidylinositol-4-phosphate 5-kinases synthesize the novel lipids phosphatidylinositol 3,5-bisphosphate and phosphatidylinositol 5-phosphate	J Biol Chem	1998	9660759	- pathway for synthesis of PtdIns5P is unclear, but cpd has been detected in mammalian fibroblasts [Tolias, Chem Phys Lipids 1999] - 8394 & 8395 have been shown to catalyze PtdIns -> PtdIns5P rxn in vitro [Tolias, J Biol Chem 1998] - 23396 has not been fully characterized but is inferred to catalyze reaction as well
PIt2m	3	Palmieri, F.	The mitochondrial transporter family (SLC25): physiological and pathological implications.	Pflugers Archive	2004	14598172	- Added by RS/TV Mitochondrial according to Entrez Gene Database Four transcript variants according to RefSeq found on Entrez Gene Database 1) Substrate specificity: Phosphate 2) Transport mechanism: Proton antiport 3) Tissue Localization: Variant 1(isoform a: heart, muscle, skeletal muscle, diaphragm), Variant 2&3(isoform b: liver, kidney, brain, thymus, lung, heart, skeletal muscle, diaphragm), Variant 4 (isoform c: unknown) 4) GPR association as shown 1 through 4 according to Table 1 in Palmieri, F. The mitochondrial transporter family (SLC25): physiological and pathological implications. Pflugers Arch. 2004 Feb. (PMID: 14598172)
PIt7	3	Murer H, Forster I, Biber J.	The sodium phosphate cotransporter family SLC34.		2004	12750889	- A1 and A2 transporters are electrogenic w/ probably 3:1 Na:Pi cotransport MM
PIt7ir	2	Murer H, Biber J	Molecular mechanisms of renal apical Na/phosphate cotransport	Annu Rev Physiol	1996	8815811	The 3:1 ratio Na to Pi is from tentative data gathered for the type II transporter, which is NOT SLC17A1!! The ratio for the type I transporter (SLC17A1-4) is not known. From PMID 8815811: The calculated Hill coefficients of these interactions suggest a 3:l coupling ratio of Na vs Pi. The discrepancy of the coupling ratio of 2 1, as derived from Pi transport studies in brush-border membrane vesicles (40), may be explained by factors such as heterogeneity and electrical properties of the vesicle population Three other proteins closely related to NPT1 have been identified through genomic analysis, and designated NPT3 (SLC17A2), NPT4 (SLC17A3) and Na+/PO4 cotransporter homologue (SLC17A4) [36, 38]. As of yet, there has been no functional characterization of SLC17A2 4.

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
Plt7ir	2	Reimer RJ, Edwards RH	Organic anion transport is the primary function of the SLC17/type I phosphate transporter family	Pflugers Arch	2004	12811560	The 3:1 ratio Na to Pi is from tentative data gathered for the type II transporter, which is NOT SLC17A1!! The ratio for the type I transporter (SLC17A1-4) is not known. From PMID 8815811: The calculated Hill coefficients of these interactions suggest a 3:l coupling ratio of Na vs Pi. The discrepancy of the coupling ratio of 2 1, as derived from Pi transport studies in brush-borde membrane vesicles (40), may be explained by factors such as heterogeneity and electrical properties of the vesicle population Three other proteins closely related to NPT1 have been identified through genomic analysis, and designated NPT3 (SLC17A2), NPT4 (SLC17A3) and Na+/PO4 cotransporter homologue (SLC17A4) [36, 38]. As of yet, there has been no functional characterization of SLC17A2 4.
Plt8	3	Collins JF, Bai L, Ghishan FK.	The SLC20 family of proteins: dual functions as sodium-phosphate cotransporters and viral receptors.		2003	12759754	-paper states that stoichiometry is >1 Na per Pi cotransported, but no other papers specified the actual number. 1.5:1 was used as an estimated average value between 1 and 2 MM
PLA2_2	3	Nimmrich I, Friedl W, Kruse R, Pietsch S, Hentsch S, Deuter R, Winde G, Muller O.	Loss of the PLA2G2A gene in a sporadic colorectal tumor of a patient with a PLA2G2A germline mutation and absence of PLA2G2A germline alterations in patients with FAP.	Hum Genet	1997	9272153	cytoplasm - for group VI by uniport, other variants: by default The protein encoded by this gene is an A2 phospholipase, a class of enzyme that catalyzes the release of fatty acids from phospholipids. The encoded protein may play a role in phospholipid remodelling, arachidonic acid release, leukotriene and prostaglandin synthesis, fas-mediated apoptosis, and transmembrane ion flux in glucose-stimulated B-cells. Several transcript variants encoding multiple isoforms have been described, but the full-length nature of only two of them have been determined to date. group VI variant has been sequenced and described, others have not been identified yet (genetically) PLA2G2A: see PMID: 9272153. Membrane associated. Group II phospholipase A2 is found in many cells and also extracellularly. The membrane-bound and secreted forms are identical and are encoded by a single gene. NJ
PLA2_2	3	Larsson PK, Claesson HE, Kennedy BP.	Multiple splice variants of the human calcium-independent phospholipase A2 and their effect on enzyme activity.	J Biol Chem	1998	9417066	cytoplasm - for group VI by uniport, other variants: by default The protein encoded by this gene is an A2 phospholipase, a class of enzyme that catalyzes the release of fatty acids from phospholipids. The encoded protein may play a role in phospholipid remodelling, arachidonic acid release, leukotriene and prostaglandin synthesis, fas-mediated apoptosis, and transmembrane ion flux in glucose-stimulated B-cells. Several transcript variants encoding multiple isoforms have been described, but the full-length nature of only two of them have been determined to date. group VI variant has been sequenced and described, others have not been identified yet (genetically) PLA2G2A: see PMID: 9272153. Membrane associated. Group II phospholipase A2 is found in many cells and also extracellularly. The membrane-bound and secreted forms are identical and are encoded by a single gene. NJ

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
PLA2_2e	3	Nardelli B, Tiffany HL, Bong GW, Yourey PA, Morahan DK, Li Y, Murphy PM, Alderson RF.	Characterization of the signal transduction pathway activated in human monocytes and dendritic cells by MPIF-1, a specific ligand for CC chemokine receptor 1.	J Immunol	1999		secreted enzyme -> extracellular designation: uniprot PA2 catalyzes the calcium-dependent hydrolysis of the 2- acyl groups in 3-sn-phosphoglycerides. Pla2g1b: specificity: pancreas role in signaling pathways, etc (Nardelli ref) Pla2g12a: Abundantly expressed in heart, skeletal muscle, kidney, liver and pancreas. (see Gelb et al ref) Pla2g2e: specificity: Restricted to the brain, heart, lung, and placenta. Promotes stimulus-induced arachidonic acid release and prostaglandin (PG) production similar to those elicited by HSPG-dependent sPLA(2)s, suggesting that this enzyme plays a role in the inflammatory process. see PMID: 10681567. PLA2G2A: see PMID: 9272153. Membrane associated. Group II phospholipase A2 is found in many cells and also extracellularly. The membrane-bound and secreted forms are identical and are encoded by a single gene. PLA2G5: PMID: 8300559. Localization: extracellular because enzyme is secreted (uniprot). Specificity: Heart, placenta and less abundantly, in lung. May be involved in the production of lung surfactant, the remodeling or regulation of cardiac muscle. PLA2G2F: PMID: 11112443. Localization: extracellular - secre PLA2G10: PMID: 9188469 Localization: extracellular - secrete PLA2G2D: PMID: 10455175. Localization: extracellular - secr
PLA2_2e	3	Cupillard L, Koumanov K, Mattei MG, Lazdunski M, Lambeau G.	Cloning, chromosomal mapping, and expression of a novel human secretory phospholipase A2.	J Biol Chem	1997	9188469	secreted enzyme -> extracellular designation: uniprot PA2 catalyzes the calcium-dependent hydrolysis of the 2- acyl groups in 3-sn-phosphoglycerides. Pla2g1b: specificity: pancreas role in signaling pathways, etc (Nardelli ref) Pla2g12a: Abundantly expressed in heart, skeletal muscle, kidney, liver and pancreas. (see Gelb et al ref) Pla2g2e: specificity: Restricted to the brain, heart, lung, and placenta. Promotes stimulus-induced arachidonic acid release and prostaglandin (PG) production similar to those elicited by HSPG-dependent sPLA(2)s, suggesting that this enzyme plays a role in the inflammatory process. see PMID: 10681567. PLA2G2A: see PMID: 9272153. Membrane associated. Group II phospholipase A2 is found in many cells and also extracellularly. The membrane-bound and secreted forms are identical and are encoded by a single gene. PLA2G5: PMID: 8300559. Localization: extracellular because enzyme is secreted (uniprot). Specificity: Heart, placenta and less abundantly, in lung. May be involved in the production of lung surfactant, the remodeling or regulation of cardiac muscle. PLA2G2F: PMID: 11112443. Localization: extracellular - secre PLA2G10: PMID: 9188469 Localization: extracellular - secrete PLA2G2D: PMID: 10455175. Localization: extracellular - secr

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PLA2_2e	3	Ishizaki J, Suzuki N, Higashino K, Yokota Y, Ono T, Kawamoto K, Fujii N, Arita H, Hanasaki K.	Cloning and characterization of novel mouse and human secretory phospholipase A(2)s.	J Biol Chem	1999	10455175	secreted enzyme -> extracellular designation: uniprot PA2 catalyzes the calcium-dependent hydrolysis of the 2- acyl groups in 3-sn-phosphoglycerides. Pla2g1b: specificity: pancreas role in signaling pathways, etc (Nardelli ref) Pla2g12a: Abundantly expressed in heart, skeletal muscle, kidney, liver and pancreas. (see Gelb et al ref) Pla2g2e: specificity: Restricted to the brain, heart, lung, and placenta. Promotes stimulus-induced arachidonic acid release and prostaglandin (PG) production similar to those elicited by HSPG-dependent sPLA(2)s, suggesting that this enzyme plays a role in the inflammatory process. see PMID: 10681567. PLA2G2A: see PMID: 9272153. Membrane associated. Group II phospholipase A2 is found in many cells and also extracellularly. The membrane-bound and secreted forms are identical and are encoded by a single gene. PLA2G5: PMID: 8300559. Localization: extracellular because enzyme is secreted (uniprot). Specificity: Heart, placenta and less abundantly, in lung. May be involved in the production of lung surfactant, the remodeling or regulation of cardiac muscle. PLA2G2F: PMID: 11112443. Localization: extracellular - secre PLA2G10: PMID: 9188469 Localization: extracellular - secrete PLA2G2D: PMID: 10455175. Localization: extracellular - secr
PLA2_2e	3	Suzuki N, Ishizaki J, Yokota Y, Higashino K, Ono T, Ikeda M, Fujii N, Kawamoto K, Hanasaki K.	Structures, enzymatic properties, and expression of novel human and mouse secretory phospholipase A(2)s.	J Biol Chem	2000	10681567	secreted enzyme -> extracellular designation: uniprot PA2 catalyzes the calcium-dependent hydrolysis of the 2- acyl groups in 3-sn-phosphoglycerides. Pla2g1b: specificity: pancreas role in signaling pathways, etc (Nardelli ref) Pla2g12a: Abundantly expressed in heart, skeletal muscle, kidney, liver and pancreas. (see Gelb et al ref) Pla2g2e: specificity: Restricted to the brain, heart, lung, and placenta. Promotes stimulus-induced arachidonic acid release and prostaglandin (PG) production similar to those elicited by HSPG-dependent sPLA(2)s, suggesting that this enzyme plays a role in the inflammatory process. see PMID: 10681567. PLA2G2A: see PMID: 9272153. Membrane associated. Group II phospholipase A2 is found in many cells and also extracellularly. The membrane-bound and secreted forms are identical and are encoded by a single gene. PLA2G5: PMID: 8300559. Localization: extracellular because enzyme is secreted (uniprot). Specificity: Heart, placenta and less abundantly, in lung. May be involved in the production of lung surfactant, the remodeling or regulation of cardiac muscle. PLA2G2F: PMID: 11112443. Localization: extracellular - secre PLA2G10: PMID: 9188469 Localization: extracellular - secrete PLA2G2D: PMID: 10455175. Localization: extracellular - secr

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PLA2_2e	3	Gelb MH, Valentin E, Ghomashchi F, Lazdunski M, Lambeau G.	Cloning and recombinant expression of a structurally novel human secreted phospholipase A2.	J Biol Chem	2000	11031251	secreted enzyme -> extracellular designation: uniprot PA2 catalyzes the calcium-dependent hydrolysis of the 2- acyl groups in 3-sn-phosphoglycerides. Pla2g1b: specificity: pancreas role in signaling pathways, etc (Nardelli ref) Pla2g12a: Abundantly expressed in heart, skeletal muscle, kidney, liver and pancreas. (see Gelb et al ref) Pla2g2e: specificity: Restricted to the brain, heart, lung, and placenta. Promotes stimulus-induced arachidonic acid release and prostaglandin (PG) production similar to those elicited by HSPG-dependent sPLA(2)s, suggesting that this enzyme plays a role in the inflammatory process. see PMID: 10681567. PLA2G2A: see PMID: 9272153. Membrane associated. Group II phospholipase A2 is found in many cells and also extracellularly. The membrane-bound and secreted forms are identical and are encoded by a single gene. PLA2G5: PMID: 8300559. Localization: extracellular because enzyme is secreted (uniprot). Specificity: Heart, placenta and less abundantly, in lung. May be involved in the production of lung surfactant, the remodeling or regulation of cardiac muscle. PLA2G2F: PMID: 11112443. Localization: extracellular - secre PLA2G10: PMID: 9188469 Localization: extracellular - secrete PLA2G2D: PMID: 10455175. Localization: extracellular - secr
PLA2_2e	3	Valentin E, Singer AG, Ghomashchi F, Lazdunski M, Gelb MH, Lambeau G.	Cloning and recombinant expression of human group IIF-secreted phospholipase A(2).	Biochem Biophys Res Commun	2000	11112443	secreted enzyme -> extracellular designation: uniprot PA2 catalyzes the calcium-dependent hydrolysis of the 2- acyl groups in 3-sn-phosphoglycerides. Pla2g1b: specificity: pancreas role in signaling pathways, etc (Nardelli ref) Pla2g12a: Abundantly expressed in heart, skeletal muscle, kidney, liver and pancreas. (see Gelb et al ref) Pla2g2e: specificity: Restricted to the brain, heart, lung, and placenta. Promotes stimulus-induced arachidonic acid release and prostaglandin (PG) production similar to those elicited by HSPG-dependent sPLA(2)s, suggesting that this enzyme plays a role in the inflammatory process. see PMID: 10681567. PLA2G2A: see PMID: 9272153. Membrane associated. Group II phospholipase A2 is found in many cells and also extracellularly. The membrane-bound and secreted forms are identical and are encoded by a single gene. PLA2G5: PMID: 8300559. Localization: extracellular because enzyme is secreted (uniprot). Specificity: Heart, placenta and less abundantly, in lung. May be involved in the production of lung surfactant, the remodeling or regulation of cardiac muscle. PLA2G2F: PMID: 11112443. Localization: extracellular - secre PLA2G10: PMID: 9188469 Localization: extracellular - secrete PLA2G2D: PMID: 10455175. Localization: extracellular - secr

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PLA2_2e	3	Chen J, Engle SJ, Seilhamer JJ, Tischfield JA.	Cloning and recombinant expression of a novel human low molecular weight Ca(2+)-dependent phospholipase A2.	J Biol Chem	1994	8300559 [	secreted enzyme -> extracellular designation: uniprot PA2 catalyzes the calcium-dependent hydrolysis of the 2- acyl groups in 3-sn-phosphoglycerides. Pla2g1b: specificity: pancreas role in signaling pathways, etc (Nardelli ref) Pla2g12a: Abundantly expressed in heart, skeletal muscle, kidney, liver and pancreas. (see Gelb et al ref) Pla2g2e: specificity: Restricted to the brain, heart, lung, and placenta. Promotes stimulus-induced arachidonic acid release and prostaglandin (PG) production similar to those elicited by HSPG-dependent sPLA(2)s, suggesting that this enzyme plays a role in the inflammatory process. see PMID: 10681567. PLA2G2A: see PMID: 9272153. Membrane associated. Group II phospholipase A2 is found in many cells and also extracellularly. The membrane-bound and secreted forms are identical and are encoded by a single gene. PLA2G5: PMID: 8300559. Localization: extracellular because enzyme is secreted (uniprot). Specificity: Heart, placenta and less abundantly, in lung. May be involved in the production of lung surfactant, the remodeling or regulation of cardiac muscle. PLA2G2F: PMID: 11112443. Localization: extracellular - secre PLA2G10: PMID: 9188469 Localization: extracellular - secrete PLA2G2D: PMID: 10455175. Localization: extracellular - secr
PMI12346PH	3	Saiardi A, Nagata E, Luo HR, Snowman AM, Snyder SH	Identification and characterization of a novel inositol hexakisphosphate kinase	J Biol Chem	2001	11502751	has the activity [RefSeq, [Saiardi, J Biol Chem 2001]]: InsP6 -> PP-Ins(1,2,3,4,6)P5 Ins(1,3,4,5,6)P5 -> PP-Ins(1,3,4,6)P4 - nuclear (predominant) and cytoplasmic [UniProt], [Saiardi, J Biol Chem 2001] - gene was cloned; 50, 45% identity to isozymes [Saiardi, J Biol Chem 2001]
PNP	3	Wielgus-Kutrowska B, Kulikowska E, Wierzchowski J, Bzowska A, Shugar D.	Nicotinamide riboside, an unusual, non-typical, substrate of purified purine-nucleoside phosphorylases.	Eur J Biochem	1997	9030766	IT
PNP	3	Magni G, Amici A, Emanuelli M, Orsomando G, Raffaelli N, Ruggieri S.	Enzymology of NAD+ homeostasis in man.	Cell Mol Life Sci	2004	14704851	IT
PNTEH	3	Maras B, Barra D, Dupre S, Pitari G.	Is pantetheinase the actual identity of mouse and human vanin-1 proteins?	FEBS Lett	1999	10567687	IT I am not 100 % sure if all three genes are necessary for pantetheinase activity.
PNTEH	3	Martin F, Malergue F, Pitari G, Philippe JM, Philips S, Chabret C, Granjeaud S, Mattei MG, Mungall AJ, Naquet P, Galland F.	Vanin genes are clustered (human 6q22-24 and mouse 10A2B1) and encode isoforms of pantetheinase ectoenzymes.	Immunogenetics	2001	11491533	IT I am not 100 % sure if all three genes are necessary for pantetheinase activity.
PNTK	3	Zhou B, Westaway SK, Levinson B, Johnson MA, Gitschier J, Hayflick SJ.	A novel pantothenate kinase gene (PANK2) is defective in Hallervorden-Spatz syndrome.	Nat Genet	2001	11479594	This gene is defective in Hallervorden-Spatz syndrome (PanK2) 01-24-05 IT Expression: PanK1: heart, liver, kidney PanK2: ubiquitously, inluding retina and infant basal ganglia PanK3: mostly liver PanK4: most abundant in muscle, but expressed in all tissues There are 2 other reactions of this enzyme - I did not included them yet
PNTK	3	Daugherty M, Polanuyer B, Farrell M, Scholle M, Lykidis A, de Crecy-Lagard V, Osterman A.	Complete reconstitution of the human coenzyme A biosynthetic pathway via comparative genomics.	J Biol Chem	2002	11923312	This gene is defective in Hallervorden-Spatz syndrome (PanK2) 01-24-05 IT Expression: PanK1: heart, liver, kidney PanK2: ubiquitously, inluding retina and infant basal ganglia PanK3: mostly liver PanK4: most abundant in muscle, but expressed in all tissues There are 2 other reactions of this enzyme - I did not included them yet

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PNTK	3	Ching KH, Westaway SK, Gitschier J, Higgins JJ, Hayflick SJ.	HARP syndrome is allelic with pantothenate kinase-associated neurodegeneration.	Neurology	2002	Neurology	This gene is defective in Hallervorden-Spatz syndrome (PanK2) 01-24-05 IT Expression: PanK1: heart, liver, kidney PanK2: ubiquitously, inluding retina and infant basal ganglia PanK3: mostly liver PanK4: most abundant in muscle, but expressed in all tissues There are 2 other reactions of this enzyme - I did not included them yet
PNTKm	3	Hortnagel K, Prokisch H, Meitinger T.	An isoform of hPANK2, deficient in pantothenate kinase-associated neurodegeneration, localizes to mitochondria.	Hum Mol Genet	2003	12554685	01-24-05 I am not quite sure if this is a new isoform or not, however the isoforms listed in Locuslink do not cover the same CDS (7..1711). In Hoertnagel et al, 2003, Human Mol. genetics, 12(3), 321-327, it seems as they identified this as new transcript. IT They also proposed that a complete intramitochondrial pathway for de novo synthesis of CoA exists
PPA	3	Fairchild TA, Patejunas G.	Cloning and expression profile of human inorganic pyrophosphatase.	Biochim Biophys Acta	1999	10542310	- Added by RS/TV Catalytic Activity: Inorganic phosphatase catalyzes the hydrolysis of pyrophosphate to form orthophosphate. There are two groups of Ppases (type I and type 2). Both catalyzes the same aforementioned reaction, however vary in their kinetic information, co-factor usuage. More differences described Fabrichniy IP, Lehtio L, Salminen A, Zyryanov AB, Baykov AA, Lahti R, Goldman A.Biochemistry. 2004 Nov 16;43(45):14403-11. There are four transcriptional variants according to Entrez for PPA2 Subcellular Localization: Ppa2.1-4: Located in mitochondria according to GeneCards Pp.1: Located in cytosol according to Gene Cards Tissue Localization: Both are distributed fairly ubquitiously throughout the body. There is a slightly greater concentration in the heart and brain. Catalytic activity and tissue localization according to Fairchild TA, Patejunas G.iochim Biophys Acta. 1999 Oct 28;1447(2-3):133-6.
PPA	3	Fabrichniy IP, Lehtio L, Salminen A, Zyryanov AB, Baykov AA, Lahti R, Goldman A.	Structural studies of metal ions in family II pyrophosphatases: the requirement for a Janus ion.	Biochemistry	2004	15533045	- Added by RS/TV Catalytic Activity: Inorganic phosphatase catalyzes the hydrolysis of pyrophosphate to form orthophosphate. There are two groups of Ppases (type I and type 2). Both catalyzes the same aforementioned reaction, however vary in their kinetic information, co-factor usuage. More differences described Fabrichniy IP, Lehtio L, Salminen A, Zyryanov AB, Baykov AA, Lahti R, Goldman A.Biochemistry. 2004 Nov 16;43(45):14403-11. There are four transcriptional variants according to Entrez for PPA2 Subcellular Localization: Ppa2.1-4: Located in mitochondria according to GeneCards Pp.1: Located in cytosol according to Gene Cards Tissue Localization: Both are distributed fairly ubquitiously throughout the body. There is a slightly greater concentration in the heart and brain. Catalytic activity and tissue localization according to Fairchild TA, Patejunas G.iochim Biophys Acta. 1999 Oct 28;1447(2-3):133-6.
PPAP	3	Coleman RA, Lee DP	Enzymes of triacylglycerol synthesis and their regulation	Prog in Lipid Research	2004		ER - external ER surface (see refs) multiple substrate specificities NJ
PPAP	3	Roberts R, Sciorra VA, Morris AJ	Human type 2 phosphatidic acid phosphohydrolases	The Journal of Biological Chemistry	1998		ER - external ER surface (see refs) multiple substrate specificities NJ
PPAP	3	Coleman RA, Lee DP	Enzymes of triacylglycerol synthesis and their regulation	Prog in Lipid Research	2004		ER - external ER surface (see refs) multiple substrate specificities NJ
PPAt	2	Tassani V, Cattapan F, Magnanimi L, Peschechera A.	Anaplerotic effect of propionyl carnitine in rat heart mitochondria.	Biochem Biophys Res Commun	1994	8135845	Tassani, 1994 Anaplerotic effect of propionyl carnintine in rat heart mitochondria - reference and description taken from Thuy's mitochondrial model ("Heart Mito Isotopomer"); ND

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PPBNGS	3	Ishida N, Fujita H, Fukuda Y, Noguchi T, Doss M, Kappas A, Sassa S.	Cloning and expression of the defective genes from a patient with delta-aminolevulinate dehydratase porphyria.	J Clin Invest	1992		- Aminolevulinate dehydratase (ALAD), the second enzyme in the heme biosyntheic pathway, catalyzes the asymmetric condensation of two molecules of 5-aminolevulic acid to form the monopyrrole, porphobilinogen. (Ishida N, Fujita H, Fukuda Y, Noguchi T, Doss M, Kappas A, Sassa S. J Clin Invest. 1992 May;89(5):1431-7.) Added by RS/TV
PPCOACm	3	Lamhonwah AM, Barankiewicz TJ, Willard HF, Mahuran DJ, Quan F, Gravel RA	Isolation of cDNA clones coding for the alpha and beta chains of human propionyl-CoA carboxylase: chromosomal assignments and DNA polymorphisms associated with PCCA and PCCB genes	Proc Natl Acad Sci U S A	1986	3460076	- enzyme is heterodimer of PCCA & PCCB [RefSeq], [UniProt], [Lamhonwah, PNAS 1986] - mitochondrial [UniProt], [RefSeq], [Lamhonwah, Genomics 1994] - reaction described in Devlin p. 637, Orten p. 262
PPCOACm	3	Lamhonwah AM, Leclerc D, Loyer M, Clarizio R, Gravel RA	Correction of the metabolic defect in propionic acidemia fibroblasts by microinjection of a full-length cDNA or RNA transcript encoding the propionyl-CoA carboxylase beta subunit	Genomics	1994	8188292	- enzyme is heterodimer of PCCA & PCCB [RefSeq], [UniProt], [Lamhonwah, PNAS 1986] - mitochondrial [UniProt], [RefSeq], [Lamhonwah, Genomics 1994] - reaction described in Devlin p. 637, Orten p. 262
PPCOAOm	3	Rozen R, Vockley J, Zhou L, Milos R, Willard J, Fu K, Vicanek C, Low-Nang L, Torban E, Fournier B	Isolation and expression of a cDNA encoding the precursor for a novel member (ACADSB) of the acyl-CoA dehydrogenase gene family	Genomics	1994	7698750	chains can also act on propinoyl-CoA 34: - mitochondrial [RefSeq], [UniProt] - functions on C4 to C12 fatty acyl-CoA chains [RefSeq] - functions on C4 to C16 fatty acyl-CoA chains [UniProt] - 88% sequence identity w/ porcine gene [Kelly, PNAS 1987] 35: - mitochondrial [RefSeq], [UniProt] - specificity inferred from mouse protein [Kelly, Genomics 1993] - identification of cDNA [Naito, J Clin Invest 1985] 36: - mitochondrial [RefSeq], [UniProt] - greatest activity towards (S)-2-methylbutyryl-CoA, but also reacts significantly with other 2-methyl branched chain substrates and with short straight chain acyl-CoAs [RefSeq], [Rozen, Genomics 1994], [UniProt] -ubiquitous [UniProt] 27034: - has activity with isobutyryl-CoA, (S) 2-methylbutyryl-CoA, and n-propionyl-CoA [Ngyuen, Mol Genet Metab 2002] - mitochondrial [UniProt] - Detected at comparable levels in all tissues examined (heart, lung, brain, skeletal muscle, pancreas and placenta). Weakly expressed in liver and kidney. [UniProt] 28976: - primarily active on palmitoyl-CoA (C16) and stearoyl-CoA (C - mitochondrial (probable) [UniProt] - Ubiquitously expressed in most normal human tissues and can 80724:
PPCOAOm	3	Kelly CL, Hinsdale ME, Wood PA	Cloning and characterization of the mouse short-chain acyl-CoA dehydrogenase cDNA	Genomics	1993	8276399	chains can also act on propinoyl-CoA 34: - mitochondrial [RefSeq], [UniProt] - functions on C4 to C12 fatty acyl-CoA chains [RefSeq] - functions on C4 to C16 fatty acyl-CoA chains [UniProt] - 88% sequence identity w/ porcine gene [Kelly, PNAS 1987] 35: - mitochondrial [RefSeq], [UniProt] - specificity inferred from mouse protein [Kelly, Genomics 1993] - identification of cDNA [Naito, J Clin Invest 1985] 36: - mitochondrial [RefSeq], [UniProt] - greatest activity towards (S)-2-methylbutyryl-CoA, but also reacts significantly with other 2-methyl branched chain substrates and with short straight chain acyl-CoAs [RefSeq], [Rozen, Genomics 1994], [UniProt] -ubiquitous [UniProt] 27034: - has activity with isobutyryl-CoA, (S) 2-methylbutyryl-CoA, and n-propionyl-CoA [Ngyuen, Mol Genet Metab 2002] - mitochondrial [UniProt] - Detected at comparable levels in all tissues examined (heart, lung, brain, skeletal muscle, pancreas and placenta). Weakly expressed in liver and kidney. [UniProt] 28976: - primarily active on palmitoyl-CoA (C16) and stearoyl-CoA (C - mitochondrial (probable) [UniProt] - Ubiquitously expressed in most normal human tissues and can 80724:

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PPCOAOm	3	Nguyen TV, Andresen BS, Corydon TJ, Ghisla S, Abd-El Razik N, Mohsen AW, Cederbaum SD, Roe DS, Roe CR, Lench NJ, Vockley J	Identification of isobutyryl-CoA dehydrogenase and its deficiency in humans	Mol Genet Metab	2002	12359132	chains can also act on propinoyl-CoA 34: - mitochondrial [RefSeq], [UniProt] - functions on C4 to C12 fatty acyl-CoA chains [RefSeq] - functions on C4 to C16 fatty acyl-CoA chains [UniProt] - 88% sequence identity w/ porcine gene [Kelly, PNAS 1987] 35: - mitochondrial [RefSeq], [UniProt] - specificity inferred from mouse protein [Kelly, Genomics 1993] - identification of cDNA [Naito, J Clin Invest 1985] 36: - mitochondrial [RefSeq], [UniProt] - greatest activity towards (S)-2-methylbutyryl-CoA, but also reacts significantly with other 2-methyl branched chain substrates and with short straight chain acyl-CoAs [RefSeq], [Rozen, Genomics 1994], [UniProt] -ubiquitous [UniProt] 27034: - has activity with isobutyryl-CoA, (S) 2-methylbutyryl-CoA, and n-propionyl-CoA [Ngyuen, Mol Genet Metab 2002] - mitochondrial [UniProt] - Detected at comparable levels in all tissues examined (heart, lung, brain, skeletal muscle, pancreas and placenta). Weakly expressed in liver and kidney. [UniProt] 28976: - primarily active on palmitoyl-CoA (C16) and stearoyl-CoA (C - mitochondrial (probable) [UniProt] - Ubiquitously expressed in most normal human tissues and can 80724:
PPCOAOm	3	Zhang J, Zhang W, Zou D, Chen G, Wan T, Zhang M, Cao X	Cloning and functional characterization of ACAD-9, a novel member of human acyl-CoA dehydrogenase family	Biochem Biophys Res Commun	2002	12359260	chains can also act on propinoyl-CoA 34: - mitochondrial [RefSeq], [UniProt] - functions on C4 to C12 fatty acyl-CoA chains [RefSeq] - functions on C4 to C16 fatty acyl-CoA chains [UniProt] - 88% sequence identity w/ porcine gene [Kelly, PNAS 1987] 35: - mitochondrial [RefSeq], [UniProt] - specificity inferred from mouse protein [Kelly, Genomics 1993] - identification of cDNA [Naito, J Clin Invest 1985] 36: - mitochondrial [RefSeq], [UniProt] - greatest activity towards (S)-2-methylbutyryl-CoA, but also reacts significantly with other 2-methyl branched chain substrates and with short straight chain acyl-CoAs [RefSeq], [Rozen, Genomics 1994], [UniProt] -ubiquitous [UniProt] 27034: - has activity with isobutyryl-CoA, (S) 2-methylbutyryl-CoA, and n-propionyl-CoA [Ngyuen, Mol Genet Metab 2002] - mitochondrial [UniProt] - Detected at comparable levels in all tissues examined (heart, lung, brain, skeletal muscle, pancreas and placenta). Weakly expressed in liver and kidney. [UniProt] 28976: - primarily active on palmitoyl-CoA (C16) and stearoyl-CoA (C - mitochondrial (probable) [UniProt] - Ubiquitously expressed in most normal human tissues and can 80724:

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PPCOAOm	3	Ye X, Ji C, Zhou C, Zeng L, Gu S, Ying K, Xie Y, Mao Y	Cloning and characterization of a human cDNA ACAD10 mapped to chromosome 12q24.1	Mol Biol Rep	2004	15560374	chains can also act on propinoyl-CoA 34: - mitochondrial [RefSeq], [UniProt] - functions on C4 to C12 fatty acyl-CoA chains [RefSeq] - functions on C4 to C16 fatty acyl-CoA chains [UniProt] - 88% sequence identity w/ porcine gene [Kelly, PNAS 1987] 35: - mitochondrial [RefSeq], [UniProt] - specificity inferred from mouse protein [Kelly, Genomics 1993] - identification of cDNA [Naito, J Clin Invest 1985] 36: - mitochondrial [RefSeq], [UniProt] - greatest activity towards (S)-2-methylbutyryl-CoA, but also reacts significantly with other 2-methyl branched chain substrates and with short straight chain acyl-CoAs [RefSeq], [Rozen, Genomics 1994], [UniProt] -ubiquitous [UniProt] 27034: - has activity with isobutyryl-CoA, (S) 2-methylbutyryl-CoA, and n-propionyl-CoA [Ngyuen, Mol Genet Metab 2002] - mitochondrial [UniProt] - Detected at comparable levels in all tissues examined (heart, lung, brain, skeletal muscle, pancreas and placenta). Weakly expressed in liver and kidney. [UniProt] 28976: - primarily active on palmitoyl-CoA (C16) and stearoyl-CoA (C - mitochondrial (probable) [UniProt] - Ubiquitously expressed in most normal human tissues and can 80724:
PPNCL3	3	Manoj N, Strauss E, Begley TP, Ealick SE.	Structure of human phosphopantothenoylcysteine synthetase at 2.3 A resolution.	Structure (Camb)	2003	12906824	01-24-05 IT The functional enzyme is a homodimer
PPPGOm	2	Dailey TA, Dailey HA.	Human protoporphyrinogen oxidase: expression, purification, and characterization of the cloned enzyme.	Protein Sci	1996	8771201	- Added by RS/TV Proteome - Mitochondrial according to Entrez Gene database. - Protoporphyrinogen oxidase catalyzes the oxygen-dependent oxidation of protoporphyrinogen IX to protoporphyrin IX. Northern blot analysis of of eight different human tissues show evidence for only a single transcript in all tissue types. (Dailey TA, Dailey HA. Protein Sci. 1996 Jan;5(1):98-105.)
PRAGSr	3	Schild D, Brake AJ, Kiefer MC, Young D, Barr PJ.	Cloning of three human multifunctional de novo purine biosynthetic genes by functional complementation of yeast mutations.	Proc Natl Acad Sci U S A	1990	2183217	IT no infos about compartiment
PRAGSr	3	Brodsky G, Barnes T, Bleskan J, Becker L, Cox M, Patterson D.	The human GARS-AIRS-GART gene encodes two proteins which are differentially expressed during human brain development and temporally overexpressed in cerebellum of individuals with Down syndrome.	Hum Mol Genet	1997	9328467	IT no infos about compartiment
PRAGSr	3	Poch MT, Qin W, Caperelli CA.	The human trifunctional enzyme of de novo purine biosynthesis: heterologous expression, purification, and preliminary characterization.	Protein Expr Purif	1998	9473452	IT no infos about compartiment
PRAGSr	3	Zhang Y, Desharnais J, Greasley SE, Beardsley GP, Boger DL, Wilson IA.	Crystal structures of human GAR Tfase at low and high pH and with substrate beta-GAR.	Biochemistry	2002	12450384	IT no infos about compartiment
PRDX	0	Wu W, Chen Y, Hazen SL.	Eosinophil peroxidase nitrates protein tyrosyl residues. Implications for oxidative damage by nitrating intermediates in eosinophilic inflammatory disorders.	J Biol Chem	1999	10464338	- RS/TV (6/3/2005) - cytosolic accoding to GeneCards - EPX belongs to the peroxidase family. It has the ability to reduce hydrogen peroxide while simultaneously using a co-substrate which is consequently oxidized. Studies thus far have shown that EPX is able to use bromide, SCN salts; Furthermore it is also shown that EPX readily uses NO2(1-) as substrate to generate a reactive intermediate that nitrates protein tyrosyl residues in high yield. (Wu W, Chen Y, Hazen SL. J Biol Chem. 1999 Sep 3;274(36):25933-44.) - Based on this observation as well as GO annotation this GPR association has been made. - the catalase-peroxidase system is used to oxidize methanol in non-primates whereas in primates the alcohol dehydrogenase system is the primary mechanism; see: http://antizol.info/mpoisono.htm

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
PRDXl	0	Burner U, Furtmuller PG, Kettle AJ, Koppenol WH, Obinger C.	Mechanism of reaction of myeloperoxidase with nitrite	J Biol Chem	2000	10777476	- RS/TV (6/3/2005) - Lysosomal according to GeneCards - MPO is a part of the peroxidase family. Generally, ferric or native myeloperoxidase reacts with hydrogen peroxide forming a redox intermediate. This redox intermediate is known to oxidize halides via a single two-electron reaction to produce the respective hypohalous acids and regenerate the native enzyme. However, halides are not the only co-substrates that MPO works with. These co-substrates include tyrosine, tryptophan, sulfhydryls, phenol and indole derivatives, nitrite, hydrogen peroxide, xenobiotics, and others. According to 1) Arnhold J.Biochemistry (Mosc). 2004 Jan;69(1):4-9. Review. 2) Burner U, Furtmuller PG, Kettle AJ, Koppenol WH, Obinger C.J Biol Chem. 2000 Jul 7;275(27):20597-601. - Based on GO annotation and known catalytic activity, this GPR association has been made. - the catalase-peroxidase system is used to oxidize methanol in non-primates whereas in primates the alcohol dehydrogenase system is the primary mechanism; see: http://antizol.info/mpoisono.htm
PRDXl	0	Arnhold J.	Properties, functions, and secretion of human myeloperoxidase	Biochemistry (Mosc)	2004	14972011	- RS/TV (6/3/2005) - Lysosomal according to GeneCards - MPO is a part of the peroxidase family. Generally, ferric or native myeloperoxidase reacts with hydrogen peroxide forming a redox intermediate. This redox intermediate is known to oxidize halides via a single two-electron reaction to produce the respective hypohalous acids and regenerate the native enzyme. However, halides are not the only co-substrates that MPO works with. These co-substrates include tyrosine, tryptophan, sulfhydryls, phenol and indole derivatives, nitrite, hydrogen peroxide, xenobiotics, and others. According to 1) Arnhold J.Biochemistry (Mosc). 2004 Jan;69(1):4-9. Review. 2) Burner U, Furtmuller PG, Kettle AJ, Koppenol WH, Obinger C.J Biol Chem. 2000 Jul 7;275(27):20597-601. - Based on GO annotation and known catalytic activity, this GPR association has been made. - the catalase-peroxidase system is used to oxidize methanol in non-primates whereas in primates the alcohol dehydrogenase system is the primary mechanism; see: http://antizol.info/mpoisono.htm
PRFGS	3	Patterson D, Bleskan J, Gardiner K, Bowersox J.	Human phosphoribosylformylglycineamide amidotransferase (FGARAT): regional mapping, complete coding sequence, isolation of a functional genomic clone, and DNA sequence analysis.	Gene	1999	10548741	cytoplasm (GeneCards) IT
PROAKGOX1r	3	Helaakoski T, Vuori K, Myllyla R, Kivirikko KI, Pihlajaniemi T.	Molecular cloning of the alpha-subunit of human prolyl 4-hydroxylase: the complete cDNA-derived amino acid sequence and evidence for alternative splicing of RNA transcripts.	Proc Natl Acad Sci U S A	1989	2543975	this is done with enzyme complex vs subunits and one enzyme because "The beta subunit (P4HB; MIM 176790) is an unusual multifunctional polypeptide identical to protein disulfide isomerase (EC 5.3.4.1). P4HA2 is one of at least 2 alpha subunit isoforms (Helaakoski et al., 1995 [PubMed 7753822])" This reaction represents proline hydroxylation in peptide likages and NOT free proline [Helaakoski et al., 1995] Collagen prolyl 4-hydroxylases (P4Hs, EC 1.14.11.2) are located within the lumen of the endoplasmic reticulum and catalyze the formation of 4-hydroxyproline by the hydroxylation of prolines in -X-Pro-Gly- sequences in collagens and more than 15 other proteins that have collagen-like domains [Myllyharju 2003] The 4hpro-L in in proline could eventually be broken down and used to form glyoxylate.

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
PROAKGOX1r	3	Pihlajaniemi T, Helaakoski T, Tasanen K, Myllyla R, Huhtala ML, Koivu J, Kivirikko KI.	Molecular cloning of the beta-subunit of human prolyl 4-hydroxylase. This subunit and protein disulphide isomerase are products of the same gene.	EMBO J	1987	3034602	this is done with enzyme complex vs subunits and one enzyme because "The beta subunit (P4HB; MIM 176790) is an unusual multifunctional polypeptide identical to protein disulfide isomerase (EC 5.3.4.1). P4HA2 is one of at least 2 alpha subunit isoforms (Helaakoski et al., 1995 [PubMed 7753822])" This reaction represents proline hydroxylation in peptide likages and NOT free proline [Helaakoski et al., 1995] Collagen prolyl 4-hydroxylases (P4Hs, EC 1.14.11.2) are located within the lumen of the endoplasmic reticulum and catalyze the formation of 4-hydroxyproline by the hydroxylation of prolines in -X-Pro-Gly- sequences in collagens and more than 15 other proteins that have collagen-like domains [Myllyharju 2003] The 4hpro-L in in proline could eventually be broken down and used to form glyoxylate.
PROAKGOX1r	3	Myllyharju J	Prolyl 4-hydroxylases, the key enzymes of collagen biosynthesis	Matrix Biol	2003	12714038	this is done with enzyme complex vs subunits and one enzyme because "The beta subunit (P4HB; MIM 176790) is an unusual multifunctional polypeptide identical to protein disulfide isomerase (EC 5.3.4.1). P4HA2 is one of at least 2 alpha subunit isoforms (Helaakoski et al., 1995 [PubMed 7753822])" This reaction represents proline hydroxylation in peptide likages and NOT free proline [Helaakoski et al., 1995] Collagen prolyl 4-hydroxylases (P4Hs, EC 1.14.11.2) are located within the lumen of the endoplasmic reticulum and catalyze the formation of 4-hydroxyproline by the hydroxylation of prolines in -X-Pro-Gly- sequences in collagens and more than 15 other proteins that have collagen-like domains [Myllyharju 2003] The 4hpro-L in in proline could eventually be broken down and used to form glyoxylate.
PROD2	2	Gogos JA, Santha M, Takacs Z, Beck KD, Luine V, Lucas LR, Nadler JV, Karayiorgou M.	The gene encoding proline dehydrogenase modulates sensorimotor gating in mice.	Nat Genet	1999	10192398	unclear which acceptors are used for this reaction (NADPH specifically excluded at this point because it would cause a loop that could turn NADH into NADPH) (right now a loop can turn NADH into FADH2 which should be okay)
PROSTGD2t	3	Lu R, Kanai N, Bao Y, Schuster VL.	Cloning, in vitro expression, and tissue distribution of a human prostaglandin transporter cDNA(hPGT).	J Clin Invest	1996	8787677	Tissue Specificity: SLCO2A1 - ubiquitous SLCO1A2 - brain, kidney, lung, testis, liver SLCO1B1 - liver SLCO1B3 - liver SLCO2B1 - liver, placenta, spleen, lung, kidney, heart, ovary SLCO3A1 - ubiquitously SLCO4A1 - ubiquitously SLCO1C1 - brain, testis May mediate the release of newly synthesized prostaglandins from cells, the transepithelial transport of prostaglandins, and the clearance of prostaglandins from the circulation. NJ
PROSTGD2t	3	Satlin LM, Amin V, Wolkoff AW.	Organic anion transporting polypeptide mediates organic anion/HCO3- exchange.	J Biol Chem	1997	9334206	Tissue Specificity: SLCO2A1 - ubiquitous SLCO1A2 - brain, kidney, lung, testis, liver SLCO1B1 - liver SLCO1B3 - liver SLCO2B1 - liver, placenta, spleen, lung, kidney, heart, ovary SLCO3A1 - ubiquitously SLCO4A1 - ubiquitously SLCO1C1 - brain, testis May mediate the release of newly synthesized prostaglandins from cells, the transepithelial transport of prostaglandins, and the clearance of prostaglandins from the circulation. NJ

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
PROSTGD2t	3	Hagenbuch B, Meier PJ.	The superfamily of organic anion transporting polypeptides.	Biochim Biophys Acta	2003	12507753	Tissue Specificity: SLCO2A1 - ubiquitous SLCO1A2 - brain, kidney, lung, testis, liver SLCO1B1 - liver SLCO1B3 - liver SLCO2B1 - liver, placenta, spleen, lung, kidney, heart, ovary SLCO3A1 - ubiquitously SLCO4A1 - ubiquitously SLCO1C1 - brain, testis May mediate the release of newly synthesized prostaglandins from cells, the transepithelial transport of prostaglandins, and the clearance of prostaglandins from the circulation. NJ
PROSTGE2t2	3	Zhang L, Dresser MJ, Gray AT, Yost SC, Terashita S, Giacomini KM.	Cloning and functional expression of a human liver organic cation transporter.	Mol Pharmacol	1997	9187257	Tissue specificity: kidney (basolat membrane of prox tub), brain Km and Ki listed in Koepsell 2003 (in addition to detailed info about localization and other members of organic cation transporters) PMID: 12827517 cloning in PMID 9187257 Polyspecific organic cation transporters in the liver, kidney, intestine, and other organs are critical for elimination of many endogenous small organic cations as well as a wide array of drugs and environmental toxins. This gene is one of three similar cation transporter genes located in a cluster on chromosome 6. The encoded protein contains twelve putative transmembrane domains and is a plasma integral membrane protein. Two transcript variants encoding two different isoforms have been found for this gene, but only the longer variant encodes a functional transporter. NJ
PRPNCOAHYDx	3	Hoefler G, Forstner M, McGuinness MC, Hulla W, Hiden M, Krisper P, Kenner L, Ried T, Lengauer C, Zechner R, et al.	DNA cloning of the human peroxisomal enoyl-CoA hydratase: 3-hydroxyacyl-CoA dehydrogenase bifunctional enzyme and localization to chromosome 3q26.3-3q28: a free left Alu Arm is inserted in the 3' noncoding region.	Genomics	1994	8188243	- peroxisomal [Hoefler, Genomics 1994], [UniProt] - highest expression in liver and kidney [Hoefler, Genomics 1994] lower amounts also in brain [UniProt]
PRPPS	0	Taira M, Iizasa T, Shimada H, Kudoh J, Shimizu N, Tatibana M.	A human testis-specific mRNA for phosphoribosylpyrophosphate synthetase that initiates from a non-AUG codon.	J Biol Chem	1990	2168892	221823: - testis [RefSeq, UniProt]
PRPPS	0	Becker MA, Kim M	Regulation of purine synthesis de novo in human fibroblasts by purine nucleotides and phosphoribosylpyrophosphate.	J Biol Chem	1987	2444588	221823: - testis [RefSeq, UniProt]
PSDm_hs	3	Voelker DR.	Phosphatidylserine decarboxylase.	Biochim Biophys Acta	1997	9370338	from TV model - needs to be updated w/ refs, etc Localized to inner mit membrane (PMID: 9370338). This enzyme is actually believed to be a minor contributor to the production of pe - PMID: 15052331 (hatch rev) comment on data suggesting that the pe production pathway may involve the beta ox pathway. NJ
PSDm_hs	3	Hatch GM.	Cell biology of cardiac mitochondrial phospholipids.	Biochem Cell Biol	2004	15052331	from TV model - needs to be updated w/ refs, etc Localized to inner mit membrane (PMID: 9370338). This enzyme is actually believed to be a minor contributor to the production of pe - PMID: 15052331 (hatch rev) comment on data suggesting that the pe production pathway may involve the beta ox pathway. NJ
PSERT	3	Baek,J.Y. , Jun,d. o Y , Taub,D. , Kim,Y.H.	Characterization of human phosphoserine aminotransferase involved in the phosphorylated pathway of L-serine biosynthesis		2003	12633500	irreversible according to Lehninger (pg. 844, 4th ed.)
PSP_L	3	Collet JF, Gerin I, Rider MH, Veiga-da-Cunha M, Van Schaftingen E.	Human L-3-phosphoserine phosphatase: sequence, expression and evidence for a phosphoenzyme intermediate.		1997	9188776	irreversibility based on Lehninger (4th ed.)
PSP_L	3	Planitzer SA, Machl AW, Rueckels M, Kubbies M.	Identification of a novel c-DNA overexpressed in Fanconi's anemia fibroblasts partially homologous to a putative L-3-phosphoserine-phosphatase.		1998	9573387	irreversibility based on Lehninger (4th ed.)

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PTE2x	3	Jones JM, Nau K, Geraghty MT, Erdmann R, Gould SJ.	Identification of peroxisomal acyl-CoA thioesterases in yeast and humans.	J Biol Chem	1999	10092594	localization: peroxisomal (uniprot) specificity: ubiquitous Acyl-CoA thioesterases are a group of enzymes that catalyze the hydrolysis of acyl-CoAs to the free fatty acid and coenzyme A (CoASH), providing the potential to regulate intracellular levels of acyl-CoAs, free fatty acids and CoASH. May mediate Nef-induced down-regulation of CD4. Major thioesterase in peroxisomes. Competes with BAAT (Bile acid CoA: amino acid N-acyltransferase) for bile acid-CoA substrate (such as chenodeoxycholoyl-CoA). Shows a preference for medium-length fatty acyl-CoAs (By similarity). May be involved in the metabolic regulation of peroxisome proliferation. see also PMID: 10944470 for support for Zap128 NJ
PTE3x	3	Jones JM, Gould SJ.	Identification of PTE2, a human peroxisomal long-chain acyl-CoA thioesterase.	Biochem Biophys Res Commun	2000	10944470	localization: peroxisome (uniprot) specificity: none-noted Descriptions only noted medium and long chain fatty acids, in the future re-check literature for possible addition of other FA, particularly bile acid precursors (PTE1x, PTE6x, ...) Acyl-CoA thioesterases are a group of enzymes that catalyze the hydrolysis of acyl-CoAs to the free fatty acid and coenzyme A (CoASH), providing the potential to regulate intracellular levels of acyl-CoAs, free fatty acids and CoASH. Displays high levels of activity on medium- and long chain acyl CoAs. See PMID: 10944470 for thioesterase activity and localization. NJ
PTPAT	3	Aghajanian S, Worrall DM.	Identification and characterization of the gene encoding the human phosphopantetheine adenylyltransferase and dephospho-CoA kinase bifunctional enzyme (CoA synthase).	Biochem J	2002	11994049	01-24-05 IT
PTRCAT1	3	Chen Y, Vujcic S, Liang P, Diegelman P, Kramer DL, Porter CW.	Genomic identification and biochemical characterization of a second spermidine/spermine N1-acetyltransferase	Biochem J	2003	12803540	preference is for other substrates, but citation says ptrc is acceptable
PTRCOX1	2	Imamura Y, Kubota R, Wang Y, Asakawa S, Kudoh J, Mashima Y, Oguchi Y, Shimizu N	Human retina-specific amine oxidase (RAO): cDNA cloning, tissue expression, and chromosomal mapping	Genomics	1997	9119395	physiological data based on at least one of these genes associated with ptrc degradation in some way
PUNP1	3	Williams SR, Goddard JM, Martin DW Jr.	Human purine nucleoside phosphorylase cDNA sequence and genomic clone characterization.	Nucleic Acids Res	1984	6087295	IT
PUNP1	3	Erion MD, Stoeckler JD, Guida WC, Walter RL, Ealick SE.	Purine nucleoside phosphorylase. 2. Catalytic mechanism.	Biochemistry	1997	9305963	IT
PUNP5	3	Canduri F, dos Santos DM, Silva RG, Mendes MA, Basso LA, Palma MS, de Azevedo WF, Santos DS.	Structures of human purine nucleoside phosphorylase complexed with inosine and ddI.	Biochem Biophys Res Commun	2004	14706628	IT
PYDX5Ptm	2	Lui A, Lumeng L, Li TK.	Metabolism of vitamin B6 in rat liver mitochondria.	J Biol Chem	1981	6263901	IT studies on rat hepatocytes suggests that the mitochondrial transport occurs via diffusion. A number of enzymes located in the mitochondria are using Vit B6 (either pydx5p or pyam5p) as cofactor.
PYDX5Ptm	2	Lui A, Lumeng L, Li TK.	Transport of pyridoxine and pyridoxal 5'-phosphate in isolated rat liver mitochondria.	J Biol Chem	1982	7174673	IT studies on rat hepatocytes suggests that the mitochondrial transport occurs via diffusion. A number of enzymes located in the mitochondria are using Vit B6 (either pydx5p or pyam5p) as cofactor.
PYDXK	3	Hanna MC, Turner AJ, Kirkness EF.	Human pyridoxal kinase. cDNA cloning, expression, and modulation by ligands of the benzodiazepine receptor.	J Biol Chem	1997	9099727	IT
PYDXNK	3	Chern CJ, Beutler E.	Biochemical and electrophoretic studies of erythrocyte pyridoxine kinase in white and black Americans.	Am J Hum Genet	1976	2009	IT
PYDXNK	3	Ink SL, Henderson LM.	Vitamin B6 metabolism.	Annu Rev Nutr	1984	6380540	IT
PYNP2r	3	Watanabe S, Uchida T.	Cloning and expression of human uridine phosphorylase.	Biochem Biophys Res Commun	1995	7488099	IT
PYNP2r	3	Russell RL, Cao D, Zhang D, Handschumacher RE, Pizzorno G.	Uridine phosphorylase association with vimentin. Intracellular distribution and localization.	J Biol Chem	2001	11278417	IT
PYNP2r	3	Pizzorno G, Cao D, Leffert JJ, Russell RL, Zhang D, Handschumacher RE.	Homeostatic control of uridine and the role of uridine phosphorylase: a biological and clinical update.	Biochim Biophys Acta	2002	12084455	IT
PYNP2r	3	Johansson M.	Identification of a novel human uridine phosphorylase.	Biochem Biophys Res Commun	2003	12849978	IT

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PYRt2m	0	Halestrap AP, Scott RD, Thomas AP	Mitochondrial pyruvate transport and its hormonal regulation	Int J Biochem	1980	6987111	Halestrap et al, Int J Biochem 1980 - Additional Info by RS/TV: Ferdinando Palmieri, The mitochondrial transporter family (SLC25): physiological and pathological implications. "not yet identified at the molecular level"
PYRt2p	3	McClelland GB, Khanna S, Gonzalez GF, Butz CE, Brooks GA	Peroxisomal membrane monocarboxylate transporters: evidence for a redox shuttle system?	Biochem Biophys Res Commun	2003	12705896	Mechanism based on references and yeast The associated genes probably function in the transport into/out of various compartments The first citation also has evidence that pyruvate is converted into lactate inside peroxisomes 9194: - cloned [Lin 1998] - high affinity for pyruvate [Lin 1998] - restricted expression in normal tissues but high in cancer cell lines [Lin 1998] - also transports lactate, hydroxybutrayte [Lin 1998], ketone bodies[Halestrap 2004]
RAI3	2	Gough WH, VanOoteghem S, Sint T, Kedishvili NY.	cDNA cloning and characterization of a new human microsomal NAD+-dependent dehydrogenase that oxidizes all-trans-retinol and 3alpha-hydroxysteroids.	J Biol Chem	1998	9677409	IT
RAI3	2	Chen H, Juchau MR.	Recombinant human glutathione S-transferases catalyse enzymic isomerization of 13-cis-retinoic acid to all-trans-retinoic acid in vitro.	Biochem J	1998	9806904	IT
RBFK	3	Karthikeyan S, Zhou Q, Mseeh F, Grishin NV, Osterman AL, Zhang H.	Crystal structure of human riboflavin kinase reveals a beta barrel fold and a novel active site arch.	Structure (Camb)	2003	12623014	GeneCards located enzyme in cytoplasm based on sequence. IT
RBFK	3	Karthikeyan S, Zhou Q, Osterman AL, Zhang H.	Ligand binding-induced conformational changes in riboflavin kinase: structural basis for the ordered mechanism.	Biochemistry	2003	14580199	GeneCards located enzyme in cytoplasm based on sequence. IT
RBK	2	Agranoff BW, Brady RO	Purification and properties of calf liver ribokinase	J Biol Chem	1956	13295274	- exogenous ribose enters the PPP and is converted to R-5-P by ribokinase [Segal 1958] - enzyme has been purified from calf liver [Agranoff 1956]
RBK	2	Segal S, Foley J	The metabolism of D-ribose in man.	J Clin Invest	1958	13539215	- exogenous ribose enters the PPP and is converted to R-5-P by ribokinase [Segal 1958] - enzyme has been purified from calf liver [Agranoff 1956]
RBK_D	2	Huck JH, Roos B, Jakobs C, van der Knaap MS, Verhoeven NM	Evaluation of pentitol metabolism in mammalian tissues provides new insight into disorders of human sugar metabolism	Mol Genet Metab	2004	15234337	- ribulokinase has been identified in mammals [Huck, Mol Genet Metab 2004]
RDH1	3	Jurukovski V, Markova NG, Karaman-Jurukovska N, Randolph RK, Su J, Napoli JL, Simon M.	Cloning and characterization of retinol dehydrogenase transcripts expressed in human epidermal keratinocytes.	Mol Genet Metab	1999	10329026	IT RDH5 (5959): substrate spec: 11-cis-reinal = 13-cis-retinal > 9-cis-retinal (pro-S) (not all-trans-retinal), pro-S NADH
RDH1	3	Haeseleer F, Jang GF, Imanishi Y, Driessen CA, Matsumura M, Nelson PS, Palczewski K.	Dual-substrate specificity short chain retinol dehydrogenases from the vertebrate retina.	J Biol Chem	2002	12226107	IT RDH5 (5959): substrate spec: 11-cis-reinal = 13-cis-retinal > 9-cis-retinal (pro-S) (not all-trans-retinal), pro-S NADH
RDH1	3	Lapshina EA, Belyaeva OV, Chumakova OV, Kedishvili NY.	Differential recognition of the free versus bound retinol by human microsomal retinol/sterol dehydrogenases: characterization of the holo-CRBP dehydrogenase activity of RoDH-4.	Biochemistry	2003	12534290	IT RDH5 (5959): substrate spec: 11-cis-reinal = 13-cis-retinal > 9-cis-retinal (pro-S) (not all-trans-retinal), pro-S NADH
RDH1a	3	Matsuzaka Y, Okamoto K, Tsuji H, Mabuchi T, Ozawa A, Tamiya G, Inoko H.	Identification of the hRDH-E2 gene, a novel member of the SDR family, and its increased expression in psoriatic lesion.	Biochem Biophys Res Commun	2002	12372410	all-trans-retinol is predominant form, with 100% Viatmin A activity. 13-cis-retinol has 75% relative activity. 11-cis-retinaldehyde(retinal) is the chromophore in the retina of the eye, while all-trans and 9-cis retinoic acid are active metabolitess of retinol found in most if not in all tissues. changes in the molecular state of oxidation and cis/trans isomerization are of physiological importance in modifying the biological activity of retinoids. (Ball, Vitamins, book, 2004, 1st Ed) RDH12 (145226.1): Substrate spec: 9-cis-retinal> 11-cis-retinal>all-trans-retinal, NADPH, eye, other tissue? (Haeseleer, 2002) RDH14 (57665.1): Substrate spec: : 9-cis-retinal, 11-cis-retinal,all-trans-retinal, NADPH, eye, other tissue? (Haeseleer, 2002), pancreas RDH11 (51109.1): 9-cis-retinal>all-trans-retinal>11-cis-retinal,pro-S NADPH, eye (Haeseleer, 2002), prostate RDH13 (112724):NADPH (Haeseleer, 2002) RDH8(50700.1): pro-S NADPH, pro-R all-trans=retinol>9-cis-retinal; retina (Haeseleer,2002) RHD10 (157506.1): NADPH (Wu, 2002), retinal pigment epithelium IT

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RDH1a	3	Wu BX, Chen Y, Chen Y, Fan J, Rohrer B, Crouch RK, Ma JX.	Cloning and characterization of a novel all-trans retinol short-chain dehydrogenase/reductase from the RPE.	Invest Ophthalmol Vis Sci	2002	12407145	all-trans-retinol is predominant form, with 100% Viatmin A activity. 13-cis-retinol has 75% relative activity. 11-cis-retinaldehyde(retinal) is the chromophore in the retina of the eye, while all-trans and 9-cis retinoic acid are active metabolitess of retinol found in most if not in all tissues. changes in the molecular state of oxidation and cis/trans isomerization are of physiological importance in modifying the biological activity of retinoids. (Ball, Vitamins, book, 2004, 1st Ed) RDH12 (145226.1): Substrate spec: 9-cis-retinal> 11-cis-retinal>all-trans-retinal, NADPH, eye, other tissue? (Haeseleer, 2002) RDH14 (57665.1): Substrate spec: : 9-cis-retinal, 11-cis-retinal,all-trans-retinal, NADPH, eye, other tissue? (Haeseleer, 2002), pancreas RDH11 (51109.1): 9-cis-retinal>all-trans-retinal>11-cis-retinal,pro-S NADPH, eye (Haeseleer, 2002), prostate RDH13 (112724):NADPH (Haeseleer, 2002) RDH8(50700.1): pro-S NADPH, pro-R all-trans=retinol>9-cis-retinal; retina (Haeseleer,2002) RHD10 (157506.1): NADPH (Wu, 2002), retinal pigment epithelium IT
RDH1a	3	Janecke AR, Thompson DA, Utermann G, Becker C, Hubner CA, Schmid E, McHenry CL, Nair AR, Ruschendorf F, Heckenlively J, Wissinger B, Nurnberg P, Gal	Mutations in RDH12 encoding a photoreceptor cell retinol dehydrogenase cause childhood-onset severe retinal dystrophy.	Nat Genet	2004	15258582	all-trans-retinol is predominant form, with 100% Viatmin A activity. 13-cis-retinol has 75% relative activity. 11-cis-retinaldehyde(retinal) is the chromophore in the retina of the eye, while all-trans and 9-cis retinoic acid are active metabolitess of retinol found in most if not in all tissues. changes in the molecular state of oxidation and cis/trans isomerization are of physiological importance in modifying the biological activity of retinoids. (Ball, Vitamins, book, 2004, 1st Ed) RDH12 (145226.1): Substrate spec: 9-cis-retinal> 11-cis-retinal>all-trans-retinal, NADPH, eye, other tissue? (Haeseleer, 2002) RDH14 (57665.1): Substrate spec: : 9-cis-retinal, 11-cis-retinal,all-trans-retinal, NADPH, eye, other tissue? (Haeseleer, 2002), pancreas RDH11 (51109.1): 9-cis-retinal>all-trans-retinal>11-cis-retinal,pro-S NADPH, eye (Haeseleer, 2002), prostate RDH13 (112724):NADPH (Haeseleer, 2002) RDH8(50700.1): pro-S NADPH, pro-R all-trans=retinol>9-cis-retinal; retina (Haeseleer,2002) RHD10 (157506.1): NADPH (Wu, 2002), retinal pigment epithelium IT
RDH1a	3	Perrault I, Hanein S, Gerber S, Barbet F, Ducroq D, Dollfus H, Hamel C, Dufier JL, Munnich A, Kaplan J, Rozet JM.	Retinal dehydrogenase 12 (RDH12) mutations in leber congenital amaurosis.	Am J Hum Genet	2004	15322982	all-trans-retinol is predominant form, with 100% Viatmin A activity. 13-cis-retinol has 75% relative activity. 11-cis-retinaldehyde(retinal) is the chromophore in the retina of the eye, while all-trans and 9-cis retinoic acid are active metabolitess of retinol found in most if not in all tissues. changes in the molecular state of oxidation and cis/trans isomerization are of physiological importance in modifying the biological activity of retinoids. (Ball, Vitamins, book, 2004, 1st Ed) RDH12 (145226.1): Substrate spec: 9-cis-retinal> 11-cis-retinal>all-trans-retinal, NADPH, eye, other tissue? (Haeseleer, 2002) RDH14 (57665.1): Substrate spec: : 9-cis-retinal, 11-cis-retinal,all-trans-retinal, NADPH, eye, other tissue? (Haeseleer, 2002), pancreas RDH11 (51109.1): 9-cis-retinal>all-trans-retinal>11-cis-retinal,pro-S NADPH, eye (Haeseleer, 2002), prostate RDH13 (112724):NADPH (Haeseleer, 2002) RDH8(50700.1): pro-S NADPH, pro-R all-trans=retinol>9-cis-retinal; retina (Haeseleer,2002) RHD10 (157506.1): NADPH (Wu, 2002), retinal pigment epithelium IT
RDH2	3	Simon A, Hellman U, Wernstedt C, Eriksson U.	The retinal pigment epithelial-specific 11-cis retinol dehydrogenase belongs to the family of short chain alcohol dehydrogenases.	J Biol Chem	1995	7836368	IT RDH5 (5959): substrate spec: 11-cis-reinal = 13-cis-retinal > 9-cis-retinal (pro-S) (not all-trans-retinal), pro-S NADH
RDH2	3	Mertz JR, Shang E, Piantedosi R, Wei S, Wolgemuth DJ, Blaner WS.	Identification and characterization of a stereospecific human enzyme that catalyzes 9-cis-retinol oxidation. A possible role in 9-cis-retinoic acid formation.	J Biol Chem	1997	9115228	IT RDH5 (5959): substrate spec: 11-cis-reinal = 13-cis-retinal > 9-cis-retinal (pro-S) (not all-trans-retinal), pro-S NADH

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
RDH2a	3	Belyaeva OV, Kedishvili NY.	Human pancreas protein 2 (PAN2) has a retinal reductase activity and is ubiquitously expressed in human tissues.	FEBS Lett	2002	12435598	RDH12 (145226.1): Substrate spec: 9-cis-retinal> 11-cis-retinal>all-trans-retinal, NADPH, eye, other tissue? (Haeseleer, 2002) RDH14 (57665.1): Substrate spec: : 9-cis-retinal, 11-cis-retinal,all-trans-retinal, NADPH, eye, other tissue? (Haeseleer, 2002), pancreas RDH11 (51109.1): 9-cis-retinal>all-trans-retinal>11-cis-retinal,pro-S NADPH, eye (Haeseleer, 2002), prostate RDH13 (112724):NADPH (Haeseleer, 2002) RDH8(50700.1): pro-S NADPH, pro-R all-trans=retinol>9-cis-retinal; retina (Haeseleer,2002) IT
RETH	3	Gao J, Simon M.	Identification of a novel keratinocyte retinyl ester hydrolase as a transacylase and lipase.	J Invest Dermatol	2005	15955102	IT main R group = palminate
RETI3	3	Blaner WS.	Cellular metabolism and actions of 13-cis-retinoic acid.	J Am Acad Dermatol	2001	11606944	it
RETNGLCt2	2	Tang GW, Russell RM.	13-cis-retinoic acid is an endogenous compound in human serum.	J Lipid Res	1990	2324641	mechanism unknown. produced in ER. found in blood. IT
RETNt	2	Hodam JR, Creek KE.	Uptake and metabolism of [3H]retinoic acid delivered to human foreskin keratinocytes either bound to serum albumin or added directly to the culture medium.	Biochim Biophys Acta	1996	8630327	IT
RETt	2	Blomhoff R, Green MH, Norum KR.	Vitamin A: physiological and biochemical processing.	Annu Rev Nutr	1992	1503811	IT at pharmacological concentration levels retinol can be absorbed by passive diffusion retinol is transported (absorbed) by passive diffusion from intestinal lumen to enterocytes. there it is enclosed by chylomicron and released. In this from it can get to extrahepatic target cells. However, the most part of chylomicron with retinol is taken up by liver cells (parenchymal cells), retinol is released there and binds directly to RBP (retinol binding protein) and then either stored or transported to other extrahepatic cells via blood
RIBFLVt3	3	Said HM, Ma TY.	Mechanism of riboflavine uptake by Caco-2 human intestinal epithelial cells.	Am J Physiol	2003	8304455	IT
RNDR1	2	Shao J, Zhou B, Zhu L, Qiu W, Yuan YC, Xi B, Yen Y.	In vitro characterization of enzymatic properties and inhibition of the p53R2 subunit of human ribonucleotide reductase.	Cancer Res	2004	14729598	IT needs ATP, iron -protein (kegg note)
RNMK	3	Bieganowski P, Brenner C.	Discoveries of nicotinamide riboside as a nutrient and conserved NRK genes establish a Preiss-Handler independent route to NAD+ in fungi and humans.	Cell	2004	15137942	IT There are two human genes for this reaction however i could not identify the second gene in Entrz-Gene
S23T2g	3	Sasaki K, Watanabe E, Kawashima K, Sekine S, Dohi T, Oshima M, Hanai N, Nishi T, Hasegawa M	Expression cloning of a novel Gal beta (1-3/1-4) GlcNAc alpha 2,3-sialyltransferase using lectin resistance selection	J Biol Chem	1993	7901202	- reaction described in Varki, pg 235 6482: - most activity due to ST3Gal-1, low levels due to ST3Gal-2, -4 in vitro [Varki] - gene was cloned and expressed [Shang, Eur J Biochem 1999] - found in Golgi [RefSeq], also inferred from author statement in [Shang, Eur J Biochem 1999] - Siat4ap expressed in placenta, liver, sk muscle [Kitagawa and Paulson, JBC 1994] 6483: - most activity due to ST3Gal-1, low levels due to ST3Gal-2, -4 in vitro [Varki] - gene was cloned and expressed [Kim, Biochem, Biophys Res Commun 1996] - Golgi, see [Kolter, Brain Pathol 1998] 6484: - most activity due to ST3Gal-1, low levels due to ST3Gal-2, -4 in vitro [Varki] - gene was cloned [Sasaki, J Biol Chem 1993], [Kitagawa, J Biol Chem 1994]

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
S23T2g	3	Kitagawa H, Paulson JC	Cloning of a novel alpha 2,3-sialyltransferase that sialylates glycoprotein and glycolipid carbohydrate groups	J Biol Chem	1994	8288606	- reaction described in Varki, pg 235 6482: - most activity due to ST3Gal-1, low levels due to ST3Gal-2, -4 in vitro [Varki] - gene was cloned and expressed [Shang, Eur J Biochem 1999] - found in Golgi [RefSeq], also inferred from author statement in [Shang, Eur J Biochem 1999] - Siat4ap expressed in placenta, liver, sk muscle [Kitagawa and Paulson, JBC 1994] 6483: - most activity due to ST3Gal-1, low levels due to ST3Gal-2, -4 in vitro [Varki] - gene was cloned and expressed [Kim, Biochem, Biophys Res Commun 1996] - Golgi, see [Kolter, Brain Pathol 1998] 6484: - most activity due to ST3Gal-1, low levels due to ST3Gal-2, -4 in vitro [Varki] - gene was cloned [Sasaki, J Biol Chem 1993], [Kitagawa, J Biol Chem 1994]
S23T2g	3	Kim YJ, Kim KS, Kim SH, Kim CH, Ko JH, Choe IS, Tsuji S, Lee YC	Molecular cloning and expression of human Gal beta 1,3GalNAc alpha 2,3-sialytransferase (hST3Gal II)	Biochem Biophys Res Commun	1996	8920913	- reaction described in Varki, pg 235 6482: - most activity due to ST3Gal-1, low levels due to ST3Gal-2, -4 in vitro [Varki] - gene was cloned and expressed [Shang, Eur J Biochem 1999] - found in Golgi [RefSeq], also inferred from author statement in [Shang, Eur J Biochem 1999] - Siat4ap expressed in placenta, liver, sk muscle [Kitagawa and Paulson, JBC 1994] 6483: - most activity due to ST3Gal-1, low levels due to ST3Gal-2, -4 in vitro [Varki] - gene was cloned and expressed [Kim, Biochem, Biophys Res Commun 1996] - Golgi, see [Kolter, Brain Pathol 1998] 6484: - most activity due to ST3Gal-1, low levels due to ST3Gal-2, -4 in vitro [Varki] - gene was cloned [Sasaki, J Biol Chem 1993], [Kitagawa, J Biol Chem 1994]
S23T3g	3	Kitagawa H, Paulson JC	Cloning and expression of human Gal beta 1,3(4)GlcNAc alpha 2,3-sialyltransferase	Biochem Biophys Res Commun	1993	8333853	- normally found in Golgi [RefSeq] - gene was cloned and expressed [Kitagawa, Biochem Biophys Res Commun 1993] - 91% similiarity w/ rat cDNA [Kitagawa, Biochem Biophys Res Commun 1993] - abundant in sk muscle & fetal tissues, low exp in placenta [Kitagawa, Biochem Biophys Res Commun 1993]
S23Tg	3	Shang J, Qiu R, Wang J, Liu J, Zhou R, Ding H, Yang S, Zhang S, Jin C	Molecular cloning and expression of Galbeta1,3GalNAc alpha2, 3-sialyltransferase from human fetal liver	Eur J Biochem	1999	10504389	- reaction described in Varki, pg 235 - gene was cloned and expressed [Shang, Eur J Biochem 1999] - found in Golgi [RefSeq], also inferred from author statement in [Shang, Eur J Biochem 1999] - Siat4ap expressed in placenta, liver, sk muscle [Kitagawa and Paulson, JBC 1994]
S26Tg	0	Kitagawa H, Paulson JC	Differential expression of five sialyltransferase genes in human tissues	J Biol Chem	1994	8027041	The protein encoded by SIAT1 is a type II membrane protein that catalyzes the transfer of sialic acid from CMP-sialic acid to galactose-containing substrates. The encoded protein, which is normally found in the Golgi but which can be proteolytically processed to a soluble form, is involved in the generation of the cell-surface carbohydrate determinants and differentiation antigens HB-6, CDw75, and CD76. This protein is a member of glycosyltransferase family 29. Three transcript variants encoding two different isoforms have been found for this gene. [RefSeq] Siat1p expressed in sk muscle, liver, placenta [Kitagawa and Paulson, JBC 1994]
S2T1g	3	Kobayashi M, Sugumaran G, Liu J, Shworak NW, Silbert JE, Rosenberg RD	Molecular cloning and characterization of a human uronyl 2-sulfotransferase that sulfates iduronyl and glucuronyl residues in dermatan/chondroitin sulfate	J Biol Chem	1999	10187838	- Golgi localization [Silbert, IUBMB LIfe 2002] - identified based on sequence homology to heparan sulfate IdA 6-sulfotransferase [Kobayashi, J Biol Chem 1999] - gene was cloned and expressed [Kobayashi, J Biol Chem 1999] - ubiquitously expressed [Kobayashi, J Biol Chem 1999] - substantial sulfotransferase activity w/ dermatan sulfate, small degree of activity w/ chondroitin sulfate [Kobayashi, J Biol Chem 1999]
S2T4g	3	Seki N, Ohira M, Nagase T, Ishikawa K, Miyajima N, Nakajima D, Nomura N, Ohara O	Characterization of cDNA clones in size-fractionated cDNA libraries from human brain.	DNA Res	1997	9455484	- 2-sulfation of IdoA and GlcA in heparan sulfate is catalyzed by the same enzyme [Rong, Biochem J 2000], but has higher affinity for transfer to IdoA [Sugahara, IUBMB Life 2002] - distinct from uronyl-2-O-sulfotransferase for synthesis of chondroitin and dermatan sulfate [Kobayashi, J Biol Chem 1999] - gene was identified via high-throughput study [Seki, DNA Res 1997]

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
S2T4g	3	Rong J, Habuchi H, Kimata K, Lindahl U, Kusche-Gullberg M	Expression of heparan sulphate L-iduronyl 2-O-sulphotransferase in human kidney 293 cells results in increased D-glucuronyl 2-O-sulphation	Biochem J	2000	10677367	- 2-sulfation of IdoA and GlcA in heparan sulfate is catalyzed by the same enzyme [Rong, Biochem J 2000], but has higher affinity for transfer to IdoA [Sugahara, IUBMB Life 2002] - distinct from uronyl-2-O-sulfotransferase for synthesis of chondroitin and dermatan sulfate [Kobayashi, J Biol Chem 1999] - gene was identified via high-throughput study [Seki, DNA Res 1997]
S2TASE1ly	3	Wilson PJ, Morris CP, Anson DS, Occhiodoro T, Bielicki J, Clements PR, Hopwood JJ	Hunter syndrome: isolation of an iduronate-2-sulfatase cDNA clone and analysis of patient DNA	Proc Natl Acad Sci U S A	1990	2122463	- hexuronic acids have to be desulfated before the hexuronidic linkage is hydrolyzed [Winchester 1996] 3423: - cloned isolated [Wilson 1990] - genomic sequence identified [Wilson 1993] - enzyme has been isolated from human placenta, serum, urine, liver (see refs in [Malmgren 1985]) - alternative transcript identified [Malmgren 1985])
S2TASE1ly	3	Wilson PJ, Meaney CA, Hopwood JJ, Morris CP	Sequence of the human iduronate 2-sulfatase (IDS) gene	Genomics	1993	8244397	- hexuronic acids have to be desulfated before the hexuronidic linkage is hydrolyzed [Winchester 1996] 3423: - cloned isolated [Wilson 1990] - genomic sequence identified [Wilson 1993] - enzyme has been isolated from human placenta, serum, urine, liver (see refs in [Malmgren 1985]) - alternative transcript identified [Malmgren 1985])
S2TASE1ly	3	Malmgren H, Carlberg BM, Pettersson U, Bondeson ML	dentification of an alternative transcript from the human iduronate-2-sulfatase (IDS) gene	Genomics	1995	8530090	- hexuronic acids have to be desulfated before the hexuronidic linkage is hydrolyzed [Winchester 1996] 3423: - cloned isolated [Wilson 1990] - genomic sequence identified [Wilson 1993] - enzyme has been isolated from human placenta, serum, urine, liver (see refs in [Malmgren 1985]) - alternative transcript identified [Malmgren 1985])
S2TASE4ly	3	Freeman C, Hopwood JJ	Human liver glucuronate 2-sulphatase. Purification, characterization and catalytic properties	Biochem J	1989	2497731	- hexuronic acids have to be desulfated before the hexuronidic linkage is hydrolyzed [Winchester 1996] - cultured human skin fibroblasts were shown to have glucuronate 2-sulfatase activity [Shaklee 1985] - glucuronate 2-sulfatase was purified from human liver, but it was unstable w/o the addition of BSA [Freeman 1989]
S2TASE4ly	3	Shaklee PN, Glaser JH, Conrad HE	A sulfatase specific for glucuronic acid 2-sulfate residues in glycosaminoglycans	J Biol Chem	1985	4019466	- hexuronic acids have to be desulfated before the hexuronidic linkage is hydrolyzed [Winchester 1996] - cultured human skin fibroblasts were shown to have glucuronate 2-sulfatase activity [Shaklee 1985] - glucuronate 2-sulfatase was purified from human liver, but it was unstable w/o the addition of BSA [Freeman 1989]
S3T1g	3	Shworak NW, Liu J, Fritze LM, Schwartz JJ, Zhang L, Logeart D, Rosenberg RD	Molecular cloning and expression of mouse and human cDNAs encoding heparan sulfate D-glucosaminyl 3-O-sulfotransferase	J Biol Chem	1997	9346953	9957: - Golgi [RefSeq], [Shworak, J Biol Chem 1997] - cDNA was cloned; protein has 93% similarity to mouse homolog [Shworak, J Biol Chem 1997] - expressed highly in kidney and brain, intermediately in heart and lung, and lowly in other tissues [Shworak, J Biol Chem 1999], [Sugahara, IUBMB Life 2002] - transfers sulfate to C3 position of NSGlcNAc and NSGLcNAc(6S) adjacent to the reducing side of GlcA [Sugahara, IUBMB Life 2002] 222537: - cDNA was isolated and expressed [Xia, J Biol Chem 2002] - major products of recombinantly expressed protein were: DeltaHexA-GlcN(NS,3S,6S), DeltaHexA(2S)-GlcN(NS,3S), and DeltaHexA(2S)-GlcN(NS,3S,6S) [Mochizuki, J Biol Chem 2003], [Sugahara, IUBMB Life 2002] - highly expressed in fetal brain, adult brain and spinal cord, low or undetectable in other tissues [Mochizuki, J Biol Chem 2003] 9951: - partial length clone identified (incomplete coding sequence) [Shworak, J Biol Chem 1999] - exclusively expressed in brain [Shworak, J Biol Chem 1999]

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
S3T1g	3	Shworak NW, Liu J, Petros LM, Zhang L, Kobayashi M, Copeland NG, Jenkins NA, Rosenberg RD	Multiple isoforms of heparan sulfate D-glucosaminyl 3-O-sulfotransferase. Isolation, characterization, and expression of human cdnas and identification of distinct genomic loci	J Biol Chem	1999	9988767	9957: - Golgi [RefSeq], [Shworak, J Biol Chem 1997] - cDNA was cloned; protein has 93% similarity to mouse homolog [Shworak, J Biol Chem 1997] - expressed highly in kidney and brain, intermediately in heart and lung, and lowly in other tissues [Shworak, J Biol Chem 1999], [Sugahara, IUBMB Life 2002] - transfers sulfate to C3 position of NSGlcNAc and NSGLcNAc(6S) adjacent to the reducing side of GlcA [Sugahara, IUBMB Life 2002] 222537: - cDNA was isolated and expressed [Xia, J Biol Chem 2002] - major products of recombinantly expressed protein were: DeltaHexA-GlcN(NS,3S,6S), DeltaHexA(2S)-GlcN(NS,3S), and DeltaHexA(2S)-GlcN(NS,3S,6S) [Mochizuki, J Biol Chem 2003], [Sugahara, IUBMB Life 2002] - highly expressed in fetal brain, adult brain and spinal cord, low or undetectable in other tissues [Mochizuki, J Biol Chem 2003] 9951: - partial length clone identified (incomplete coding sequence) [Shworak, J Biol Chem 1999] - exclusively expressed in brain [Shworak, J Biol Chem 1999]
S3T1g	3	Xia G, Chen J, Tiwari V, Ju W, Li JP, Malmstrom A, Shukla D, Liu J	Heparan sulfate 3-O-sulfotransferase isoform 5 generates both an antithrombin-binding site and an entry receptor for herpes simplex virus, type 1	J Biol Chem	2002	12138164	9957: - Golgi [RefSeq], [Shworak, J Biol Chem 1997] - cDNA was cloned; protein has 93% similarity to mouse homolog [Shworak, J Biol Chem 1997] - expressed highly in kidney and brain, intermediately in heart and lung, and lowly in other tissues [Shworak, J Biol Chem 1999], [Sugahara, IUBMB Life 2002] - transfers sulfate to C3 position of NSGlcNAc and NSGLcNAc(6S) adjacent to the reducing side of GlcA [Sugahara, IUBMB Life 2002] 222537: - cDNA was isolated and expressed [Xia, J Biol Chem 2002] - major products of recombinantly expressed protein were: DeltaHexA-GlcN(NS,3S,6S), DeltaHexA(2S)-GlcN(NS,3S), and DeltaHexA(2S)-GlcN(NS,3S,6S) [Mochizuki, J Biol Chem 2003], [Sugahara, IUBMB Life 2002] - highly expressed in fetal brain, adult brain and spinal cord, low or undetectable in other tissues [Mochizuki, J Biol Chem 2003] 9951: - partial length clone identified (incomplete coding sequence) [Shworak, J Biol Chem 1999] - exclusively expressed in brain [Shworak, J Biol Chem 1999]
S3T1g	3	Mochizuki H, Yoshida K, Gotoh M, Sugioka S, Kikuchi N, Kwon YD, Tawada A, Maeyama K, Inaba N, Hiruma T, Kimata K, Narimatsu H	Characterization of a heparan sulfate 3-O-sulfotransferase-5, an enzyme synthesizing a tetrasulfated disaccharide	J Biol Chem	2003	12740361	9957: - Golgi [RefSeq], [Shworak, J Biol Chem 1997] - cDNA was cloned; protein has 93% similarity to mouse homolog [Shworak, J Biol Chem 1997] - expressed highly in kidney and brain, intermediately in heart and lung, and lowly in other tissues [Shworak, J Biol Chem 1999], [Sugahara, IUBMB Life 2002] - transfers sulfate to C3 position of NSGlcNAc and NSGLcNAc(6S) adjacent to the reducing side of GlcA [Sugahara, IUBMB Life 2002] 222537: - cDNA was isolated and expressed [Xia, J Biol Chem 2002] - major products of recombinantly expressed protein were: DeltaHexA-GlcN(NS,3S,6S), DeltaHexA(2S)-GlcN(NS,3S), and DeltaHexA(2S)-GlcN(NS,3S,6S) [Mochizuki, J Biol Chem 2003], [Sugahara, IUBMB Life 2002] - highly expressed in fetal brain, adult brain and spinal cord, low or undetectable in other tissues [Mochizuki, J Biol Chem 2003] 9951: - partial length clone identified (incomplete coding sequence) [Shworak, J Biol Chem 1999] - exclusively expressed in brain [Shworak, J Biol Chem 1999]

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
S3T2g	3	Liu J, Shworak NW, Sinay P, Schwartz JJ, Zhang L, Fritze LM, Rosenberg RD	Expression of heparan sulfate D-glucosaminyl 3-O-sulfotransferase isoforms reveals novel substrate specificities	J Biol Chem	1999	9988768	222537: - cDNA was isolated and expressed [Xia, J Biol Chem 2002] - major products of recombinantly expressed protein were: DeltaHexA-GlcN(NS,3S,6S), DeltaHexA(2S)-GlcN(NS,3S), and DeltaHexA(2S)-GlcN(NS,3S,6S) [Mochizuki, J Biol Chem 2003], [Sugahara, IUBMB Life 2002] - highly expressed in fetal brain, adult brain and spinal cord, low or undetectable in other tissues [Mochizuki, J Biol Chem 2003] 9956: - cDNA was isolated, characterized, and expressed [Shworak, J Biol Chem 1999] - predominantly expressed in the brain, low expression in heart and placenta [Shworak, J Biol Chem 1999] - transfers sulfate to C3 position of GlcA2S-GlcNS and IdoA2S-GlcNS [Liu, J Biol Chem 1999], [Sugahara, IUBMB Life 2002] 9951: - partial length clone identified (incomplete coding sequence) [Shworak, J Biol Chem 1999] - exclusively expressed in brain [Shworak, J Biol Chem 1999] 9953:
S3T3g	3	Liu J, Shriver Z, Blaiklock P, Yoshida K, Sasisekharan R, Rosenberg RD	Heparan sulfate D-glucosaminyl 3-O-sulfotransferase 3A sulfates N-unsubstituted glucosamine residues	J Biol Chem	1999	10608887	- cDNA was isolated, characterized, and expressed [Shworak, J Biol Chem 1999] - highly expressed in heart and placenta, moderately expressed in liver and kidney, lowly expressed in lung and pancreas [Shworak, J Biol Chem 1999] - transfers sulfate to C3 position of IdoA2S-GlcNH2 [Liu, J Biol Chem 1999], [Liu, J Biol Chem 1999], [Sugahara, J Biol Chem 2002] 9954: - cDNA was isolated and expressed [Shworak, J Biol Chem 1999] - functionality remains to be established [Shworak, J Biol Chem 1999]; assumed to have same functionality as HS3ST3A1 9953: - cDNA was isolated, characterized, and expressed [Shworak, J Biol Chem 1999] - highly expressed in placenta and liver, moderately expressed in heart, kidney, and pancreas, lowly expressed in brain, lung, skeletal muscle [Shworak, J Biol Chem 1999] - transfers sulfate to C3 position of IdoA2S-GlcNH2 [Sugahara, IUBMB Life 2002] 9952: - cDNA was isolated and expressed [Shworak, J Biol Chem 1999] - functionality remains to be established [Shworak, J Biol Chem 1999]; assumed to have same functionality as HS3ST3B1 64711:
S3T3g	3	Xu D, Tiwari V, Xia G, Clement C, Shukla D, Liu J	Characterization of heparan sulphate 3-O-sulphotransferase isoform 6 and its role in assisting the entry of herpes simplex virus type 1	Biochem J	2005	15303968	9953: - cDNA was isolated, characterized, and expressed [Shworak, J Biol Chem 1999] - highly expressed in heart and placenta, moderately expressed in liver and kidney, lowly expressed in lung and pancreas [Shworak, J Biol Chem 1999] - transfers sulfate to C3 position of IdoA2S-GlcNH2 [Liu, J Biol Chem 1999], [Liu, J Biol Chem 1999], [Sugahara, J Biol Chem 2002] 9954: - cDNA was isolated and expressed [Shworak, J Biol Chem 1999] - functionality remains to be established [Shworak, J Biol Chem 1999]; assumed to have same functionality as HS3ST3A1 9953: - cDNA was isolated, characterized, and expressed [Shworak, J Biol Chem 1999] - highly expressed in placenta and liver, moderately expressed in heart, kidney, and pancreas, lowly expressed in brain, lung, skeletal muscle [Shworak, J Biol Chem 1999] - transfers sulfate to C3 position of IdoA2S-GlcNH2 [Sugahara, IUBMB Life 2002] 9952: - cDNA was isolated and expressed [Shworak, J Biol Chem 1999] - functionality remains to be established [Shworak, J Biol Chem 1999]; assumed to have same functionality as HS3ST3B1 64711:
S3TASE3ly	2	Leder IG	A novel 3-O sulfatase from human urine acting on methyl-2-deoxy-2-sulfamino-alphs-D-glucopyranoside 3-sulfate	Biochem Biophys Res Commun	1980	7396957	- heparan sulfate contains a small amount of glucosamine O-sulfated at the C3 position, but it is not known which sulfatase is responsible for the hydrolysis of this sulfate ester [Winchester 1996] - the 3-O-sulfatase described by [Leder 1980] would not function on this residue since it is not N-sulfated

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
S4T1g	3	Evers MR, Xia G, Kang HG, Schachner M, Baenziger JU	Molecular cloning and characterization of a dermatan specific N-acetylgalactosamine 4-O-sulfotransferase	J Biol Chem	2001	1147079	- Golgi localization [Silbert, IUBMB LIfe 2002] - sulfation of Gal residues may be catalyzed byt the same sulfotransferases that add sulfate to GalNAc of chondroitin [Silbert, IUBMB LIfe 2002] 50515: - gene was cloned [Yamauchi, J Biol Chem 2000], [Okuda, J Biochem (Tokyo) 2000], [Hiraoka, J Biol Chem 2000] - protein has 29% identity and 48% similarity to rat protein [Yamauchi, J Biol Chem 2000], 96% similarity to mouse protein [Okuda, J Biochem (Tokyo) 2000] - expressed ubiquitously [Okuda, J Biochem (Tokyo) 2000]; mainly expressed in brain and kidney [Yamauchi, J Biol Chem 2000]; predominantly expressed in peripheral leukocytes and hematopoietic tissues [Hiraoka, J Biol Chem 2000] - 4-sulfotransferase activity verified for chondroitin sulfate and desulfated dermatan sulfate [Yamauchi, J Biol Chem 2000], [Okuda, J Biochem (Tokyo) 2000] 55501: - gene was cloned and expressed [Hiraoka, J Biol Chem 2000] - widely expressed in various tissues [Hiraoka, J Biol Chem 2000] 166012: - gene was identified based on sequence homology with other HNK-1 family members; was cloned and expressed [Kang, J Bi - expressed in adult liver and at lower levels in adult kidney, lyn - similar specificty to C4ST-1 [Kang, J Biol Chem 2002] 113189: - identified based on sequence homology to HNK-1 family [Eve - transfers sulfate to 4 position of GalNAc that is next to IdoA - sulfation occurs after epimerization of GlcA to IdoA [Evers, J
S4T1g	3	Yamauchi S, Mita S, Matsubara T, Fukuta M, Habuchi H, Kimata K, Habuchi O	Molecular cloning and expression of chondroitin 4-sulfotransferase	J Biol Chem	2000	10722746	- Golgi localization [Silbert, IUBMB LIfe 2002] - sulfation of Gal residues may be catalyzed byt the same sulfotransferases that add sulfate to GalNAc of chondroitin [Silbert, IUBMB LIfe 2002] 50515: - gene was cloned [Yamauchi, J Biol Chem 2000], [Okuda, J Biochem (Tokyo) 2000], [Hiraoka, J Biol Chem 2000] - protein has 29% identity and 48% similarity to rat protein [Yamauchi, J Biol Chem 2000], 96% similarity to mouse protein [Okuda, J Biochem (Tokyo) 2000] - expressed ubiquitously [Okuda, J Biochem (Tokyo) 2000]; mainly expressed in brain and kidney [Yamauchi, J Biol Chem 2000]; predominantly expressed in peripheral leukocytes and hematopoietic tissues [Hiraoka, J Biol Chem 2000] - 4-sulfotransferase activity verified for chondroitin sulfate and desulfated dermatan sulfate [Yamauchi, J Biol Chem 2000], [Okuda, J Biochem (Tokyo) 2000] 55501: - gene was cloned and expressed [Hiraoka, J Biol Chem 2000] - widely expressed in various tissues [Hiraoka, J Biol Chem 2000] 166012: - gene was identified based on sequence homology with other HNK-1 family members; was cloned and expressed [Kang, J Bi - expressed in adult liver and at lower levels in adult kidney, lyn - similar specificty to C4ST-1 [Kang, J Biol Chem 2002] 113189: - identified based on sequence homology to HNK-1 family [Eve - transfers sulfate to 4 position of GalNAc that is next to IdoA - sulfation occurs after epimerization of GlcA to IdoA [Evers, J
S4T1g	3	Hiraoka N, Nakagawa H, Ong E, Akama TO, Fukuda MN, Fukuda M	Molecular cloning and expression of two distinct human chondroitin 4-O-sulfotransferases that belong to the HNK-1 sulfotransferase gene family	J Biol Chem	2000	10781601	- Golgi localization [Silbert, IUBMB LIfe 2002] - sulfation of Gal residues may be catalyzed byt the same sulfotransferases that add sulfate to GalNAc of chondroitin [Silbert, IUBMB LIfe 2002] 50515: - gene was cloned [Yamauchi, J Biol Chem 2000], [Okuda, J Biochem (Tokyo) 2000], [Hiraoka, J Biol Chem 2000] - protein has 29% identity and 48% similarity to rat protein [Yamauchi, J Biol Chem 2000], 96% similarity to mouse protein [Okuda, J Biochem (Tokyo) 2000] - expressed ubiquitously [Okuda, J Biochem (Tokyo) 2000]; mainly expressed in brain and kidney [Yamauchi, J Biol Chem 2000]; predominantly expressed in peripheral leukocytes and hematopoietic tissues [Hiraoka, J Biol Chem 2000] - 4-sulfotransferase activity verified for chondroitin sulfate and desulfated dermatan sulfate [Yamauchi, J Biol Chem 2000], [Okuda, J Biochem (Tokyo) 2000] 55501: - gene was cloned and expressed [Hiraoka, J Biol Chem 2000] - widely expressed in various tissues [Hiraoka, J Biol Chem 2000] 166012: - gene was identified based on sequence homology with other HNK-1 family members; was cloned and expressed [Kang, J Bi - expressed in adult liver and at lower levels in adult kidney, lyn - similar specificty to C4ST-1 [Kang, J Biol Chem 2002] 113189: - identified based on sequence homology to HNK-1 family [Eve - transfers sulfate to 4 position of GalNAc that is next to IdoA - sulfation occurs after epimerization of GlcA to IdoA [Evers, J

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S4T1g	3	Okuda T, Mita S, Yamauchi S, Matsubara T, Yagi F, Yamamori D, Fukuta M, Kuroiwa A, Matsuda Y, Habuchi O	Molecular cloning, expression, and chromosomal mapping of human chondroitin 4-sulfotransferase, whose expression pattern in human tissues is different from that of chondroitin 6-sulfotransferase	J Biochem (Tokyo)	2000	11056388	- Golgi localization [Silbert, IUBMB LIfe 2002] - sulfation of Gal residues may be catalyzed byt the same sulfotransferases that add sulfate to GalNAc of chondroitin [Silbert, IUBMB LIfe 2002] 50515: - gene was cloned [Yamauchi, J Biol Chem 2000], [Okuda, J Biochem (Tokyo) 2000], [Hiraoka, J Biol Chem 2000] - protein has 29% identity and 48% similarity to rat protein [Yamauchi, J Biol Chem 2000], 96% similarity to mouse protein [Okuda, J Biochem (Tokyo) 2000] - expressed ubiquitously [Okuda, J Biochem (Tokyo) 2000]; mainly expressed in brain and kidney [Yamauchi, J Biol Chem 2000]; predominantly expressed in peripheral leukocytes and hematopoietic tissues [Hiraoka, J Biol Chem 2000] - 4-sulfotransferase activity verified for chondroitin sulfate and desulfated dermatan sulfate [Yamauchi, J Biol Chem 2000], [Okuda, J Biochem (Tokyo) 2000] 55501: - gene was cloned and expressed [Hiraoka, J Biol Chem 2000] - widely expressed in various tissues [Hiraoka, J Biol Chem 2000] 166012: - gene was identified based on sequence homology with other HNK-1 family members; was cloned and expressed [Kang, J Bi - expressed in adult liver and at lower levels in adult kidney, lyn - similar specificty to C4ST-1 [Kang, J Biol Chem 2002] 113189: - identified based on sequence homology to HNK-1 family [Eve - transfers sulfate to 4 position of GalNAc that is next to IdoA - sulfation occurs after epimerization of GlcA to IdoA [Evers, J
S4T1g	3	Kang HG, Evers MR, Xia G, Baenziger JU, Schachner M	Molecular cloning and characterization of chondroitin-4-O-sulfotransferase-3. A novel member of the HNK-1 family of sulfotransferases	J Biol Chem	2002	12080076	- Golgi localization [Silbert, IUBMB LIfe 2002] - sulfation of Gal residues may be catalyzed byt the same sulfotransferases that add sulfate to GalNAc of chondroitin [Silbert, IUBMB LIfe 2002] 50515: - gene was cloned [Yamauchi, J Biol Chem 2000], [Okuda, J Biochem (Tokyo) 2000], [Hiraoka, J Biol Chem 2000] - protein has 29% identity and 48% similarity to rat protein [Yamauchi, J Biol Chem 2000], 96% similarity to mouse protein [Okuda, J Biochem (Tokyo) 2000] - expressed ubiquitously [Okuda, J Biochem (Tokyo) 2000]; mainly expressed in brain and kidney [Yamauchi, J Biol Chem 2000]; predominantly expressed in peripheral leukocytes and hematopoietic tissues [Hiraoka, J Biol Chem 2000] - 4-sulfotransferase activity verified for chondroitin sulfate and desulfated dermatan sulfate [Yamauchi, J Biol Chem 2000], [Okuda, J Biochem (Tokyo) 2000] 55501: - gene was cloned and expressed [Hiraoka, J Biol Chem 2000] - widely expressed in various tissues [Hiraoka, J Biol Chem 2000] 166012: - gene was identified based on sequence homology with other HNK-1 family members; was cloned and expressed [Kang, J Bi - expressed in adult liver and at lower levels in adult kidney, lyn - similar specificty to C4ST-1 [Kang, J Biol Chem 2002] 113189: - identified based on sequence homology to HNK-1 family [Eve - transfers sulfate to 4 position of GalNAc that is next to IdoA - sulfation occurs after epimerization of GlcA to IdoA [Evers, J
S4T1g	3	Mikami T, Mizumoto S, Kago N, Kitagawa H, Sugahara K.	Specificities of three distinct human chondroitin/dermatan N-acetylgalactosamine 4-O-sulfotransferases demonstrated using partially desulfated dermatan sulfate as an acceptor: implication of differential roles in dermatan sulfate biosynthesis.	J Biol Chem	2003	12847091	- Golgi localization [Silbert, IUBMB LIfe 2002] - sulfation of Gal residues may be catalyzed byt the same sulfotransferases that add sulfate to GalNAc of chondroitin [Silbert, IUBMB LIfe 2002] 50515: - gene was cloned [Yamauchi, J Biol Chem 2000], [Okuda, J Biochem (Tokyo) 2000], [Hiraoka, J Biol Chem 2000] - protein has 29% identity and 48% similarity to rat protein [Yamauchi, J Biol Chem 2000], 96% similarity to mouse protein [Okuda, J Biochem (Tokyo) 2000] - expressed ubiquitously [Okuda, J Biochem (Tokyo) 2000]; mainly expressed in brain and kidney [Yamauchi, J Biol Chem 2000]; predominantly expressed in peripheral leukocytes and hematopoietic tissues [Hiraoka, J Biol Chem 2000] - 4-sulfotransferase activity verified for chondroitin sulfate and desulfated dermatan sulfate [Yamauchi, J Biol Chem 2000], [Okuda, J Biochem (Tokyo) 2000] 55501: - gene was cloned and expressed [Hiraoka, J Biol Chem 2000] - widely expressed in various tissues [Hiraoka, J Biol Chem 2000] 166012: - gene was identified based on sequence homology with other HNK-1 family members; was cloned and expressed [Kang, J Bi - expressed in adult liver and at lower levels in adult kidney, lyn - similar specificty to C4ST-1 [Kang, J Biol Chem 2002] 113189: - identified based on sequence homology to HNK-1 family [Eve - transfers sulfate to 4 position of GalNAc that is next to IdoA - sulfation occurs after epimerization of GlcA to IdoA [Evers, J

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S4TASE1ly	3	Schuchman EH, Jackson CE, Desnick RJ	Human arylsulfatase B: MOPAC cloning, nucleotide sequence of a full-length cDNA, and regions of amino acid identity with arylsulfatases A and C	Genomics	1990	1968043	411: - hydrolyzes sulfate groups of GalNAc in chondroitin sulfate and dermatan sulfate [RefSeq] - lysosomal [RefSeq], [Peters 1990] - isolated from hepatoma cell cDNA library; seq used to isolate ORF from human testis library [Schuchman 1990] - isolated and overexpressed in baby hamster kidney cellls [Peters 1990]
S4TASE1ly	3	Peters C, Schmidt B, Rommerskirch W, Rupp K, Zuhlsdorf M, Vingron M, Meyer HE, Pohlmann R, von Figura K	Phylogenetic conservation of arylsulfatases. cDNA cloning and expression of human arylsulfatase B.	J Biol Chem	1990	2303452	411: - hydrolyzes sulfate groups of GalNAc in chondroitin sulfate and dermatan sulfate [RefSeq] - lysosomal [RefSeq], [Peters 1990] - isolated from hepatoma cell cDNA library; seq used to isolate ORF from human testis library [Schuchman 1990] - isolated and overexpressed in baby hamster kidney cellls [Peters 1990]
S6T19g	3	Tsutsumi K, Shimakawa H, Kitagawa H, Sugahara K	Functional expression and genomic structure of human chondroitin 6-sulfotransferase	FEBS Lett	1998	9883891	- Golgi localization [Silbert, IUBMB LIfe 2002] - sulfation of Gal residues may be catalyzed byt the same sulfotransferases that add sulfate to GalNAc of chondroitin [Silbert, IUBMB LIfe 2002] 9469: - Golgi [UniProt] - gene identified and cDNA isolated, has 74% identity to chick ortholog [Fukuda, Biochim Biophys Acta 1998] - highly expressed in sk muscle, lower levels in heart, placenta, pancreas [Fukuda, Biochim Biophys Acta 1998] - keratan sulfate was sulfated by C6ST at position 6 of Gal residues [Habuchi, Glycobiology 1996] - sulfates GalNAc residues in GlcAGalNAc disaccharides, but not IdoAGalNAc or GlcAGalNAc4S [Tsutsumi, FEBS Lett 1998] 56548: - gene identified by BLAST [Kitagawa, J Biol Chem 2000], [Bhakta, J Biol Chem 2000] - gene was cloned and expressed [Kitagawa, J Biol Chem 2000], [Uchimura, Biochem Biophys Res Commun 2000], [Bhakta, J Biol Chem 2000] - predominant activity is 6-sulfation of GalNAc in chondroitin, little to no activity w/ keratan sulfate [Kitagawa, J Biol Chem 2000] - expression varied during development, persisted through adulthood in spleen [Kitagawa, J Biol Chem 2000], primarily in
S6T19g	3	Kitagawa H, Fujita M, Ito N, Sugahara K	Molecular cloning and expression of a novel chondroitin 6-O-sulfotransferase	J Biol Chem	2000	10781596	- Golgi localization [Silbert, IUBMB LIfe 2002] - sulfation of Gal residues may be catalyzed byt the same sulfotransferases that add sulfate to GalNAc of chondroitin [Silbert, IUBMB LIfe 2002] 9469: - Golgi [UniProt] - gene identified and cDNA isolated, has 74% identity to chick ortholog [Fukuda, Biochim Biophys Acta 1998] - highly expressed in sk muscle, lower levels in heart, placenta, pancreas [Fukuda, Biochim Biophys Acta 1998] - keratan sulfate was sulfated by C6ST at position 6 of Gal residues [Habuchi, Glycobiology 1996] - sulfates GalNAc residues in GlcAGalNAc disaccharides, but not IdoAGalNAc or GlcAGalNAc4S [Tsutsumi, FEBS Lett 1998] 56548: - gene identified by BLAST [Kitagawa, J Biol Chem 2000], [Bhakta, J Biol Chem 2000] - gene was cloned and expressed [Kitagawa, J Biol Chem 2000], [Uchimura, Biochem Biophys Res Commun 2000], [Bhakta, J Biol Chem 2000] - predominant activity is 6-sulfation of GalNAc in chondroitin, little to no activity w/ keratan sulfate [Kitagawa, J Biol Chem 2000] - expression varied during development, persisted through adulthood in spleen [Kitagawa, J Biol Chem 2000], primarily in

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S6T19g	3	Bhakta S, Bartes A, Bowman KG, Kao WM, Polsky I, Lee JK, Cook BN, Bruehl RE, Rosen SD, Bertozzi CR, Hemmerich S	Sulfation of N-acetylglucosamine by chondroitin 6-sulfotransferase 2 (GST-5)	J Biol Chem	2000	10956661	- Golgi localization [Silbert, IUBMB LIfe 2002] - sulfation of Gal residues may be catalyzed byt the same sulfotransferases that add sulfate to GalNAc of chondroitin [Silbert, IUBMB LIfe 2002] 9469: - Golgi [UniProt] - gene identified and cDNA isolated, has 74% identity to chick ortholog [Fukuda, Biochim Biophys Acta 1998] - highly expressed in sk muscle, lower levels in heart, placenta, pancreas [Fukuda, Biochim Biophys Acta 1998] - keratan sulfate was sulfated by C6ST at position 6 of Gal residues [Habuchi, Glycobiology 1996] - sulfates GalNAc residues in GlcAGalNAc disaccharides, but not IdoAGalNAc or GlcAGalNAc4S [Tsutsumi, FEBS Lett 1998] 56548: - gene identified by BLAST [Kitagawa, J Biol Chem 2000], [Bhakta, J Biol Chem 2000] - gene was cloned and expressed [Kitagawa, J Biol Chem 2000], [Uchimura, Biochem Biophys Res Commun 2000], [Bhakta, J Biol Chem 2000] - predominant activity is 6-sulfation of GalNAc in chondroitin, little to no activity w/ keratan sulfate [Kitagawa, J Biol Chem 2000] - expression varied during development, persisted through adulthood in spleen [Kitagawa, J Biol Chem 2000], primarily in
S6T1g	3	Uchimura K, Muramatsu H, Kaname T, Ogawa H, Yamakawa T, Fan QW, Mitsuoka C, Kannagi R, Habuchi O, Yokoyama I, Yamamura K, Ozaki T, Nakagawara A, Kadomatsu K, Muramatsu T	Human N-acetylglucosamine-6-O-sulfotransferase involved in the biosynthesis of 6-sulfo sialyl Lewis X: molecular cloning, chromosomal mapping, and expression in various organs and tumor cells	J Biochem (Tokyo)	1998	9722682	- refs, substrate specificity, and tissue distribution of GlcNac/Gal-6-O-sulfotransferases [Grunwell, Biochemistry 2002] 4166: - gene was cloned [Uchimura, Biochem Biophys Res Commun 2000] and biochemically characterized [Akama, J Biol Chem 2001] - highly expressed in heart, spleen, and ovary [Uchimura, Biochem Biophys Res Commun 2000] 9435: - Golgi [de Graffenried, J Biol Chem 2003] - gene was identified and cloned, 99% identical to mouse ortholog [Uchimura, J Biochem (Tokyo) 1998] - strongly expressed in the bone marrow, peripheral blood leukocytes, spleen, brain, spinal cord, ovary, and placenta, and moderately expressed in many organs including lymph nodes and thymus [Uchimura, J Biochem (Tokyo) 1998] 10164: - Golgi [de Graffenried, J Biol Chem 2003] - gene was cloned [Bistrup, J Cell Biol 1999] 23563: - Golgi [de Graffenried, J Biol Chem 2003] - gene was cloned and characterized [Lee Biochem Biophys Res Commun 1999] - expressed in small intestine and colon [Lee Biochem Biophys Res Commun 1999]
S6T1g	3	Bistrup A, Bhakta S, Lee JK, Belov YY, Gunn MD, Zuo FR, Huang CC, Kannagi R, Rosen SD, Hemmerich S	Sulfotransferases of two specificities function in the reconstitution of high endothelial cell ligands for L-selectin	J Cell Biol	1999	10330415	- refs, substrate specificity, and tissue distribution of GlcNac/Gal-6-O-sulfotransferases [Grunwell, Biochemistry 2002] 4166: - gene was cloned [Uchimura, Biochem Biophys Res Commun 2000] and biochemically characterized [Akama, J Biol Chem 2001] - highly expressed in heart, spleen, and ovary [Uchimura, Biochem Biophys Res Commun 2000] 9435: - Golgi [de Graffenried, J Biol Chem 2003] - gene was identified and cloned, 99% identical to mouse ortholog [Uchimura, J Biochem (Tokyo) 1998] - strongly expressed in the bone marrow, peripheral blood leukocytes, spleen, brain, spinal cord, ovary, and placenta, and moderately expressed in many organs including lymph nodes and thymus [Uchimura, J Biochem (Tokyo) 1998] 10164: - Golgi [de Graffenried, J Biol Chem 2003] - gene was cloned [Bistrup, J Cell Biol 1999] 23563: - Golgi [de Graffenried, J Biol Chem 2003] - gene was cloned and characterized [Lee Biochem Biophys Res Commun 1999] - expressed in small intestine and colon [Lee Biochem Biophys Res Commun 1999]

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S6T1g	3	Lee JK, Bhakta S, Rosen SD, Hemmerich S	Cloning and characterization of a mammalian N-acetylglucosamine-6-sulfotransferase that is highly restricted to intestinal tissue	Biochem Biophys Res Commun	1999	10491328	- refs, substrate specificity, and tissue distribution of GlcNac/Gal-6-O-sulfotransferases [Grunwell, Biochemistry 2002] 4166: - gene was cloned [Uchimura, Biochem Biophys Res Commun 2000] and biochemically characterized [Akama, J Biol Chem 2001] - highly expressed in heart, spleen, and ovary [Uchimura, Biochem Biophys Res Commun 2000] 9435: - Golgi [de Graffenried, J Biol Chem 2003] - gene was identified and cloned, 99% identical to mouse ortholog [Uchimura, J Biochem (Tokyo) 1998] - strongly expressed in the bone marrow, peripheral blood leukocytes, spleen, brain, spinal cord, ovary, and placenta, and moderately expressed in many organs including lymph nodes and thymus [Uchimura, J Biochem (Tokyo) 1998] 10164: - Golgi [de Graffenried, J Biol Chem 2003] - gene was cloned [Bistrup, J Cell Biol 1999] 23563: - Golgi [de Graffenried, J Biol Chem 2003] - gene was cloned and characterized [Lee Biochem Biophys Res Commun 1999] - expressed in small intestine and colon [Lee Biochem Biophys Res Commun 1999]
S6T1g	3	Uchimura K, Fasakhany F, Kadomatsu K, Matsukawa T, Yamakawa T, Kurosawa N, Muramatsu T	Diversity of N-acetylglucosamine-6-O-sulfotransferases: molecular cloning of a novel enzyme with different distribution and specificities	Biochem Biophys Res Commun	2000	10913333	- refs, substrate specificity, and tissue distribution of GlcNac/Gal-6-O-sulfotransferases [Grunwell, Biochemistry 2002] 4166: - gene was cloned [Uchimura, Biochem Biophys Res Commun 2000] and biochemically characterized [Akama, J Biol Chem 2001] - highly expressed in heart, spleen, and ovary [Uchimura, Biochem Biophys Res Commun 2000] 9435: - Golgi [de Graffenried, J Biol Chem 2003] - gene was identified and cloned, 99% identical to mouse ortholog [Uchimura, J Biochem (Tokyo) 1998] - strongly expressed in the bone marrow, peripheral blood leukocytes, spleen, brain, spinal cord, ovary, and placenta, and moderately expressed in many organs including lymph nodes and thymus [Uchimura, J Biochem (Tokyo) 1998] 10164: - Golgi [de Graffenried, J Biol Chem 2003] - gene was cloned [Bistrup, J Cell Biol 1999] 23563: - Golgi [de Graffenried, J Biol Chem 2003] - gene was cloned and characterized [Lee Biochem Biophys Res Commun 1999] - expressed in small intestine and colon [Lee Biochem Biophys Res Commun 1999]
S6T1g	3	Akama TO, Nakayama J, Nishida K, Hiraoka N, Suzuki M, McAuliffe J, Hindsgaul O, Fukuda M, Fukuda MN	Human corneal GlcNac 6-O-sulfotransferase and mouse intestinal GlcNac 6-O-sulfotransferase both produce keratan sulfate	J Biol Chem	2001	11278593	- refs, substrate specificity, and tissue distribution of GlcNac/Gal-6-O-sulfotransferases [Grunwell, Biochemistry 2002] 4166: - gene was cloned [Uchimura, Biochem Biophys Res Commun 2000] and biochemically characterized [Akama, J Biol Chem 2001] - highly expressed in heart, spleen, and ovary [Uchimura, Biochem Biophys Res Commun 2000] 9435: - Golgi [de Graffenried, J Biol Chem 2003] - gene was identified and cloned, 99% identical to mouse ortholog [Uchimura, J Biochem (Tokyo) 1998] - strongly expressed in the bone marrow, peripheral blood leukocytes, spleen, brain, spinal cord, ovary, and placenta, and moderately expressed in many organs including lymph nodes and thymus [Uchimura, J Biochem (Tokyo) 1998] 10164: - Golgi [de Graffenried, J Biol Chem 2003] - gene was cloned [Bistrup, J Cell Biol 1999] 23563: - Golgi [de Graffenried, J Biol Chem 2003] - gene was cloned and characterized [Lee Biochem Biophys Res Commun 1999] - expressed in small intestine and colon [Lee Biochem Biophys Res Commun 1999]

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S6T1g	3	Grunwell JR, Bertozzi CR	Carbohydrate sulfotransferases of the GalNAc/Gal/GlcNAc6ST family	Biochemistry	2002	12403612	- refs, substrate specificity, and tissue distribution of GlcNac/Gal-6-O-sulfotransferases [Grunwell, Biochemistry 2002] 4166: - gene was cloned [Uchimura, Biochem Biophys Res Commun 2000] and biochemically characterized [Akama, J Biol Chem 2001] - highly expressed in heart, spleen, and ovary [Uchimura, Biochem Biophys Res Commun 2000] 9435: - Golgi [de Graffenried, J Biol Chem 2003] - gene was identified and cloned, 99% identical to mouse ortholog [Uchimura, J Biochem (Tokyo) 1998] - strongly expressed in the bone marrow, peripheral blood leukocytes, spleen, brain, spinal cord, ovary, and placenta, and moderately expressed in many organs including lymph nodes and thymus [Uchimura, J Biochem (Tokyo) 1998] 10164: - Golgi [de Graffenried, J Biol Chem 2003] - gene was cloned [Bistrup, J Cell Biol 1999] 23563: - Golgi [de Graffenried, J Biol Chem 2003] - gene was cloned and characterized [Lee Biochem Biophys Res Commun 1999] - expressed in small intestine and colon [Lee Biochem Biophys Res Commun 1999]
S6T1g	3	de Graffenried CL, Bertozzi CR	Golgi localization of carbohydrate sulfotransferases is a determinant of L-selectin ligand biosynthesis	J Biol Chem	2003	12855678	- refs, substrate specificity, and tissue distribution of GlcNac/Gal-6-O-sulfotransferases [Grunwell, Biochemistry 2002] 4166: - gene was cloned [Uchimura, Biochem Biophys Res Commun 2000] and biochemically characterized [Akama, J Biol Chem 2001] - highly expressed in heart, spleen, and ovary [Uchimura, Biochem Biophys Res Commun 2000] 9435: - Golgi [de Graffenried, J Biol Chem 2003] - gene was identified and cloned, 99% identical to mouse ortholog [Uchimura, J Biochem (Tokyo) 1998] - strongly expressed in the bone marrow, peripheral blood leukocytes, spleen, brain, spinal cord, ovary, and placenta, and moderately expressed in many organs including lymph nodes and thymus [Uchimura, J Biochem (Tokyo) 1998] 10164: - Golgi [de Graffenried, J Biol Chem 2003] - gene was cloned [Bistrup, J Cell Biol 1999] 23563: - Golgi [de Graffenried, J Biol Chem 2003] - gene was cloned and characterized [Lee Biochem Biophys Res Commun 1999] - expressed in small intestine and colon [Lee Biochem Biophys Res Commun 1999]
S6T25g	3	Habuchi H, Kobayashi M, Kimata K	Molecular characterization and expression of heparan sulfate 6-sulfotransferase. Complete cDNA cloning in human and partial cloning in Chinese hamster ovary cells	J Biol Chem	1998	9535912	- transfers sulfate to C6-position of NSGlcNAc residues im HS but not GlcNAc [Sugahara, IUBMB Life 2002] - all 3 isoforms transfer sulfate to heparan sulfate / heparin but not chondoroitin or keratan sulfate [Sugahara, IUBMB Life 2002] 9394: - mouse protein preferentially sulfates IdoA-NSGlcNAc [Sugahara, IUBMB Life 2002] - cDNA was cloned and expressed [Habuchi, J Biol Chem 1998] - expressed ubiquitously, but highest levels in adrenal gland, kidney, liver, intestine, foetal brain and fetal kidney [Habuchi, Biochem J 2003] 90161: - mouse protein preferentially sulfates GlcA residue [Sugahara, IUBMB Life 2002] - cDNA was cloned and expressed [Habuchi, Biochem J 2003] - encodes two transcripts -- a long and short form [Habuchi, Biochem J 2003] - long form xclusively expressed in adult and foetal brain tissues, short form preferentially expressed in ovary, placenta and foetal kidney [Habuchi, Biochem J 2003] 26672: - mouse protein sulfates IdoA-NSGlcNAc and GlcA equally [Sugahara, IUBMB Life 2002] - cDNA was identified through high-throughput study [Ota, Nat Genet 2004]

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S6T25g	3	Habuchi H, Miyake G, Nogami K, Kuroiwa A, Matsuda Y, Kusche-Gullberg M, Habuchi O, Tanaka M, Kimata K	Biosynthesis of heparan sulphate with diverse structures and functions: two alternatively spliced forms of human heparan sulphate 6-O-sulphotransferase-2 having different expression patterns and properties	Biochem J	2003	12492399	- transfers sulfate to C6-position of NSGlcNAc residues im HS but not GlcNAc [Sugahara, IUBMB Life 2002] - all 3 isoforms transfer sulfate to heparan sulfate / heparin but not chondoroitin or keratan sulfate [Sugahara, IUBMB Life 2002] 9394: - mouse protein preferentially sulfates IdoA-NSGlcNAc [Sugahara, IUBMB Life 2002] - cDNA was cloned and expressed [Habuchi, J Biol Chem 1998] - expressed ubiquitously, but highest levels in adrenal gland, kidney, liver, intestine, foetal brain and fetal kidney [Habuchi, Biochem J 2003] 90161: - mouse protein preferentially sulfates GlcA residue [Sugahara, IUBMB Life 2002] - cDNA was cloned and expressed [Habuchi, Biochem J 2003] - encodes two transcripts -- a long and short form [Habuchi, Biochem J 2003] - long form xclusively expressed in adult and foetal brain tissues, short form preferentially expressed in ovary, placenta and foetal kidney [Habuchi, Biochem J 2003] 26672: - mouse protein sulfates IdoA-NSGlcNAc and GlcA equally [Sugahara, IUBMB Life 2002] - cDNA was identified through high-throughput study [Ota, Nat Genet 2004]
S6T25g	3	Ota T, Suzuki Y, Nishikawa T, Otsuki T, Sugiyama T, Irie R, Wakamatsu A, Hayashi K, Sato H, Nagai K, Kimura K, et al	Complete sequencing and characterization of 21,243 full-length human cDNAs.	Nat Genet	2004	14702039	- transfers sulfate to C6-position of NSGlcNAc residues im HS but not GlcNAc [Sugahara, IUBMB Life 2002] - all 3 isoforms transfer sulfate to heparan sulfate / heparin but not chondoroitin or keratan sulfate [Sugahara, IUBMB Life 2002] 9394: - mouse protein preferentially sulfates IdoA-NSGlcNAc [Sugahara, IUBMB Life 2002] - cDNA was cloned and expressed [Habuchi, J Biol Chem 1998] - expressed ubiquitously, but highest levels in adrenal gland, kidney, liver, intestine, foetal brain and fetal kidney [Habuchi, Biochem J 2003] 90161: - mouse protein preferentially sulfates GlcA residue [Sugahara, IUBMB Life 2002] - cDNA was cloned and expressed [Habuchi, Biochem J 2003] - encodes two transcripts -- a long and short form [Habuchi, Biochem J 2003] - long form xclusively expressed in adult and foetal brain tissues, short form preferentially expressed in ovary, placenta and foetal kidney [Habuchi, Biochem J 2003] 26672: - mouse protein sulfates IdoA-NSGlcNAc and GlcA equally [Sugahara, IUBMB Life 2002] - cDNA was identified through high-throughput study [Ota, Nat Genet 2004]
S6T3g	3	Habuchi O, Hirahara Y, Uchimura K, Fukuta M	Enzymatic sulfation of galactose residue of keratan sulfate by chondroitin 6-sulfotransferase	Glycobiology	1996	8991509	- refs, substrate specificity, and tissue distribution of GlcNac/Gal-6-O-sulfotransferases [Grunwell, Biochemistry 2002] 9469: - Golgi [UniProt] - gene identified and cDNA isolated, has 74% identity to chick ortholog [Fukuda, Biochim Biophys Acta 1998] - highly expressed in sk muscle, lower levels in heart, placenta, pancreas [Fukuda, Biochim Biophys Acta 1998] - keratan sulfate was sulfated by C6ST at position 6 of Gal residues [Habuchi, Glycobiology 1996] 8534: - gene was cloned and characterized [Fukuta, J Biol Chem 1997] - sulfates position 6 of Gal residues [Fukuta, J Biol Chem 1997] - expressed primarily in brain [Fukuta, J Biol Chem 1997]

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
S6T3g	3	Fukuta M, Inazawa J, Torii T, Tsuzuki K, Shimada E, Habuchi O	Molecular cloning and characterization of human keratan sulfate Gal-6-sulfotransferase	J Biol Chem	1997	9405439	- refs, substrate specificity, and tissue distribution of GlcNac/Gal-6-O-sulfotransferases [Grunwell, Biochemistry 2002] 9469: - Golgi [UniProt] - gene identified and cDNA isolated, has 74% identity to chick ortholog [Fukuda, Biochim Biophys Acta 1998] - highly expressed in sk muscle, lower levels in heart, placenta, pancreas [Fukuda, Biochim Biophys Acta 1998] - keratan sulfate was sulfated by C6ST at position 6 of Gal residues [Habuchi, Glycobiology 1996] 8534: - gene was cloned and characterized [Fukuta, J Biol Chem 1997] - sulfates position 6 of Gal residues [Fukuta, J Biol Chem 1997] - expressed primarily in brain [Fukuta, J Biol Chem 1997]
S6T3g	3	Fukuta M, Kobayashi Y, Uchimura K, Kimata K, Habuchi O	Molecular cloning and expression of human chondroitin 6-sulfotransferase	Biochim Biophys Acta	1998	9714738	- refs, substrate specificity, and tissue distribution of GlcNac/Gal-6-O-sulfotransferases [Grunwell, Biochemistry 2002] 9469: - Golgi [UniProt] - gene identified and cDNA isolated, has 74% identity to chick ortholog [Fukuda, Biochim Biophys Acta 1998] - highly expressed in sk muscle, lower levels in heart, placenta, pancreas [Fukuda, Biochim Biophys Acta 1998] - keratan sulfate was sulfated by C6ST at position 6 of Gal residues [Habuchi, Glycobiology 1996] 8534: - gene was cloned and characterized [Fukuta, J Biol Chem 1997] - sulfates position 6 of Gal residues [Fukuta, J Biol Chem 1997] - expressed primarily in brain [Fukuta, J Biol Chem 1997]
S6TASE1ly	3	Robertson DA, Freeman C, Nelson PV, Morris CP, Hopwood JJ	Human glucosamine-6-sulfatase cDNA reveals homology with steroid sulfatase	Biochem Biophys Res Commun	1988	3196333	- lysosomal enzyme; ubiquitous [RefSeq] - cloned [Robertson 1988] - purified from human liver [Freeman 1987] - kinetic characterization [Freeman 1987]
S6TASE1ly	3	Freeman C, Clements PR, Hopwood JJ	Human liver N-acetylglucosamine-6-sulphate sulphatase. Purification and characterization	Biochem J	1987	3689314	- lysosomal enzyme; ubiquitous [RefSeq] - cloned [Robertson 1988] - purified from human liver [Freeman 1987] - kinetic characterization [Freeman 1987]
S6TASE1ly	3	Freeman C, Hopwood JJ	Human liver N-acetylglucosamine-6-sulphate sulphatase. Catalytic properties	Biochem J	1987	3689315	- lysosomal enzyme; ubiquitous [RefSeq] - cloned [Robertson 1988] - purified from human liver [Freeman 1987] - kinetic characterization [Freeman 1987]
SACCD3m	3	Sacksteder,K.A., Biery,B.J., Morrell,J.C., Goodman,B.K., Geisbrecht,B.V., Cox,R.P., Gould,S.J., Geraghty,M.T.,	Identification of the alpha-aminoadipic semialdehyde synthase gene, which is defective in familial hyperlysinemia.		2000	10775527	Mutations in this gene are associated with familial hyperlysinemia.
SADT	3	Fuda H, Shimizu C, Lee YC, Akita H, Strott CA.	Characterization and expression of human bifunctional 3'-phosphoadenosine 5'-phosphosulphate synthase isoforms.	Biochem J	2002	11931637	bifunctional enzyme In brain and skin PAPSS1 is the major expressed isoform, whereas in liver, cartilage and adrenal glands PAPSS2 isoform expression predominates and in various other tissues the proportions of the isoform expressions is purported to vary IT
SADT	3	Venkatachalam KV.	Human 3'-phosphoadenosine 5'-phosphosulfate (PAPS) synthase: biochemistry, molecular biology and genetic deficiency.	IUBMB Life	2003	12716056	bifunctional enzyme In brain and skin PAPSS1 is the major expressed isoform, whereas in liver, cartilage and adrenal glands PAPSS2 isoform expression predominates and in various other tissues the proportions of the isoform expressions is purported to vary IT
SALMCOM2	2	Schluckebier G, O'Gara M, Saenger W, Cheng X.	Universal catalytic domain structure of AdoMet-dependent methyltransferases.	J Mol Biol	1995	7897657	cytosol - uniprot biochem function by seq similarity. Schluckebier - PMID ref 7897657 notes ability of enzyme to methylate wide-rage of catechols NJ
SAMHISTA	3	Yamauchi K, Sekizawa K, Suzuki H, Nakazawa H, Ohkawara Y, Katayose D, Ohtsu H, Tamura G, Shibahara S, Takemura M, et al	Structure and function of human histamine N-methyltransferase: critical enzyme in histamine metabolism in airway	Am J Physiol	1994	7943261	This reaction is important in the airway and probably elsewhere as well.
SARCOXp	2	Dodt G, Kim DG, Reimann SA, Reuber BE, McCabe K, Gould SJ, Mihalik SJ.	L-Pipecolic acid oxidase, a human enzyme essential for the degradation of L-pipecolic acid, is most similar to the monomeric sarcosine oxidases.		2000	10642506	- recombinant enzyme oxidized both L-pipecolic acid and sarcosine. However, PBD patients who lack the enzyme activity accumulate only L-pipecolic acid, suggesting that in humans in vivo, this enzyme is involved mainly in the degradation of L-pipecolic acid (Dodt et. al)

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SARCStex	2	Glorieux FH, Scriver CR, Delvin E, Mohyuddin F.	Transport and metabolism of sarcosine in hypersarcosinemic and normal phenotypes.		1971	5096515	(PMID: 5096515): patients show sarcosine absorption/clearance from plasma MM
SARDHm	3	Eschenbrenner M, Jorns MS.	Cloning and mapping of the cDNA for human sarcosine dehydrogenase, a flavoenzyme defective in patients with sarcosinemia.	Genomics	1999	10444331	0
SBPP1er	3	Johnson KR, Johnson KY, Becker KP, Bielawski J, Mao C, Obeid LM.	Role of human sphingosine-1-phosphate phosphatase 1 in the regulation of intra- and extracellular sphingosine-1-phosphate levels and cell viability.	J Biol Chem	2003	12815058	ER - uniprot and johnson ref Has enzymatic activity against both sphingosine 1 phosphate (S1P) and dihydro-S1P. Regulates intracellular and extracellular S1P levels. NJ
SBTD_D2	0	El-Kabbani O, Darmanin C, Chung RP	Sorbitol dehydrogenase: structure, function and ligand design	Curr Med Chem	2004	14965227	- strictly uses NAD as cofactor [El-Kabbani et al, Curr Med Chem. 2004 Feb;11(4):465-76] - found in the liver, ovaries, sperm, and seminal vesicles [Champe, Biochemistry 2005]
SCP21x	3	Yamamoto R, Kallen CB, Babalola GO, Rennert H, Billheimer JT, Strauss JF 3rd.	Cloning and expression of a cDNA encoding human sterol carrier protein 2.	Proc Natl Acad Sci U S A	1991	1703300	This gene encodes two proteins: sterol carrier protein X (SCPx) and sterol carrier protein 2 (SCP2), as a result of transcription initiation from 2 independently regulated promoters. The transcript initiated from the proximal promoter encodes the longer SCPx protein, and the transcript initiated from the distal promoter encodes the shorter SCP2 protein, with the 2 proteins sharing a common C-terminus. Evidence suggests that the SCPx protein is a peroxisome-associated thiolase that is involved in the oxidation of branched chain fatty acids, while the SCP2 protein is thought to be an intracellular lipid transfer protein. This gene is highly expressed in organs involved in lipid metabolism, and may play a role in Zellweger syndrome, in which cells are deficient in peroxisomes and have impaired bile acid synthesis. Alternative splicing of this gene produces multiple transcript variants, some encoding different isoforms. The full-length nature of all transcript variants has not been determined. NJ
SCPx	3	Mukherji M, Kershaw NJ, Schofield CH, Wierzbicki AS, Lloyd MD	Utilization of sterol carrier protein-2 by phytanoyl-CoA 2-hydroxylase in the peroxisomal alpha oxidation of phytanic acid	Chemistry and Biology	2002		peroxisome: uniprot (SCPx) other isoforms in liver and mit - also catalyzes other reactions specificity: Liver, fibroblasts, and placenta Mediates in vitro the transfer of all common phospholipids, cholesterol and gangliosides between membranes. May play a role in regulating steroidogenesis. NJ
SELADT	1	Xu ZH, Otterness DM, Freimuth RR, Carlini EJ, Wood TC, Mitchell S, Moon E, Kim UJ, Xu JP, Siciliano MJ, Weinshilboum RM	Human 3'-phosphoadenosine 5'-phosphosulfate synthetase 1 (PAPSS1) and PAPSS2: gene cloning, characterization and chromosomal localization	Biochem Biophys Res Commun	2000	10679223	modeling evidence assuming sel is same as sulfur
SELCYSLY	1	Mihara H, Kurihara T, Watanabe T, Yoshimura T, Esaki N.	cDNA cloning, purification, and characterization of mouse liver selenocysteine lyase. Candidate for selenium delivery protein in selenoprotein synthesis	J Biol Chem	2000	10692412	second citation is mostly concerned with mouse other citation says gsh is used modeling evdience only
SELCYSLY2	3	Daher R, Van Lente F.	Characterization of selenocysteine lyase in human tissues and its relationship to tissue selenium concentrations	J Trace Elem Electrolytes Health Dis	1992	1483038	Enzymatic studies on human form state that selcys is the SOLE substrate and pdx5p is the requied cofactor. see PMID: 1483038
SELMETAT	1	Katsuhiko Nakamuro, Tomofumi Okuno, and Tatsuya Hasegawa	Metabolism of Selenoamino Acids and Contribution of Selenium Methylation to Their Toxicity	Journal of Health Science	2000	?	based on assumption that sel isn't different from sulfur, thus modeling evidence
SELNPS	3	Esaki N, Nakamura T, Tanaka H, Soda K	Selenocysteine lyase, a novel enzyme that specifically acts on selenocysteine. Mammalian distribution and purification and properties of pig liver enzyme	J Biol Chem	1982	6461656	0
SELNPS	3	Stadtman TC	Selenocysteine	Annu Rev Biochem	1996	8811175	0
SERGLYexR	2	Fukasawa Y, Segawa H, Kim JY, Chairoungdua A, Kim DK, Matsuo H, Cha SH, Endou H, Kanai Y	Identification and characterization of a Na(+)-independent neutral amino acid transporter that associates with the 4F2 heavy chain and exhibits substrate selectivity for small neutral D- and L-amino acids	J Biol Chem	2000	10734121	homology and is linked to 4F2hc via a disulphide bond [25, 41]. It mediates Na+-independent transport of small neutral amino acids such as Gly, L-Ala, L-Ser, L-Thr, L-Cys, -aminoisobutyric acid and -alanine. Asc-1-4F2hc also transports d-isomers including D-Ser with high apparent affinity. It functions preferentially, but not exclusively, in an exchange mode. These functional properties appear consistent with those of system asc. Heterogeneity in substrate selectivity has been described for this transport system and the existence of at least two subtypes has been proposed. Asc-1 corresponds to the subtype that was characterized originally in trout peripheral blood lymphocytes, which is less stereospecific and transports -aminoisobutyric acid and -alanine. Asc-1 exhibits the highest structural similarity to the L-type transporter light chain LAT2 (66% identity). In contrast to LAT2-4F2hc, which takes neutral amino acids of all sizes, and to LAT1-4F2hc, which transports only large ones, Asc-1 transports only small neutral amino acids and is not inhibited by Asc-1 mRNA is expressed in the brain, lung, small intestine and PMID 14770310

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SERGLYexR	2	Nakauchi J, Matsuo H, Kim DK, Goto A, Chairoungdua A, Cha SH, Inatomi J, Shiokawa Y, Yamaguchi K, Saito I, Endou H, Kanai Y	Cloning and characterization of a human brain Na(+)-independent transporter for small neutral amino acids that transports D-serine with high affinity	Neurosci Lett	2000	10863037	homology and is linked to 4F2hc via a disulphide bond [25, 41]. It mediates Na+-independent transport of small neutral amino acids such as Gly, L-Ala, L-Ser, L-Thr, L-Cys, -aminoisobutyric acid and -alanine. Asc-1-4F2hc also transports d-isomers including D-Ser with high apparent affinity. It functions preferentially, but not exclusively, in an exchange mode. These functional properties appear consistent with those of system asc. Heterogeneity in substrate selectivity has been described for this transport system and the existence of at least two subtypes has been proposed. Asc-1 corresponds to the subtype that was characterized originally in trout peripheral blood lymphocytes, which is less stereospecific and transports -aminoisobutyric acid and -alanine. Asc-1 exhibits the highest structural similarity to the L-type transporter light chain LAT2 (66% identity). In contrast to LAT2-4F2hc, which takes neutral amino acids of all sizes, and to LAT1-4F2hc, which transports only large ones, Asc-1 transports only small neutral amino acids and is not inhibited by Asc-1 mRNA is expressed in the brain, lung, small intestine and PMID 14770310
SERHL	3	Ogawa H, Gomi T, Konishi K, Date T, Nakashima H, Nose K, Matsuda Y, Peraino C, Pitot HC, Fujioka M.	Human liver serine dehydratase. cDNA cloning and sequence homology with hydroxyamino acid dehydratases from other sources.		1989	2674117	cytosolic according to GeneCards predominantly in liver PMID 14596599: Formation of pyruvate by SDH is a two-step reaction in which the hydroxyl group of serine is cleaved to produce aminoacrylate, and then the aminoacrylate is deaminated by nonenzymatic hydrolysis to produce pyruvate. MM
SERPT	3	Weiss B, Stoffel W	Human and murine serine-palmitoyl-CoA transferase	Eur J Biochem	1997		cytoplasm - actually associated w/ ER membrane, however given the rest of the associated pathway and the lack of specificity of location (inner vs cytoplasmic side) - uniprot NJ
SERtp	2	Xue HH, Sakaguchi T, Fujie M, Ogawa H, Ichiyama A.	Flux of the L-serine metabolism in rabbit, human, and dog livers. Substantial contributions of both mitochondrial and peroxisomal serine:pyruvate/alanine:glyoxylate aminotransferase.		1999	10347152	L-serine catabolslim can occur via SPTx pathway in the peroxisome (PMID:10347152) MM
SGPL11r	3	Van Veldhoven PP, Gijsbers S, Mannaerts GP, Vermeesch JR, Brys V.	Human sphingosine-1-phosphate lyase: cDNA cloning, functional expression studies and mapping to chromosome 10q22(1).	Biochim Biophys Acta	2000	11018465	NJ
SGPL11r	3	Reiss U, Oskouian B, Zhou J, Gupta V, Sooriyakumaran P, Kelly S, Wang E, Merrill AH Jr, Saba JD.	Sphingosine-phosphate lyase enhances stress-induced ceramide generation and apoptosis.	J Biol Chem	2004	14570870	NJ
SIAASE	0	Monti E, Preti A, Rossi E, Ballabio A, Borsani G.	Cloning and characterization of NEU2, a human gene homologous to rodent soluble sialidases.	Genomics	1999	10191093	NEU2 belongs to a family of glycohydrolytic enzymes which remove sialic acid residues from glycoproteins and glycolipids. Expression studies in COS7 cells confirmed that this gene encodes a functional sialidase. Its cytosolic localization was demonstrated by cell fractionation experiments. [RefSeq] NEU4 belongs to a family of glycohydrolytic enzymes which remove sialic acid residues from glycoproteins and glycolipids.[RefSeq] NEU4 wasidentified by searching sequence databases for entries showing homologies to the human cytosolic sialidase NEU2. Highest expression in the liver. Associated with inner cell membranes. [Monti et al, Genomics 83(3):445-453 (2004)] Neu2p expressed in sk muscle [Monti et al, Genomics 1999]
SIAT4Bg	3	Giordanengo V, Bannwarth S, Laffont C, Van Miegem V, Harduin-Lepers A, Delannoy P, Lefebvre JC.	Cloning and expression of cDNA for a human Gal(beta1-3)GalNAc alpha2,3-sialyltransferase from the CEM T-cell line.	Eur J Biochem	1997	9266697	Golgi - lumen side - see ref Kolter and Sanhoff; also noted in uniprot The protein encoded by this gene is a type II membrane protein that catalyzes the transfer of sialic acid from CMP-sialic acid to galactose-containing substrates. The encoded protein is normally found in the Golgi but can be proteolytically processed to a soluble form. This protein, which is a member of glycosyltransferase family 29, can use the same acceptor substrates as does sialyltransferase 4A. cloning, biochem, seq - Giordanengo ref NJ

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SIAT9g	3	Ishii A, Ohta M, Watanabe Y, Matsuda K, Ishiyama K, Sakoe K, Nakamura M, Inokuchi J, Sanai Y, Saito M.	Expression cloning and functional characterization of human cDNA for ganglioside GM3 synthase.	J Biol Chem	1998	9822625	Golgi - lumen side - see ref Kolter and Sanhoff; also noted in uniprot See Ishi ref -gene was found in a tissue-specific manner, with predominant expression in brain, skeletal muscle, and testis, and very low expression in liver Ganglioside GM3 is known to participate in the induction of cell differentiation, modulation of cell proliferation, maintenance of fibroblast morphology, signal transduction, and integrin-mediated cell adhesion. The protein encoded by this gene is a type II membrane protein which catalyzes the formation of GM3 using lactosylceramide as the substrate. NJ
SLCBK1	3	Liu H, Sugiura M, Nava VE, Edsall LC, Kono K, Poulton S, Milstien S, Kohama T, Spiegel S.	Molecular cloning and functional characterization of a novel mammalian sphingosine kinase type 2 isoform.	J Biol Chem	2000	10751414	no good localization info available at this point - cyt by default, temporarily - re-review in future. cloning + biochem characterization - Liu ref Sphingosine-1-phosphate (SPP) has diverse biological functions acting inside cells as a second messenger to regulate proliferation and survival, and extracellularly, as a ligand for G protein-coupled receptors of the endothelial differentiation gene 1 subfamily. Based on sequence homology to murine and human sphingosine kinase-1 (SPHK1), which we recently cloned - ref exerpt tissue spec (Liu ref): liver, heart, kideny, testis, brain. NJ
SLDx	2	Weinstein CL, Griffith OW.	Cysteinesulfonate and beta-sulfopyruvate metabolism. Partitioning between decarboxylation, transamination, and reduction pathways.		1988	3346220	- catalysed by mammalian malate dehydrogenase (EC 1.1.1.37), where the resulting sulfolactate is excreted (PMID: 15758220) - direct evidence found in rat (PMID:3346220) MM
SLDx	2	Rein U, Gueta R, Denger K, Ruff J, Hollemeyer K, Cook AM.	Dissimilation of cysteate via 3-sulfolactate sulfo-lyase and a sulfate exporter in Paracoccus pantotrophus NKNCYSA.		2005	15758220	- catalysed by mammalian malate dehydrogenase (EC 1.1.1.37), where the resulting sulfolactate is excreted (PMID: 15758220) - direct evidence found in rat (PMID:3346220) MM
SMPD3l	3	Hofmann K, Tomiuk S, Wolff G, Stoffel W.	Cloning and characterization of the mammalian brain specific, Mg2+-dependent neutral sphingomyelinase.	Proc Natl Acad Sci	2000	10823942	lysosomal - uniprot
SMPD4	2	Rodriguez-Lafrasse C, Vanier MT.	Sphingosylphosphorylcholine in Niemann-Pick disease brain: accumulation in type A but not in type B.	Neurochem Res	1999	9972865	see PMID: 12069827, 9972865 for evidence - noted accumulation of spc_hs in deficiencies of sphingomyelinase, so although not enough evidence can be inferred for gene assocations, there must be a sphingomyelinase with spc_hs specificity in the cell. IC localization not known, added to cytosol as default and also as part of model gap filling. NJ
SMS	3	Huitema K, van den Dikkenberg J, Brouwers JF, Holthuis JC.	Identification of a family of animal sphingomyelin synthases.	EMBO J	2003	14685263	Golgi - lumen side - see ref Kolter and Sanhoff; also noted in uniprot - also in Huitema ref Note: Huitema notes SMS1 and SMS2 - golgi and cytoplasmic versions respectively TMEM23 = SMS1 SMS2 for humans not found yet in Entrez gene Bidirectional lipid cholinephosphotransferases capable of converting phosphatidylcholine (PC) and ceramide to sphingomyelin (SM) and diacylglycerol (DAG) and vice versa. Direction is dependent on the relative concentrations of DAG and ceramide as phosphocholine acceptors. Directly and specifically recognizes the choline head group on the substrate. Also requires two fatty chains on the choline-P donor molecule in order to be recognized efficiently as a substrate. Does not function strictly as a SM synthase. NJ

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SO4HCOtex	2	Mount DB, Romero MF	The SLC26 gene family of multifunctional anion exchangers	Pflugers Arch	2004	12759755	These anion exchange reactions are all somewhat suspect in some regard. Stoichiometry of exchange is probably least certain. Reversibility is also questionable in some cases, and more substrates almost certainly exist than are indicated in these reactions. From PMID 12759755: The ten-member SLC26 gene family encodes anion exchangers capable of transporting a wide variety of monovalent and divalent anions. The physiological role(s) of individual paralogs is evidently due to variation in both anion specificity and expression pattern. Three members of the gene family are involved in genetic disease; SLC26A2 in chondrodysplasias, SLC26A3 in chloride-losing diarrhea, and SLC26A4 in Pendred syndrome and hereditary deafness (DFNB4). The analysis of Slc26a4-null mice has significantly enhanced the understanding of the roles of this gene in both health and disease. Targeted deletion of Slc26a5 has in turn revealed that this paralog is essential for electromotor activity of cochlear outer hair cells and thus for cochlear amplification. Anions transported by the SLC26 family, with variable specificity, include the chloride, su
SO4t4_2	3	Girard JP, Baekkevold ES, Feliu J, Brandtzaeg P, Amalric F	Molecular cloning and functional analysis of SUT-1, a sulfate transporter from human high endothelial venules	Proc Natl Acad Sci U S A	1999	10535998	26266: - cloned [Girard 1999] -high in placenta and testis; intermediate in brain; low in heart, thymus, liver [Markovich 2005] - 40-50% amino acid identity w/ rat NaS1, human & rat NaC1, NaC3 [Girard 1999] - 2 Na+:1 anion stoichiometry [Markovich 2005]
SO4t4_2	3	Markovich D, Regeer RR, Kunzelmann K, Dawson PA	Functional characterization and genomic organization of the human Na(+)-sulfate cotransporter hNaS2 gene (SLC13A4)	Biochem Biophys Res Commun	2005	15607730	26266: - cloned [Girard 1999] -high in placenta and testis; intermediate in brain; low in heart, thymus, liver [Markovich 2005] - 40-50% amino acid identity w/ rat NaS1, human & rat NaC1, NaC3 [Girard 1999] - 2 Na+:1 anion stoichiometry [Markovich 2005]
SO4t4_3	3	Pajor AM	Molecular properties of sodium/dicarboxylate cotransporters	J Membr Biol	2000	10811962	6561: - cloned [Lee 2000] - ortholog cotransports sulfate, thiosulfate, selenate with Na+; molybdate, tungstate are also competitively transported but not included in model [Lee 2000] - kidney [Lee 2000] - 3 Na+:1 anion stoichiometry [Pajor 2000]
SO4t4_3	3	Lee A, Beck L, Markovich D	The human renal sodium sulfate cotransporter (SLC13A1; hNaSi-1) cDNA and gene: organization, chromosomal localization, and functional characterization	Genomics	2000	11161786	6561: - cloned [Lee 2000] - ortholog cotransports sulfate, thiosulfate, selenate with Na+; molybdate, tungstate are also competitively transported but not included in model [Lee 2000] - kidney [Lee 2000] - 3 Na+:1 anion stoichiometry [Pajor 2000]
SOAT11	3	Chang CC, Huh HY, Cadigan KM, Chang TY.	Molecular cloning and functional expression of human acyl-coenzyme A:cholesterol acyltransferase cDNA in mutant Chinese hamster ovary cells.	J Biol Chem	1993	8407899	Guo et al (PMID: 15850387) have evidence that the transmembrane protein SOAT1 is likely able to catalyze esterification of cholesterol diffusing from the cytosol into the ER membrane or from the ER lumen into the ER membrane. Expression, sequence and function in Change et al (PMID: 8407899). NJ
SOAT11	3	Guo ZY, Chang CC, Lu X, Chen J, Li BL, Chang TY.	The disulfide linkage and the free sulfhydryl accessibility of acyl-coenzyme A:cholesterol acyltransferase 1 as studied by using mPEG5000-maleimide.	Biochemistry	2005	15850387	Guo et al (PMID: 15850387) have evidence that the transmembrane protein SOAT1 is likely able to catalyze esterification of cholesterol diffusing from the cytosol into the ER membrane or from the ER lumen into the ER membrane. Expression, sequence and function in Change et al (PMID: 8407899). NJ
SPH1Ptr	2	Quest AF, Leyton L, Parraga M.	Caveolins, caveolae, and lipid rafts in cellular transport, signaling, and disease.	Biochem Cell Biol	2004	15052333	Unknown mechanism - may or may not be energy dependen - may be vesicular/caveolor/other... However these metabolites must be able to be transported intracellularly and exported outside of the cell. NJ
SPHMDAc	0	Meyer zu Heringdorf D, Himmel HM, Jakobs KH.	Sphingosylphosphorylcholine-biological functions and mechanisms of action.	Biochim Biophys Acta	2002	12069827	Details about localization not known, gene not found. It's biochemical function however has been described. Presently left as cytosolic by default, likely to occur in other compartments. See PMID: 12069827 NJ
SPMDOX	2	Salim EI, Wanibuchi H, Morimura K, Kim S, Yano Y, Yamamoto S, Fukushima S	Inhibitory effects of 1,3-diaminopropane, an ornithine decarboxylase inhibitor, on rat two-stage urinary bladder carcinogenesis initiated by N-butyl-N-(4-hydroxybutyl)nitrosamine	Carcinogenesis	2000	10657958	This reaction added based on the physiological evidence that 13dampp inhibits the ODC reaction, which is upstream.
SPMS	3	Myohanen S, Kauppinen L, Wahlfors J, Alhonen L, Janne J	Human spermidine synthase gene: structure and chromosomal localization	DNA Cell Biol	1991	2069720	Well-accepted gene and enzyme function.
SPMS	3	Kauppinen L, Myohanen S, Halmekyto M, Alhonen L, Janne J	Transgenic mice over-expressing the human spermidine synthase gene	Biochem J	1993	8343131	Well-accepted gene and enzyme function.

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
SPODM	3	Crapo JD, Oury T, Rabouille C, Slot JW, Chang LY	Copper,zinc superoxide dismutase is primarily a cytosolic protein in human cells	Proc Natl Acad Sci U S A	1992	1332049	6647: - homodimer, soluble cytosolic protein [UniProt] - widely expressed in cytosol of all mammalian cells - primarily cytosolic, but also found in nucleus and peroxisome [Crapo 1992] - cloned & expressed [Hallewell 1985]
SPODM	3	Hallewell RA, Masiarz FR, Najarian RC, Puma JP, Quiroga MR, Randolph A, Sanchez-Pescador R, Scandella CJ, Smith B, Steimer KS, et al	Human Cu/Zn superoxide dismutase cDNA: isolation of clones synthesising high levels of active or inactive enzyme from an expression library	Nucleic Acids Res	1985	3889846	6647: - homodimer, soluble cytosolic protein [UniProt] - widely expressed in cytosol of all mammalian cells - primarily cytosolic, but also found in nucleus and peroxisome [Crapo 1992] - cloned & expressed [Hallewell 1985]
SPODMe	3	Hjalmarsson K, Marklund SL, Engstrom A, Edlund T	Isolation and sequence of complementary DNA encoding human extracellular superoxide dismutase	Proc Natl Acad Sci U S A	1987	3476950	6649: - homotetrameric protein, secreted [Fridovich 1997] - exhibits affinity for sulfated polysaccharides, such as heparin or heparan sulfate [Fridovich 1997] - cloned [Hjalmarsson 1987] - Highly expressed in alveolar type II cells, proximal renal tubular cells, vascular smooth muscular cells, lung macrophages, cultured fibroblast cell lines (see refs in [Zelko 2002]); also detectable in blood plasma, mostly bound onto the extracellular matrix (see [Fridovich 1997] for refs)
SPODMe	3	Fridovich I	Superoxide anion radical (O2-.), superoxide dismutases, and related matters	J Biol Chem	1997	9228011	6649: - homotetrameric protein, secreted [Fridovich 1997] - exhibits affinity for sulfated polysaccharides, such as heparin or heparan sulfate [Fridovich 1997] - cloned [Hjalmarsson 1987] - Highly expressed in alveolar type II cells, proximal renal tubular cells, vascular smooth muscular cells, lung macrophages, cultured fibroblast cell lines (see refs in [Zelko 2002]); also detectable in blood plasma, mostly bound onto the extracellular matrix (see [Fridovich 1997] for refs)
SPODMe	3	Zelko IN, Mariani TJ, Folz RJ	Superoxide dismutase multigene family: a comparison of the CuZn-SOD (SOD1), Mn-SOD (SOD2), and EC-SOD (SOD3) gene structures, evolution, and expression	Free Radic Biol Med	2002	12126755	6649: - homotetrameric protein, secreted [Fridovich 1997] - exhibits affinity for sulfated polysaccharides, such as heparin or heparan sulfate [Fridovich 1997] - cloned [Hjalmarsson 1987] - Highly expressed in alveolar type II cells, proximal renal tubular cells, vascular smooth muscular cells, lung macrophages, cultured fibroblast cell lines (see refs in [Zelko 2002]); also detectable in blood plasma, mostly bound onto the extracellular matrix (see [Fridovich 1997] for refs)
SPODMm	2	Folz RJ, Guan J, Seldin MF, Oury TD, Enghild JJ, Crapo JD.	Mouse extracellular superoxide dismutase: primary structure, tissue-specific gene expression, chromosomal localization, and lung in situ hybridization.	Am J Respir Cell Mol Biol	1997	9376114	proteome Shlafer M, Myers CL, Adkins S.; Mitochondrial hydrogen peroxide generation and activities of glutathione peroxidase and superoxide dismutase following global ischemia.; J Mol Cell Cardiol. 1987 Dec;19(12):1195-206 Mitochondriral catalase and oxidative injury, Bai J. Catalytic activity: Copper-zinc superoxide dismutase (SOD) is a 32-kDa homodimeric protein that catalyzes the disproportionation of superoxide anion into dioxygen and hydrogen peroxide through redox cycling of its catalytic copper ion. This was according to Elam J. J Biol Chem. 2003 Jun 6;278(23):21032-9. Subcellular localization: 1) Sod1.1 - cytoplasmic & nuclear 2) Sod2.1 - mitochondrial 3) Sod3.1 - extracellular according to Entrez Gene Database Tissue Localization Extracellular SOD (Sod3.1) is found in trace amounts in almost all tissues, but can be found predominantly in the lung and kidney. Tissue localization for the cytoplasmic and mitochondrial was not specified. This was according to Figure 4 in Folz RJ. Am J Respir Cell Mol Biol. 1997 Oct;17(4):393-403. Review.

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SPODMm	2	Elam JS, Malek K, Rodriguez JA, Doucette PA, Taylor AB, Hayward LJ, Cabelli DE, Valentine JS, Hart PJ.	An alternative mechanism of bicarbonate-mediated peroxidation by copper-zinc superoxide dismutase: rates enhanced via proposed enzyme-associated peroxycarbonate intermediate.	J Biol Chem	2003	12649272	proteome Shlafer M, Myers CL, Adkins S.; Mitochondrial hydrogen peroxide generation and activities of glutathione peroxidase and superoxide dismutase following global ischemia.; J Mol Cell Cardiol. 1987 Dec;19(12):1195-206 Mitochondriral catalase and oxidative injury, Bai J. Catalytic activity: Copper-zinc superoxide dismutase (SOD) is a 32-kDa homodimeric protein that catalyzes the disproportionation of superoxide anion into dioxygen and hydrogen peroxide through redox cycling of its catalytic copper ion. This was according to Elam J. J Biol Chem. 2003 Jun 6;278(23):21032-9. Subcellular localization: 1) Sod1.1 - cytoplasmic & nuclear 2) Sod2.1 - mitochondrial 3) Sod3.1 - extracellular according to Entrez Gene Database Tissue Localization Extracellular SOD (Sod3.1) is found in trace amounts in almost all tissues, but can be found predominantly in the lung and kidney. Tissue localization for the cytoplasmic and mitochondrial was not specified. This was according to Figure 4 in Folz RJ. Am J Respir Cell Mol Biol. 1997 Oct;17(4):393-403. Review.
SPRMS	3	Korhonen VP, Halmekyto M, Kauppinen L, Myohanen S, Wahlfors J, Keinanen T, Hyvonen T, Alhonen L, Eloranta T, Janne J	Molecular cloning of a cDNA encoding human spermine synthase	DNA Cell Biol	1995	7546290	Well-accepted gene for this function.
SPRn	3	Elzaouk L, Laufs S, Heerklotz D, Leimbacher W, Blau N, Resibois A, Thony B.	Nuclear localization of tetrahydrobiopterin biosynthetic enzymes.	Biochim Biophys Acta	2004	14729142	IT only ~1% of total SPR could be found in nucleus. however, i included this nuclear reaction. gap: no one knows why GTPCIn, PTHPSn, SPRn are located in nucleus - and what the function of thbpt could be
SPTix	3	Lumb MJ, Danpure CJ.	Functional synergism between the most common polymorphism in human alanine:glyoxylate aminotransferase and four of the most common disease-causing mutations.		2000	10960483	-catalyzed by same gene product as AGTx, although at lower activity (see ref.) MM
SQLSr	3	Cohen LH, Griffioen M, vanRoermund CW, Wanders RJ	Subcellular localization of squalene synthase in human hepatoa cell line Hep G2	Biochim Biophys Acta	1992		ER - according to lit refs (need to check more thoroughly in the literature if on outer side of ER membrane or inside no tissue specificity NJ
SR5ARr	3	Wigley WC, Prihoda JS, Mowaszowicz I, Mendonca BB, New MI, Wilson JD, Russell DW	Natural mutagenesis study of the human steroid 5-alpha-reductase 2 isozyme	Biochemistry	1994		ER/microsomal - uniprot + refs specificity: prostate, liver Converts testosterone into 5-alpha-dihydrotestosterone and progesterone or corticosterone into their corresponding 5- alpha 3-oxosteroids. It plays a central role in sexual differentiation and androgen physiology. NJ
SR5ARr	3	Andersson S, Berman DM, Jenkins EP, Russel DW	Deletion of steroid 5-alpha-reductase 2 gene in male pseudohermaphroditism	Nature	1991		ER/microsomal - uniprot + refs specificity: prostate, liver Converts testosterone into 5-alpha-dihydrotestosterone and progesterone or corticosterone into their corresponding 5- alpha 3-oxosteroids. It plays a central role in sexual differentiation and androgen physiology. NJ
SRTN23OX	3	Okuma M, Tokuyama T, Senoh S, Hirata F, Hayaishi O	Antagonism of 5-hydroxykynurenamine against serotonin action on platelet aggregation	Proc Natl Acad Sci U S A	1976	1061163	Enzyme name connected to reaction in citation.
SRTNACT	3	Coon SL, Mazuruk K, Bernard M, Roseboom PH, Klein DC, Rodriguez IR	The human serotonin N-acetyltransferase (EC 2.3.1.87) gene (AANAT): structure, chromosomal localization, and tissue expression	Genomics	1996	8661026	Enzyme and reaction characterized.
SSALxm	3	Chambliss KL, Caudle DL, Hinson DD, Moomaw CR, Slaughter CA, Jakobs C, Gibson KM.	Molecular cloning of the mature NAD(+)-dependent succinic semialdehyde dehydrogenase from rat and human. cDNA isolation, evolutionary homology, and tissue expression.		1995	7814412	- (SSADH) deficiency causes a rare metabolic disorder of 4-aminobutyric acid degradation (Chambliss et. al. 1998) -mitochondrial (GeneCards) -brain, pancreas, heart, liver, skeletal muscle and kidney. lower in placenta.
SSALxm	3	Chambliss KL, Hinson DD, Trettel F, Malaspina P, Novelletto A, Jakobs C, Gibson KM.	Two exon-skipping mutations as the molecular basis of succinic semialdehyde dehydrogenase deficiency (4-hydroxybutyric aciduria).		1998	9683595	- (SSADH) deficiency causes a rare metabolic disorder of 4-aminobutyric acid degradation (Chambliss et. al. 1998) -mitochondrial (GeneCards) -brain, pancreas, heart, liver, skeletal muscle and kidney. lower in placenta.

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ST3GAL61g	3	Okajima T, Fukumoto S, Miyazaki H, Ishida H, Kiso M, Furukawa K, Urano T, Furukawa K.	Molecular cloning of a novel alpha2,3-sialyltransferase (ST3Gal VI) that sialylates type II lactosamine structures on glycoproteins and glycolipids.	J Biol Chem	1999	10206952	localization: golgi: uniprot and PMID: 10206952 sequence, function, cloning: PMID: 10206952 Sialyltransferases catalyze the transfer of sialic acid from cytidine 5-prime monophospho-N-acetylneuraminic acid (CMP NeuAc) to terminal positions of glycoprotein and glycolipid carbohydrate groups. Terminal NeuAc residues are key determinants of carbohydrate structures, such as the sialyl-Lewis X determinants, and are widely distributed in many cell types.[supplied by OMIM] Involved in the synthesis of sialyl-paragloboside, a precursor of sialyl-Lewis X determinant. Has a alpha-2,3- sialyltransferase activity toward Gal-beta1,4-GlcNAc structure on glycoproteins and glycolipids. Has a restricted substrate specificity, it utilizes Gal-beta1,4-GlcNAc on glycoproteins, and neolactotetraosylceramide and neolactohexaosylceramide, but not lactotetraosylceramide, lactosylceramide or asialo-GM1. NJ
ST8SIA11	3	Kim YJ, Kim KS, Do S, Kim CH, Kim SK, Lee YC.	Molecular cloning and expression of human alpha2,8-sialyltransferase (hST8Sia V).	Biochem Biophys Res Commun	1997	9199191	Golgi - lumen side - see ref Kolter and Sanhoff; also noted in uniprot The protein encoded by this gene is a type II membrane protein that may be present in the Golgi apparatus. The encoded protein, which is a member of glycosyltransferase family 29, may be involved in the synthesis of gangliosides GD1c, GT1a, GQ1b, and GT3 from GD1a, GT1b, GM1b, and GD3, respectively. NJ
ST8SIA11	3	Takashima S, Tsuji S, Tsujimoto	Characterization of second type of human beta-galactoside alpha2,6-sialyltransferase which sialates gal-beta1,4GlcNAc structures on oligosaccharides preferentially	Journal of Biological Chemistry	2002		Golgi - lumen side - see ref Kolter and Sanhoff; also noted in uniprot The protein encoded by this gene is a type II membrane protein that may be present in the Golgi apparatus. The encoded protein, which is a member of glycosyltransferase family 29, may be involved in the synthesis of gangliosides GD1c, GT1a, GQ1b, and GT3 from GD1a, GT1b, GM1b, and GD3, respectively. NJ
ST8SIA12	3	Sasaki K, Kurata K, Kojima N, Kurosawa N, Ohta S, Hanai N, Tsuji S, Nishi T	Expression cloning of a Gm3-specific alpha-2,8-sialyltransferase (GD3 synthase)	Journal of Biological Chemistry	1994		Golgi - lumen side - see ref Kolter and Sanhoff The protein encoded by this gene is a type II membrane protein that may be present in the Golgi apparatus. The encoded protein, which is a member of glycosyltransferase family 29, may be involved in the synthesis of gangliosides GD1c, GT1a, GQ1b, and GT3 from GD1a, GT1b, GM1b, and GD3, respectively. cloning and function: PMID: 9199191 NJ
ST8SIA51g	3	Harduin-Lepers A, Vallejo-Ruiz V, Krzewinski-Recchi MA, Smyn-Petit B, Julien S, Delannoy P	The human sialyltransferase family	Biochimie	2001		Golgi - lumen side - see ref Kolter and Sanhoff; also noted in uniprot The protein encoded by this gene is a type II membrane protein that may be present in the Golgi apparatus. The encoded protein, which is a member of glycosyltransferase family 29, may be involved in the synthesis of gangliosides GD1c, GT1a, GQ1b, and GT3 from GD1a, GT1b, GM1b, and GD3, respectively. cloning and function: PMID: 9199191 NJ
ST8SIA55g	3	Sandhoff K, Kolter T	Biosynthesis and degradation of mammalian glycosphingolipids	Phil Trans R Soc Lond B	2003		golgi inner lumenal side - uniport and refs The protein encoded by this gene is a type II membrane protein that may be present in the Golgi apparatus. The encoded protein, which is a member of glycosyltransferase family 29, may be involved in the synthesis of gangliosides GD1c, GT1a, GQ1b, and GT3 from GD1a, GT1b, GM1b, and GD3, respectively. cloning and function: PMID: 9199191 NJ

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STS1r	3	Migeon BR, Shapiro LJ, Norum RA, Mohandas T, Axelman J, Dabora RL.	Differential expression of steroid sulphatase locus on active and inactive human X chromosome.	Nature	1982		ER membrane - lumen side - ref and uniprot Stein ref also notes: "STS expressed in BHK-21 cells is located predominantly in the endoplasmic reticulum; smaller fractions are found in the Golgi, at the cell surface, multivesicular endosomes, as well as in lysosomes." The protein encoded by this gene catalyzes the conversion of sulfated steroid precursors to estrogens during pregnancy. The encoded protein is found in the endoplasmic reticulum, where it acts as a homodimer. Mutations in this gene are known to cause X-linked ichthyosis (XLI). NJ
STS1r	3	Stein C, Hille A, Seidel J, Rijnbout S, Waheed A, Schmidt B, Geuze H, von Figura K.	Cloning and expression of human steroid-sulfatase. Membrane topology, glycosylation, and subcellular distribution in BHK-21 cells.	J Biol Chem	1989	2668275	ER membrane - lumen side - ref and uniprot Stein ref also notes: "STS expressed in BHK-21 cells is located predominantly in the endoplasmic reticulum; smaller fractions are found in the Golgi, at the cell surface, multivesicular endosomes, as well as in lysosomes." The protein encoded by this gene catalyzes the conversion of sulfated steroid precursors to estrogens during pregnancy. The encoded protein is found in the endoplasmic reticulum, where it acts as a homodimer. Mutations in this gene are known to cause X-linked ichthyosis (XLI). NJ
SUCCt4_3	3	Wang H, Fei YJ, Kekuda R, Yang-Feng TL, Devoe LD, Leibach FH, Prasad PD, Ganapathy V	Structure, function, and genomic organization of human Na(+)-dependent high-affinity dicarboxylate transporter	Am J Physiol Cell Physiol	2000	794676	64849: - cloned [Wang 2000] - high affinty cotransport of Na+ w/ succinate, dimethylsuccinate, aKG [Wang 2000] - basolateral membrane of renal proximal tubular epithelial cells, sinusoidal membrane of hepatocytes, and brain synaptosome [Pajor 1999] - high in kidney, also in placenta, brain, liver, pancreas [Wang 2000] - Na(+)-to-succinate stoichiometry is 3:1 [Wang 2000]
SUCCt4_3	3	Pajor AM	Sodium-coupled transporters for Krebs cycle intermediates	Annu Rev Physiol	1999	10099705	64849: - cloned [Wang 2000] - high affinty cotransport of Na+ w/ succinate, dimethylsuccinate, aKG [Wang 2000] - basolateral membrane of renal proximal tubular epithelial cells, sinusoidal membrane of hepatocytes, and brain synaptosome [Pajor 1999] - high in kidney, also in placenta, brain, liver, pancreas [Wang 2000] - Na(+)-to-succinate stoichiometry is 3:1 [Wang 2000]
SUCOAS1m	0	Johnson JD, Mehus JG, Tews K, Milavetz BI, Lambeth DO	Genetic evidence for the expression of ATP- and GTP-specific succinyl-CoA synthetases in multicellular eucaryotes	J Biol Chem	1998	9765291	- Highly ATP- and GTP-specific isoforms of succinyl-CoA synthetase in pigeon incorporate the same alpha -subunit, but different beta -subunits [Johnson et al, J Biol Chem 1998] - heterodimer of an alpha and a beta chain [UniProt] - mitochondrial [UniProt]
SUCRe	3	Wu GD, Wang W, Traber PG	Isolation and characterization of the human sucrase-isomaltase gene and demonstration of intestine-specific transcriptional elements	J Biol Chem	1992	1560017	8972: - brush border enzyme [RefSeq], [Naim, J Biol Chem 1988] - expressed in small intestine and kidney [UniProt] 6476: - brush border enzyme [GO], [Wu et al, J Biol Chem 1992] -sm intestine [Wu et al, J Biol Chem 1992], [Devlin, Textbook of Biochemistry]
SUCRe	3	Naim HY, Sterchi EE, Lentze MJ	Structure, biosynthesis, and glycosylation of human small intestinal maltase-glucoamylase	J Biol Chem	1988	3143729	8972: - brush border enzyme [RefSeq], [Naim, J Biol Chem 1988] - expressed in small intestine and kidney [UniProt] 6476: - brush border enzyme [GO], [Wu et al, J Biol Chem 1992] -sm intestine [Wu et al, J Biol Chem 1992], [Devlin, Textbook of Biochemistry]
TAURtcx	1	Ramamoorthy S, Leibach FH, Mahesh VB, Han H, Yang-Feng T, Blakely RD, Ganapathy V	Functional characterization and chromosomal localization of a cloned taurine transporter from human placenta	Biochem J	1994	8010975	Mechanism isn't as certain as it could be--sodium symport is commonly thought to be the transport method from outside to inside cell no specific evidence located regarding transport from cytosol to peroxisome, so only modeling confidence for now
TDP	3	Laforenza U, Mazzarello P, Patrini C, Poloni M, Casadei GP, Rindi G.	Different distribution of thiaminpyrophosphatase activity in neuronal and glial cell enriched fractions from human and rat brain: an isoelectric focusing investigation.	Basic Appl Histochem	1990	2171493	IT activity has been measured by Bettendorf et al 1996 vmax=130+-19 nmmol/mg.30 min(at pH=7.4) Laforenza et al, 1990, might have found multiple isoforms of this enzyme extracted from humna neuronal and glial cells - check reference

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TDPDRE	1	Tonetti M, Sturla L, Bisso A, Zanardi D, Benatti U, De Flora A	The metabolism of 6-deoxyhexoses in bacterial and animal cells	Biochimie	1998	9893952	- L-rhamnose has been observed mainly in bacteria; however, there have been a few acttered reports which suggest its presence in animals (see refs in [Tonetti 1998]) - conversion of dTDP-glucose to dTDP-rhamnose is described as a mammalian pathway by Devlin, pgs. 671-672 - these facts together with the putative annotation of a human dTDPglucose 4,6-dehydratase (the first step in dTDP-rhamnose production) prompted the inclusion of this rxn
TDPGDH	2	Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD, et al.	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	Proc Natl Acad Sci U S A	2002	12477932	- discovered as part of high-througput study; function inferred from electronic annotation [Strausberg 2002]
TDPm	2	Barile M, Valenti D, Brizio C, Quagliariello E, Passarella S.	Rat liver mitochondria can hydrolyse thiamine pyrophosphate to thiamine monophosphate which can cross the mitochondrial membrane in a carrier-mediated process.	FEBS Lett	1998	9755848	based on rat data (liver cell). It seems that the mitochondrial thmpp is degraded to thmmp in the mitochondria and than exported to be degraded to thiamine in cytosol. IT it seems that thmmp can also be taken up by mitochondria but I do not see the sense in this uptake since there is no possible conversion of this compound reported (rxn has not been included)
THD1m	3	Hatefi Y, Yamaguchi M.	Nicotinamide nucleotide transhydrogenase: a model for utilization of substrate binding energy for proton translocation.	FASEB	1996	8647343	IT - Additional information added by RS/TV: White SA, Peake SJ, McSweeney S, Leonard G, Cotton NP, Jackson JB., The high-resolution structure of the NADP(H)-binding component (dIII) of proton-translocating transhydrogenase from human heart mitochondria., Structure Fold Des. 2000 Jan 15;8(1):1-12 (Jackson, Peake et al. 1999; Peake, Jackson et al. 2000;) There are two isozymes, both of which are mitochondrial, according to Entrez Gene Database. Catalytic Activity: Proton-pumping nicotinamide transhydrogenases are membrane proteins and proton pumps which catalyze the reversible reduction of NADP+ byd NADH linked to proton translocation across the membrane. The NADPH generate may be then used for detoxification of peroxides. According to Arkblad EL. Comp Biochem Physiol B Biochem Mol Biol. 2002 Sep;133(1):13-21.
THD1m	3	Zieger B, Ware J.	Cloning and deduced amino acid sequence of human nicotinamide nucleotide transhydrogenase.	DNA Seq	1997	9524818	IT - Additional information added by RS/TV: White SA, Peake SJ, McSweeney S, Leonard G, Cotton NP, Jackson JB., The high-resolution structure of the NADP(H)-binding component (dIII) of proton-translocating transhydrogenase from human heart mitochondria., Structure Fold Des. 2000 Jan 15;8(1):1-12 (Jackson, Peake et al. 1999; Peake, Jackson et al. 2000;) There are two isozymes, both of which are mitochondrial, according to Entrez Gene Database. Catalytic Activity: Proton-pumping nicotinamide transhydrogenases are membrane proteins and proton pumps which catalyze the reversible reduction of NADP+ byd NADH linked to proton translocation across the membrane. The NADPH generate may be then used for detoxification of peroxides. According to Arkblad EL. Comp Biochem Physiol B Biochem Mol Biol. 2002 Sep;133(1):13-21.
THD1m	3	Arkblad EL, Egorov M, Shakhparonov M, Romanova L, Polzikov M, Rydstrom J.	Expression of proton-pumping nicotinamide nucleotide transhydrogenase in mouse, human brain and C elegans.	Comp Biochem Physiol B Biochem Mol Biol	2002	12223207	IT - Additional information added by RS/TV: White SA, Peake SJ, McSweeney S, Leonard G, Cotton NP, Jackson JB., The high-resolution structure of the NADP(H)-binding component (dIII) of proton-translocating transhydrogenase from human heart mitochondria., Structure Fold Des. 2000 Jan 15;8(1):1-12 (Jackson, Peake et al. 1999; Peake, Jackson et al. 2000;) There are two isozymes, both of which are mitochondrial, according to Entrez Gene Database. Catalytic Activity: Proton-pumping nicotinamide transhydrogenases are membrane proteins and proton pumps which catalyze the reversible reduction of NADP+ byd NADH linked to proton translocation across the membrane. The NADPH generate may be then used for detoxification of peroxides. According to Arkblad EL. Comp Biochem Physiol B Biochem Mol Biol. 2002 Sep;133(1):13-21.
THFtm	2	Suh JR, Herbig AK, Stover PJ.	New perspectives on folate catabolism.	Annu Rev Nutr	2001	11375437	IT

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THMMPt4	3	Dutta B, Huang W, Molero M, Kekuda R, Leibach FH, Devoe LD, Ganapathy V, Prasad PD.	Cloning of the human thiamine transporter, a member of the folate transporter family.	J Biol Chem	1999	10542220	IT reactions is based on the fact that Ganapathy et al mentioned that folate is transported via OH- antiport. Since the same gene product has also been found to transport the thiamine derivates, the same mechanism of transport was concluded
THMMPt4	3	Ganapathy V, Smith SB, Prasad PD.	SLC19: the folate/thiamine transporter family.	Pflugers Arch	2004	14770311	IT reactions is based on the fact that Ganapathy et al mentioned that folate is transported via OH- antiport. Since the same gene product has also been found to transport the thiamine derivates, the same mechanism of transport was concluded
THMP	1	Zhao R, Gao F, Goldman ID.	Reduced folate carrier transports thiamine monophosphate: an alternative route for thiamine delivery into mammalian cells.	Am J Physiol Cell Physiol	2002	11997266	I did not found any biochemical studies on this enzyme, however, Bettendorff et al, 1996, proposed this reaction beyond others. Zhao et al., 2002, reported that the majority of uptaken TMP was hydrolysed to thiamine. IT In kegg they assigned locus 8776 with this function, however, there is no evidence that this is the case
THMt2m	3	Song Q, Singleton CK.	Mitochondria from cultured cells derived from normal and thiamine-responsive megaloblastic anemia individuals efficiently import thiamine diphosphate.	BMC Biochem	2005	12014993	It is thought that this SLC19A2 is also reponsible for the mitochondrial transport since cells of TRMA patients (thiamine responive megaloblastic anemia) in this gene show no mitochondrial transport of thiamine. Role of thiamine in mitochondria is not clear (therefore will be a gap) since there is no mitochondrial thiamine (diphosphokinase) IT
THMt3	3	Eudy JD, Spiegelstein O, Barber RC, Wlodarczyk BJ, Talbot J, Finnell RH.	Identification and characterization of the human and mouse SLC19A3 gene: a novel member of the reduced folate family of micronutrient transporter genes.	Mol Genet Metab	2000	11136550	It has been shown that the transport is soudium independent and is stimulated by an outwardly directed H+ gradient. SLC19A2: The gene is highky expressed in skeletal muscle, less in hear and placenta, and very low in intestine and kidney although the uptake there is very high. SLC19A3: most abundant in placenta, follwed by liver, kidney, and heart. IT
THMt3	3	Rajgopal A, Edmondnson A, Goldman ID, Zhao R.	SLC19A3 encodes a second thiamine transporter ThTr2.	Biochim Biophys Acta	2001	11731220	It has been shown that the transport is soudium independent and is stimulated by an outwardly directed H+ gradient. SLC19A2: The gene is highky expressed in skeletal muscle, less in hear and placenta, and very low in intestine and kidney although the uptake there is very high. SLC19A3: most abundant in placenta, follwed by liver, kidney, and heart. IT
THMTP	3	Lakaye B, Makarchikov AF, Wins P, Margineanu I, Roland S, Lins L, Aichour R, Lebeau L, El Moualij B, Zorzi W, Coumans B, Grisar T, Bettendorff L.	Human recombinant thiamine triphosphatase: purification, secondary structure and catalytic properties.	Int J Biochem Cell Biol	2004	15109578	IT In locusLink there is only one isoform marked instead of two as in the gene index based on GeneCards the reaction thakes place in cytoplasm activity has been measured by Bettendorff et al, 1996: vmax= 29+-5 nmol/mg/5min thmtp may modulate ion channel regulation (PMID:11899071). - is dead-end in model
THRD_L	3	Edgar AJ.	The human L-threonine 3-dehydrogenase gene is an expressed pseudogene.		2002	12361482	-catalyzed by same enzyme for serine deaminase -shown in Lehninger Biochemistry (4th ed.) pg. 682 MM
THYMDtm	3	Lai Y, Tse CM, Unadkat JD.	Mitochondrial expression of the human equilibrative nucleoside transporter 1 (hENT1) results in enhanced mitochondrial toxicity of antiviral drugs.	J Biol Chem	2004	14607828	IT liver mitochondria
THYOXt2	3	Lafreniere RG, Carrel L, Willard HF.	A novel transmembrane transporter encoded by the XPCT gene in Xq13.2.	Hum Mol Genet	1994	7981683	- cloned [Lafreniere 1994] - rat ortholog transports T3, T4 by Na- and H-independent facilitated diffusion [Friesema 2003]
THYOXt2	3	Friesema EC, Ganguly S, Abdalla A, Manning Fox JE, Halestrap AP, Visser TJ	Identification of monocarboxylate transporter 8 as a specific thyroid hormone transporter	J Biol Chem	2003	12871948	- cloned [Lafreniere 1994] - rat ortholog transports T3, T4 by Na- and H-independent facilitated diffusion [Friesema 2003]
TMABADH	3	Kikonyogo,A. , Pietruszko,R.	Aldehyde dehydrogenase from adult human brain that dehydrogenates gamma-aminobutyraldehyde: purification, characterization, cloning and distribution.		1996	8645224	-irreversible due to direction in KEGG
TMABADH	3	Vaz,F.M. , Fouchier,S.W. , Ofman,R. , Sommer,M. , Wanders,R.J.	Molecular and biochemical characterization of rat gamma-trimethylaminobutyraldehyde dehydrogenase and evidence for the involvement of human aldehyde dehydrogenase 9 in carnitine biosynthesis.		2000	10702312	-irreversible due to direction in KEGG

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
TMDK1	3	Johansson M, Brismar S, Karlsson A.	Human deoxycytidine kinase is located in the cell nucleus.	Proc Natl Acad Sci U S A	1997	9342341	activity of TK2 has been detected in both cytosol and mito. The fluorescence study could not identify a mito TK2, therefore, it is thought that there different transcript. TK2 seems also to act on dCyt but higher concentration is needed --> therefore rxn is not included IT
TMDK1	3	Krawiec K, Kierdaszuk B, Shugar D.	Inorganic tripolyphosphate (PPP(i)) as a phosphate donor for human deoxyribonucleoside kinases.	Biochem Biophys Res Commun	2003	12535661	activity of TK2 has been detected in both cytosol and mito. The fluorescence study could not identify a mito TK2, therefore, it is thought that there different transcript. TK2 seems also to act on dCyt but higher concentration is needed --> therefore rxn is not included IT
TMDPK	3	Zhao R, Gao F, Goldman ID.	Molecular cloning of human thiamin pyrophosphokinase.	Biochim Biophys Acta	2001	11342117	IT activity has been measured by Bettendorff et al, 1996: vmax=11 +- 2pmol/mg/min
TMDPP	3	Kubilus J, Lee LD, Baden HP	Purification of thymidine phosphorylase from human amniochorion	Biochim Biophys Acta	1978	718961	in cytoplasm or in mitochondria - not really clear. In patient with Mitochondrial neurogastrointestinal encephalomyopathy (MNGIE) the thymidine phosphorylase shows only 10% activity:"We hypothesize that, in patients with TP deficiency, increased levels of dThd and dUrd cause mitochondrial nucleotide pool imbalances, which, in turn, lead to mtDNA abnormalities including site-specific point mutations." - not included as mitochondrial reaction yet IT - first purified to homogeneity from human amniochorion [Kubilus 1978], [Gan 1981] - reversible [Brown 1998] - clears thymidine from the cytoplasm [Brown 1998]
TMDPP	3	Gan TE, Hallam L, Pilkington GR, Van der Weyden MB	A rapid and simple radiometric assay for thymidine phosphorylase of human peripheral blood cells	Clin Chim Acta	1981	7028324	in cytoplasm or in mitochondria - not really clear. In patient with Mitochondrial neurogastrointestinal encephalomyopathy (MNGIE) the thymidine phosphorylase shows only 10% activity:"We hypothesize that, in patients with TP deficiency, increased levels of dThd and dUrd cause mitochondrial nucleotide pool imbalances, which, in turn, lead to mtDNA abnormalities including site-specific point mutations." - not included as mitochondrial reaction yet IT - first purified to homogeneity from human amniochorion [Kubilus 1978], [Gan 1981] - reversible [Brown 1998] - clears thymidine from the cytoplasm [Brown 1998]
TMDPP	3	Brown NS, Bicknell R.	Thymidine phosphorylase, 2-deoxy-D-ribose and angiogenesis	Biochem J	1998	9693094	in cytoplasm or in mitochondria - not really clear. In patient with Mitochondrial neurogastrointestinal encephalomyopathy (MNGIE) the thymidine phosphorylase shows only 10% activity:"We hypothesize that, in patients with TP deficiency, increased levels of dThd and dUrd cause mitochondrial nucleotide pool imbalances, which, in turn, lead to mtDNA abnormalities including site-specific point mutations." - not included as mitochondrial reaction yet IT - first purified to homogeneity from human amniochorion [Kubilus 1978], [Gan 1981] - reversible [Brown 1998] - clears thymidine from the cytoplasm [Brown 1998]
TMDPPK	2	Bettendorff L, Mastrogiacomo F, Kish SJ, Grisar T.	Thiamine, thiamine phosphates, and their metabolizing enzymes in human brain.	J Neurochem	1996	8522961	IT proposed by Bettendorf et al., 1996 Such a function has to be pressent based on the fact that intracellular concentration of Thmtp has been measured (Bettendorf et al., 1996) thmtp is used by: - mitochondria: - PDHm - alpha-ketoglutarate deh.(1.2.4.2) - alpha-keto acid deh. (1.2.4.4) - cytosol: - transketolase (2.2.1.1)
TMDS	3	Kaneda S, Nalbantoglu J, Takeishi K, Shimizu K, Gotoh O, Seno T, Ayusawa D.	Structural and functional analysis of the human thymidylate synthase gene.	J Biol Chem	1990	2243092	IT homodimer (Genecards)
TMDS	3	Forsthoefel AM, Pena MM, Xing YY, Rafique Z, Berger FG.	Structural determinants for the intracellular degradation of human thymidylate synthase.	Biochemistry	2004	14967037	IT homodimer (Genecards)

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TMLYSOX	3	Hulse JD, Ellis SR, Henderson LM.	Carnitine biosynthesis. beta-Hydroxylation of trimethyllysine by an alpha-ketoglutarate-dependent mitochondrial dioxygenase.		1978	627563	-paper that states that this enzyme's localisation has not been resolved (may or may not be located in the mitochondrial matrix), so will assume it is in the inner membrane space (PMID:11802770) -sequence similar to purified rat enzyme; mitochondrial (see citation) -from Reactome: Carnitine is synthesized in four steps from trimethyllysine (generated in turn by the S-adenosyl-methionine mediated methylation of lysine residues in proteins, followed by protein hydrolysis). The enzymes that catalyze the first three steps of carnitine synthesis, converting trimethyllysine to gamma-butyrobetaine, are widely distributed in human tissues. The enzyme that catalyzes the last reaction, converting gamma-butyrobetaine to carnitine, is found only in liver and kidney cells, and at very low levels in brain tissues. Other tissues that require carnitine, such as muscle, are dependent on transport systems that mediate its export from the liver and uptake by other tissues. [Kerner & Hoppel 1998] MM
TMLYSOX	3	Vaz,F.M. , Ofman,R. , Westinga,K. , Back,J.W. , Wanders,R.J.	Molecular and Biochemical Characterization of Rat epsilon -N-Trimethyllysine Hydroxylase, the First Enzyme of Carnitine Biosynthesis.		2001	11431483	-paper that states that this enzyme's localisation has not been resolved (may or may not be located in the mitochondrial matrix), so will assume it is in the inner membrane space (PMID:11802770) -sequence similar to purified rat enzyme; mitochondrial (see citation) -from Reactome: Carnitine is synthesized in four steps from trimethyllysine (generated in turn by the S-adenosyl-methionine mediated methylation of lysine residues in proteins, followed by protein hydrolysis). The enzymes that catalyze the first three steps of carnitine synthesis, converting trimethyllysine to gamma-butyrobetaine, are widely distributed in human tissues. The enzyme that catalyzes the last reaction, converting gamma-butyrobetaine to carnitine, is found only in liver and kidney cells, and at very low levels in brain tissues. Other tissues that require carnitine, such as muscle, are dependent on transport systems that mediate its export from the liver and uptake by other tissues. [Kerner & Hoppel 1998] MM
TMLYSOX	3	Vaz FM, Wanders RJ.	Carnitine biosynthesis in mammals.		2002	11802770	-paper that states that this enzyme's localisation has not been resolved (may or may not be located in the mitochondrial matrix), so will assume it is in the inner membrane space (PMID:11802770) -sequence similar to purified rat enzyme; mitochondrial (see citation) -from Reactome: Carnitine is synthesized in four steps from trimethyllysine (generated in turn by the S-adenosyl-methionine mediated methylation of lysine residues in proteins, followed by protein hydrolysis). The enzymes that catalyze the first three steps of carnitine synthesis, converting trimethyllysine to gamma-butyrobetaine, are widely distributed in human tissues. The enzyme that catalyzes the last reaction, converting gamma-butyrobetaine to carnitine, is found only in liver and kidney cells, and at very low levels in brain tissues. Other tissues that require carnitine, such as muscle, are dependent on transport systems that mediate its export from the liver and uptake by other tissues. [Kerner & Hoppel 1998] MM
TRDR	3	Tamura T, Stadtman TC.	A new selenoprotein from human lung adenocarcinoma cells: purification, properties, and thioredoxin reductase activity.	Proc Natl Acad Sci U S A	1996	8577704	Genecards: activity with NADPH as acceptor homordimer acts on a number of substrates - 5,5'-dithiobis(2-nitrobenzoic acid), insulin (both in presence of thioredoxin, NADPH) - Tamura + Stadtman, 1996
TRDR	3	Koishi R, Kawashima I, Yoshimura C, Sugawara M, Serizawa N.	Cloning and characterization of a novel oxidoreductase KDRF from a human bone marrow-derived stromal cell line KM-102.	J Biol Chem	1997	8999974	Genecards: activity with NADPH as acceptor homordimer acts on a number of substrates - 5,5'-dithiobis(2-nitrobenzoic acid), insulin (both in presence of thioredoxin, NADPH) - Tamura + Stadtman, 1996
TRDR2	3	Xia L, Nordman T, Olsson JM, Damdimopoulos A, Bjorkhem-Bergman L, Nalvarte I, Eriksson LC, Arner ES, Spyrou G, Bjornstedt M.	The mammalian cytosolic selenoenzyme thioredoxin reductase reduces ubiquinone. A novel mechanism for defense against oxidative stress.	J Biol Chem	2003	12435734	IT reaction has been experimentally shown. apparently there are 3 important extra-mitochondrial ubiquinone reductase; lipoamide dehydrogenas, glutathionine reductase and thioredoxdin reductase. the question is how ubiquinone come into cytosol (and liposome). There might be a ubiquinol release from mitochondria but i did not found literature on it - will leave as gap for the moment.
TRDRm	3	Miranda-Vizuete A, Damdimopoulos AE, Pedrajas JR, Gustafsson JA, Spyrou G.	Human mitochondrial thioredoxin reductase cDNA cloning, expression and genomic organization.	Eur J Biochem	1999	10215850	IT

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TRDRm	3	Sun QA, Kirnarsky L, Sherman S, Gladyshev VN.	Selenoprotein oxidoreductase with specificity for thioredoxin and glutathione systems.	Proc Natl Acad Sci U S A	2001	11259642	IT
TRDRm	3	Kim MR, Chang HS, Kim BH, Kim S, Baek SH, Kim JH, Lee SR, Kim JR.	Involvements of mitochondrial thioredoxin reductase (TrxR2) in cell proliferation.	Biochem Biophys Res Commun	2003	12705894	IT
TREHe	3	Ishihara R, Taketani S, Sasai-Takedatsu M, Kino M, Tokunaga R, Kobayashi Y	Molecular cloning, sequencing and expression of cDNA encoding human trehalase	Gene	1997	9427547	- extrinsic to plasma membrane, GPI anchored [GO],[UniProt] - trehalose is broken down into glucose at the brush border [Richards et al, Food Chem Toxicol 2002] - mainly found in kidney, liver and small intestine [Ishihara, Gene 1997]
TREHe	3	Richards AB, Krakowka S, Dexter LB, Schmid H, Wolterbeek AP, Waalkens-Berendsen DH, Shigoyuki A, Kurimoto M	Trehalose: a review of properties, history of use and human tolerance, and results of multiple safety studies	Food Chem Toxicol	2002	12065209	- extrinsic to plasma membrane, GPI anchored [GO],[UniProt] - trehalose is broken down into glucose at the brush border [Richards et al, Food Chem Toxicol 2002] - mainly found in kidney, liver and small intestine [Ishihara, Gene 1997]
TRPHYDRO2	3	Wang L, Erlandsen H, Haavik J, Knappskog PM, Stevens RC	Three-dimensional structure of human tryptophan hydroxylase and its implications for the biosynthesis of the neurotransmitters serotonin and melatonin	Biochemistry	2002	12379098	Citations give this reaction.
TRPO2	3	Comings DE, Muhleman D, Dietz G, Sherman M, Forest GL	Sequence of human tryptophan 2,3-dioxygenase (TDO2): presence of a glucocorticoid response-like element composed of a GTT repeat and an intronic CCCCT repeat	Genomics	1995	8666386	Rate-limiting enzyme.
TSTSTERONESULT	3	Chatterjee B, Echchgadda I, Song CS	Vitamin D receptor regulation of the steroid/bile acid sulfotransferase SULT2A1	Methods Enzymol	2005	16399349	localization cytosol by swiss-prot specificity: liver, adrenal glands. Sulfotransferase enzymes catalyze the sulfate conjugation of many hormones, neurotransmitters, drugs, and xenobiotic compounds. These cytosolic enzymes are different in their tissue distributions and substrate specificities. The gene structure (number and length of exons) is similar among family members. This gene is primarily expressed in liver and adrenal tissues where the encoded protein sulfates steroids and bile acids. NJ
TYR3MO2	3	Bodeau-Pean S, Ravassard P, Neuner-Jehle M, Faucheux B, Mallet J, Dumas S	A human tyrosine hydroxylase isoform associated with progressive supranuclear palsy shows altered enzymatic activity	J Biol Chem	1999	9920892	This enzyme is the rate limiting step in catecholamine biosynthesis.
TYRASE	2	Box NF, Wyeth JR, Mayne CJ, O'Gorman LE, Martin NG, Sturm RA	Complete sequence and polymorphism study of the human TYRP1 gene encoding tyrosinase-related protein 1	Mamm Genome	1998	9434945	There may be a parallel pathway (as indicated in KEGG) that is involved in the synthesis of melanin. These reactions should take place exclusively in the melanosomes of melanocytes, but they are localized in the cytoplasm in this reconstruction because that specialized compartment is not available. The reference provides some physiological data. The other tyr gene (7299) may also be involved.
TYRDOPO	3	Pomerantz SH	The tyrosine hydroxylase activity of mammalian tyrosinase	J Biol Chem	1968	5294951	reaction mechanism (2 of each) questionable
TYRDOPO	3	Aaron Bunsen Lerner, Thomas B. Fitzpatrick, Evan Calkins, and William H. Summerson	MAMMALIAN TYROSINASE: PREPARATION AND PROPERTIES	J Biol Chem	1949		reaction mechanism (2 of each) questionable
TYROXDAc	3	Anderson MC, Hasan F, McCrodden JM, Tipton KF	Monoamine oxidase inhibitors and the cheese effect	Neurochem Res	1993	8255365	Biochemical data for this reaction is from the references which discuss the cheese effect. In short, certain Mao inhibitors (with clinical applications in treating depression) also inhibit the degradation of tyramine which is found in cheese, among other foods.
TYROXDAc	3	Humphrey SJ, Curry JT, Turman CN, Stryd RP	Cardiovascular sympathomimetic amine interactions in rats treated with monoamine oxidase inhibitors and the novel oxazolidinone antibiotic linezolid	J Cardiovasc Pharmacol	2001	11336106	Biochemical data for this reaction is from the references which discuss the cheese effect. In short, certain Mao inhibitors (with clinical applications in treating depression) also inhibit the degradation of tyramine which is found in cheese, among other foods.
TYROXDAc	3	Youdim MB, Weinstock M	Therapeutic applications of selective and non-selective inhibitors of monoamine oxidase A and B that do not cause significant tyramine potentiation	Neurotoxicology	2004	14697899	Biochemical data for this reaction is from the references which discuss the cheese effect. In short, certain Mao inhibitors (with clinical applications in treating depression) also inhibit the degradation of tyramine which is found in cheese, among other foods.
TYRTAm	3	Rettenmeier R, Natt E, Zentgraf H, Scherer G.	Isolation and characterization of the human tyrosine aminotransferase gene.	Nucleic Acids Res	1990	1973834	- Additional information added by RS/TV: 1) Tyrosine aminotransferase is a liver-specific enzyme that converts tyrosine to p-hydroxyphenylpyruvate in a pyridoxal phosphate-dependent transamination reaction according to Rettenmeier R, Natt E, Zentgraf H, Scherer G. Isolation and characterization of the human tyrosine aminotransferase gene. Nucleic Acids Res. 1990 Jul 11;18(13):3853-61. PMID: 1973834 mitochondrial according to Entrez gene database catalytic activity specified by GeneCards

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UAGDP	3	Mio T, Yabe T, Arisawa M, Yamada-Okabe H	The eukaryotic UDP-N-acetylglucosamine pyrophosphorylases. Gene cloning, protein expression, and catalytic mechanism	J Biol Chem	1998	9603950	- shown as irreversible in Devlin p. 672, Orten p. 244, Varki p. 74 6675: - cytoplasmic [UniProt] 91373: - only annotated as UDP-GlcNAc pyrophosphorylase in H-Inv Db
UDPDOLPT_L	0	Bossuyt X, Blanckaert N.	Topology of nucleotide-sugar:dolichyl phosphate glycosyltransferases involved in the dolichol pathway for protein glycosylation in native rat liver microsomes	Biochem J	1993	8280060	active centres of the transferases are cytoplasmically oriented Bossuyt X, Blanckaert N. Biochem J. 1993 Dec 15;296 (Pt 3):627-32.
UDPDOLPT_U	0	Imbach T, Burda P, Kuhnert P, Wevers RA, Aebi M, Berger EG, Hennet T.	A mutation in the human ortholog of the Saccharomyces cerevisiae ALG6 gene causes carbohydrate-deficient glycoprotein syndrome type-Ic.	Proc Natl Acad Sci USA	1999	10359825	active centres of the transferases are cytoplasmically oriented Bossuyt X, Blanckaert N. Biochem J. 1993 Dec 15;296 (Pt 3):627-32. Alg5p is ubiquitously expressed [Imbach et al, PNAS 1999]
UDPGALtg	3	Miura N, Ishida N, Hoshino M, Yamauchi M, Hara T, Ayusawa D, Kawakita M	Human UDP-galactose translocator: molecular cloning of a complementary DNA that complements the genetic defect of a mutant cell line deficient in UDP-galactose translocator	J Biochem (Tokyo)	1996	8889805	- cloned [Miura 1996], [Ishida 1996] - complemented UDPGal Golgi transport defect [Miura 1996] - expressed [Yoshioka 1997], [Sun-Wada 1998] - specific for UDPGal [Yoshioka 1997], [Sun-Wada 1998] and UDPGalNAc [Segawa 2002] - localized in Golgi [Yoshioka 1997], [Sun-Wada 1998]
UDPGALtg	3	Yoshioka S, Sun-Wada GH, Ishida N, Kawakita M	Expression of the human UDP-galactose transporter in the Golgi membranes of murine Had-1 cells that lack the endogenous transporter	J Biochem (Tokyo)	1997	9399569	- cloned [Miura 1996], [Ishida 1996] - complemented UDPGal Golgi transport defect [Miura 1996] - expressed [Yoshioka 1997], [Sun-Wada 1998] - specific for UDPGal [Yoshioka 1997], [Sun-Wada 1998] and UDPGalNAc [Segawa 2002] - localized in Golgi [Yoshioka 1997], [Sun-Wada 1998]
UDPGALtg	3	Sun-Wada GH, Yoshioka S, Ishida N, Kawakita M	Functional expression of the human UDP-galactose transporters in the yeast Saccharomyces cerevisiae	J Biochem (Tokyo)	1998	9562625	- cloned [Miura 1996], [Ishida 1996] - complemented UDPGal Golgi transport defect [Miura 1996] - expressed [Yoshioka 1997], [Sun-Wada 1998] - specific for UDPGal [Yoshioka 1997], [Sun-Wada 1998] and UDPGalNAc [Segawa 2002] - localized in Golgi [Yoshioka 1997], [Sun-Wada 1998]
UDPGALtg	3	Segawa H, Kawakita M, Ishida N	Human and Drosophila UDP-galactose transporters transport UDP-N-acetylgalactosamine in addition to UDP-galactose	Eur J Biochem	2002	11784306	- cloned [Miura 1996], [Ishida 1996] - complemented UDPGal Golgi transport defect [Miura 1996] - expressed [Yoshioka 1997], [Sun-Wada 1998] - specific for UDPGal [Yoshioka 1997], [Sun-Wada 1998] and UDPGalNAc [Segawa 2002] - localized in Golgi [Yoshioka 1997], [Sun-Wada 1998]
UDPGD	2	Banhegyi G, Braun L, Csala M, Puskas F, Mandl J	Ascorbate metabolism and its regulation in animals	Free Radic Biol Med	1997	9296457	- reaction described in Devlin pp 611-612 - shown as irreversible in Orten p 241 - thought to be important for hyaluronan biosynthesis, which is occurs on inner side of plasma membrane - occurs in the cytosol [Banhegyi 1997]
UDPGD	2	Spicer AP, Kaback LA, Smith TJ, Seldin MF	Molecular cloning and characterization of the human and mouse UDP-glucose dehydrogenase genes	J Biol Chem	1998	9737970	- reaction described in Devlin pp 611-612 - shown as irreversible in Orten p 241 - thought to be important for hyaluronan biosynthesis, which is occurs on inner side of plasma membrane - occurs in the cytosol [Banhegyi 1997]
UDPGLCAter	3	Muraoka M, Kawakita M, Ishida N	Molecular characterization of human UDP-glucuronic acid/UDP-N-acetylgalactosamine transporter, a novel nucleotide sugar transporter with dual substrate specificity	FEBS Lett	2001	11322953	- cloned [Muraoka 2001] - UDP-GlcA and UDP-GalNAc transport activity determined by expression in yeast [Muraoka 2001] - ER [Muraoka 2001]
UDPGLCter	2	Trombetta ES, Helenius A.	Glycoprotein reglucosylation and nucleotide sugar utilization in the secretory pathway: identification of a nucleoside diphosphatase in the endoplasmic reticulum.	EMBO J	1999	10369669	- there is a UDP-Glc transporter in both the ER and Golgi [Varki, p. 79-80] - UDP-Glc is transported from the cytosol where it is synthesized into the ER lumen where it is used by UDP-Glc:glycoprotein glucosyltransferase (see refs in [Trombetta 1999])

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UDPGLCtg	3	Milla ME, Clairmont CA, Hirschberg CB	Reconstitution into proteoliposomes and partial purification of the Golgi apparatus membrane UDP-galactose, UDP-xylose, and UDP-glucuronic acid transport activities	J Biol Chem	1992	1730575	23443: - cloned [Ishida 1999] - ubiquitous [Ishida 1999] - Golgi [Ishida 1999] - transports UDPGlc [Ishida 1999] 11046: - cloned [Ishida 2005], [Suda 2004] - 50% similarity w/ human SLC35D1, fruitfly fringe connection (frc) transporter, nematode SQV-7 transporter [Ishida 2005] - expression in yeast yielded significant (but only slightly higher) transport of UDPGlcNAc [Ishida 2005], [Suda 2004], UDPGlc & UDPMan [Suda 2004]; in mammalian cells only transported UDPGlcNAc and UDPGlc [Suda 2004] - Golgi [Ishida 2005], [Suda 2004] - high in colon, lung, stomach; moderate in WBC, pancreas; low in thyroid, uterus, placenta, sk muscle, testis, adrenal glands; barely detectable in liver, kidney, mammary, salivary, spinal cord, trachea [Suda 2004] 84912: - Golgi [Ashikov 2005] - demonstrated UDP-Glc, UDP-Xyl transport activity by expressing genes in yeast and measuring transport in vitro from Golgi fractions [Ashikov 2005] - earlier results in rat showed that UDP-Xyl can access Golgi but protein had not been characterized at molecular level [Nuwayhid 1986], [Milla 1992]
UDPGLCtg	3	Nuwayhid N, Glaser JH, Johnson JC, Conrad HE, Hauser SC, Hirschberg CB	Xylosylation and glucuronosylation reactions in rat liver Golgi apparatus and endoplasmic reticulum	J Biol Chem	1986	3093474	23443: - cloned [Ishida 1999] - ubiquitous [Ishida 1999] - Golgi [Ishida 1999] - transports UDPGlc [Ishida 1999] 11046: - cloned [Ishida 2005], [Suda 2004] - 50% similarity w/ human SLC35D1, fruitfly fringe connection (frc) transporter, nematode SQV-7 transporter [Ishida 2005] - expression in yeast yielded significant (but only slightly higher) transport of UDPGlcNAc [Ishida 2005], [Suda 2004], UDPGlc & UDPMan [Suda 2004]; in mammalian cells only transported UDPGlcNAc and UDPGlc [Suda 2004] - Golgi [Ishida 2005], [Suda 2004] - high in colon, lung, stomach; moderate in WBC, pancreas; low in thyroid, uterus, placenta, sk muscle, testis, adrenal glands; barely detectable in liver, kidney, mammary, salivary, spinal cord, trachea [Suda 2004] 84912: - Golgi [Ashikov 2005] - demonstrated UDP-Glc, UDP-Xyl transport activity by expressing genes in yeast and measuring transport in vitro from Golgi fractions [Ashikov 2005] - earlier results in rat showed that UDP-Xyl can access Golgi but protein had not been characterized at molecular level [Nuwayhid 1986], [Milla 1992]
UDPGLCtg	3	Ishida N, Yoshioka S, Chiba Y, Takeuchi M, Kawakita M	Molecular cloning and functional expression of the human Golgi UDP-N-acetylglucosamine transporter	J Biochem (Tokyo)	1999	10393322	23443: - cloned [Ishida 1999] - ubiquitous [Ishida 1999] - Golgi [Ishida 1999] - transports UDPGlc [Ishida 1999] 11046: - cloned [Ishida 2005], [Suda 2004] - 50% similarity w/ human SLC35D1, fruitfly fringe connection (frc) transporter, nematode SQV-7 transporter [Ishida 2005] - expression in yeast yielded significant (but only slightly higher) transport of UDPGlcNAc [Ishida 2005], [Suda 2004], UDPGlc & UDPMan [Suda 2004]; in mammalian cells only transported UDPGlcNAc and UDPGlc [Suda 2004] - Golgi [Ishida 2005], [Suda 2004] - high in colon, lung, stomach; moderate in WBC, pancreas; low in thyroid, uterus, placenta, sk muscle, testis, adrenal glands; barely detectable in liver, kidney, mammary, salivary, spinal cord, trachea [Suda 2004] 84912: - Golgi [Ashikov 2005] - demonstrated UDP-Glc, UDP-Xyl transport activity by expressing genes in yeast and measuring transport in vitro from Golgi fractions [Ashikov 2005] - earlier results in rat showed that UDP-Xyl can access Golgi but protein had not been characterized at molecular level [Nuwayhid 1986], [Milla 1992]

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UDPGLCtg	3	Suda T, Kamiyama S, Suzuki M, Kikuchi N, Nakayama K, Narimatsu H, Jigami Y, Aoki T, Nishihara S	Molecular cloning and characterization of a human multisubstrate specific nucleotide-sugar transporter homologous to Drosophila fringe connection	J Biol Chem	2004	15082721	23443: - cloned [Ishida 1999] - ubiquitous [Ishida 1999] - Golgi [Ishida 1999] - transports UDPGlc [Ishida 1999] 11046: - cloned [Ishida 2005], [Suda 2004] - 50% similarity w/ human SLC35D1, fruitfly fringe connection (frc) transporter, nematode SQV-7 transporter [Ishida 2005] - expression in yeast yielded significant (but only slightly higher) transport of UDPGlcNAc [Ishida 2005], [Suda 2004], UDPGlc & UDPMan [Suda 2004]; in mammalian cells only transported UDPGlcNAc and UDPGlc [Suda 2004] - Golgi [Ishida 2005], [Suda 2004] - high in colon, lung, stomach; moderate in WBC, pancreas; low in thyroid, uterus, placenta, sk muscle, testis, adrenal glands; barely detectable in liver, kidney, mammary, salivary, spinal cord, trachea [Suda 2004] 84912: - Golgi [Ashikov 2005] - demonstrated UDP-Glc, UDP-Xyl transport activity by expressing genes in yeast and measuring transport in vitro from Golgi fractions [Ashikov 2005] - earlier results in rat showed that UDP-Xyl can access Golgi but protein had not been characterized at molecular level [Nuwayhid 1986], [Milla 1992]
UDPGLCtg	3	Ishida N, Kuba T, Aoki K, Miyatake S, Kawakita M, Sanai Y	Identification and characterization of human Golgi nucleotide sugar transporter SLC35D2, a novel member of the SLC35 nucleotide sugar transporter family	Genomics	2005	15607426	23443: - cloned [Ishida 1999] - ubiquitous [Ishida 1999] - Golgi [Ishida 1999] - transports UDPGlc [Ishida 1999] 11046: - cloned [Ishida 2005], [Suda 2004] - 50% similarity w/ human SLC35D1, fruitfly fringe connection (frc) transporter, nematode SQV-7 transporter [Ishida 2005] - expression in yeast yielded significant (but only slightly higher) transport of UDPGlcNAc [Ishida 2005], [Suda 2004], UDPGlc & UDPMan [Suda 2004]; in mammalian cells only transported UDPGlcNAc and UDPGlc [Suda 2004] - Golgi [Ishida 2005], [Suda 2004] - high in colon, lung, stomach; moderate in WBC, pancreas; low in thyroid, uterus, placenta, sk muscle, testis, adrenal glands; barely detectable in liver, kidney, mammary, salivary, spinal cord, trachea [Suda 2004] 84912: - Golgi [Ashikov 2005] - demonstrated UDP-Glc, UDP-Xyl transport activity by expressing genes in yeast and measuring transport in vitro from Golgi fractions [Ashikov 2005] - earlier results in rat showed that UDP-Xyl can access Golgi but protein had not been characterized at molecular level [Nuwayhid 1986], [Milla 1992]
UDPGLCtg	3	Ashikov A, Routier F, Fuhlrott J, Helmus Y, Wild M, Gerardy Schahn R, Bakker H	The Human Solute Carrier Gene SLC35B4 Encodes a Bifunctional Nucleotide Sugar Transporter with Specificity for UDP-Xylose and UDP-N-Acetylglucosamine	J Biol Chem	2005	15911612	23443: - cloned [Ishida 1999] - ubiquitous [Ishida 1999] - Golgi [Ishida 1999] - transports UDPGlc [Ishida 1999] 11046: - cloned [Ishida 2005], [Suda 2004] - 50% similarity w/ human SLC35D1, fruitfly fringe connection (frc) transporter, nematode SQV-7 transporter [Ishida 2005] - expression in yeast yielded significant (but only slightly higher) transport of UDPGlcNAc [Ishida 2005], [Suda 2004], UDPGlc & UDPMan [Suda 2004]; in mammalian cells only transported UDPGlcNAc and UDPGlc [Suda 2004] - Golgi [Ishida 2005], [Suda 2004] - high in colon, lung, stomach; moderate in WBC, pancreas; low in thyroid, uterus, placenta, sk muscle, testis, adrenal glands; barely detectable in liver, kidney, mammary, salivary, spinal cord, trachea [Suda 2004] 84912: - Golgi [Ashikov 2005] - demonstrated UDP-Glc, UDP-Xyl transport activity by expressing genes in yeast and measuring transport in vitro from Golgi fractions [Ashikov 2005] - earlier results in rat showed that UDP-Xyl can access Golgi but protein had not been characterized at molecular level [Nuwayhid 1986], [Milla 1992]

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UDPGLDCg	3	Silbert JE, DeLuca S	The synthesis of uridine diphosphate xylose by particulate preparations from mouse mast-cell tumors	Biochim Biophys Acta	1967	4293108	- reaction described in Devlin p. 672, Varki p.74 - occurs in the lumen of ER or Golgi [Silbert, Biochim Biophy Acta, 1967], [Kearns, J Biol Chem 1993] - cloned and expressed, had UDP-glucuronate decarboxylase activity [Moriarity 2002] - perinuclear Golgi [Moriarity 2002] - highest expression levels in heart, brain, and testes; moderate levels in kidney, liver, lung, lower levels in spleen, sk muscle; immunochemical studies showed significant staining in kidney, liver, and brain [Moriarity 2002] - 75-80% amino acid sequence identity and 90% similarity between plants and mammals [Moriarity 2002]
UDPGLDCg	3	Moriarity JL, Hurt KJ, Resnick AC, Storm PB, Laroy W, Schnaar RL, Snyder SH	UDP-glucuronate decarboxylase, a key enzyme in proteoglycan synthesis: cloning, characterization, and localization	J Biol Chem	2002	11877387	- reaction described in Devlin p. 672, Varki p.74 - occurs in the lumen of ER or Golgi [Silbert, Biochim Biophy Acta, 1967], [Kearns, J Biol Chem 1993] - cloned and expressed, had UDP-glucuronate decarboxylase activity [Moriarity 2002] - perinuclear Golgi [Moriarity 2002] - highest expression levels in heart, brain, and testes; moderate levels in kidney, liver, lung, lower levels in spleen, sk muscle; immunochemical studies showed significant staining in kidney, liver, and brain [Moriarity 2002] - 75-80% amino acid sequence identity and 90% similarity between plants and mammals [Moriarity 2002]
UGCG	3	Ichikawa S, Sakiyama H, Suzuki G, Hidari KI, Hirabayashi Y.	Expression cloning of a cDNA for human ceramide glucosyltransferase that catalyzes the first glycosylation step of glycosphingolipid synthesis.	Proc Natl Acad Sci	1996	8643456	ER - uniprot May serve as a "flippase" as well as a glucosyltransferase that transfers glucose to ceramide. --> dual fxn as transporter also Glycosphingolipids (GSLs) are a group of membrane components that contain lipid and sugar moieties. They are present in essentially all animal cells and are believed to have important roles in various cellular processes. UDP-glucose ceramide glucosyltransferase catalyzes the first glycosylation step in glycosphingolipid biosynthesis. The product, glucosylceramide, is the core structure of more than 300 GSLs. UGCG is widely expressed and transciption is upregulated during keratinocyte differentiation. NJ
UGLT	0	Holden HM, Rayment I, Thoden JB	Structure and function of enzymes of the Leloir pathway for galactose metabolism	J Biol Chem	2003	12923184	- UGLT reaction is reversible [Holden et al, J Biol Chem, 2003]
UGT1A1r	3	Basu NK, Kubota S, Meselhy MR, Ciotti M, Chowdhury B, Hartori M, Owens IS.	Gastrointestinally distributed UDP-glucuronosyltransferase 1A10, which metabolizes estrogens and nonsteroidal anti-inflammatory drugs, depends upon phosphorylation.	J Biol Chem	2004		specificity: microsomal - uniprot specificity: Liver and colon. This gene encodes a UDP-glucuronosyltransferase, an enzyme of the glucuronidation pathway that transforms small lipophilic molecules, such as steroids, bilirubin, hormones, and drugs, into water-soluble, excretable metabolites. This gene is part of a complex locus that encodes several UDP-glucuronosyltransferases. The locus includes thirteen unique alternate first exons followed by four common exons. Four of the alternate first exons are considered pseudogenes. Each of the remaining nine 5' exons may be spliced to the four common exons, resulting in nine proteins with different N-termini and identical C-termini. Each first exon encodes the substrate binding site, and is regulated by its own promoter. The enzyme encoded by this gene has glucuronidase activity on mycophenolic acid, coumarins, and quinolines. NJ
UGT1A1r	3	Mackenzie PI, Owens IS, Burchell B, Bock KW, Bairoch A, Belanger A, Fournel-Gigleux S, Green M, Hum DW, Iyanagi T, Lancet D, Louisot P, Magdalou J, Chowdhury JR, Ritter JK, Schachter H, Tephly TR, Tipton KF, Nebert DW.	The UDP glycosyltransferase gene superfamily: recommended nomenclature update based on evolutionary divergence.	Pharmacogenetics	1997	9295054	specificity: microsomal - uniprot specificity: Liver and colon. This gene encodes a UDP-glucuronosyltransferase, an enzyme of the glucuronidation pathway that transforms small lipophilic molecules, such as steroids, bilirubin, hormones, and drugs, into water-soluble, excretable metabolites. This gene is part of a complex locus that encodes several UDP-glucuronosyltransferases. The locus includes thirteen unique alternate first exons followed by four common exons. Four of the alternate first exons are considered pseudogenes. Each of the remaining nine 5' exons may be spliced to the four common exons, resulting in nine proteins with different N-termini and identical C-termini. Each first exon encodes the substrate binding site, and is regulated by its own promoter. The enzyme encoded by this gene has glucuronidase activity on mycophenolic acid, coumarins, and quinolines. NJ

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UGT1A3r	3	Levesque E, Turgeon D, Carrier JS, Montminy V, Beaulieu M, Belanger A.	Isolation and characterization of the UGT2B28 cDNA encoding a novel human steroid conjugating UDP-glucuronosyltransferase.	Biochemistry	2001	11300766	specificity: microsomal - uniprot specificity: Liver and colon. This gene encodes a UDP-glucuronosyltransferase, an enzyme of the glucuronidation pathway that transforms small lipophilic molecules, such as steroids, bilirubin, hormones, and drugs, into water-soluble, excretable metabolites. This gene is part of a complex locus that encodes several UDP-glucuronosyltransferases. The locus includes thirteen unique alternate first exons followed by four common exons. Four of the alternate first exons are considered pseudogenes. Each of the remaining nine 5' exons may be spliced to the four common exons, resulting in nine proteins with different N-termini and identical C-termini. Each first exon encodes the substrate binding site, and is regulated by its own promoter. The enzyme encoded by this gene has glucuronidase activity on mycophenolic acid, coumarins, and quinolines. UGT2B28: PMID: 11300766. TISSUE SPECIFICITY: High expression in the liver and pancreas, lower in the skeletal muscle and kidney. See also PMID: 14643063 and 15666817 - for more about UGT2B7/17 - high expression in prostate gland (epithelium). NJ
UGT1A3r	3	Belanger A, Pelletier G, Labrie F, Barbier O, Chouinard S.	Inactivation of androgens by UDP-glucuronosyltransferase enzymes in humans.	Trends Endocrinol Metab	2003	14643063	specificity: microsomal - uniprot specificity: Liver and colon. This gene encodes a UDP-glucuronosyltransferase, an enzyme of the glucuronidation pathway that transforms small lipophilic molecules, such as steroids, bilirubin, hormones, and drugs, into water-soluble, excretable metabolites. This gene is part of a complex locus that encodes several UDP-glucuronosyltransferases. The locus includes thirteen unique alternate first exons followed by four common exons. Four of the alternate first exons are considered pseudogenes. Each of the remaining nine 5' exons may be spliced to the four common exons, resulting in nine proteins with different N-termini and identical C-termini. Each first exon encodes the substrate binding site, and is regulated by its own promoter. The enzyme encoded by this gene has glucuronidase activity on mycophenolic acid, coumarins, and quinolines. UGT2B28: PMID: 11300766. TISSUE SPECIFICITY: High expression in the liver and pancreas, lower in the skeletal muscle and kidney. See also PMID: 14643063 and 15666817 - for more about UGT2B7/17 - high expression in prostate gland (epithelium). NJ
UGT1A5r2	2	Barua AB, Sidell N.	Retinoyl beta-glucuronide: a biologically active interesting retinoid.	J Nutr	2004	14704335	IT
UGT1A8r	3	Jin CJ, Miners JO, Lillywhite KJ, Mackenzie PI.	cDNA cloning and expression of two new members of the human liver UDP-glucuronosyltransferase 2B subfamily.	Biochem Biophys Res Commun	1993	8333863	specificity: microsomal - uniprot specificity: Liver and colon. This gene encodes a UDP-glucuronosyltransferase, an enzyme of the glucuronidation pathway that transforms small lipophilic molecules, such as steroids, bilirubin, hormones, and drugs, into water-soluble, excretable metabolites. This gene is part of a complex locus that encodes several UDP-glucuronosyltransferases. The locus includes thirteen unique alternate first exons followed by four common exons. Four of the alternate first exons are considered pseudogenes. Each of the remaining nine 5' exons may be spliced to the four common exons, resulting in nine proteins with different N-termini and identical C-termini. Each first exon encodes the substrate binding site, and is regulated by its own promoter. The enzyme encoded by this gene has glucuronidase activity on mycophenolic acid, coumarins, and quinolines. UGT2B28: PMID: 11300766. TISSUE SPECIFICITY: High expression in the liver and pancreas, lower in the skeletal muscle and kidney. UGT2B4: PMID: 11300766. PMID: 8333863 NJ
UPP3S	0	Tsai SF, Bishop DF, Desnick RJ.	Human uroporphyrinogen III synthase: molecular cloning, nucleotide sequence, and expression of a full length cDNA.	Proc Natl Acad Sci U S A	1988	3174619	- Added by RS/TV Proteome - Uroporphyrinogen-III synthase (UROS), hmb is rapidly converted to uroporphyrinogen III by an intramolecular rearrangment of the D-pyrrole group and ring closure. (Tsai SF, Bishop DF, Desnick RJ. Proc Natl Acad Sci U S A. 1988 Oct;85(19):7049-53) - Although expressed in multiple tissues, prominently expressed in liver, heart, and skeletal muscle. (Aizencang G, Solis C, Bishop DF, Warner C, Desnick RJ. Genomics. 2000 Dec 1;70(2):223-31.) - Catalytic activity also specified by GeneCards.

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UPPDC1	3	Romeo PH, Raich N, Dubart A, Beaupain D, Pryor M, Kushner J, Cohen-Solal M, Goossens M.	Molecular cloning and nucleotide sequence of a complete human uroporphyrinogen decarboxylase cDNA.	J Biol Chem	1986	3015909	- Added by RS/TV Biochem textbook - Cytoplasmic according to GeneCards - Uroporphyrinogen decarboxylase is a cytosolic enzyme involved in the biosynthesis of heme. It catalyzes the sequential removal of the four carboxyl groups of the carboxymethyl side chains of uroporphyrinogen to yield coproporphyrinogen. (Romeo PH, Raich N, Dubart A, Beaupain D, Pryor M, Kushner J, Cohen-Solal M, Goossens M. J Biol Chem. 1986 Jul 25;261(21):9825-31)
UPPN	3	Vreken P, van Kuilenburg AB, Hamajima N, Meinsma R, van Lenthe H, Gohlich-Ratmann G, Assmann BE, Wevers RA, van Gennip AH	cDNA cloning, genomic structure and chromosomal localization of the human BUP-1 gene encoding beta-ureidopropionase	Biochim Biophys Acta	1999	10542323	Standard degradation pathway of uracil, which also works for a related drug according to the first citation. Pyrimidine Catabolism
UPPN	3	Kuhara T	Diagnosis and monitoring of inborn errors of metabolism using urease-pretreatment of urine, isotope dilution, and gas chromatography-mass spectrometry	J Chromatogr B Analyt Technol Biomed Life Sci	2002	12450676	Standard degradation pathway of uracil, which also works for a related drug according to the first citation. Pyrimidine Catabolism
URCN	3	Kessler D, Retey J, Schulz GE	Structure and action of urocanase	J Mol Biol	2004	15313616	Common enzyme.
UREAt	3	Dai G, Levy O, Carrasco N	Cloning and characterization of the thyroid iodide transporter	Nature	1996	8559252	-cloned [Hediger 1989] - cotransports Glc/2 Na+, Gal/2 Na+ [Quick 2001] - H+ can replace Na+ [Hirayama 1994] - behaves as urea channel in the absence of substrates; cotransports urea under substrate-transporting conditions [Leung 2000] - Na+ transport occurs by a saturable uniport mechanism; water permeation is through a low conductance water channel [Loo 1999] - brush border membrane [Wright 1994] - plasma membrane; see [Wright 2004] for refs 6563,8170 - In mammalian cells, urea is the chief end-product of nitrogen catabolism and plays an important role in the urinary concentration mechanism. Thus, the plasma membrane of erythrocytes and some renal epithelial cells exhibit an elevated urea permeability that is mediated by highly selective urea transporters. In mammals, 2 urea transporters have been identified: the renal tubular urea transporter, UT2, and the erythrocyte urea transporter, UT11 (SLC14A1; MIM 111000).[supplied by OMIM] 6528: - cloned [Dai 1996] - gene has 84% identity to the rat homolog [Smanik 1996] - sodium iodide cotransport [Dai 1996]; 2 Na+ per I- [Eskandar - primarily in thyroid gland [De La Vieja 2000], also expressed - also transports ClO3-, SCN-, SeCN-, NO3-, Br-, BF4-, IO4-, I - basolateral plasma membrane; see [Wright 2004] for refs
UREAt	3	Smanik PA, Liu Q, Furminger TL, Ryu K, Xing S, Mazzaferri EL, Jhiang SM	Cloning of the human sodium lodide symporter	Biochem Biophys Res Commun	1996	8806637	-cloned [Hediger 1989] - cotransports Glc/2 Na+, Gal/2 Na+ [Quick 2001] - H+ can replace Na+ [Hirayama 1994] - behaves as urea channel in the absence of substrates; cotransports urea under substrate-transporting conditions [Leung 2000] - Na+ transport occurs by a saturable uniport mechanism; water permeation is through a low conductance water channel [Loo 1999] - brush border membrane [Wright 1994] - plasma membrane; see [Wright 2004] for refs 6563,8170 - In mammalian cells, urea is the chief end-product of nitrogen catabolism and plays an important role in the urinary concentration mechanism. Thus, the plasma membrane of erythrocytes and some renal epithelial cells exhibit an elevated urea permeability that is mediated by highly selective urea transporters. In mammals, 2 urea transporters have been identified: the renal tubular urea transporter, UT2, and the erythrocyte urea transporter, UT11 (SLC14A1; MIM 111000).[supplied by OMIM] 6528: - cloned [Dai 1996] - gene has 84% identity to the rat homolog [Smanik 1996] - sodium iodide cotransport [Dai 1996]; 2 Na+ per I- [Eskandar - primarily in thyroid gland [De La Vieja 2000], also expressed - also transports ClO3-, SCN-, SeCN-, NO3-, Br-, BF4-, IO4-, I - basolateral plasma membrane; see [Wright 2004] for refs

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UREAt	3	Eskandari S, Loo DD, Dai G, Levy O, Wright EM, Carrasco N.	Thyroid Na+/I- symporter. Mechanism, stoichiometry, and specificity	J Biol Chem	1997	9341168	-cloned [Hediger 1989] - cotransports Glc/2 Na+, Gal/2 Na+ [Quick 2001] - H+ can replace Na+ [Hirayama 1994] - behaves as urea channel in the absence of substrates; cotransports urea under substrate-transporting conditions [Leung 2000] - Na+ transport occurs by a saturable uniport mechanism; water permeation is through a low conductance water channel [Loo 1999] - brush border membrane [Wright 1994] - plasma membrane; see [Wright 2004] for refs 6563,8170 - In mammalian cells, urea is the chief end-product of nitrogen catabolism and plays an important role in the urinary concentration mechanism. Thus, the plasma membrane of erythrocytes and some renal epithelial cells exhibit an elevated urea permeability that is mediated by highly selective urea transporters. In mammals, 2 urea transporters have been identified: the renal tubular urea transporter, UT2, and the erythrocyte urea transporter, UT11 (SLC14A1; MIM 111000).[supplied by OMIM] 6528: - cloned [Dai 1996] - gene has 84% identity to the rat homolog [Smanik 1996] - sodium iodide cotransport [Dai 1996]; 2 Na+ per I- [Eskandar - primarily in thyroid gland [De La Vieja 2000], also expressed - also transports ClO3-, SCN-, SeCN-, NO3-, Br-, BF4-, IO4-, I - basolateral plasma membrane; see [Wright 2004] for refs
UREAt	3	De La Vieja A, Dohan O, Levy O, Carrasco N	Molecular analysis of the sodium/iodide symporter: impact on thyroid and extrathyroid pathophysiology	Physiol Rev	2000	10893432	-cloned [Hediger 1989] - cotransports Glc/2 Na+, Gal/2 Na+ [Quick 2001] - H+ can replace Na+ [Hirayama 1994] - behaves as urea channel in the absence of substrates; cotransports urea under substrate-transporting conditions [Leung 2000] - Na+ transport occurs by a saturable uniport mechanism; water permeation is through a low conductance water channel [Loo 1999] - brush border membrane [Wright 1994] - plasma membrane; see [Wright 2004] for refs 6563,8170 - In mammalian cells, urea is the chief end-product of nitrogen catabolism and plays an important role in the urinary concentration mechanism. Thus, the plasma membrane of erythrocytes and some renal epithelial cells exhibit an elevated urea permeability that is mediated by highly selective urea transporters. In mammals, 2 urea transporters have been identified: the renal tubular urea transporter, UT2, and the erythrocyte urea transporter, UT11 (SLC14A1; MIM 111000).[supplied by OMIM] 6528: - cloned [Dai 1996] - gene has 84% identity to the rat homolog [Smanik 1996] - sodium iodide cotransport [Dai 1996]; 2 Na+ per I- [Eskandar - primarily in thyroid gland [De La Vieja 2000], also expressed - also transports ClO3-, SCN-, SeCN-, NO3-, Br-, BF4-, IO4-, I - basolateral plasma membrane; see [Wright 2004] for refs
UREAt	3	Wapnir IL, van de Rijn M, Nowels K, Amenta PS, Walton K, Montgomery K, Greco RS, Dohan O, Carrasco N	Immunohistochemical profile of the sodium/iodide symporter in thyroid, breast, and other carcinomas using high density tissue microarrays and conventional sections	J Clin Endocrinol Metab	2003	12679487	-cloned [Hediger 1989] - cotransports Glc/2 Na+, Gal/2 Na+ [Quick 2001] - H+ can replace Na+ [Hirayama 1994] - behaves as urea channel in the absence of substrates; cotransports urea under substrate-transporting conditions [Leung 2000] - Na+ transport occurs by a saturable uniport mechanism; water permeation is through a low conductance water channel [Loo 1999] - brush border membrane [Wright 1994] - plasma membrane; see [Wright 2004] for refs 6563,8170 - In mammalian cells, urea is the chief end-product of nitrogen catabolism and plays an important role in the urinary concentration mechanism. Thus, the plasma membrane of erythrocytes and some renal epithelial cells exhibit an elevated urea permeability that is mediated by highly selective urea transporters. In mammals, 2 urea transporters have been identified: the renal tubular urea transporter, UT2, and the erythrocyte urea transporter, UT11 (SLC14A1; MIM 111000).[supplied by OMIM] 6528: - cloned [Dai 1996] - gene has 84% identity to the rat homolog [Smanik 1996] - sodium iodide cotransport [Dai 1996]; 2 Na+ per I- [Eskandar - primarily in thyroid gland [De La Vieja 2000], also expressed - also transports ClO3-, SCN-, SeCN-, NO3-, Br-, BF4-, IO4-, I - basolateral plasma membrane; see [Wright 2004] for refs

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UREAt	3	Shayakul C, Hediger MA.	The SLC14 gene family of urea transporters.		2004	12856182	-cloned [Hediger 1989] - cotransports Glc/2 Na+, Gal/2 Na+ [Quick 2001] - H+ can replace Na+ [Hirayama 1994] - behaves as urea channel in the absence of substrates; cotransports urea under substrate-transporting conditions [Leung 2000] - Na+ transport occurs by a saturable uniport mechanism; water permeation is through a low conductance water channel [Loo 1999] - brush border membrane [Wright 1994] - plasma membrane; see [Wright 2004] for refs 6563,8170 - In mammalian cells, urea is the chief end-product of nitrogen catabolism and plays an important role in the urinary concentration mechanism. Thus, the plasma membrane of erythrocytes and some renal epithelial cells exhibit an elevated urea permeability that is mediated by highly selective urea transporters. In mammals, 2 urea transporters have been identified: the renal tubular urea transporter, UT2, and the erythrocyte urea transporter, UT11 (SLC14A1; MIM 111000).[supplied by OMIM] 6528: - cloned [Dai 1996] - gene has 84% identity to the rat homolog [Smanik 1996] - sodium iodide cotransport [Dai 1996]; 2 Na+ per I- [Eskandar - primarily in thyroid gland [De La Vieja 2000], also expressed - also transports ClO3-, SCN-, SeCN-, NO3-, Br-, BF4-, IO4-, I - basolateral plasma membrane; see [Wright 2004] for refs
UREAtm	2	Tsukaguchi H, Shayakul C, Berger UV, Mackenzie B, Devidas S, Guggino WB, van Hoek AN, Hediger MA	Molecular characterization of a broad selectivity neutral solute channel	J Biol Chem	1998	9733774	Citations indicate that this aquaporin can transport urea into the mitochondria. There is no explicit information that it is reversible, but the reversibility fills a gap in the model and is thus assumed. This transporter can supposedly also transport lactate into the mitochondria, but that functionality has been omitted for now due to loop issues. Also, this transporter takes many other neutral solutes, probably more prominently into and out of the cell rather than the mitochondria.
UREAtm	2	Agre P, King LS, Yasui M, Guggino WB, Ottersen OP, Fujiyoshi Y, Engel A, Nielsen S	Aquaporin water channels--from atomic structure to clinical medicine	J Physiol	2002	12096044	Citations indicate that this aquaporin can transport urea into the mitochondria. There is no explicit information that it is reversible, but the reversibility fills a gap in the model and is thus assumed. This transporter can supposedly also transport lactate into the mitochondria, but that functionality has been omitted for now due to loop issues. Also, this transporter takes many other neutral solutes, probably more prominently into and out of the cell rather than the mitochondria.
UREAtm	2	Amiry-Moghaddam M, Lindland H, Zelenin S, Roberg BA, Gundersen BB, Petersen P, Rinvik E, Torgner IA, Ottersen OP	Brain mitochondria contain aquaporin water channels: evidence for the expression of a short AQP9 isoform in the inner mitochondrial membrane	FASEB J	2005	16126913	Citations indicate that this aquaporin can transport urea into the mitochondria. There is no explicit information that it is reversible, but the reversibility fills a gap in the model and is thus assumed. This transporter can supposedly also transport lactate into the mitochondria, but that functionality has been omitted for now due to loop issues. Also, this transporter takes many other neutral solutes, probably more prominently into and out of the cell rather than the mitochondria.
URIK1	3	Ozaki K, Kuroki T, Hayashi S, Nakamura Y.	Isolation of three testis-specific genes (TSA303, TSA806, TSA903) by a differential mRNA display method.	Genomics	1996	8812458	IT Kashuba 2002 found 7371 product predominately in cytoplasme but when cell was infected with Epstein-Barr virus, the protein was located in nucleus --> I did not account for this observation yet. Found protein expressed in most tissues. Ozaki et al, 1996 found mRNA expressed in testis UCK2: interestingly the papers differ in their results of expression of the corresponding mRNA. While Ozaki et al, 1996, found the mRNA only in testis, and Van Rompay et al 2001 only in placenta, Kashuba et al 2002 detected the mRNA in most tissues they investigated ...??? UCK1,UCK2: Van Rompay et al., 2001:The enzymes phosphorylated several of the analogs, such as 6-azauridine, 5-fluorouridine, 4-thiouridine, 5-bromouridine, N(4)-acetylcytidine, N(4)-benzoylcytidine, 5-fluorocytidine, 2-thiocytidine, 5-methylcytidine, and N(4)-anisoylcytidine

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
URIK1	3	Van Rompay AR, Norda A, Linden K, Johansson M, Karlsson A.	Phosphorylation of uridine and cytidine nucleoside analogs by two human uridine-cytidine kinases.	Mol Pharmacol	2001	11306702	IT Kashuba 2002 found 7371 product predominately in cytoplasme but when cell was infected with Epstein-Barr virus, the protein was located in nucleus --> I did not account for this observation yet. Found protein expressed in most tissues. Ozaki et al, 1996 found mRNA expressed in testis UCK2: interestingly the papers differ in their results of expression of the corresponding mRNA. While Ozaki et al, 1996, found the mRNA only in testis, and Van Rompay et al 2001 only in placenta, Kashuba et al 2002 detected the mRNA in most tissues they investigated ...??? UCK1,UCK2: Van Rompay et al., 2001:The enzymes phosphorylated several of the analogs, such as 6-azauridine, 5-fluorouridine, 4-thiouridine, 5-bromouridine, N(4)-acetylcytidine, N(4)-benzoylcytidine, 5-fluorocytidine, 2-thiocytidine, 5-methylcytidine, and N(4)-anisoylcytidine
URIK1	3	Kashuba E, Kashuba V, Sandalova T, Klein G, Szekely L	Epstein-Barr virus encoded nuclear protein EBNA-3 binds a novel human uridine kinase/uracil phosphoribosyltransferase.	BMC Cell Biol	2002	12199906	IT Kashuba 2002 found 7371 product predominately in cytoplasme but when cell was infected with Epstein-Barr virus, the protein was located in nucleus --> I did not account for this observation yet. Found protein expressed in most tissues. Ozaki et al, 1996 found mRNA expressed in testis UCK2: interestingly the papers differ in their results of expression of the corresponding mRNA. While Ozaki et al, 1996, found the mRNA only in testis, and Van Rompay et al 2001 only in placenta, Kashuba et al 2002 detected the mRNA in most tissues they investigated ...??? UCK1,UCK2: Van Rompay et al., 2001:The enzymes phosphorylated several of the analogs, such as 6-azauridine, 5-fluorouridine, 4-thiouridine, 5-bromouridine, N(4)-acetylcytidine, N(4)-benzoylcytidine, 5-fluorocytidine, 2-thiocytidine, 5-methylcytidine, and N(4)-anisoylcytidine
Uritl	3	Pisoni RL, Thoene JG.	Detection and characterization of a nucleoside transport system in human fibroblast lysosomes.	J Biol Chem	1989	2925670	IT it is not clear whether H+ is co-transported or not. since influx has low affinity it is more likely that transporter serve to remove nucleosides from lysosome rather then importing them (baldwin, 2005)
Uritl	3	Baldwin SA, Yao SY, Hyde RJ, Ng AM, Foppolo S, Barnes K, Ritzel MW, Cass CE, Young JD.	Functional characterization of novel human and mouse equilibrative nucleoside transporters (hENT3 and mENT3) located in intracellular membranes.	J Biol Chem	2005	15701636	IT it is not clear whether H+ is co-transported or not. since influx has low affinity it is more likely that transporter serve to remove nucleosides from lysosome rather then importing them (baldwin, 2005)
UROLACer	1	Winkelman J, Lehninger AL	Aldono- and uronolactonases of animal tissues.	J Biol Chem	1958	13587494	-found in the ER of rat livers; also found in several other animals (including monkey) [Winkelman, J Biol Chem 1958]
VALt5m	3	Porter RK.	Mammalian mitochondrial inner membrane cationic and neutral amino acid carriers.		2000	11004451	PMID 11004451: Non-respiring mitochondria swell when suspended in isotonic solutions of each of several different amino acids, indicating that these compounds can penetrate the mitochondrial inner membrane [5 and 6]. Gamble and Lehninger [12] showed that rat liver mitochondria swell in glycine, alanine, proline, valine and citrulline, but rat heart mitochondria do not swell in citrulline. Halling et al. [13] also showed that a variety of neutral amino acids, including non-metabolisable amino acids, could penetrate the mitochondrial inner membrane; Further advances were made when Cybulski and Fisher [15] found that mitochondrial swelling in neutral amino acids showed L-stereoisomer specificity
VITD3Hm	3	Guo YD, Strugnell S, Back DW, Jones G.	Transfected human liver cytochrome P-450 hydroxylates vitamin D analogs at different side-chain positions.	Proc Natl Acad Sci U S A	1993	7690968	This reaction takes place only in liver moeglich dass gleiche reaktion auch in microsome stattfindet based on Vitamins, G.F.M. Ball,2004, Blackwell publishing, 1st ed (book) pg.194 IT plasma conc: 10-40 ng/ml blood most of 25hvitd is in blood since tissue uptake is small
VLCSp	3	Mihalik SJ, Steinberg SJ, Pei Z, Park J, Kim DG, Heinzer AK, Dacremont G, Wanders JAR, Cuebas DA, Smith KD, Watkins PA	Participation of two members of the veryl long-chain acyl-CoA synthetase family in bile acid synthesis and recycling	Journal of Biological Chemistry	2002		peroxisome + ER: uniprot + literature references integral membrane protein specificity: Expressed in liver, kidney, placenta and pancreas NJ
VLCSp	3	Kelley M, Vessey DA	Dual role of diavlent cations in the bile acid: CoA ligase catalyzed reaction	Biochimica et Biophysica Acta	1994		peroxisome + ER: uniprot + literature references integral membrane protein specificity: Expressed in liver, kidney, placenta and pancreas NJ
VLCSp	3	Steinberg SJ, Mihalik SJ, Kim DG, Cuebas DA, Watkins PA	The human liver-specific homolog of very long-chain acyl-CoA synthetase is cholate: CoA ligase	Journal of Biological Chemistry	2000		peroxisome + ER: uniprot + literature references integral membrane protein specificity: Expressed in liver, kidney, placenta and pancreas NJ

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VLCSp	3	Mihalik SJ, Steinberg SJ, Pei Z, Park J, Kim DG, Heinzer AK, Dacremont G, Wanders JAR, Cuebas DA, Smith KD, Watkins PA	Participation of two members of the veryl long-chain acyl-CoA synthetase family in bile acid synthesis and recycling	Journal of Biological Chemistry	2002		peroxisome + ER: uniprot + literature references integral membrane protein specificity: Expressed in liver, kidney, placenta and pancreas NJ
VLCSp	3	Kelley M, Vessey DA	Dual role of diavlent cations in the bile acid: CoA ligase catalyzed reaction	Biochimica et Biophysica Acta	1994		peroxisome + ER: uniprot + literature references integral membrane protein specificity: Expressed in liver, kidney, placenta and pancreas NJ
VLCSp	3	Mihalik SJ, Steinberg SJ, Pei Z, Park J, Kim DG, Heinzer AK, Dacremont G, Wanders JAR, Cuebas DA, Smith KD, Watkins PA	Participation of two members of the veryl long-chain acyl-CoA synthetase family in bile acid synthesis and recycling	Journal of Biological Chemistry	2002		peroxisome + ER: uniprot + literature references integral membrane protein specificity: Expressed in liver, kidney, placenta and pancreas NJ
VLCSp	3	Steinberg SJ, Mihalik SJ, Kim DG, Cuebas DA, Watkins PA	The human liver-specific homolog of very long-chain acyl-CoA synthetase is cholate: CoA ligase	Journal of Biological Chemistry	2000		peroxisome + ER: uniprot + literature references integral membrane protein specificity: Expressed in liver, kidney, placenta and pancreas NJ
VLCSp	3	Kelley M, Vessey DA	Dual role of diavlent cations in the bile acid: CoA ligase catalyzed reaction	Biochimica et Biophysica Acta	1994		peroxisome + ER: uniprot + literature references integral membrane protein specificity: Expressed in liver, kidney, placenta and pancreas NJ
VLCSp	3	Steinberg SJ, Mihalik SJ, Kim DG, Cuebas DA, Watkins PA	The human liver-specific homolog of very long-chain acyl-CoA synthetase is cholate: CoA ligase	Journal of Biological Chemistry	2000		peroxisome + ER: uniprot + literature references integral membrane protein specificity: Expressed in liver, kidney, placenta and pancreas NJ
VLCSp	3	Mihalik SJ, Steinberg SJ, Pei Z, Park J, Kim DG, Heinzer AK, Dacremont G, Wanders JAR, Cuebas DA, Smith KD, Watkins PA	Participation of two members of the veryl long-chain acyl-CoA synthetase family in bile acid synthesis and recycling	Journal of Biological Chemistry	2002		peroxisome + ER: uniprot + literature references integral membrane protein specificity: Expressed in liver, kidney, placenta and pancreas NJ
XANDp	3	Saksela M, Raivio KO.	Cloning and expression in vitro of human xanthine dehydrogenase/oxidase.	Biochem J	1996	8670112	GeneCards: peroxisome homodimer. dehydrogenase form can be reversibly converted oxidase through oxidation of sulhydryl group needs molybdenum as cofactor IT
XANDp	3	Linder N, Martelin E, Lapatto R, Raivio KO.	Posttranslational inactivation of human xanthine oxidoreductase by oxygen under standard cell culture conditions.	Am J Physiol Cell Physiol	2003	12637268	GeneCards: peroxisome homodimer. dehydrogenase form can be reversibly converted oxidase through oxidation of sulhydryl group needs molybdenum as cofactor IT
XYLt	3	Kayano T, Fukumoto H, Eddy RL, Fan YS, Byers MG, Shows TB, Bell GI	Evidence for a family of human glucose transporter-like proteins. Sequence and gene localization of a protein expressed in fetal skeletal muscle and other tissues	J Biol Chem	1988	3170580	6515: - major substrates are Glc (high affinity), Gal, Man, Xyl, maltose, dehydroascorbic acid [Uldry, Pflugers Arch 2004] - protein localized to brain (neurons), testis (spermatozoa) [Haber, Endocrinology 1993], [Uldry, Pflugers Arch 2004], sk muscle (slow twitch fibers) [Stuart, Metabolism 1999], platelets (alpha-granules) [Heijen, J Cell Biol 1997] - cDNA was cloned [Kayano, J Biol Chem 1988]
XYLt	3	Haber RS, Weinstein SP, O'Boyle E, Morgello S	Tissue distribution of the human GLUT3 glucose transporte	Endocrinology	1993	8504756	6515: - major substrates are Glc (high affinity), Gal, Man, Xyl, maltose, dehydroascorbic acid [Uldry, Pflugers Arch 2004] - protein localized to brain (neurons), testis (spermatozoa) [Haber, Endocrinology 1993], [Uldry, Pflugers Arch 2004], sk muscle (slow twitch fibers) [Stuart, Metabolism 1999], platelets (alpha-granules) [Heijen, J Cell Biol 1997] - cDNA was cloned [Kayano, J Biol Chem 1988]
XYLt	3	Heijnen HF, Oorschot V, Sixma JJ, Slot JW, James DE	Thrombin stimulates glucose transport in human platelets via the translocation of the glucose transporter GLUT-3 from alpha-granules to the cell surface	J Cell Biol	1997	9230074	6515: - major substrates are Glc (high affinity), Gal, Man, Xyl, maltose, dehydroascorbic acid [Uldry, Pflugers Arch 2004] - protein localized to brain (neurons), testis (spermatozoa) [Haber, Endocrinology 1993], [Uldry, Pflugers Arch 2004], sk muscle (slow twitch fibers) [Stuart, Metabolism 1999], platelets (alpha-granules) [Heijen, J Cell Biol 1997] - cDNA was cloned [Kayano, J Biol Chem 1988]
XYLt	3	Stuart CA, Wen G, Jiang J	GLUT3 protein and mRNA in autopsy muscle specimens	Metabolism	1999	10421229	6515: - major substrates are Glc (high affinity), Gal, Man, Xyl, maltose, dehydroascorbic acid [Uldry, Pflugers Arch 2004] - protein localized to brain (neurons), testis (spermatozoa) [Haber, Endocrinology 1993], [Uldry, Pflugers Arch 2004], sk muscle (slow twitch fibers) [Stuart, Metabolism 1999], platelets (alpha-granules) [Heijen, J Cell Biol 1997] - cDNA was cloned [Kayano, J Biol Chem 1988]

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
XYLt	3	Uldry M, Thorens B	The SLC2 family of facilitated hexose and polyol transporters	Pflugers Arch	2004	12750891	6515: - major substrates are Glc (high affinity), Gal, Man, Xyl, maltose, dehydroascorbic acid [Uldry, Pflugers Arch 2004] - protein localized to brain (neurons), testis (spermatozoa) [Haber, Endocrinology 1993], [Uldry, Pflugers Arch 2004], sk muscle (slow twitch fibers) [Stuart, Metabolism 1999], platelets (alpha-granules) [Heijen, J Cell Biol 1997] - cDNA was cloned [Kayano, J Biol Chem 1988]
XYLTer	3	Kearns AE, Vertel BM, Schwartz NB	Topography of glycosylation and UDP-xylose production	J Biol Chem	1993	8496172	- immunocytochemistry, subcellular fractionation, and electron microscopy have demonstrated that xylosylation begins in the ER and continues in the early Golgi [Kearns, J Biol Chem 1993] - ER localization [Silbert, IUBMB LIfe 2002] 64131: - catalyzes the transfer of UDP-xylose to serine residues within XT recognition sequences of target proteins [OMIM] - protein was isolated, partial aa seq identified [Kuhn, J Biol Chem 2001] - cDNA was cloned and expressed, 94% identity to rat homolog [Gotting, J Mol Biol 2000] - ubiquitously expressed [Gotting, J Mol Biol 2000] 64132: - transfers xylose from UDP-xylose to specific serine residues of the core protein [RefSeq] - cDNA was isolated [Gotting, J Mol Biol 2000] - ubiquitously expressed [Gotting, J Mol Biol 2000] ** May need to also add a Golgi reaction since UDPXyl is now produced in Golgi instead of ER ***
XYLTer	3	Kuhn J, Gotting C, Schnolzer M, Kempf T, Brinkmann T, Kleesiek K	First isolation of human UDP-D-xylose: proteoglycan core protein beta-D-xylosyltransferase secreted from cultured JAR choriocarcinoma cells	J Biol Chem	2001	11087729	- immunocytochemistry, subcellular fractionation, and electron microscopy have demonstrated that xylosylation begins in the ER and continues in the early Golgi [Kearns, J Biol Chem 1993] - ER localization [Silbert, IUBMB LIfe 2002] 64131: - catalyzes the transfer of UDP-xylose to serine residues within XT recognition sequences of target proteins [OMIM] - protein was isolated, partial aa seq identified [Kuhn, J Biol Chem 2001] - cDNA was cloned and expressed, 94% identity to rat homolog [Gotting, J Mol Biol 2000] - ubiquitously expressed [Gotting, J Mol Biol 2000] 64132: - transfers xylose from UDP-xylose to specific serine residues of the core protein [RefSeq] - cDNA was isolated [Gotting, J Mol Biol 2000] - ubiquitously expressed [Gotting, J Mol Biol 2000] ** May need to also add a Golgi reaction since UDPXyl is now produced in Golgi instead of ER ***
XYLTer	3	Gotting C, Kuhn J, Zahn R, Brinkmann T, Kleesiek K	Molecular cloning and expression of human UDP-d-Xylose:proteoglycan core protein beta-d-xylosyltransferase and its first isoform XT-II	J Mol Biol	2000	11099377	- immunocytochemistry, subcellular fractionation, and electron microscopy have demonstrated that xylosylation begins in the ER and continues in the early Golgi [Kearns, J Biol Chem 1993] - ER localization [Silbert, IUBMB LIfe 2002] 64131: - catalyzes the transfer of UDP-xylose to serine residues within XT recognition sequences of target proteins [OMIM] - protein was isolated, partial aa seq identified [Kuhn, J Biol Chem 2001] - cDNA was cloned and expressed, 94% identity to rat homolog [Gotting, J Mol Biol 2000] - ubiquitously expressed [Gotting, J Mol Biol 2000] 64132: - transfers xylose from UDP-xylose to specific serine residues of the core protein [RefSeq] - cDNA was isolated [Gotting, J Mol Biol 2000] - ubiquitously expressed [Gotting, J Mol Biol 2000] ** May need to also add a Golgi reaction since UDPXyl is now produced in Golgi instead of ER ***

Reaction Abbreviation	Score	Authors	Article or Book Title	Journal	Year	PubMed ID	Curation Notes
XYLTer	3	Silbert JE, Sugumaran G	Biosynthesis of chondroitin/dermatan sulfate	IUBMB Life	2002	12512856	- immunocytochemistry, subcellular fractionation, and electron microscopy have demonstrated that xylosylation begins in the ER and continues in the early Golgi [Kearns, J Biol Chem 1993] - ER localization [Silbert, IUBMB LIfe 2002] 64131: - catalyzes the transfer of UDP-xylose to serine residues within XT recognition sequences of target proteins [OMIM] - protein was isolated, partial aa seq identified [Kuhn, J Biol Chem 2001] - cDNA was cloned and expressed, 94% identity to rat homolog [Gotting, J Mol Biol 2000] - ubiquitously expressed [Gotting, J Mol Biol 2000] 64132: - transfers xylose from UDP-xylose to specific serine residues of the core protein [RefSeq] - cDNA was isolated [Gotting, J Mol Biol 2000] - ubiquitously expressed [Gotting, J Mol Biol 2000] ** May need to also add a Golgi reaction since UDPXyl is now produced in Golgi instead of ER ***
XYLTt	1	Wang YM, van Eys J	Nutritional significance of fructose and sugar alcohols	Annu Rev Nutr	1981	6821187	- most likely absorbed by intestinal mucosa through passive or facilitated diffusion (see refs in [Wang 1981])
XYLUR	3	Nakagawa J, Ishikura S, Asami J, Isaji T, Usami N, Hara A, Sakurai T, Tsuritani K, Oda K, Takahashi M, Yoshimoto M, Otsuka N, Kitamura K	Molecular characterization of mammalian dicarbonyl/L-xylulose reductase and its localization in kidney	J Biol Chem	2002	11882650	- rxn described in Devlin p. 676, Orten p. 243, [Wang 1981] - pathway operates in adipose tissue [Devlin, Textbook of Biochem 2001] - highly expressed in kidney and liver [Nakagawa, J Biol Chem 2002]

Table 11: Expression changes in glycolysis/gluconeogenesis for the gastric bypass study. Alphabetized list of reactions in glycolysis/gluconeogenesis (as defined by Recon 1). Ratio is the average log10 expression ratio (*n*=3) of post-/pregene expression measurements (see text for details). Negative ratios (green) indicate a decrease in expression postsurgery whereas positive ratios indicate an increase (red). Values denoted with "n/a" indicate that gene expression values were unavailable, or that expression ratios conflicted at the probe or patient levels.

Reaction	Putative function	Locus	Ratio
ACS	acetyl-CoA synthetase	65985.1	n/a
ACS	acetyl-CoA synthetase	55902.1	n/a
ACS	acetyl-CoA synthetase	55902.2	n/a
ACSm	acetyl-CoA synthetase	84532.1	n/a
ACYP	acylphosphatase	98.1	-0.16
ACYP	acylphosphatase	97.2	n/a
ACYP	acylphosphatase	112611.1	n/a
ACYP	acylphosphatase	97.1	n/a
ALCD2if	alcohol dehydrogenase, forward rxn (ethanol -> acetaldehyde)	125.1	0.233
ALCD2if	alcohol dehydrogenase, forward rxn (ethanol -> acetaldehyde)	124.1	0.233
ALCD2if	alcohol dehydrogenase, forward rxn (ethanol -> acetaldehyde)	126.1	0.233
ALCD2if	alcohol dehydrogenase, forward rxn (ethanol -> acetaldehyde)	130.1	0.32
ALCD2if	alcohol dehydrogenase, forward rxn (ethanol -> acetaldehyde)	131.1	n/a
ALCD2if	alcohol dehydrogenase, forward rxn (ethanol -> acetaldehyde)	137872.1	n/a
ALCD2if	alcohol dehydrogenase, forward rxn (ethanol -> acetaldehyde)	127.1	n/a
ALCD2if	alcohol dehydrogenase, forward rxn (ethanol -> acetaldehyde)	284273.2	n/a
ALCD2if	alcohol dehydrogenase, forward rxn (ethanol -> acetaldehyde)	284273.1	n/a
ALCD2if	alcohol dehydrogenase, forward rxn (ethanol -> acetaldehyde)	128.1	n/a
ALCD2yf	alcohol dehydrogenase (ethanol, NADP), forward reaction	10327.1	0.066
ALCD2yf	alcohol dehydrogenase (ethanol, NADP), forward reaction	10327.2	n/a
ALDD2x	aldehyde dehydrogenase (acetaldehyde, NAD)	218.1	-0.247
ALDD2x	aldehyde dehydrogenase (acetaldehyde, NAD)	8854.1	0.273
ALDD2x	aldehyde dehydrogenase (acetaldehyde, NAD)	222.1	0.284
ALDD2x	aldehyde dehydrogenase (acetaldehyde, NAD)	501.1	n/a
ALDD2x	aldehyde dehydrogenase (acetaldehyde, NAD)	216.1	n/a
ALDD2x	aldehyde dehydrogenase (acetaldehyde, NAD)	8854.3	n/a
ALDD2x	aldehyde dehydrogenase (acetaldehyde, NAD)	8854.2	n/a

Reaction	Putative function	Locus	Ratio
ALDD2x	aldehyde dehydrogenase (acetaldehyde, NAD)	224.1	n/a
ALDD2x	aldehyde dehydrogenase (acetaldehyde, NAD)	223.1	n/a
ALDD2x	aldehyde dehydrogenase (acetaldehyde, NAD)	220.1	n/a
ALDD2x	aldehyde dehydrogenase (acetaldehyde, NAD)	221.1	n/a
ALDD2xm	aldehyde dehydrogenase (acetylaldehyde, NAD), mitochondrial	219.1	-0.469
ALDD2xm	aldehyde dehydrogenase (acetylaldehyde, NAD), mitochondrial	217.1	-0.039
ALDD2y	aldehyde dehydrogenase (acetaldehyde, NADP)	218.1	-0.247
ALDD2y	aldehyde dehydrogenase (acetaldehyde, NADP)	8854.1	0.273
ALDD2y	aldehyde dehydrogenase (acetaldehyde, NADP)	222.1	0.284
ALDD2y	aldehyde dehydrogenase (acetaldehyde, NADP)	8854.3	n/a
ALDD2y	aldehyde dehydrogenase (acetaldehyde, NADP)	8854.2	n/a
ALDD2y	aldehyde dehydrogenase (acetaldehyde, NADP)	224.1	n/a
ALDD2y	aldehyde dehydrogenase (acetaldehyde, NADP)	223.1	n/a
ALDD2y	aldehyde dehydrogenase (acetaldehyde, NADP)	221.1	n/a
CAT2p	catalase A, peroxisomal (ethanol)	847.1	n/a
CBPPer	Carbamoyl phosphate phosphotransferase, endoplasmic reticulum	92579.1	-0.133
CBPPer	Carbamoyl phosphate phosphotransferase, endoplasmic reticulum	57818.1	n/a
CBPPer	Carbamoyl phosphate phosphotransferase, endoplasmic reticulum	2538.1	n/a
DPGase	Diphosphoglycerate phosphatase	5223.1	0.125
DPGase	Diphosphoglycerate phosphatase	5224.1	n/a
DPGase	Diphosphoglycerate phosphatase	669.2	n/a
DPGase	Diphosphoglycerate phosphatase	5224.2	n/a
DPGase	Diphosphoglycerate phosphatase	669.1	n/a
DPGM	Diphosphoglyceromutase	5223.1	0.125
DPGM	Diphosphoglyceromutase	5224.1	n/a
DPGM	Diphosphoglyceromutase	669.2	n/a
DPGM	Diphosphoglyceromutase	5224.2	n/a
DPGM	Diphosphoglyceromutase	669.1	n/a
ENO	enolase	2023.1	0.075
ENO	enolase	26237.1	0.186

Reaction	Putative function	Locus	Ratio
ENO	enolase	2027.1	n/a
ENO	enolase	2027.2	n/a
ENO	enolase	2026.1	n/a
ETOHMO	ethanol monooxygenase	1571.1	-0.258
FBA	fructose-bisphosphate aldolase	229.1	0.188
FBA	fructose-bisphosphate aldolase	226.1	n/a
FBA	fructose-bisphosphate aldolase	230.1	n/a
FBA	fructose-bisphosphate aldolase	226.2	n/a
FBA	fructose-bisphosphate aldolase	226.3	n/a
FBP	fructose-bisphosphatase	2203.1	n/a
FBP	fructose-bisphosphatase	8789.1	n/a
G3PD2m	glycerol-3-phosphate dehydrogenase (FAD), mitochondrial	2820.1	n/a
G6PPer	glucose-6-phosphate phosphatase, edoplasmic reticular	92579.1	-0.133
G6PPer	glucose-6-phosphate phosphatase, edoplasmic reticular	57818.1	n/a
G6PPer	glucose-6-phosphate phosphatase, edoplasmic reticular	2538.1	n/a
GAPD	glyceraldehyde-3-phosphate dehydrogenase	26330.1	n/a
GAPD	glyceraldehyde-3-phosphate dehydrogenase	2597.1	n/a
HEX1	hexokinase (D-glucose:ATP)	3098.4	n/a
HEX1	hexokinase (D-glucose:ATP)	2645.3	n/a
HEX1	hexokinase (D-glucose:ATP)	3098.1	n/a
HEX1	hexokinase (D-glucose:ATP)	3098.2	n/a
HEX1	hexokinase (D-glucose:ATP)	3099.1	n/a
HEX1	hexokinase (D-glucose:ATP)	2645.2	n/a
HEX1	hexokinase (D-glucose:ATP)	80201.1	n/a
HEX1	hexokinase (D-glucose:ATP)	3098.5	n/a
HEX1	hexokinase (D-glucose:ATP)	3098.3	n/a
HEX1	hexokinase (D-glucose:ATP)	2645.1	n/a
HEX1	hexokinase (D-glucose:ATP)	3101.1	n/a
LDH_L	L-lactate dehydrogenase	92483.1	-0.437
LDH_L	L-lactate dehydrogenase	3948.2	n/a
LDH_L	L-lactate dehydrogenase	160287.1	n/a
LDH_L	L-lactate dehydrogenase	3945.1	n/a
LDH_L	L-lactate dehydrogenase	3948.1	n/a
LDH_L	L-lactate dehydrogenase	3939.1	n/a
LDH_L	L-lactate dehydrogenase	55293.1	n/a
PDHm	pyruvate dehydrogenase	8050.1	-0.128
PDHm	pyruvate dehydrogenase	1738.1	-0.051
PDHm	pyruvate dehydrogenase	5160.1	-0.042
PDHm	pyruvate dehydrogenase	1737.1	n/a
PDHm	pyruvate dehydrogenase	5161.1	n/a
PDHm	pyruvate dehydrogenase	5162.1	n/a
PEPCK	Phosphoenolpyruvate carboxykinase (GTP)	5105.1	0.567
PEPCKm	Phosphoenolpyruvate carboxykinase (GTP)	5106.1	n/a

Reaction	Putative function	Locus	Ratio
PFK	phosphofructokinase	5211.1	0.163
PFK	phosphofructokinase	5213.1	n/a
PFK	phosphofructokinase	5211.2	n/a
PFK	phosphofructokinase	5214.1	n/a
PGI	glucose-6-phosphate isomerase	2821.1	n/a
PGK	phosphoglycerate kinase	5230.1	0.099
PGK	phosphoglycerate kinase	348477.1	n/a
PGK	phosphoglycerate kinase	5232.1	n/a
PGM	phosphoglycerate mutase	5223.1	0.125
PGM	phosphoglycerate mutase	5224.1	n/a
PGM	phosphoglycerate mutase	669.2	n/a
PGM	phosphoglycerate mutase	5224.2	n/a
PGM	phosphoglycerate mutase	669.1	n/a
PGMT	phosphoglucomutase	55276.1	n/a
PGMT	phosphoglucomutase	5236.1	n/a
PYK	pyruvate kinase	5315.1	0.481
PYK	pyruvate kinase	5315.2	n/a
PYK	pyruvate kinase	5313.2	n/a
PYK	pyruvate kinase	5315.3	n/a
PYK	pyruvate kinase	5313.1	n/a
PYK	pyruvate kinase	113452.1	n/a
TPI	triose-phosphate isomerase	286016.1	n/a
TPI	triose-phosphate isomerase	7167.1	n/a

Table 12: Expression changes in pentose phosphate pathway for the gastric bypass study. Alphabetized list of reactions in pentose phosphate pathway (as defined by Recon 1). Ratio is the average log10 expression ratio (*n*=3) of post-/pregene expression measurements (see text for details). Negative ratios (green) indicate a decrease in expression postsurgery, whereas positive ratios indicate an increase (red). Values denoted with "n/a" indicate that gene expression values were unavailable, or that expression ratios conflicted at the probe or patient levels.

Reaction	Putative function	Locus	Ratio
DRBK	Deoxyribokinase	64080.1	-0.137
G6PDH1er	glucose-6-phosphate dehydrogenase, endoplasmic reticulum	9563.1	n/a
G6PDH1rer	glucose-6-phosphate dehydrogenase, endoplasmic reticulum	9563.1	n/a
G6PDH2r	glucose 6-phosphate dehydrogenase	2539.1	-0.094
G6PDH2rer	glucose 6-phosphate dehydrogenase, endoplasmic reticulum	9563.1	n/a
GND	phosphogluconate dehydrogenase	5226.1	n/a
PGL	6-phosphogluconolactonase	25796.1	-0.19
PGLer	6-phosphogluconolactonase, endoplasmic reticulum	9563.1	n/a
PPM	phosphopentomutase	5236.1	n/a
PRPPS	phosphoribosylpyrophosphate synthetase	5631.1	n/a
PRPPS	phosphoribosylpyrophosphate synthetase	221823.1	n/a
PRPPS	phosphoribosylpyrophosphate synthetase	5634.1	n/a
PRPPS	phosphoribosylpyrophosphate synthetase	221823.2	n/a
RBK	ribokinase	64080.1	-0.137
RPE	ribulose 5-phosphate 3-epimerase	6120.1	n/a
RPE	ribulose 5-phosphate 3-epimerase	6120.2	n/a
RPI	ribose-5-phosphate isomerase	22934.1	n/a
TALA	transaldolase	6888.1	n/a
TKT1	transketolase	8277.1	-0.063
TKT1	transketolase	84076.1	n/a
TKT1	transketolase	7086.1	n/a
TKT2	transketolase	8277.1	-0.063
TKT2	transketolase	84076.1	n/a
TKT2	transketolase	7086.1	n/a

Table 13: Expression changes in pyruvate metabolism for the gastric bypass study. Alphabetized list of reactions in pyruvate metabolism (as defined by Recon 1). Ratio is the average log10 expression ratio (*n*=3) of post-/pregene expression measurements (see text for details). Negative ratios (green) indicate a decrease in expression postsurgery, whereas positive ratios indicate an increase (red). Values denoted with "n/a" indicate that gene expression values were unavailable, or that expression ratios conflicted at the probe or patient levels.

Reaction	Putative function	Locus	Ratio
ACOAHi	acetyl-CoA hydrolase	134526.1	n/a
ACTLMO	acetol monooxygenase	1571.1	-0.258
ACTNMO	acetone monooxygenase	1571.1	-0.258
ALCD21_D	alcohol dehydrogenase (D-1,2-propanediol)	125.1	0.233
ALCD21_D	alcohol dehydrogenase (D-1,2-propanediol)	124.1	0.233
ALCD21_D	alcohol dehydrogenase (D-1,2-propanediol)	126.1	0.233
ALCD21_D	alcohol dehydrogenase (D-1,2-propanediol)	130.1	0.32
ALCD21_D	alcohol dehydrogenase (D-1,2-propanediol)	131.1	n/a
ALCD21_D	alcohol dehydrogenase (D-1,2-propanediol)	137872.1	n/a
ALCD21_D	alcohol dehydrogenase (D-1,2-propanediol)	127.1	n/a
ALCD21_D	alcohol dehydrogenase (D-1,2-propanediol)	284273.2	n/a
ALCD21_D	alcohol dehydrogenase (D-1,2-propanediol)	284273.1	n/a
ALCD21_D	alcohol dehydrogenase (D-1,2-propanediol)	128.1	n/a
ALCD21_L	alcohol dehydrogenase (L-1,2-propanediol)	125.1	0.233
ALCD21_L	alcohol dehydrogenase (L-1,2-propanediol)	124.1	0.233
ALCD21_L	alcohol dehydrogenase (L-1,2-propanediol)	126.1	0.233
ALCD21_L	alcohol dehydrogenase (L-1,2-propanediol)	130.1	0.32
ALCD21_L	alcohol dehydrogenase (L-1,2-propanediol)	131.1	n/a
ALCD21_L	alcohol dehydrogenase (L-1,2-propanediol)	137872.1	n/a
ALCD21_L	alcohol dehydrogenase (L-1,2-propanediol)	127.1	n/a
ALCD21_L	alcohol dehydrogenase (L-1,2-propanediol)	284273.2	n/a
ALCD21_L	alcohol dehydrogenase (L-1,2-propanediol)	284273.1	n/a
ALCD21_L	alcohol dehydrogenase (L-1,2-propanediol)	128.1	n/a
ALCD22_D	alcohol dehydrogenase (D-lactaldehyde)	125.1	0.233
ALCD22_D	alcohol dehydrogenase (D-lactaldehyde)	124.1	0.233

Reaction	Putative function	Locus	Ratio
ALCD22_D	alcohol dehydrogenase (D-lactaldehyde)	126.1	0.233
ALCD22_D	alcohol dehydrogenase (D-lactaldehyde)	130.1	0.32
ALCD22_D	alcohol dehydrogenase (D-lactaldehyde)	131.1	n/a
ALCD22_D	alcohol dehydrogenase (D-lactaldehyde)	137872.1	n/a
ALCD22_D	alcohol dehydrogenase (D-lactaldehyde)	127.1	n/a
ALCD22_D	alcohol dehydrogenase (D-lactaldehyde)	284273.2	n/a
ALCD22_D	alcohol dehydrogenase (D-lactaldehyde)	284273.1	n/a
ALCD22_D	alcohol dehydrogenase (D-lactaldehyde)	128.1	n/a
ALCD22_L	alcohol dehydrogenase (L-lactaldehyde)	125.1	0.233
ALCD22_L	alcohol dehydrogenase (L-lactaldehyde)	124.1	0.233
ALCD22_L	alcohol dehydrogenase (L-lactaldehyde)	126.1	0.233
ALCD22_L	alcohol dehydrogenase (L-lactaldehyde)	130.1	0.32
ALCD22_L	alcohol dehydrogenase (L-lactaldehyde)	131.1	n/a
ALCD22_L	alcohol dehydrogenase (L-lactaldehyde)	137872.1	n/a
ALCD22_L	alcohol dehydrogenase (L-lactaldehyde)	127.1	n/a
ALCD22_L	alcohol dehydrogenase (L-lactaldehyde)	284273.2	n/a
ALCD22_L	alcohol dehydrogenase (L-lactaldehyde)	284273.1	n/a
ALCD22_L	alcohol dehydrogenase (L-lactaldehyde)	128.1	n/a
ALR2	aldose reductase (methylglyoxal)	10327.1	0.066
ALR2	aldose reductase (methylglyoxal)	231.1	n/a
ALR2	aldose reductase (methylglyoxal)	10327.2	n/a
ALR2	aldose reductase (methylglyoxal)	8574.1	n/a
ALR3	aldose reductase (acetol)	10327.1	0.066
ALR3	aldose reductase (acetol)	231.1	n/a
ALR3	aldose reductase (acetol)	10327.2	n/a
ALR3	aldose reductase (acetol)	8574.1	n/a

Reaction	Putative function	Locus	Ratio
GLYOX	hydroxyacylglutathione hydrolase	84264.1	n/a
GLYOX	hydroxyacylglutathione hydrolase	84264.2	n/a
GLYOX	hydroxyacylglutathione hydrolase	3029.1	n/a
GLYOXm	hydroxyacylglutathione hydrolase, mitochondrial	3029.1	n/a
LALDD	D-lactaldehyde dehydrogenase	9380.1	n/a
LALDO	D-Lactaldehyde:NAD+ oxidoreductase (glutathione-formylating)	128.1	n/a
LALDO2	D-Lactaldehyde:NADP+ 1-oxidoreductase	10327.1	0.066
LALDO2	D-Lactaldehyde:NADP+ 1-oxidoreductase	231.1	n/a
LALDO2	D-Lactaldehyde:NADP+ 1-oxidoreductase	10327.2	n/a
LALDO2	D-Lactaldehyde:NADP+ 1-oxidoreductase	8574.1	n/a
LALDO2x	D-Lactaldehyde:NAD+ 1-oxidoreductase	8574.1	n/a
LCADi	lactaldehyde dehydrogenase	218.1	-0.247
LCADi	lactaldehyde dehydrogenase	8854.1	0.273
LCADi	lactaldehyde dehydrogenase	222.1	0.284
LCADi	lactaldehyde dehydrogenase	501.1	n/a
LCADi	lactaldehyde dehydrogenase	216.1	n/a
LCADi	lactaldehyde dehydrogenase	8854.3	n/a
LCADi	lactaldehyde dehydrogenase	8854.2	n/a
LCADi	lactaldehyde dehydrogenase	224.1	n/a
LCADi	lactaldehyde dehydrogenase	223.1	n/a
LCADi	lactaldehyde dehydrogenase	220.1	n/a
LCADi	lactaldehyde dehydrogenase	221.1	n/a
LCADi_D	lactaldehyde dehydrogenase	218.1	-0.247
LCADi_D	lactaldehyde dehydrogenase	8854.1	0.273
LCADi_D	lactaldehyde dehydrogenase	222.1	0.284
LCADi_D	lactaldehyde dehydrogenase	501.1	n/a
LCADi_D	lactaldehyde dehydrogenase	216.1	n/a
LCADi_D	lactaldehyde dehydrogenase	8854.3	n/a
LCADi_D	lactaldehyde dehydrogenase	8854.2	n/a
LCADi_D	lactaldehyde dehydrogenase	224.1	n/a
LCADi_D	lactaldehyde dehydrogenase	223.1	n/a
LCADi_D	lactaldehyde dehydrogenase	220.1	n/a
LCADi_D	lactaldehyde dehydrogenase	221.1	n/a
LCADi_Dm	lactaldehyde dehydrogenase, mitochondrial	219.1	-0.469

Reaction	Putative function	Locus	Ratio
LCADi_Dm	lactaldehyde dehydrogenase, mitochondrial	8659.1	-0.337
LCADi_Dm	lactaldehyde dehydrogenase, mitochondrial	4329.1	-0.084
LCADi_Dm	lactaldehyde dehydrogenase, mitochondrial	217.1	-0.039
LCADi_Dm	lactaldehyde dehydrogenase, mitochondrial	5832.1	n/a
LCADi_Dm	lactaldehyde dehydrogenase, mitochondrial	8659.2	n/a
LCADi_Dm	lactaldehyde dehydrogenase, mitochondrial	7915.1	n/a
LCADi_Dm	lactaldehyde dehydrogenase, mitochondrial	7915.2	n/a
LCADim	lactaldehyde dehydrogenase, mitochondrial	219.1	-0.469
LCADim	lactaldehyde dehydrogenase, mitochondrial	8659.1	-0.337
LCADim	lactaldehyde dehydrogenase, mitochondrial	4329.1	-0.084
LCADim	lactaldehyde dehydrogenase, mitochondrial	217.1	-0.039
LCADim	lactaldehyde dehydrogenase, mitochondrial	5832.1	n/a
LCADim	lactaldehyde dehydrogenase, mitochondrial	8659.2	n/a
LCADim	lactaldehyde dehydrogenase, mitochondrial	7915.1	n/a
LCADim	lactaldehyde dehydrogenase, mitochondrial	7915.2	n/a
LDH_D	D-lactate dehydrogenase	197257.1	n/a
LDH_D	D-lactate dehydrogenase	197257.2	n/a
LDH_Lm	L-lactate dehydrogenase	3939.1	n/a
LGTHL	lactoylglutathione lyase	2739.1	n/a
L-LACDcm	L-Lactate dehydrogenase, cytosolic/mitochondrial	124637.1	n/a
ME1m	malic enzyme (NAD), mitochondrial	4200.1	n/a
ME2	malic enzyme (NADP)	4199.1	-0.208
ME2m	malic enzyme (NADP), mitochondrial	10873.1	n/a
ME2m	malic enzyme (NADP), mitochondrial	4200.1	n/a
PCm	pyruvate carboxylase	5091.1	n/a
PCm	pyruvate carboxylase	5091.2	n/a
PPDOx	Propane-1,2-diol:NAD+ 1-oxidoreductase	8574.1	n/a

Reaction	Putative function	Locus	Ratio
PPDOy	Propane-1,2-diol:NADP+ 1-oxidoreductase	10327.1	0.066
PPDOy	Propane-1,2-diol:NADP+ 1-oxidoreductase	231.1	n/a
PPDOy	Propane-1,2-diol:NADP+ 1-oxidoreductase	10327.2	n/a
PPDOy	Propane-1,2-diol:NADP+ 1-oxidoreductase	8574.1	n/a

Table 14: Expression changes in TCA cycle for the gastric bypass study. Alphabetized list of reactions in TCA cycle (as defined by Recon 1). Ratio is the average log10 expression ratio (*n*=3) of post-/pregene expression measurements (see text for details). Negative ratios (green) indicate a decrease in expression postsurgery whereas positive ratios indicate an increase (red). Values denoted with "n/a" indicate that gene expression values were unavailable, or that expression ratios conflicted at the probe or patient levels.

Reaction	Putative function	Locus	Ratio
ACITL	ATP-Citrate lyase	47.1	0.254
ACITL	ATP-Citrate lyase	47.2	n/a
ACONT	aconitase	48.1	-0.075
ACONT	aconitase	3658.1	-0.065
ACONTm	Aconitate hydratase	50.1	-0.06
AKGDm	2-oxoglutarate dehydrogenase	8050.1	-0.128
AKGDm	2-oxoglutarate dehydrogenase	1738.1	-0.051
AKGDm	2-oxoglutarate dehydrogenase	4967.2	n/a
AKGDm	2-oxoglutarate dehydrogenase	1743.1	n/a
AKGDm	2-oxoglutarate dehydrogenase	4967.1	n/a
CITL	Citrate lyase	171425.1	n/a
CITL	Citrate lyase	171425.2	n/a
CSm	citrate synthase	1431.1	n/a
CSm	citrate synthase	1431.2	n/a
FUM	fumarase	2271.1	n/a
FUMm	fumarase, mitochondrial	2271.1	n/a
ICDHxm	Isocitrate dehydrogenase (NAD+)	3421.1	n/a
ICDHxm	Isocitrate dehydrogenase (NAD+)	3421.2	n/a
ICDHxm	Isocitrate dehydrogenase (NAD+)	3419.1	n/a
ICDHxm	Isocitrate dehydrogenase (NAD+)	3420.3	n/a
ICDHxm	Isocitrate dehydrogenase (NAD+)	3420.1	n/a
ICDHxm	Isocitrate dehydrogenase (NAD+)	3420.2	n/a
ICDHy	isocitrate dehydrogenase (NADP)	3417.1	-0.118
ICDHyp	Isocitrate dehydrogenase (NADP+)	3417.1	-0.118
ICDHyrm	Isocitrate dehydrogenase (NADP+)	3418.1	n/a
MDH	malate dehydrogenase	4190.1	-0.059
MDH	malate dehydrogenase	130752.1	n/a
MDHm	malate dehydrogenase, mitochondrial	4191.1	n/a
SUCD1m	succinate dehydrogenase	6392.1	-0.252
SUCD1m	succinate dehydrogenase	6391.1	-0.069
SUCD1m	succinate dehydrogenase	6390.1	n/a
SUCD1m	succinate dehydrogenase	6389.1	n/a
SUCOAS1m	Succinate--CoA ligase (GDP-forming)	8802.1	-0.058
SUCOAS1m	Succinate--CoA ligase (GDP-forming)	8801.1	0.028
SUCOASm	Succinate--CoA ligase (ADP-forming)	8802.1	-0.058
SUCOASm	Succinate--CoA ligase (ADP-forming)	8803.1	n/a

Table 15: Expression changes in oxidative phosphorylation for the gastric bypass study. Alphabetized list of reactions in oxidative phosphorylation (as defined by Recon 1). Ratio is the average log10 expression ratio (*n*=3) of post-/pregene expression measurements (see text for details). Negative ratios (green) indicate a decrease in expression postsurgery, whereas positive ratios indicate an increase (red). Values denoted with "n/a" indicate that gene expression values were unavailable, or that expression ratios conflicted at the probe or patient levels.

Reaction	Putative function	Locus	Ratio
ATPS4m	ATP synthase (four protons for one ATP)	517.1	-0.111
ATPS4m	ATP synthase (four protons for one ATP)	514.1	-0.104
ATPS4m	ATP synthase (four protons for one ATP)	518.1	-0.102
ATPS4m	ATP synthase (four protons for one ATP)	522.1	-0.093
ATPS4m	ATP synthase (four protons for one ATP)	4905.1	-0.08
ATPS4m	ATP synthase (four protons for one ATP)	516.1	-0.057
ATPS4m	ATP synthase (four protons for one ATP)	521.1	-0.042
ATPS4m	ATP synthase (four protons for one ATP)	509.1	-0.04
ATPS4m	ATP synthase (four protons for one ATP)	10632.1	0.201
ATPS4m	ATP synthase (four protons for one ATP)	513.1	n/a
ATPS4m	ATP synthase (four protons for one ATP)	515.3	n/a
ATPS4m	ATP synthase (four protons for one ATP)	513.2	n/a
ATPS4m	ATP synthase (four protons for one ATP)	9551.1	n/a
ATPS4m	ATP synthase (four protons for one ATP)	522.5	n/a
ATPS4m	ATP synthase (four protons for one ATP)	522.4	n/a
ATPS4m	ATP synthase (four protons for one ATP)	506.1	n/a
ATPS4m	ATP synthase (four protons for one ATP)	515.2	n/a
ATPS4m	ATP synthase (four protons for one ATP)	509.2	n/a
ATPS4m	ATP synthase (four protons for one ATP)	522.2	n/a
ATPS4m	ATP synthase (four protons for one ATP)	518.2	n/a
ATPS4m	ATP synthase (four protons for one ATP)	514.2	n/a
ATPS4m	ATP synthase (four protons for one ATP)	522.3	n/a
ATPS4m	ATP synthase (four protons for one ATP)	517.2	n/a
ATPS4m	ATP synthase (four protons for one ATP)	518.3	n/a
ATPS4m	ATP synthase (four protons for one ATP)	10476.2	n/a
ATPS4m	ATP synthase (four protons for one ATP)	9551.3	n/a
ATPS4m	ATP synthase (four protons for one ATP)	515.1	n/a
ATPS4m	ATP synthase (four protons for one ATP)	498.1	n/a
ATPS4m	ATP synthase (four protons for one ATP)	10476.1	n/a
ATPS4m	ATP synthase (four protons for one ATP)	498.2	n/a
ATPS4m	ATP synthase (four protons for one ATP)	516.2	n/a
ATPS4m	ATP synthase (four protons for one ATP)	498.3	n/a
ATPS4m	ATP synthase (four protons for one ATP)	9551.2	n/a
CYOOm3	cytochrome c oxidase, mitochondrial Complex IV	1329.1	-0.218
CYOOm3	cytochrome c oxidase, mitochondrial Complex IV	1339.1	-0.193
CYOOm3	cytochrome c oxidase, mitochondrial Complex IV	1349.1	-0.073
CYOOm3	cytochrome c oxidase, mitochondrial Complex IV	1327.1	-0.03
CYOOm3	cytochrome c oxidase, mitochondrial Complex IV	9167.1	0.045
CYOOm3	cytochrome c oxidase, mitochondrial Complex IV	1347.1	n/a
CYOOm3	cytochrome c oxidase, mitochondrial Complex IV	1345.1	n/a

Reaction	Putative function	Locus	Ratio
CYOOm3	cytochrome c oxidase, mitochondrial Complex IV	4512.1	n/a
CYOOm3	cytochrome c oxidase, mitochondrial Complex IV	1340.1	n/a
CYOOm3	cytochrome c oxidase, mitochondrial Complex IV	4514.1	n/a
CYOOm3	cytochrome c oxidase, mitochondrial Complex IV	84701.1	n/a
CYOOm3	cytochrome c oxidase, mitochondrial Complex IV	1346.1	n/a
CYOOm3	cytochrome c oxidase, mitochondrial Complex IV	1350.1	n/a
CYOOm3	cytochrome c oxidase, mitochondrial Complex IV	1337.1	n/a
CYOOm3	cytochrome c oxidase, mitochondrial Complex IV	170712.1	n/a
CYOOm3	cytochrome c oxidase, mitochondrial Complex IV	1351.1	n/a
CYOOm3	cytochrome c oxidase, mitochondrial Complex IV	4513.1	n/a
CYOOm3	cytochrome c oxidase, mitochondrial Complex IV	341947.1	n/a
CYOOm3	cytochrome c oxidase, mitochondrial Complex IV	125965.1	n/a
CYOOm3	cytochrome c oxidase, mitochondrial Complex IV	9377.1	n/a
CYOR-u10m	ubiquinol-6 cytochrome c reductase, Complex III	7381.1	-0.242
CYOR-u10m	ubiquinol-6 cytochrome c reductase, Complex III	29796.1	-0.102
CYOR-u10m	ubiquinol-6 cytochrome c reductase, Complex III	10975.1	n/a
CYOR-u10m	ubiquinol-6 cytochrome c reductase, Complex III	7388.1	n/a
CYOR-u10m	ubiquinol-6 cytochrome c reductase, Complex III	1537.1	n/a
CYOR-u10m	ubiquinol-6 cytochrome c reductase, Complex III	4519.1	n/a
CYOR-u10m	ubiquinol-6 cytochrome c reductase, Complex III	29796.2	n/a
CYOR-u10m	ubiquinol-6 cytochrome c reductase, Complex III	7384.1	n/a
CYOR-u10m	ubiquinol-6 cytochrome c reductase, Complex III	7385.1	n/a
CYOR-u10m	ubiquinol-6 cytochrome c reductase, Complex III	27089.1	n/a
CYOR-u10m	ubiquinol-6 cytochrome c reductase, Complex III	7386.1	n/a

Reaction	Putative function	Locus	Ratio
NADH2-u10m	NADH dehydrogenase, mitochondrial	4728.1	-0.219
NADH2-u10m	NADH dehydrogenase, mitochondrial	51079.1	-0.176
NADH2-u10m	NADH dehydrogenase, mitochondrial	7991.1	-0.133
NADH2-u10m	NADH dehydrogenase, mitochondrial	4729.1	-0.129
NADH2-u10m	NADH dehydrogenase, mitochondrial	4696.1	-0.101
NADH2-u10m	NADH dehydrogenase, mitochondrial	4694.1	-0.101
NADH2-u10m	NADH dehydrogenase, mitochondrial	4717.1	-0.091
NADH2-u10m	NADH dehydrogenase, mitochondrial	4719.1	-0.087
NADH2-u10m	NADH dehydrogenase, mitochondrial	4718.1	-0.086
NADH2-u10m	NADH dehydrogenase, mitochondrial	4709.1	-0.076
NADH2-u10m	NADH dehydrogenase, mitochondrial	4708.1	-0.073
NADH2-u10m	NADH dehydrogenase, mitochondrial	4702.1	-0.064
NADH2-u10m	NADH dehydrogenase, mitochondrial	4714.1	-0.055
NADH2-u10m	NADH dehydrogenase, mitochondrial	4711.1	-0.053
NADH2-u10m	NADH dehydrogenase, mitochondrial	4713.1	0.118
NADH2-u10m	NADH dehydrogenase, mitochondrial	7991.2	n/a
NADH2-u10m	NADH dehydrogenase, mitochondrial	4712.1	n/a
NADH2-u10m	NADH dehydrogenase, mitochondrial	4697.1	n/a
NADH2-u10m	NADH dehydrogenase, mitochondrial	4695.1	n/a
NADH2-u10m	NADH dehydrogenase, mitochondrial	4725.1	n/a
NADH2-u10m	NADH dehydrogenase, mitochondrial	4716.1	n/a
NADH2-u10m	NADH dehydrogenase, mitochondrial	4698.1	n/a
NADH2-u10m	NADH dehydrogenase, mitochondrial	4720.1	n/a
NADH2-u10m	NADH dehydrogenase, mitochondrial	4538.1	n/a
NADH2-u10m	NADH dehydrogenase, mitochondrial	126328.1	n/a
NADH2-u10m	NADH dehydrogenase, mitochondrial	4710.1	n/a
NADH2-u10m	NADH dehydrogenase, mitochondrial	4539.1	n/a
NADH2-u10m	NADH dehydrogenase, mitochondrial	4535.1	n/a
NADH2-u10m	NADH dehydrogenase, mitochondrial	4704.1	n/a
NADH2-u10m	NADH dehydrogenase, mitochondrial	4701.1	n/a
NADH2-u10m	NADH dehydrogenase, mitochondrial	4724.1	n/a
NADH2-u10m	NADH dehydrogenase, mitochondrial	4541.1	n/a
NADH2-u10m	NADH dehydrogenase, mitochondrial	4722.1	n/a
NADH2-u10m	NADH dehydrogenase, mitochondrial	4700.1	n/a
NADH2-u10m	NADH dehydrogenase, mitochondrial	4726.1	n/a
NADH2-u10m	NADH dehydrogenase, mitochondrial	4723.1	n/a
NADH2-u10m	NADH dehydrogenase, mitochondrial	4536.1	n/a
NADH2-u10m	NADH dehydrogenase, mitochondrial	4715.1	n/a
NADH2-u10m	NADH dehydrogenase, mitochondrial	374291.1	n/a
NADH2-u10m	NADH dehydrogenase, mitochondrial	4731.1	n/a
NADH2-u10m	NADH dehydrogenase, mitochondrial	55967.1	n/a
NADH2-u10m	NADH dehydrogenase, mitochondrial	4537.1	n/a
NADH2-u10m	NADH dehydrogenase, mitochondrial	4706.1	n/a
NADH2-u10m	NADH dehydrogenase, mitochondrial	4712.2	n/a
NADH2-u10m	NADH dehydrogenase, mitochondrial	4707.1	n/a
NADH2-u10m	NADH dehydrogenase, mitochondrial	4705.1	n/a
NADH2-u10m	NADH dehydrogenase, mitochondrial	4540.1	n/a
NADH2-u10m	NADH dehydrogenase, mitochondrial	4731.2	n/a

Reaction	Putative function	Locus	Ratio
PPA	inorganic diphosphatase	5464.1	n/a
PPAm	inorganic diphosphatase	27068.1	-0.106
PPAm	inorganic diphosphatase	27068.2	n/a
PPAm	inorganic diphosphatase	27068.4	n/a
PPAm	inorganic diphosphatase	27068.3	n/a

1. Determination of initial component list

2. Manual curation of network components

1500+ citations

5x

280+ metabolic functions

3. Functional testing and validation

4. Dissemination of network content

BiGG Human Database

- Browse and search tools
- Human-specific network maps
- Stoichiometric matrix
- Reaction, metabolite & gap lists

5. Possible research applications

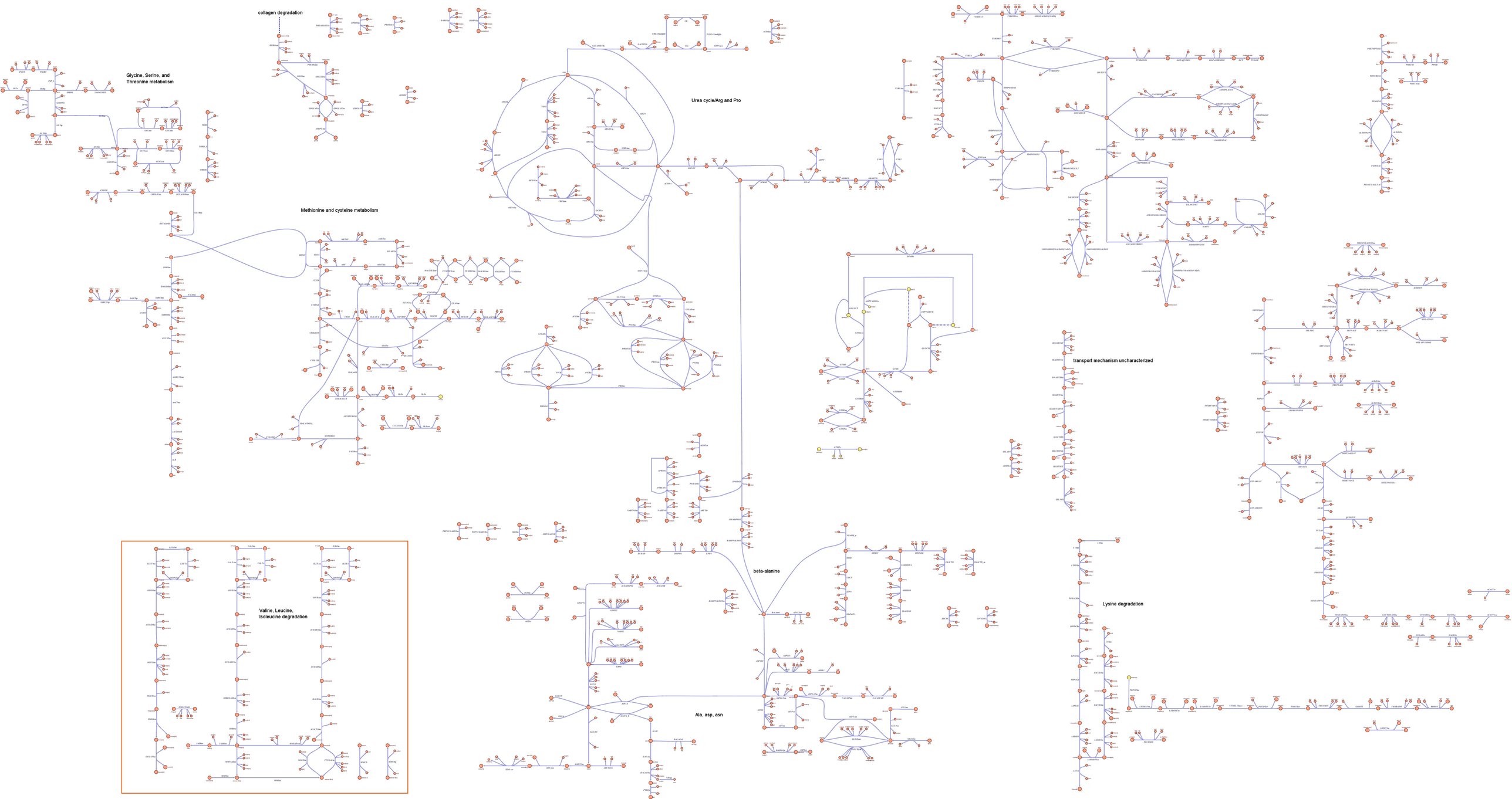
Visualizing genome-scale data (e.g., transcriptomic proteomic, fluxomic)

Identifying and investigating knowledge gaps

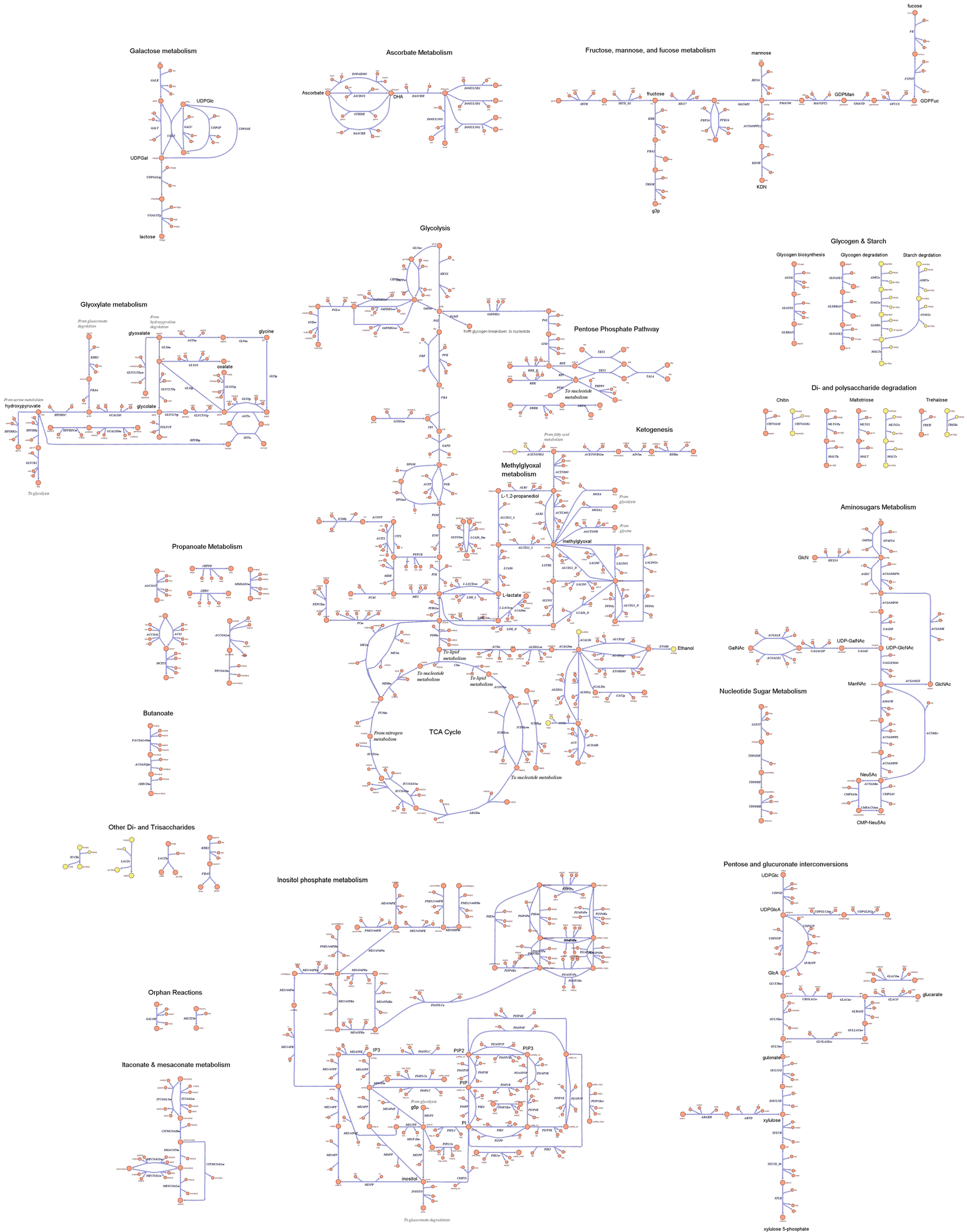
Modeling specific cell types and diseases

Analyzing network structure

Homo sapiens Recon 1 AMINO ACID METABOLISM

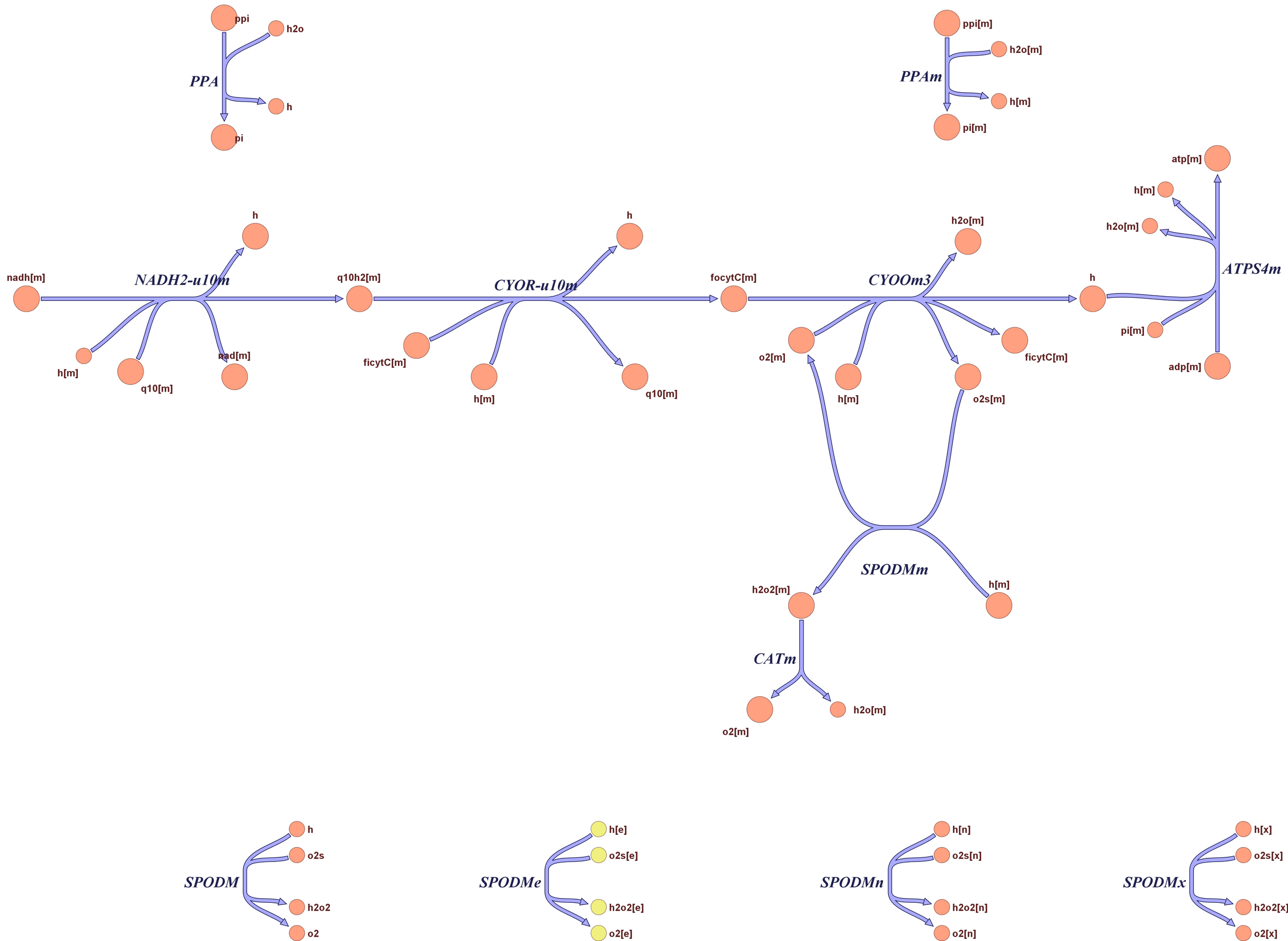


Homo sapiens Recon 1 CARBOHYDRATE METABOLISM

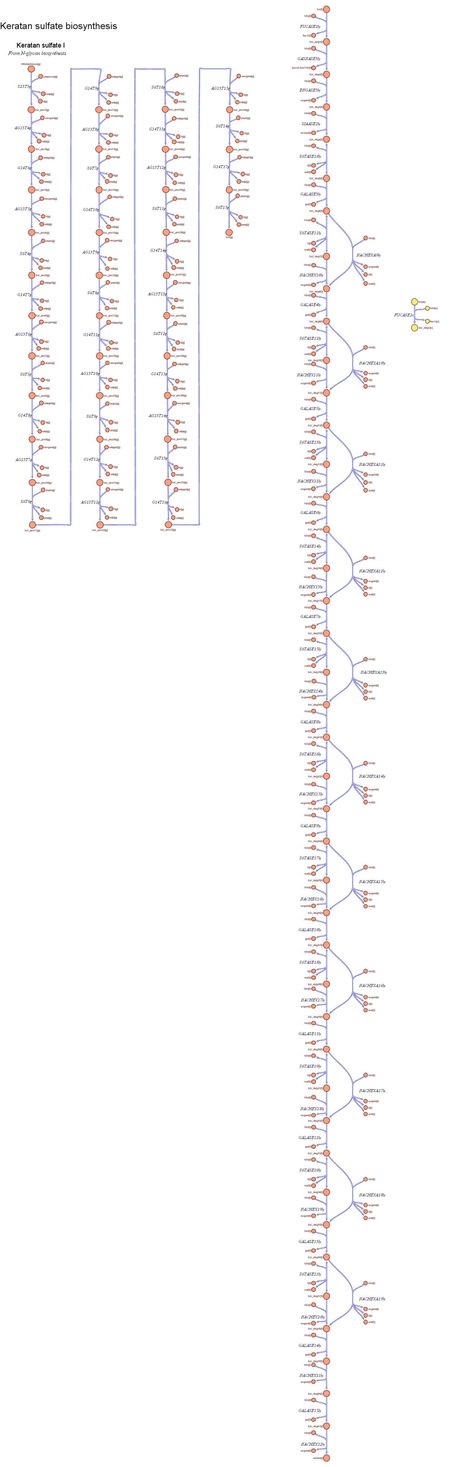


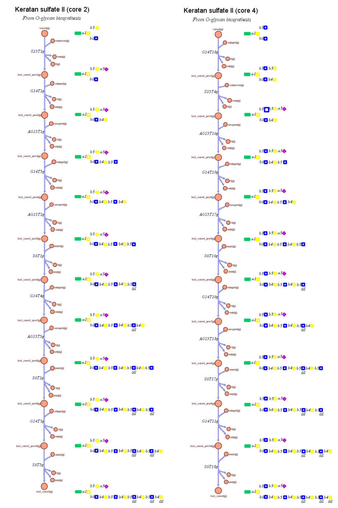
Homo sapiens Recon 1 ENERGY METABOLISM

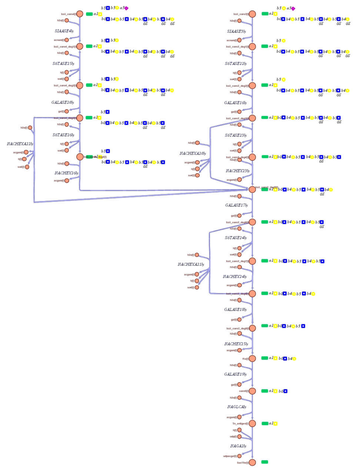
Oxidative Phosphorylation & ROS Detoxification

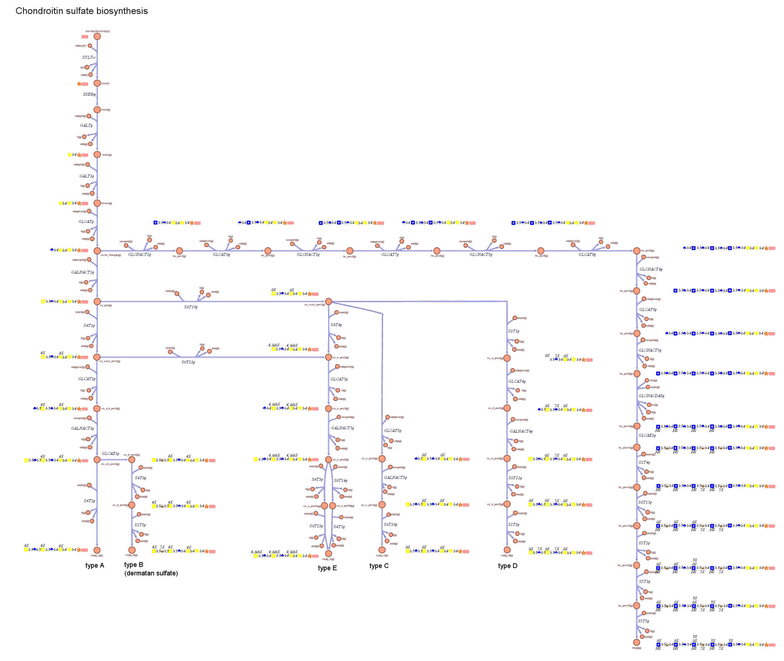


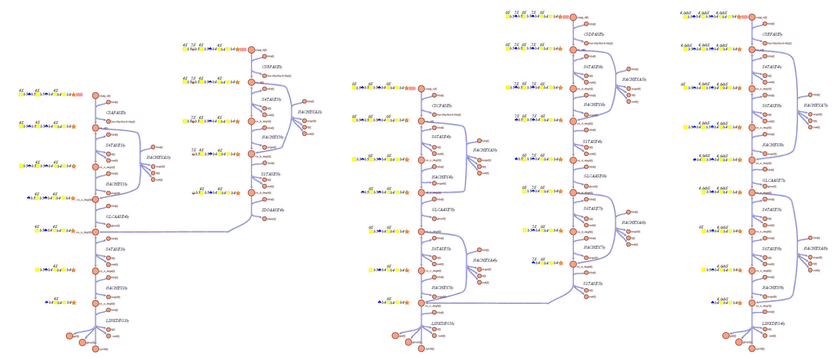
Homo sapiens Recon 1 GLYCAN METABOLISM

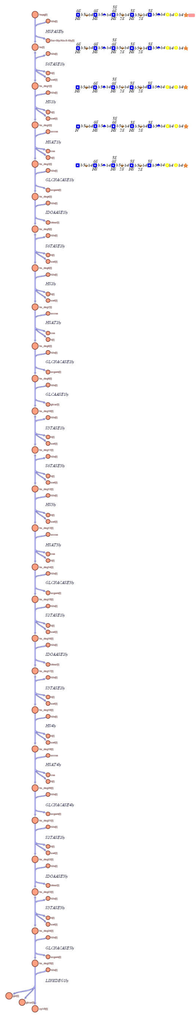


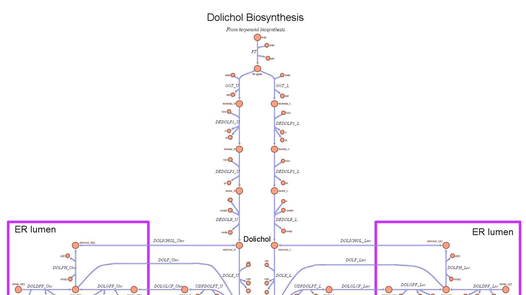


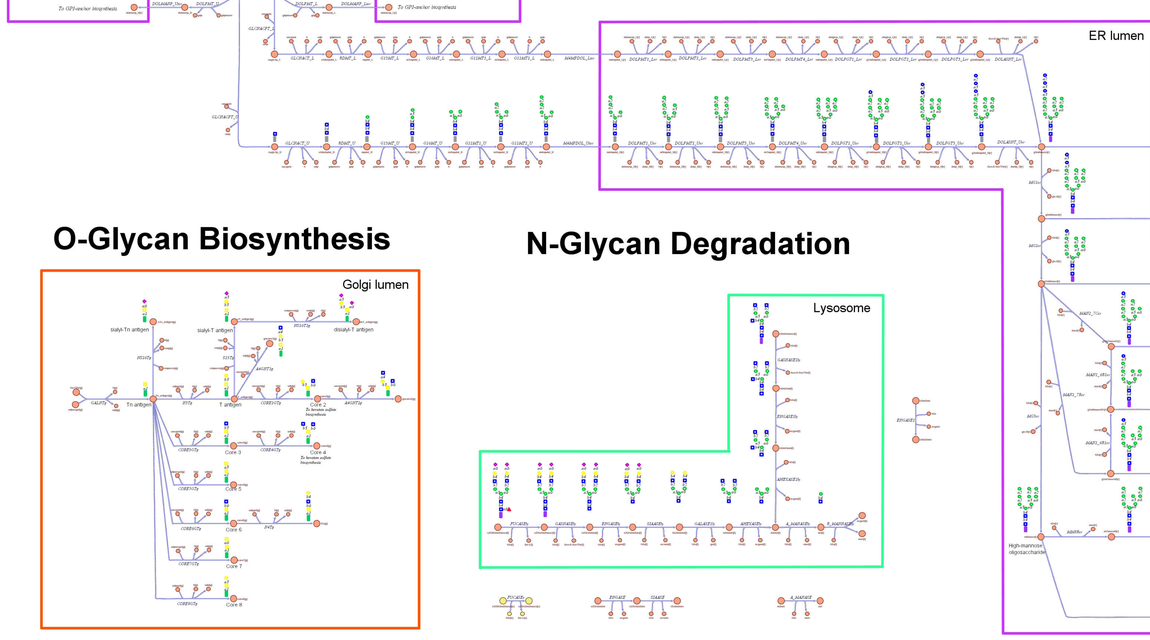


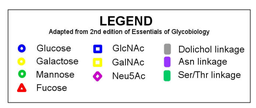


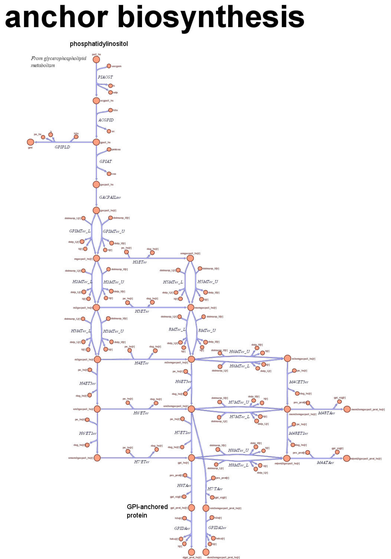




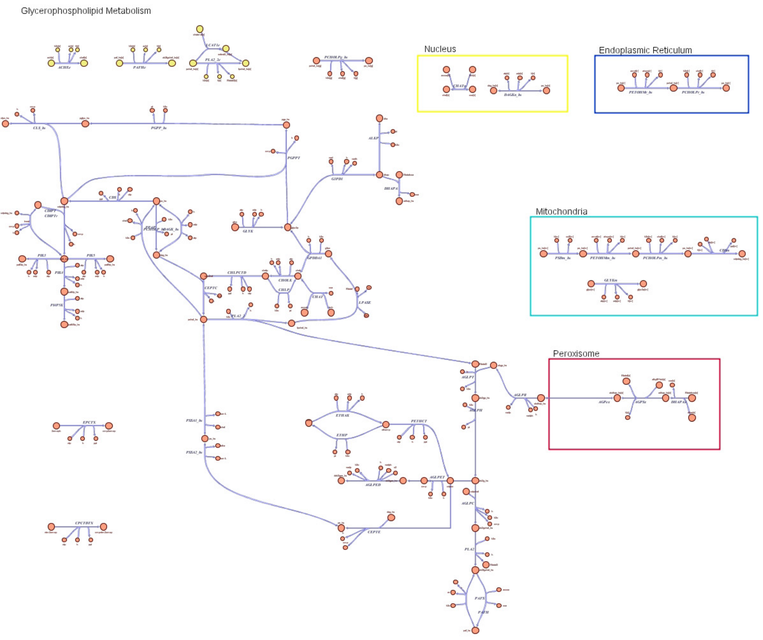


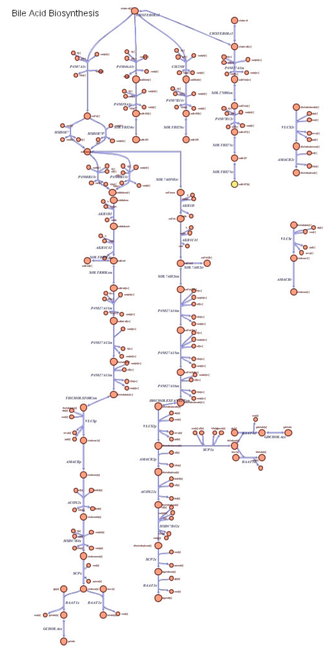


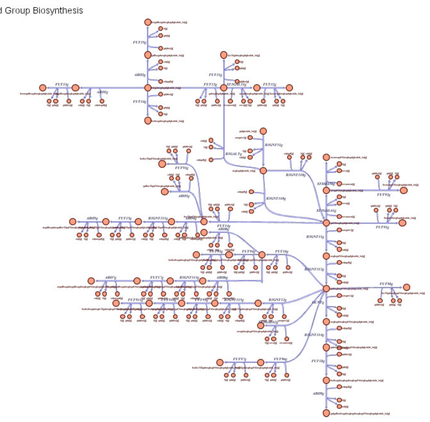


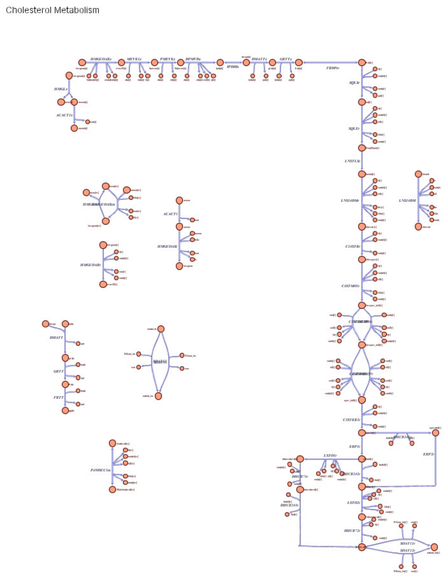


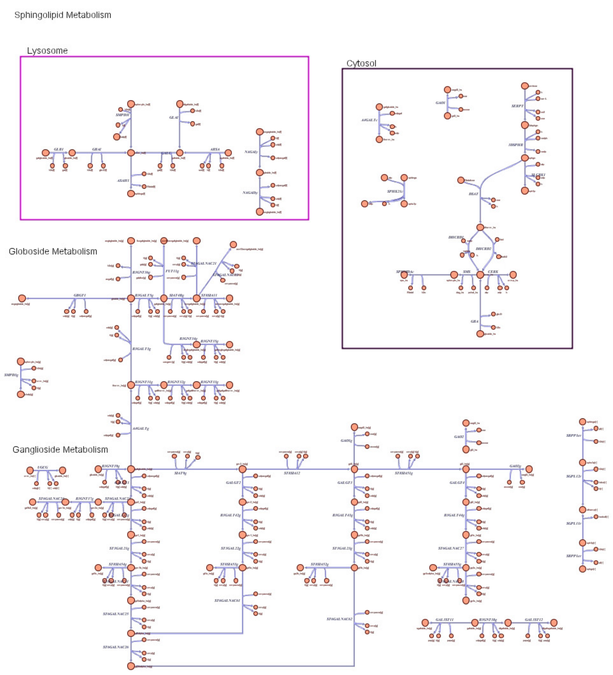
Homo sapiens Recon 1 LIPID METABOLISM

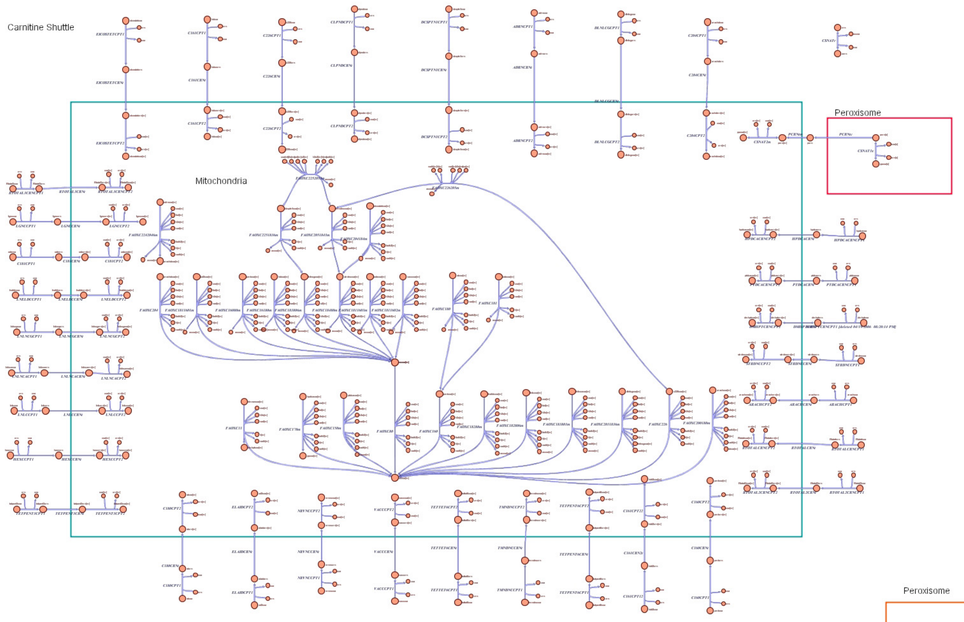


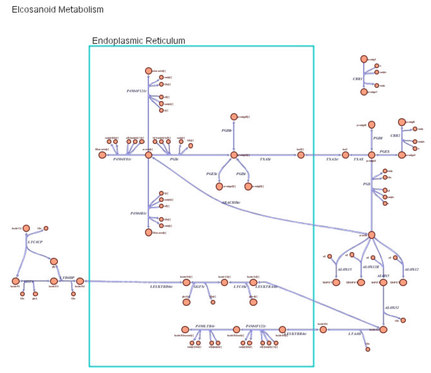


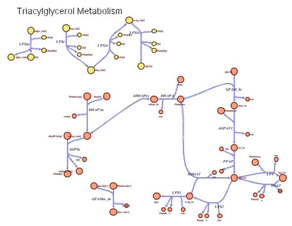


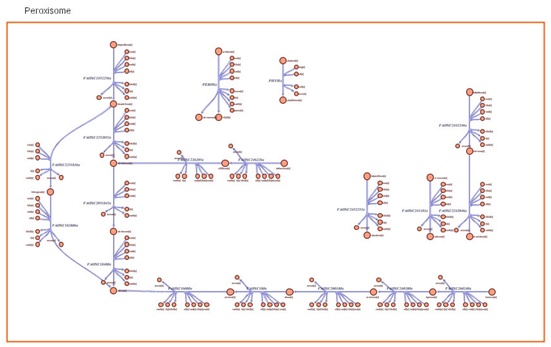


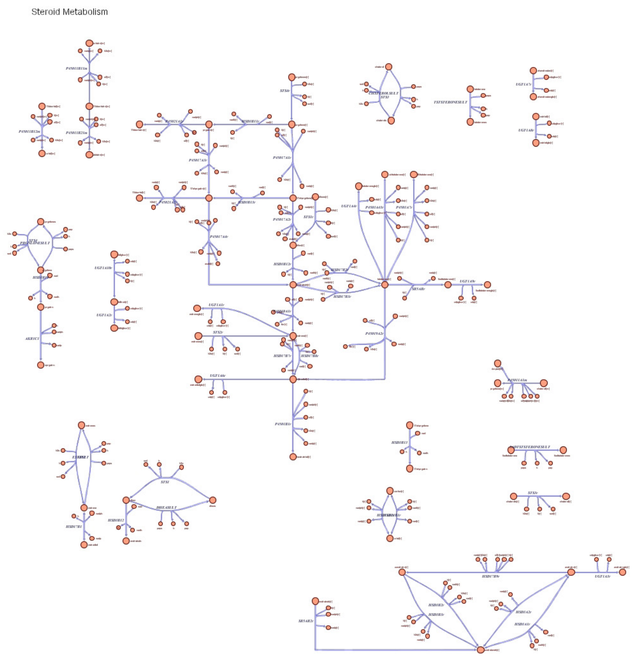


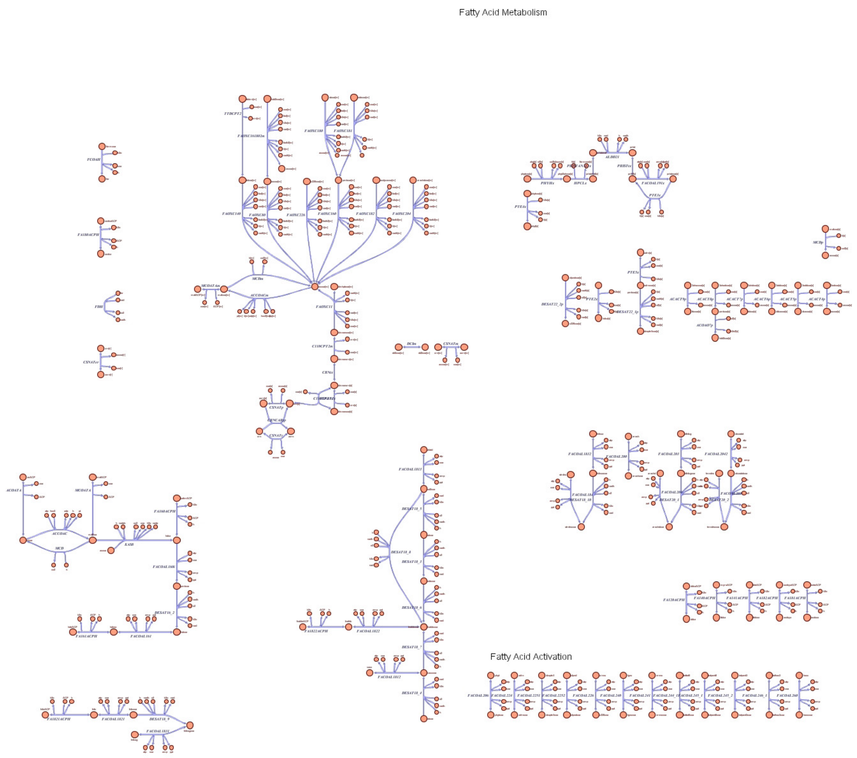


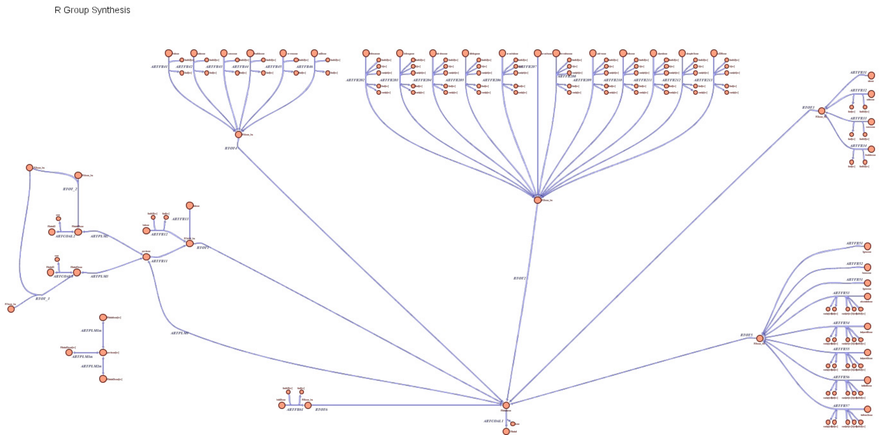




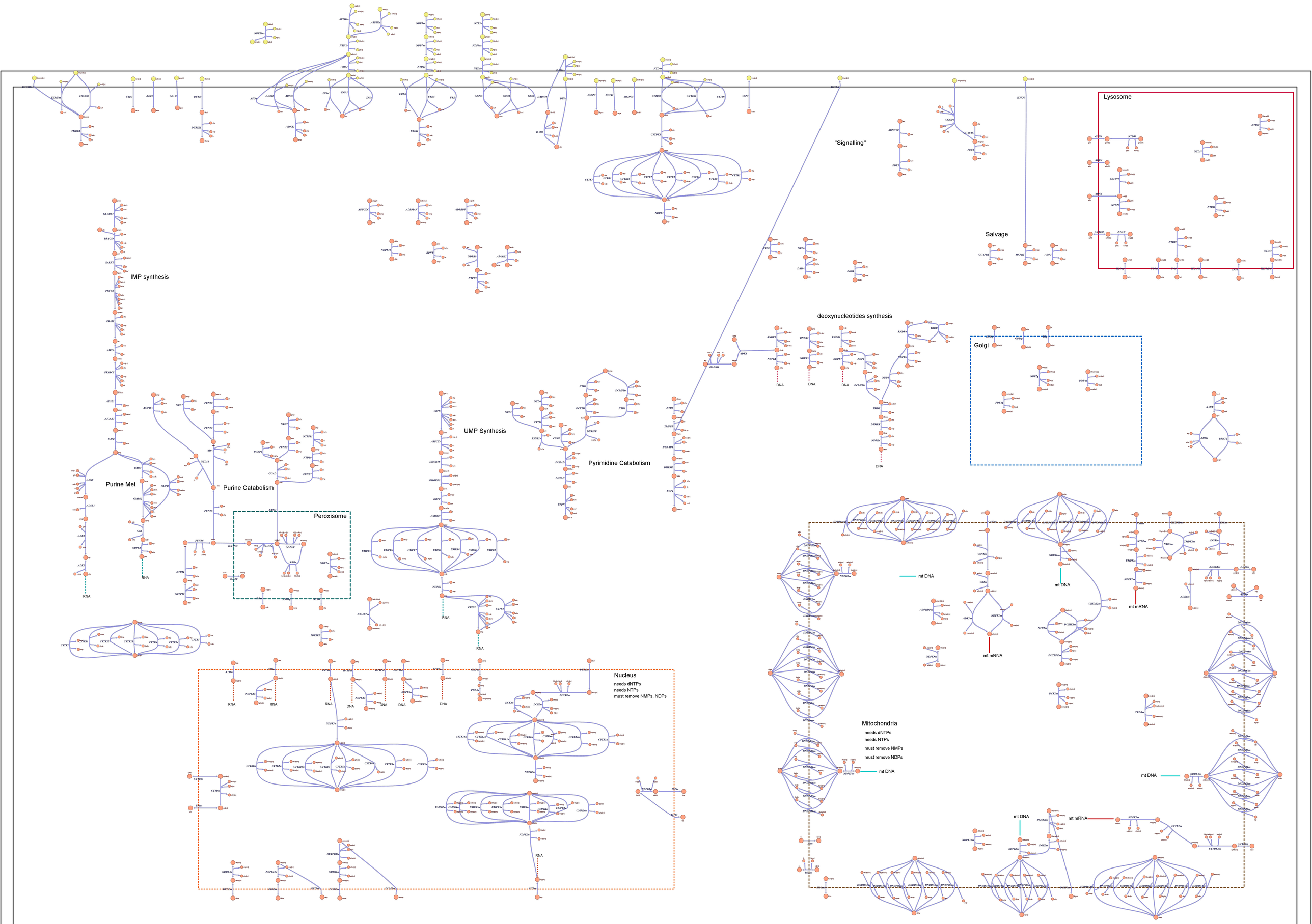




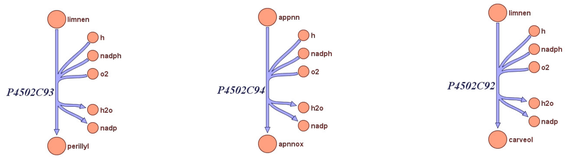




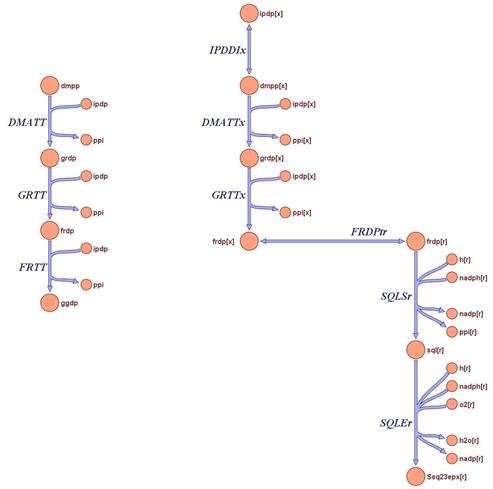
Homo sapiens Recon 1 NUCLEOTIDE METABOLISM



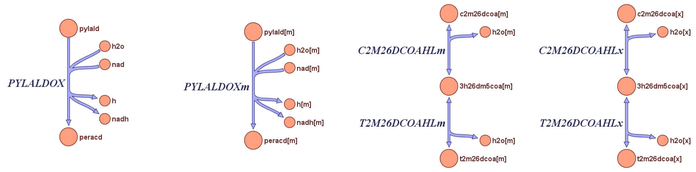
Homo sapiens Recon 1 SECONDARY METABOLITES



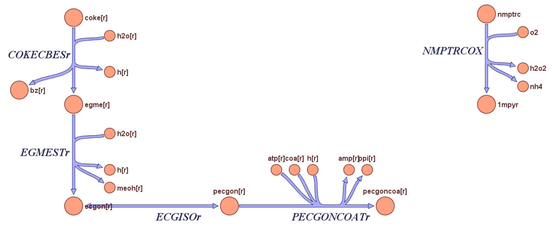
Terpenoid Biosynthesis



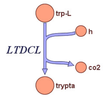
Limonene and pinene degradation



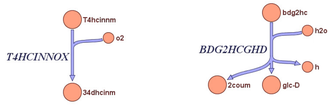
Alkaloid biosynthesis II



Indole and ipecac alkaloid biosynthesis

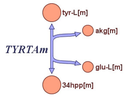


Stilbene, coumarine and lignin biosynthesis

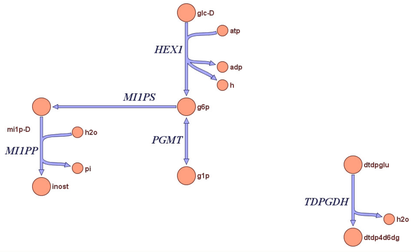


Alkaloid biosynthesis I

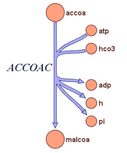
Novobiocin biosynthesis



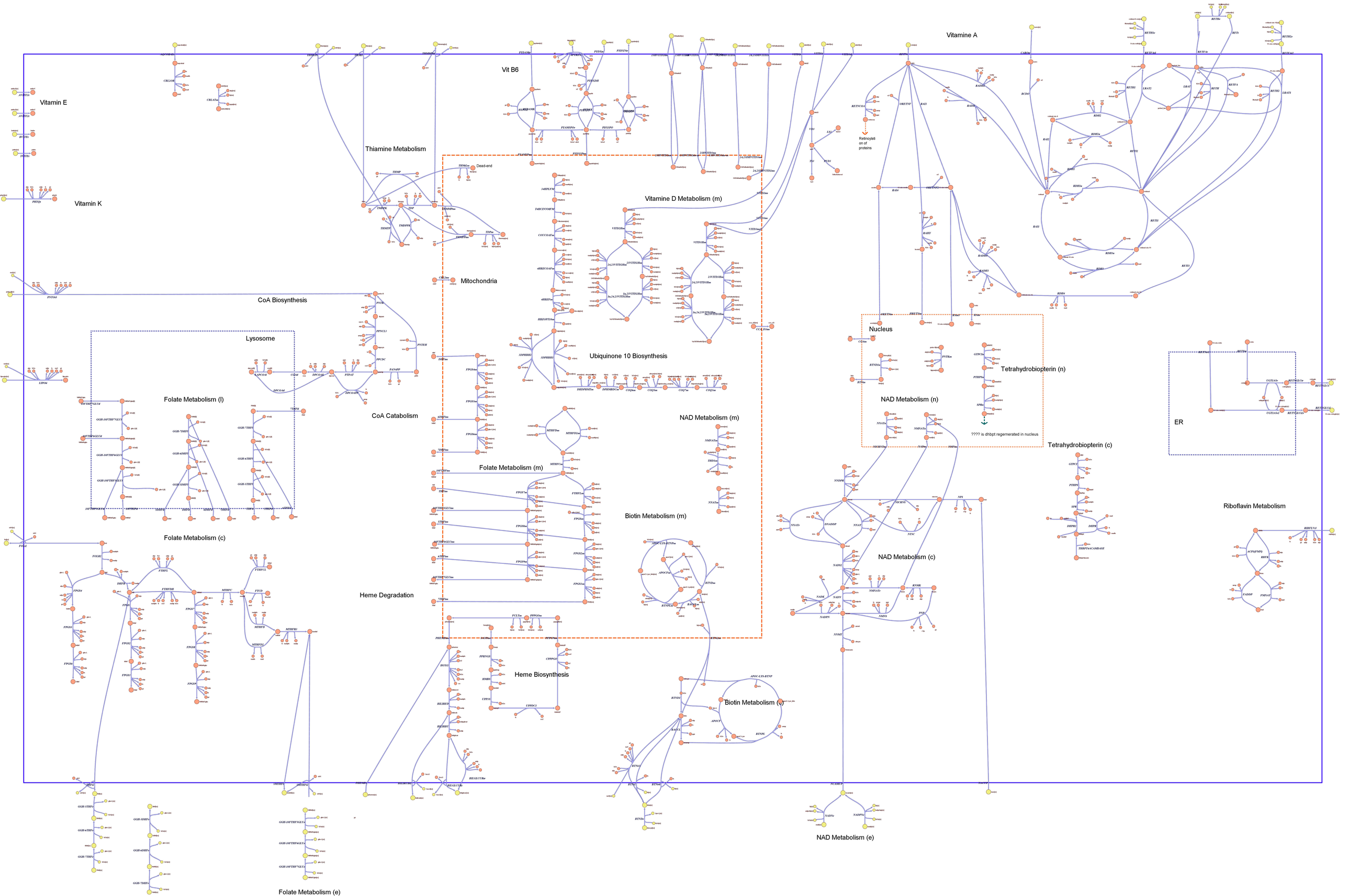
Streptomycin biosynthesis

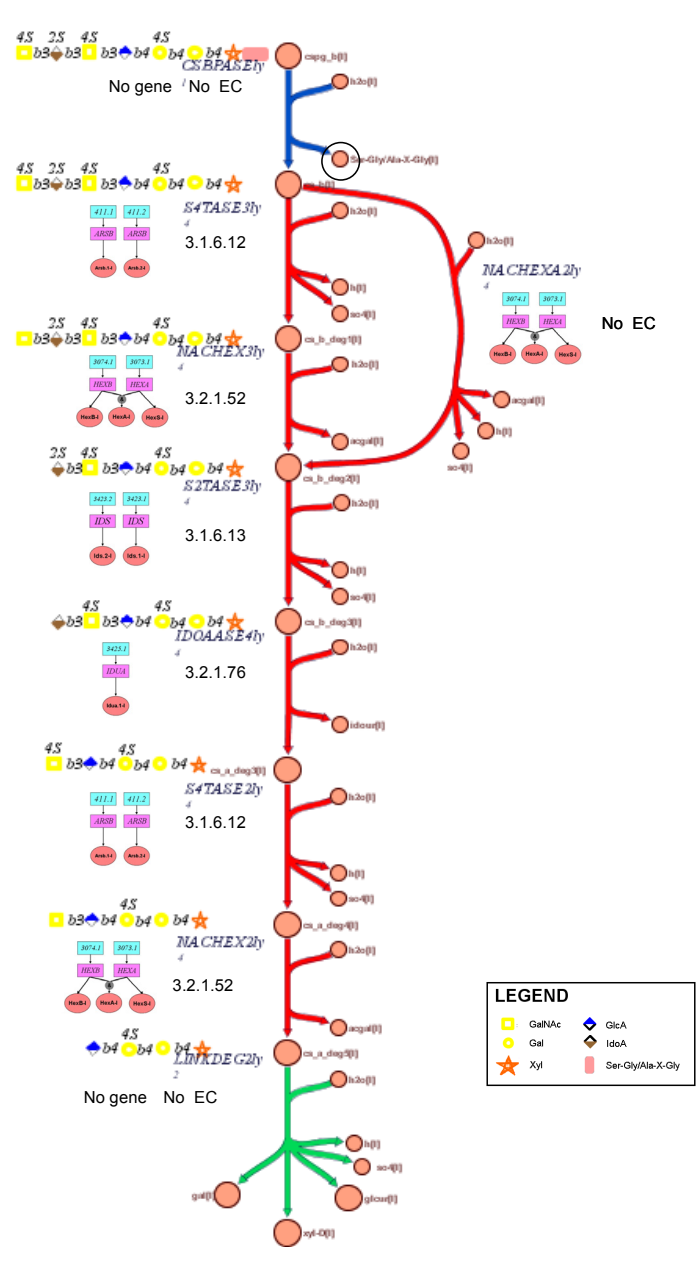


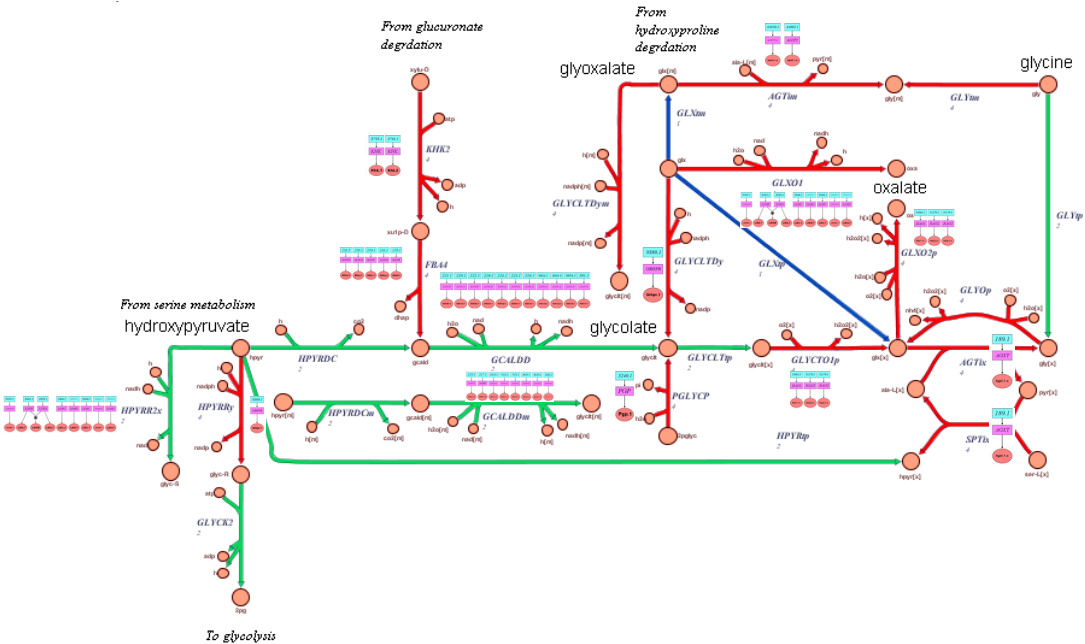
Tetracycline biosynthesis

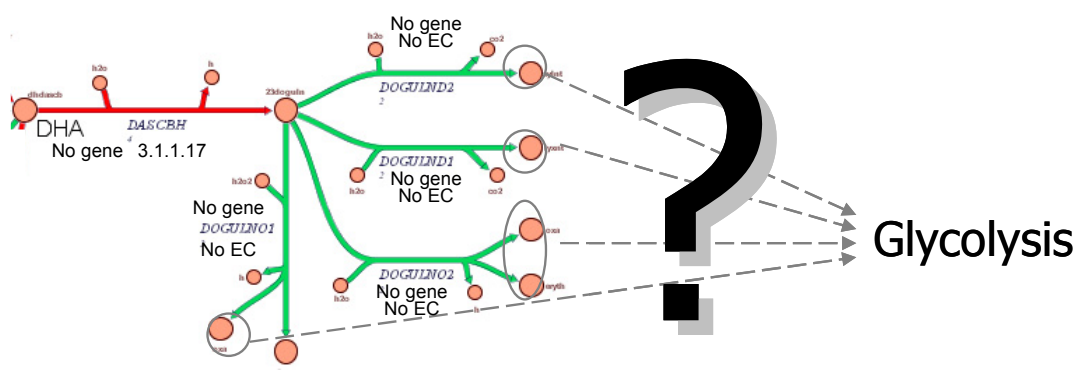


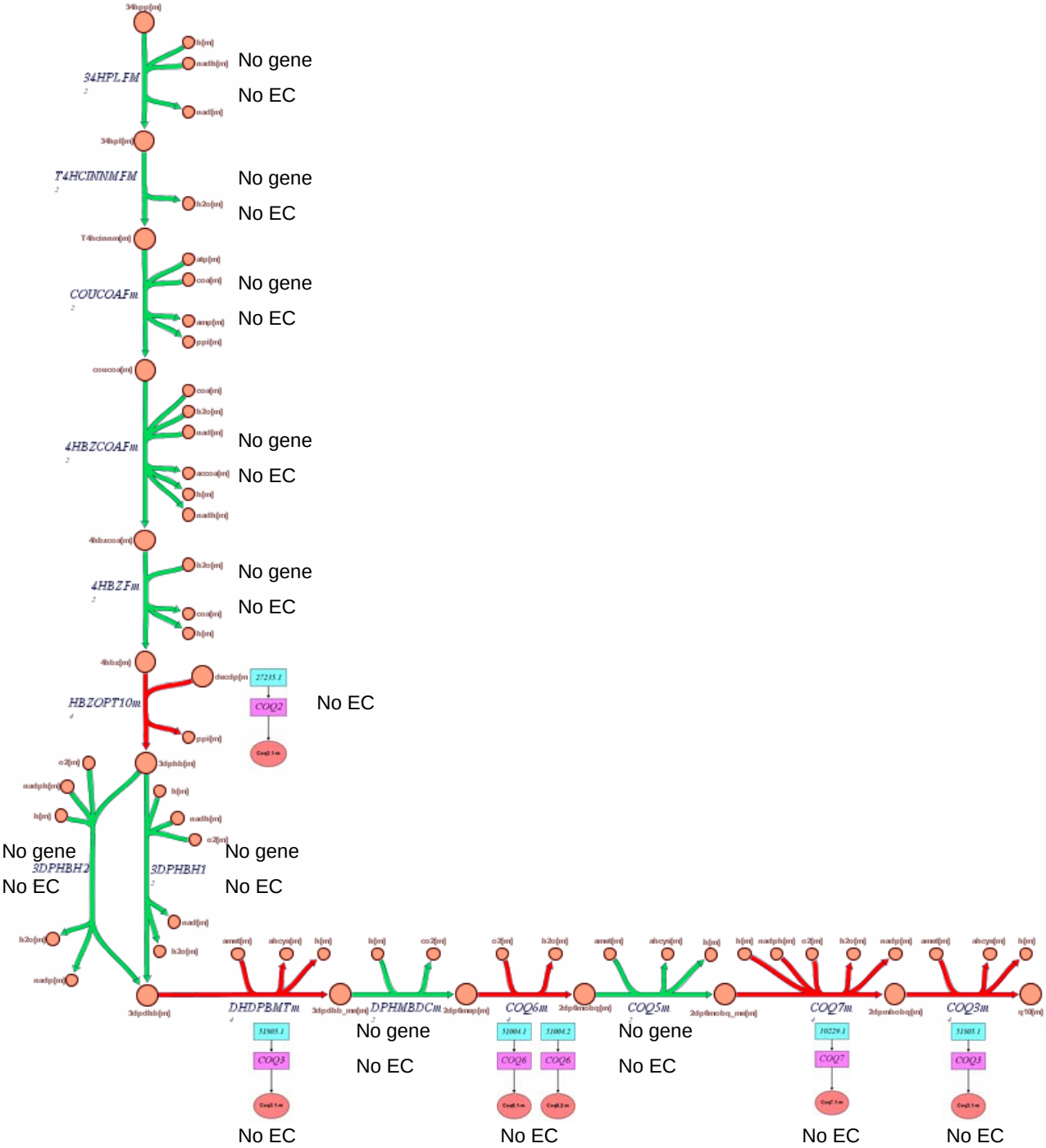
Homo sapiens Recon 1 VITAMIN & COFACTOR METABOLISM

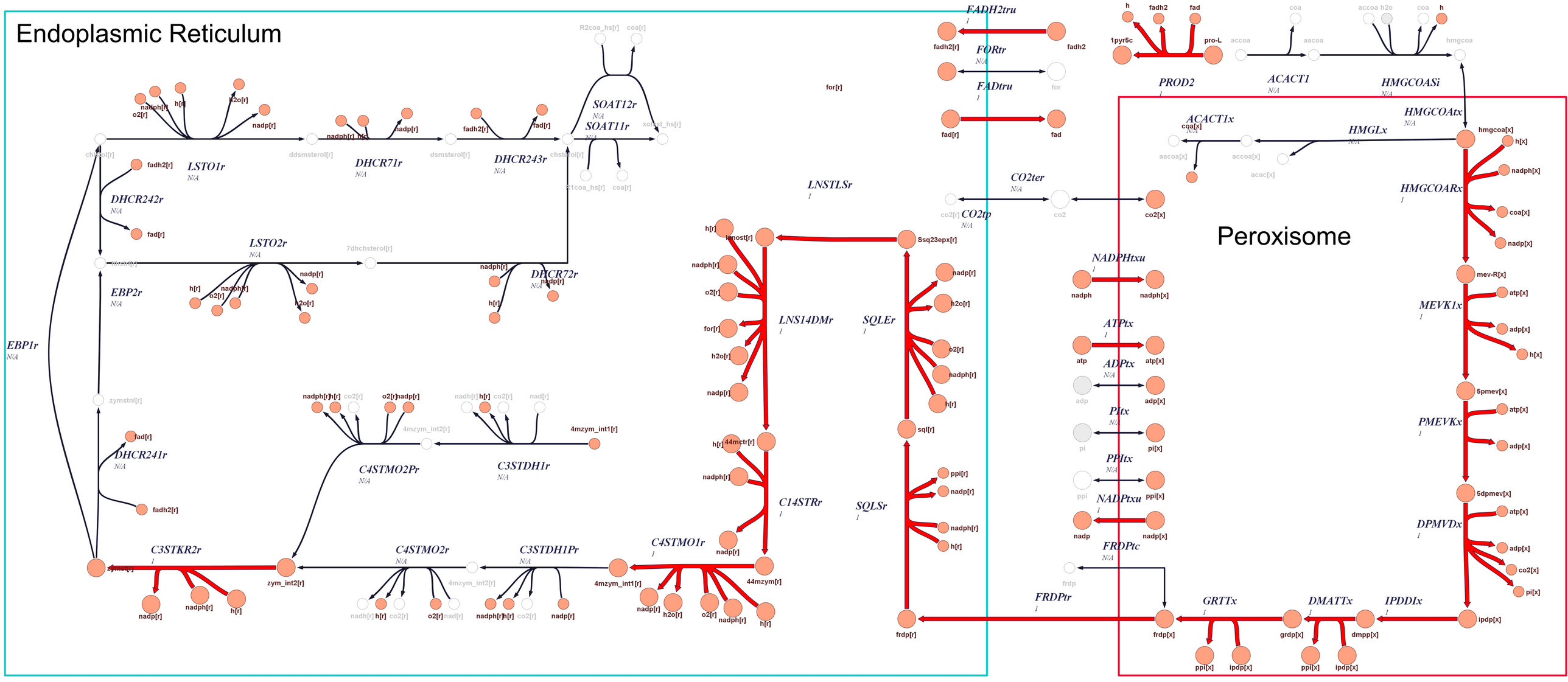


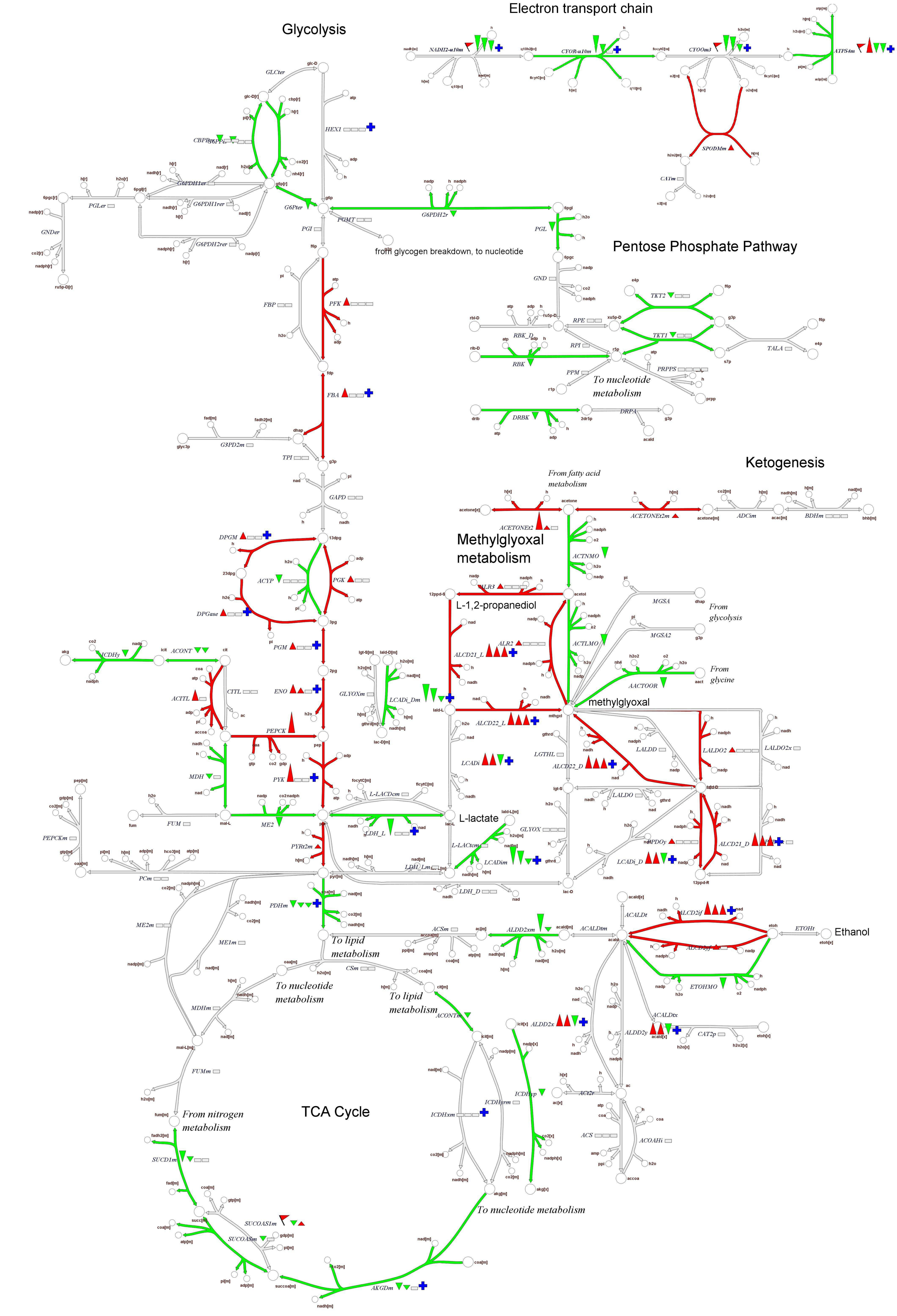

CSBPASE1ly
No gene
No EC
S4TASE3ly
3.1.6.12
NACHEXA2ly
No EC
NACHEX3ly
3.2.1.52
S2TASE3ly
3.1.6.13
IDOAASE4ly
3.2.1.76
S4TASE2ly
3.1.6.12
NACHEX2ly
3.2.1.52
LINKDEG2ly
No gene
No EC
LEGEND
GalNAc
Gal
Xyl
GlcA
IdoA
Ser-Gly/Ala-X-Gly

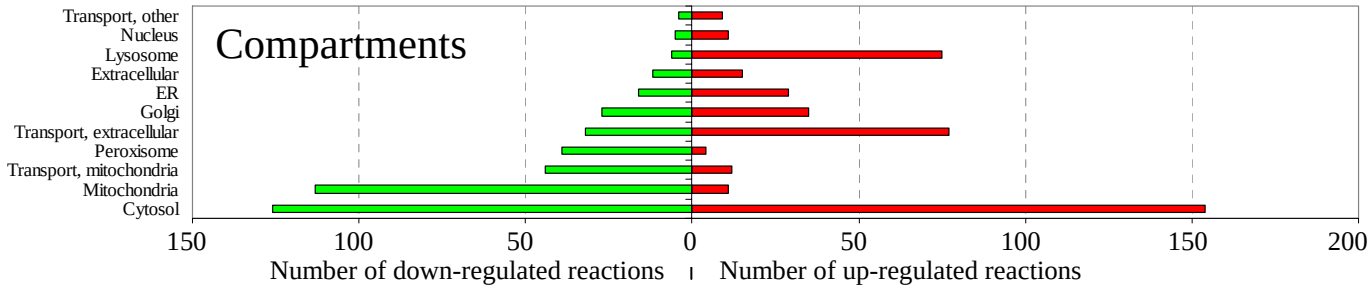

From glucuronate degrdation
From hydroxyproline degrdation
glyoxalate
glycine
AGTim
GLYim
GLXim
GLXO1
oxalate
GLYtp
GLYCLTDym
GLYCLTDy
GLXtp
GLXO2p
GLYOp
From serine metabolism
hydroxypyruvate
glycolate
HPYRDC
GCALDD
GLYCLTtp
GLYCTO1p
AGTix
HPYRR2x
HPYRRy
HPYRDCm
GCALDDm
PGLYCP
HPYRtp
SPTix
GLYCK2
KHK2
FBA4
To glycolysis

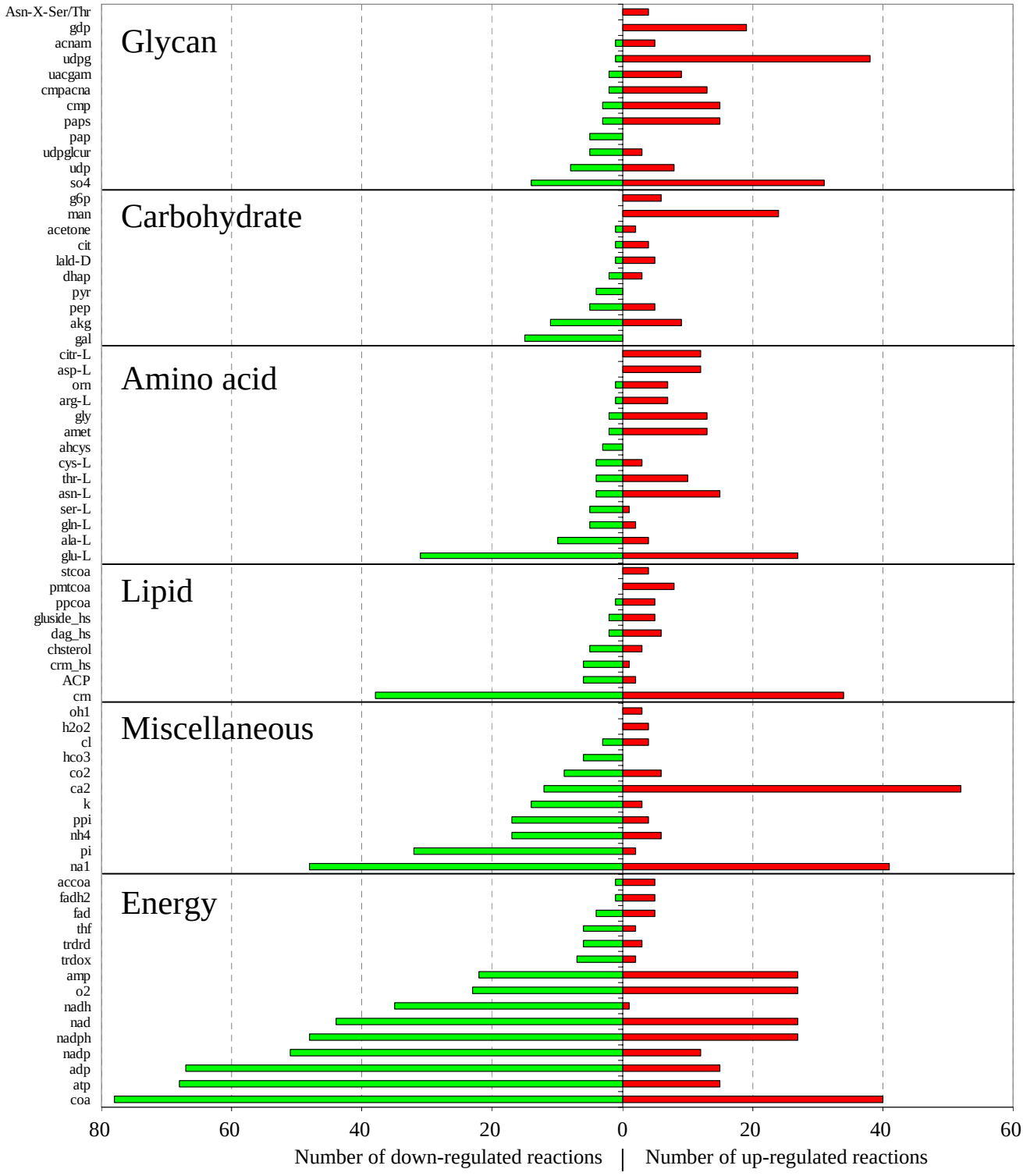

No gene
No EC
DOGULND2
DHA
DASCBH
No gene
3.1.1.17
DOGULND1
No gene
No EC
No gene
DOGULNO1
No EC
DOGULNO2
No gene
No EC
Glycolysis


34HPLFM
No gene
No EC
T4HCINNMFM
No gene
No EC
COUCOAFm
No gene
No EC
4HBZCOAFm
No gene
No EC
4HBZFm
No gene
No EC
HBZOPT10m
No EC
27235.1
COQ2
3DPHBH2
No gene
No EC
3DPHBH1
No gene
No EC
DHDPBMTm
51505.1
COQ3
No EC
DPHMBDCm
No gene
No EC
COQ6m
51004.1
51004.2
COQ6
COQ6
No EC
COQ5m
No gene
No EC
COQ7m
10229.1
COQ7
No EC
COQ3m
51505.1
COQ3
No EC


Endoplasmic Reticulum
Peroxisome
LSTO1r
DHCR71r
DHCR243r
SOAT12r
SOAT11r
DHCR242r
LSTO2r
DHCR72r
EBP2r
EBP1r
DHCR241r
C3STKR2r
C4STMO2Pr
C3STDH1r
C4STMO2r
C3STDH1Pr
C4STMO1r
LNS14DMr
SQLEr
C14STRr
SQLSr
LNSTLSr
FADH2tru
FORtr
FADtru
CO2ter
CO2tp
NADPHtxu
ATPtx
ADPtx
PItx
PPItx
NADPtxu
FRDPtc
FRDPtr
PROD2
ACACT1
HMGCOASi
HMGCOAtx
ACACT1x
HMGLx
HMGCOARx
MEVK1x
PMEVKx
DPMVDx
GRTTx
DMATTx
IPDDIx


Electron transport chain
Glycolysis
Pentose Phosphate Pathway
Ketogenesis
Methylglyoxal metabolism
L-1,2-propanediol
From fatty acid metabolism
From glycolysis
From glycine
methylglyoxal
L-lactate
Ethanol
TCA Cycle
From nitrogen metabolism
To nucleotide metabolism
To lipid metabolism
from glycogen breakdown, to nucleotide
GLCter
HEX1
PGLer
G6PDH1er
G6PDH1rer
G6PDH2rer
G6Pter
PGMT
G6PDH2r
PGI
PGL
GND
RPE
TKT2
TKT1
RPI
RBK
PPM
PRPPS
DRBK
DRPA
TALA
PFK
FBP
FBA
TPI
G3PD2m
GAPD
DPGM
DPGase
ACYP
PGK
PGM
ENO
PEPCK
PYK
PYRt2m
ACONT
ICDHy
CITL
ACITL
MDH
FUM
ME2
PEPCKm
PCm
PDHm
ME2m
ME1m
MDHm
FUMm
L-LACDcm
LDH_L
LDH_Lm
LDH_D
L-LACtcm
LCADim
GLYOX
LCADi
LCADi_Dm
GLYOXm
ACETONEt2
ACETONEt2m
ACTNMO
ALR3
ALR2
ALCD21_L
ALCD22_L
ACTLMO
MGSA
MGSA2
AACTOOR
LGTHL
ALCD22_D
LALDD
LALDO2
LALDO2x
LALDO
ALCD21_D
LCADi_D
ADCim
BDHm
ACALDt
ACALDtm
ALDD2xm
ACSm
CSm
ALCD2if
ALCD2ifj
ETOHt
ETOHMO
ACALDtx
ALDD2y
CAT2p
ALDD2x
ACONTm
ICDHyp
ICDHyrm
ICDHxm
ACt2r
ACS
ACOAHi
AKGDm
SUCOAS1m
SUCOASm
SUCD1m


Compartments
Transport, other
Nucleus
Lysosome
Extracellular
ER
Golgi
Transport, extracellular
Peroxisome
Transport, mitochondria
Mitochondria
Cytosol
150
100
50
0
50
100
150
200
Number of down-regulated reactions
Number of up-regulated reactions


Glycan
Asn-X-Ser/Thr
gdp
acnam
udpg
uacgam
cmpacna
cmp
paps
pap
udpglcur
udp
so4
Carbohydrate
g6p
man
acetone
cit
lald-D
dhap
pyr
pep
akg
gal
Amino acid
citr-L
asp-L
orn
arg-L
gly
amet
ahcys
cys-L
thr-L
asn-L
ser-L
gln-L
ala-L
glu-L
Lipid
stcoa
pmtcoa
ppcoa
gluside_hs
dag_hs
chsterol
crm_hs
ACP
crn
Miscellaneous
oh1
h2o2
cl
hco3
co2
ca2
k
ppi
nh4
pi
na1
Energy
accoa
fadh2
fad
thf
trdrd
trdox
amp
o2
nadh
nad
nadph
nadp
adp
atp
coa
80
60
40
20
0
20
40
60
Number of down-regulated reactions
Number of up-regulated reactions