"Reconstruction and Validation of Saccharomyces cerevisiae iND750, a Fully Compartmentalized Genome-scale Metabolic Model" Natalie C. Duarte, Markus J. Herrgard, Bernhard O. Palsson

Supplementary Material

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		REACTION Reactions that occur entirely within one compartment have a compartmental abbreviation at the				
		beginning of the equation. Otherwise, metabolite location is noted immediately after its abbreviation.				
ABBREVIATION	REACTION NAME	Compartment Abbreviations [c]: cytosol [e]: extracellular [g]: Golgi appratus [m]: mitochondrion [n]: nucleus [r]: endoplasmic reticulum [v]: vacoule [x]: peroxisome	E.C.#	SUBSYSTEM	ORF	PROTEIN
HCO3En	HCO3 equilibrium reaction, nuclear	[n]: co2 + h2o <==> h + hco3	2.0. //			
HCO3Em	HCO3 equilibration reaction, mitochondrial	[m]: co2 + h2o <==> h + hco3				1
HCO3E	HCO3 equilibration reaction	[c] : co2 + h2o <==> h + hco3				(Com 1) or /
HCYSMT	homocysteine S-methyltransferase	[c] : amet + hcys-L> ahcys + h + met-L	FC-2.1.1.10	Alanine and aspartate metabolism	(YPL273W or YLL062C)	(Sam4) or (Mht1)
CSNATirm	carnitine O-acetyltransferase, reverse direction, mitochondrial	[m] : accoa + crn> acrn + coa		Alanine and aspartate metabolism	YML042W	Cat2-m
CSNATifm	carnitine O-aceyltransferase, forward reaction, mitochondrial	[m]: acrn + coa> accoa + cm		Alanine and aspartate metabolism	YAR035W	Yat1-m
CSNAT	carnitine O-acetyltransferase	[c] : accoa + crn -> acrn + coa		Alanine and aspartate metabolism	VDI 40 4M	NA - da
ASPTRSm ASPTRS	Aspartyl-tRNA synthetase, mitochondrial Aspartyl-tRNA synthetase	[m]: asp-L + atp + tmaasp> amp + asptrna + ppi [c]: asp-L + atp + trnaasp> amp + asptrna + ppi		Alanine and aspartate metabolism Alanine and aspartate metabolism	YPL104W YLL018C	Msd1-m Dps1
ASPTAp	aspartate transaminase, peroxisomal	[x] : akg + asp-L <==> glu-L + oaa		Alanine and aspartate metabolism	YLR027C	Aat2-p
ASPTAm	aspartate transaminase, mitochondrial	[m] : akg + asp-L <==> glu-L + oaa	EC-2.6.1.1	Alanine and aspartate metabolism	YKL106W	Aat1-m
ASPTA	aspartate transaminase	[c] : akg + asp-L <==> glu-L + oaa	EC-2.6.1.1	Alanine and aspartate metabolism	YLR027C	Aat2
ASPKi	aspartate kinase, irreversible	[c] : asp-L + atp> 4pasp + adp	EC-2.7.2.4	Alanine and aspartate metabolism	YER052C (YGR124W or YPR145W	Hom3 (Asn2) or (Asn1) or (
ASNS1	asparagine synthase (glutamine-hydrolysing)	[c] : asp-L + atp + gln-L + h2o> amp + asn-L + glu-L + h + ppi	EC-6.3.5.4	Alanine and aspartate metabolism	or YML096W)	Asn3)
ASNS1 ASADi	aspartate-semialdehyde dehydrogenase, irreversible	[c]: 4pasp + h + nadph> aspsa + nadp + pi	EC-1.2.1.11	Alanine and aspartate metabolism	YDR158W	Hom2
ALATRS	Alanyl-tRNA synthetase	[c] : ala-L + atp + trnaala> alatrna + amp + ppi		Alanine and aspartate metabolism	YOR335C	Ala1
ALATA_Lm ALATA_L	L-alanine transaminase, mitochondrial L-alanine transaminase	[m] : akg + ala-L <==> glu-L + pyr [c] : akg + ala-L <==> glu-L + pyr		Alanine and aspartate metabolism Alanine and aspartate metabolism	YLR089C YDR111C	Alt2-m Alt1
TREHV	alpha.alpha-trehalase, vacuolar	[c] . akg + ala-L <==> glu-L + pyl [v] : h2o + tre> (2) glc-D		Alternate Carbon Metabolism	YPR026W	Ath1-v
IIXLIIV	alpria, alpria-ti criatase, vacuotai	[v] . 1120 + tie> (2) gio-b	LC-3.2.1.20	Alternate Carbon Metabolism	11 1X020VV	(Nth1) or (
TREH	alpha,alpha-trehalase	[c]: h2o + tre> (2) glc-D	EC-3.2.1.28	Alternate Carbon Metabolism	(YDR001C or YBR001C) ((YBR126C and YDR074W and YML100W)	Nth2)
					or (YBR126C and YDR074W and YMR261C)) (Tpsl) or (
TRE6PS	alpha,alpha-trehalose-phosphate synthase (UDP-forming)	[c] : g6p + udpg> h + tre6p + udp	EC-2.4.1.15	Alternate Carbon Metabolism) (/ VDD126C and	Tps3)
					((YBR126C and YDR074W and YML100W) or (YBR126C and YDR074W and YMR261C)) (Tpsl) or (
TRE6PP SUCRe	trehalose-phosphatase sucrose hydrolyzing enxyme, extracellular	[c] : h2o + tre6p> pi + tre [e] : h2o + sucr> fru + glc-D		Alternate Carbon Metabolism Alternate Carbon Metabolism	YIL162W	Tps3) Suc2-e
SBTR	D-sorbitol reductase	[c] : glc-D + h + nadph> nadp + sbt-D		Alternate Carbon Metabolism	YHR104W	Gre3
SBTD_L	L-sorbitol dehydrogenase (L-sorbose-producing)	[c] : nad + sbt-L> h + nadh + srb-L		Alternate Carbon Metabolism	YJR159W	Sor1
SBTD_D2	D-sorbitol dehydrogenase (D-fructose producing)	[c] : nad + sbt-D> fru + h + nadh		Alternate Carbon Metabolism	YJR159W	Sor1
LGTHL	lactoylglutathione lyase	[c] : gthrd + mthgxl> lgt-S		Alternate Carbon Metabolism	YML004C	Glo1
L-LACDm GLYOXm	L-Lactate dehydrogenase, mitochondrial hydroxyacylglutathione hydrolase, mitochondrial	[m] : (2) ficytc + lac-L> (2) focytc + pyr [m] : h2o + lgt-S> gthrd + h + lac-D	EC-1.1.2.3 EC-3.1.2.6	Alternate Carbon Metabolism Alternate Carbon Metabolism	YML054C YOR040W	Cyb2-m Glo4-m
GLYOX	hydroxyacylglutathione hydrolase	[c]: h2o + lgt-S> gthrd + h + lac-D		Alternate Carbon Metabolism	YDR272W	Glo2
GLYGS	glycogen (starch) synthase	[c] : h2o + udpg> 14glun + h + udp		Alternate Carbon Metabolism	(YFR015C or YLR258W)	(Gsy1) or (Gsy2)
GLCS2	glycogen synthase (UDPGIc)	[c] : udpg> glycogen + h + udp	EC-2 / 1 11	Alternate Carbon Metabolism	(YFR015C or YLR258W)	(Gsy1) or (Gsy2)
GLCS2	glycogen phosphorylase	[c]: ddpg === grycogen + n + ddp [c]: glycogen + pi ==> g1p		Alternate Carbon Metabolism	YPR160W	Gph1
GBEZ	1,4-alpha-glucan branching enzyme	[c] : 14glun> glycogen + h2o		Alternate Carbon Metabolism	YEL011W	Glc3
D-LACDm	D-lactate dehydrogenase, mitochondrial	[m] : (2) ficytc + lac-D> (2) focytc + pyr	EC-1.1.2.4	Alternate Carbon Metabolism	YDL174C ((YCR034W and YGR032W) or (YCR034W	
13GS	1,3-beta-glucan synthase	[c] : udpg> 13BDglcn + h + udp	EC-2.4.1.34	Alternate Carbon Metabolism	and YLR342W) or (YCR034W and YMR306W))	Bdgs3)
CHTNDA	chitin deacetylase	[c] : chitin + h2o> ac + chitos + h	EC-3 5 1 41	Aminosugars Metabolism	(YLR307W or YLR308W)	(Cda1) or (Cda2)
PPCK	phosphoenolpyruvate carboxykinase	[c]: atp + oaa> adp + co2 + pep		Anaplerotic reactions	YKR097W	Pck1
PC	pyruvate carboxylase	[c] : atp + hco3 + pyr> adp + h + oaa + pi	EC-6.4.1.1	Anaplerotic reactions	(YGL062W or YBR218C)	(Pyc1) or (Pyc2)
ME2m	malic enzyme (NAD), mitochondrial	[m]: mal-L + nadp> co2 + nadph + pyr		Anapleratic reactions	YKL029C	Mae1-m
ME1m MCITS	malic enzyme (NAD), mitochondrial 2-methylcitrate synthase	[m] : mal-L + nad> co2 + nadh + pyr [c] : h2o + oaa + ppcoa> 2mcit + coa + h		Anaplerotic reactions Anaplerotic reactions	YKL029C	Mae1-m
MCITLm	methyisocitrate lyase, mitochondrial	[m] : 2mcit> pyr + succ	EC-4.1.3.30	Anaplerotic reactions	YPR006C	lcl2 (Dal7-p) or (
MALSp	malate synthase, peroxisomal	[x] : accoa + glx + h2o> coa + h + mal-L		Anaplerotic reactions	(YIR031C or YNL117W)	Mls1-p)
ICL FBP	Isocitrate lyase	[c] : icit> glx + succ		Anapleratic reactions	YER065C	Icl1
ARABR	fructose-bisphosphatase arabinose reductase	[c] : fdp + h2o> f6p + pi [c] : arab-L + h + nadph> abt + nadp		Anaplerotic reactions Arabinose Metabolism	YLR377C YHR104W	Fbp1 Gre3
ARAB1D2	D-arabinose 1-dehydrogenase (NADP)	[c] : arab-D + nadp> Dara14lac + h + nadph	EC-1.1.1.21	Arabinose Metabolism	YBR149W	Ara1
ARAB1D1	D-arabinose 1-dehydrogenase (NAD)	[c] : arab-D + nad> Dara14lac + h + nadh	EC-	Arabinose Metabolism	YBR149W	Ara1
SPRMS	spermine synthase	[c]: ametam + spmd> 5mta + h + sprm	EC-2.5.1.22	Arginine and Proline Metabolism	YLR146C	Spe4
SPMS	spermidine synthase	[c] : ametam + ptrc> 5mta + h + spmd	EC-2.5.1.16	Arginine and Proline Metabolism	YPR069C	Spe3
PROTES	ProlvI-tRNA synthetase	[o] - ata + ara + tragara > ama + ani + protrac	EC 6 4 4 45	Argining and Proline Metabolism	(YER087W or YHR020W)	(Prt1) or (
PROTRS PRO1xm	prolyl-tRNA synthetase proline oxidase (NAD), mitochondrial	[c] : atp + pro-L + trnapro> amp + ppi + protrna [m] : nad + pro-L> 1pyr5c + (2) h + nadh	⊆C-0.1.1.15	Arginine and Proline Metabolism Arginine and Proline Metabolism	YLR142W	Prt2) Put1-m
I KO IAIII	profite oxidase (IVAD), filloutoridiai	ini naa - bio-r> ibiioo - (2) ii - iiaan		ruginine and i rolline Metabolisiil	1 11/17/17	J. UC1-111

PHCHGSm	L-1-Pyrroline-3-hydroxy-5-carboxylate spontaneous conversion to L-4-	[m]: 1p3h5c + h + h2o <==> 4hglusa		Arginine and Proline Metabolism		1
PHCDm	L-1-pyrroline-3-hydroxy-5-carboxylate dehydrogenase, mitochondrial	[m] : 1p3h5c + (2) h2o + nad> e4hglu + h + nadh	EC-1.5.1.12	Arginine and Proline Metabolism	YHR037W	Put2-m
P5CR	pyrroline-5-carboxylate reductase	[c]: 1pyr5c + (2) h + nadph> nadp + pro-L		Arginine and Proline Metabolism	YER023W	Pro3
ORNTACim	ornithine transacetylase, irreversible, mitochondrial	[m] : acorn + glu-L> acglu + orn		Arginine and Proline Metabolism	YMR062C	Ecm40-m
ORNTA	ornithine transaminase	[c] : akg + orn> glu-L + glu5sa		Arginine and Proline Metabolism	YLR438W	Car2
ORNDC	Ornithine Decarboxylase	[c]: h + om> co2 + ptrc		Arginine and Proline Metabolism	YKL184W	Spe1
OCBTi	ornithine carbamoyltransferase, irreversible	[c] : cbp + orn> citr-L + h + pi		Arginine and Proline Metabolism	YJL088W	Arg3
HPROym	L-hydroxyproline dehydrogenase (NADP), mitochondrial	[m]: 4hpro-LT + nadp> 1p3h5c + (2) h + nadph		Arginine and Proline Metabolism	YHR037W	Put2-m
HPROxm	L-hydroxyproline dehydrogenase (NAD), mitochondrial	[m]: 4hpro-LT + nad> 1p3h5c + (2) h + nadh		Arginine and Proline Metabolism	YHR037W YER023W	Put2-m
HPROb HPROa	L-hydroxyproline reductase (NADP) L-hydroxyproline reductase (NAD)	[c] : 1p3h5c + (2) h + nadph> 4hpro-LT + nadp [c] : 1p3h5c + (2) h + nadh> 4hpro-LT + nad		Arginine and Proline Metabolism Arginine and Proline Metabolism	YER023W YER023W	Pro3 Pro3
GLU5K	glutamate 5-kinase	[c] : atp + glu-L> adp + glu5p		Arginine and Proline Metabolism	YDR300C	Pro1
G5SD2	glutamate-5-semialdehyde dehydrogenase	[c] : glu5p + h + nadh> glu5sa + nad + pi		Arginine and Proline Metabolism	YOR323C	Pro2
G5SD G5SD	glutamate-5-semialdehyde dehydrogenase	[c] : glu5p + h + nadh> glu5sa + nadp + pi		Arginine and Proline Metabolism	YOR323C	Pro2
G5SADrm	L-glutamate 5-semialdehyde dehydratase, reversible, mitochondrial	[m] : glu5sa <==> 1pyr5c + h + h2o		Arginine and Proline Metabolism		
G5SADr	L-glutamate 5-semialdehyde dehydratase, reversible	[c] : glu5sa <==> 1pyr5c + h + h2o		Arginine and Proline Metabolism		
EHGLATp	L-erythro-4-Hydroxyglutamate:2-oxoglutarate aminotransferase, peroxisomal	[x] : akg + e4hglu> 4h2oglt + glu-L	EC-2.6.1.1	Arginine and Proline Metabolism	YLR027C	Aat2-p
EHGLATm	L-erythro-4-Hydroxyglutamate:2-oxoglutarate aminotransferase, mitochondrial	[m] : akg + e4hglu> 4h2oglt + glu-L	EC-2.6.1.1	Arginine and Proline Metabolism	YKL106W	Aat1-m
EHGLAT	L-erythro-4-Hydroxyglutamate:2-oxoglutarate aminotransferase	[c] : akg + e4hglu> 4h2oglt + glu-L		Arginine and Proline Metabolism	YLR027C	Aat2
DXHPScm	deoxyhypusine synthase, cytosolic/mitochondrial	h2o[c] + q6[m] + spmd[c]> 13dampp[c] + 4abutn[c] + q6h2[m]		Arginine and Proline Metabolism	YHR068W	Dys1
CBPSn	carbamoyl-phosphate synthase (glutamine-hydrolysing), nuclear	[n]: (2) atp + gln-L + h2o + hco3> (2) adp + cbp + glu-L + (2) h + pi	EC-6.3.5.5	Arginine and Proline Metabolism	YJL130C	Ura2-n
CBPS	carbamoyl-phosphate synthase (glutamine-hydrolysing)	[c]: (2) atp + gln-L + h2o + hco3> (2) adp + cbp + glu-L + (2) h + pi	FC-6.3.5.5	Arginine and Proline Metabolism	(YJR109C and YOR303W	Сра
ARGTRSm	Arginyl-tRNA synthetase, mitochondrial	[m] : arg-L + atp + trnaarg> amp + argtrna + ppi		Arginine and Proline Metabolism	YHR091C	Msr1-m
ARGTRS	Arginyl-tRNA synthetase	[c] : arg-L + atp + trnaarg> amp + argtrna + ppi		Arginine and Proline Metabolism	YDR341C	Msr2
ARGSSr	argininosuccinate synthase, reversible	[c] : asp-L + atp + citr-L <==> amp + argsuc + h + ppi		Arginine and Proline Metabolism	YOL058W	Arg1
ARGSL	argininosuccinate lyase	[c] : argsuc <==> arg-L + fum		Arginine and Proline Metabolism	YHR018C	Arg4
ARGN	arginase	[c] : arg-L + h2o> orn + urea		Arginine and Proline Metabolism	YPL111W	Car1
						(Amd4) or (
AMID	amidase	[c] : 4gudbd + h2o> 4gudbutn + nh4		Arginine and Proline Metabolism	(YMR293C or YDR242W)	Amd2)
AGPRim	N-acetyl-g-glutamyl-phosphate reductase, irreversible, mitochondrial	[m] : acg5p + h + nadph> acg5sa + nadp + pi		Arginine and Proline Metabolism	YER069W	Arg5-m
ADMDC	adenosylmethionine decarboxylase	[c] : amet + h> ametam + co2		Arginine and Proline Metabolism	YOL052C	Spe2
ACOTAim	acteylornithine transaminase, irreversible, mitochondrial	[m] : acg5sa + glu-L> acorn + akg	EC-2.6.1.11	Arginine and Proline Metabolism	YOL140W	Arg8-m
					()4450000	(Ecm40-m)
ACGSm	N-acteylglutamate synthase, mitochondrial	[m] : accoa + glu-L> acglu + coa + h		Arginine and Proline Metabolism	(YMR062C or YJL071W)	or (Arg2-m)
ACGKm	acetylglutamate kinase, mitochondrial	[m]: acglu + atp> acg5p + adp		Arginine and Proline Metabolism	YER069W	Arg5-m
4HGLSDm	L-4-hydroxyglutamate semialdehyde dehydrogenase, mitochondrial	[m]: 4hglusa + h2o + nad <==> e4hglu + (2) h + nadh		Arginine and Proline Metabolism	YHR037W	Put2-m
ASNTRSm ASNTRS	asparaginyl-tRNA synthetase, miotchondrial Asparaginyl-tRNA synthetase	[m] : asn-L + atp + trnaasn> amp + asntrna + ppi [c] : asn-L + atp + trnaasn> amp + asntrna + ppi		Asparagine metabolism Asparagine metabolism	YCR024C YHR019C	Ded82-m Ded81
7.O.T.T.O	inputegry, and experience	to the state of th	200	, reparting metabolism	(YLR160C or YLR158C or	(Asp34-e) or (Asp33-e) or (Asp32-e) or
ASNNe	L-asparaginase, extracellular	[e]: asn-L + h2o> asp-L + nh4	EC-3.5.1.1	Asparagine metabolism	YLR157C or YLR155C)	(Asp31-e)
ASNN	L-asparaginase	[c] : asn-L + h2o> asp-L + nh4		Asparagine metabolism	YDR321W	Asp1
SUCOAS1m	SuccinateCoA ligase (ADP-forming), mitochondrial	[m] : atp + coa + succ <==> adp + pi + succoa	FC 6 2 4 4	Citrate Cycle (TCA)	(YGR244C and YOR142W	Lsc-m
					((YDR178W and YKL141W and YKL148C and YLL041C) or (YKL141W and YKL148C and YLL041C and YLR164W) or (YDR178W	
					and YKL148C and YLL041C and YMR118C) or (YDR178W and YJL045W and YKL141W	(Sdh-m) or (Sdh2-m) or (Sdh3-m) or (
SUCD2_u6m	succinate dehydrogenase (ubiquinone-6), mitochondrial	[m] : q6 + succ <==> fum + q6h2	EC-1.3.5.1	Citrate Cycle (TCA)	YLL041C and YMR118C) or (YDR178W and YJL045W and YKL141W and YLL041C))	Sdh2-m) or (
SUCD2_u6m	succinate dehydrogenase (ubiquinone-6), mitochondrial ItaconateCoA ligase (ADP-forming), mitochondrial	[m] : q6 + succ <==> fum + q6h2 [m] : atp + coa + itacon <==> adp + itaccoa + pi		Citrate Cycle (TCA) Citrate Cycle (TCA)	YLL041C and YMR118C) or (YDR178W and YJL045W and YKL141W	Sdh2-m) or (Sdh3-m) or (
ITCOALm			EC-6.2.1.5		YLL041C and YMR118C) or (YDR178W and YJL045W and YKL141W and YLL041C))	Sdh2-m) or (Sdh3-m) or (Sdh4-m)
_	ItaconateCoA ligase (ADP-forming), mitochondrial	[m]: atp + coa + itacon <==> adp + itaccoa + pi	EC-6.2.1.5 EC-1.1.1.42	Citrate Cycle (TCA)	YLL041C and YMR118C) or (YDR178W and YJL045W and YKL141W and YLL041C)) (YGR244C and YOR142W)	Sdh2-m) or (Sdh3-m) or (Sdh4-m)
ITCOALm ICDHyp	Itaconate—CoA ligase (ADP-forming), mitochondrial Isocitrate dehydrogenase (NADP+), peroxisomal	[m] : atp + coa + itacon <==> adp + itaccoa + pi [x] : loit + nadp> akg + co2 + nadph	EC-6.2.1.5 EC-1.1.1.42 EC-1.1.1.42	Citrate Cycle (TCA) Citrate Cycle (TCA)	YLL041C and YMR118C) or (YDR178W and YJL045W and YKL141W and YLL041C)) (YGR244C and YOR142W)) YNL009W YDL066W YLR174W	Sdh2-m) or (Sdh3-m) or (Sdh4-m) Lsc-m
ITCOALm ICDHyp ICDHym ICDHy	Itaconate—CoA ligase (ADP-forming), mitochondrial Isocitrate dehydrogenase (NADP+), peroxisomal Isocitrate dehydrogenase (NADP+), mitochondrial isocitrate dehydrogenase (NADP)	[m]: atp + coa + itacon <==> adp + itaccoa + pi [x]: icit + nadp> akg + co2 + nadph [m]: icit + nadp> akg + co2 + nadph	EC-6.2.1.5 EC-1.1.1.42 EC-1.1.1.42 EC-1.1.1.42	Citrate Cycle (TCA) Citrate Cycle (TCA) Citrate Cycle (TCA) Citrate Cycle (TCA)	YLL041C and YMR118C) or (YDR178W and YJL045W and YKL141W and YLL041C)) (YGR244C and YOR142W) YNL009W YDL066W	Sdh2-m) or (Sdh3-m) or (Sdh4-m) Lsc-m Idp3-p Idp1-m
ITCOALm ICDHyp ICDHym ICDHy ICDHy	ItaconateCoA ligase (ADP-forming), mitochondrial Isocitrate dehydrogenase (NADP+), peroxisomal Isocitrate dehydrogenase (NADP+), mitochondrial isocitrate dehydrogenase (NADP) Isocitrate dehydrogenase (NAD+), mitochondrial	[m]: atp + coa + itacon <==> adp + itaccoa + pi [x]: icit + nadp> akg + co2 + nadph [m]: icit + nadp> akg + co2 + nadph [c]: icit + nadp> akg + co2 + nadph [m]: icit + nadp> akg + co2 + nadph	EC-6.2.1.5 EC-1.1.1.42 EC-1.1.1.42 EC-1.1.1.42	Citrate Cycle (TCA)	YLL041C and YMR118C) or (YDR178W and YLL141W and YLL041C)) (YGR244C and YOR142W) YNL009W YDL066W YLR174W (YNE037C and YOR136W))	Sdh2-m) or (Sdh3-m) or (Sdh4-m) Lsc-m Idp3-p Idp1-m Idp2 Idh-m
ITCOALm ICDHyp ICDHym ICDHy	Itaconate—CoA ligase (ADP-forming), mitochondrial Isocitrate dehydrogenase (NADP+), peroxisomal Isocitrate dehydrogenase (NADP+), mitochondrial isocitrate dehydrogenase (NADP)	[m]: atp + coa + itacon <==> adp + itaccoa + pi [x]: icit + nadp> akg + co2 + nadph [m]: icit + nadp> akg + co2 + nadph [c]: icit + nadp> akg + co2 + nadph	EC-6.2.1.5 EC-1.1.1.42 EC-1.1.1.42 EC-1.1.1.42	Citrate Cycle (TCA) Citrate Cycle (TCA) Citrate Cycle (TCA) Citrate Cycle (TCA)	YLL041C and YMR118C) or (YDR178W and YJL045W and YKL141W and YLL041C)) (YGR244C and YOR142W)) YNL009W YDL066W YLR174W	Sdh2-m) or (Sdh3-m) or (Sdh4-m) Lsc-m Idp3-p Idp1-m Idp2 Idh-m Cit2-p
ITCOALm ICDHyp ICDHym ICDHy ICDHy	ItaconateCoA ligase (ADP-forming), mitochondrial Isocitrate dehydrogenase (NADP+), peroxisomal Isocitrate dehydrogenase (NADP+), mitochondrial isocitrate dehydrogenase (NADP) Isocitrate dehydrogenase (NAD+), mitochondrial	[m]: atp + coa + itacon <==> adp + itaccoa + pi [x]: icit + nadp> akg + co2 + nadph [m]: icit + nadp> akg + co2 + nadph [c]: icit + nadp> akg + co2 + nadph [m]: icit + nadp> akg + co2 + nadph	EC-6.2.1.5 EC-1.1.1.42 EC-1.1.1.42 EC-1.1.1.41 EC-4.1.3.7	Citrate Cycle (TCA)	YLL041C and YMR118C) or (YDR178W and YJL045W and YKL141W and YLL041C)) (YGR244C and YOR142W) YNL009W YDL066W YLR174W (YNL037C and YOR136W) YCR005C	Sdh2-m) or (Sdh3-m) or (Sdh3-m) or (Sdh4-m) Lsc-m Idp3-p Idp1-m Idp2 Idh-m Cit2-p (Cit1-m) or (Cit3-m)
ITCOALm ICDHyp ICDHym ICDHym ICDHym ICDHxm CSp CSm	Itaconate—CoA ligase (ADP-forming), mitochondrial Isocitrate dehydrogenase (NADP+), peroxisomal Isocitrate dehydrogenase (NADP+) mitochondrial isocitrate dehydrogenase (NADP) Isocitrate dehydrogenase (NAD+), mitochondrial citrate synthase, peroxisomal	[m]: atp + coa + itacon <==> adp + itaccoa + pi [x]: icit + nadp> akg + co2 + nadph [m]: icit + nadp> akg + co2 + nadph [c]: icit + nadp> akg + co2 + nadph [m]: icit + nad> akg + co2 + nadph [m]: icit + nad> akg + co2 + nadh [x]: accoa + h2o + oaa> cit + coa + h	EC-6.2.1.5 EC-1.1.1.42 EC-1.1.1.42 EC-1.1.1.41 EC-4.1.3.7 EC-4.1.3.7	Citrate Cycle (TCA)	YLL041C and YMR118C) or (YDR178W and YJL045W and YKL141W and YLL041C)) (YGR244C and YOR142W) YNL009W YDL066W YLR174W (YNL037C and YOR136W) YCR005C	Sdh2-m) or (Sdh3-m) or (Sdh3-m) or (Sdh4-m) Lsc-m Idp3-p Idp1-m Idp2 Idh-m Cit2-p (Cit1-m) or (Cit3-m) (Kgd1-m and Kgd2-m and PdE3-m)
ITCOALM ICDHyp ICDHym ICDHym ICDHym ICDHym ICDHxm CSp CSm AKGDbm	Itaconate—CoA ligase (ADP-forming), mitochondrial Isocitrate dehydrogenase (NADP+), peroxisomal Isocitrate dehydrogenase (NADP+), mitochondrial isocitrate dehydrogenase (NADP) Isocitrate dehydrogenase (NAD+), mitochondrial citrate synthase, peroxisomal citrate synthase, mitochondrial citrate dehydrogenase (dihydrolipoamide S-succinyltransferase),	[m]: atp + coa + itacon <==> adp + itaccoa + pi [x]: icit + nadp> akg + co2 + nadph [m]: icit + nadp> akg + co2 + nadph [c]: icit + nadp> akg + co2 + nadph [m]: icit + nad> akg + co2 + nadph [m]: icit + nad> akg + co2 + nadph [x]: accoa + h2o + oaa> cit + coa + h [m]: accoa + h2o + oaa> cit + coa + h	EC-6.2.1.5 EC-1.1.1.42 EC-1.1.1.42 EC-1.1.1.41 EC-4.1.3.7 EC-4.1.3.7	Citrate Cycle (TCA)	YLL041C and YMR118C) or (YDR178W and YLL141W and YLL041C)) (YGR244C and YOR142W) YNL009W YDL066W YLR174W (YNL037C and YOR136W)) YCR005C (YNR001C or YPR001W) (YIL125W and YDR148C	Sdh2-m) or (Sdh3-m) or (Sdh3-m) or (Sdh4-m) Lsc-m lidp3-p lidp1-m lidp2 ldh-m Cit2-p (Cit1-m) or (Cit3-m) (Kgd1-m and Kgd2-m and YdE3-m and Kgd2-m and YdE3-m)
ITCOALM ICDHyp ICDHym ICDHym ICDHym ICDHY ICDHXM CSp CSm AKGDbm	Itaconate—CoA ligase (ADP-forming), mitochondrial Isocitrate dehydrogenase (NADP+), peroxisomal Isocitrate dehydrogenase (NADP+), mitochondrial isocitrate dehydrogenase (NADP) Isocitrate dehydrogenase (NAD+), mitochondrial citrate synthase, peroxisomal citrate synthase, mitochondrial oxoglutarate dehydrogenase (dihydrolipoamide S-succinyltransferase), mitochondrial oxoglutarate dehydrogenase (lipoamide), mitochondrial	[m]: atp + coa + itacon <==> adp + itaccoa + pi [x]: icit + nadp> akg + co2 + nadph [m]: icit + nadp> akg + co2 + nadph [c]: icit + nadp> akg + co2 + nadph [m]: icit + nad> akg + co2 + nadph [m]: icit + nad> akg + co2 + nadph [m]: accoa + h2o + oaa> cit + coa + h [m]: accoa + h2o + oaa> cit + coa + h [m]: coa + sdhlam> dhlam + succoa [m]: akg + h + lpam <==> co2 + sdhlam	EC-6.2.1.5 EC-1.1.1.42 EC-1.1.1.42 EC-1.1.1.41 EC-4.1.3.7 EC-4.1.3.7 EC-2.3.1.61	Citrate Cycle (TCA)	YLL041C and YMR118C) or (YDR178W and YJL045W and YKL141W and YLL041C)) (YGR244C and YOR142W)) YNL009W YDL066W YLR174W (YNL037C and YOR136W)) YCR005C (YNR001C or YPR001W) (YIL125W and YDR148C and YFL018C) (YIL125W and YDR148C and YFL018C)	Sdh2-m) or (Sdh3-m) or (Sdh3-m) or (Sdh4-m) Lsc-m Idp3-p Idp1-m Idp2 Idh-m Cit2-p (Cit1-m) or (Cit3-m) (Kgd1-m and Kgd2-m and PdE3-m) (Kgd2-m and Kgd2-m a
ITCOALM ICDHyp ICDHym I	Itaconate—CoA ligase (ADP-forming), mitochondrial Isocitrate dehydrogenase (NADP+), peroxisomal Isocitrate dehydrogenase (NADP+), mitochondrial isocitrate dehydrogenase (NADP) Isocitrate dehydrogenase (NAD+), mitochondrial citrate synthase, peroxisomal citrate synthase, mitochondrial oxoglutarate dehydrogenase (dihydrolipoamide S-succinyltransferase), mitochondrial	[m]: atp + coa + itacon <==> adp + itaccoa + pi [x]: icit + nadp> akg + co2 + nadph [m]: icit + nadp> akg + co2 + nadph [c]: icit + nadp> akg + co2 + nadph [m]: icit + nad> akg + co2 + nadph [m]: icit + nad> akg + co2 + nadph [x]: accoa + h2o + oaa> cit + coa + h [m]: accoa + h2o + oaa> cit + coa + h	EC-6.2.1.5 EC-1.1.1.42 EC-1.1.1.42 EC-1.1.1.41 EC-4.1.3.7 EC-4.1.3.7 EC-2.3.1.61 EC-1.2.4.2 EC-4.2.1.3	Citrate Cycle (TCA)	YLL041C and YMR118C) or (YDR178W and YJL045W and YKL141W and YLL041C)) (YGR244C and YOR142W) YNL009W YDL066W YLR174W (YNL037C and YOR136W)) YGR005C (YNR001C or YPR001W) (YIL125W and YDR148C and YFL018C)	Sdh2-m) or (Sdh3-m) or (Sdh3-m) or (Sdh4-m) Lsc-m lidp3-p lidp1-m lidp2 ldh-m Cit2-p (Cit1-m) or (Cit3-m) (Kgd1-m and Kgd2-m and YdE3-m and Kgd2-m and YdE3-m)
ITCOALM ICDHyp ICDHym ICDHym ICDHym ICDHY ICDHXM CSp CSm AKGDbm AKGDam ACONTm	Itaconate—CoA ligase (ADP-forming), mitochondrial Isocitrate dehydrogenase (NADP+), peroxisomal Isocitrate dehydrogenase (NADP+), mitochondrial isocitrate dehydrogenase (NADP) Isocitrate dehydrogenase (NAD+), mitochondrial citrate synthase, peroxisomal citrate synthase, mitochondrial oxoglutarate dehydrogenase (dihydrolipoamide S-succinyltransferase), mitochondrial oxoglutarate dehydrogenase (lipoamide), mitochondrial Aconitate hydratase, mitochondrial aconitate	[m]: atp + coa + itacon <==> adp + itaccoa + pi [x]: icit + nadp> akg + co2 + nadph [m]: icit + nadp> akg + co2 + nadph [c]: icit + nadp> akg + co2 + nadph [m]: icit + nad> akg + co2 + nadph [m]: icit + nad> akg + co2 + nadph [m]: accoa + h2o + oaa> cit + coa + h [m]: accoa + h2o + oaa> cit + coa + h [m]: coa + sdhlam> dhlam + succoa [m]: akg + h + lpam <==> co2 + sdhlam [m]: cit <==> icit [c]: cit <==> icit	EC-6.2.1.5 EC-1.1.1.42 EC-1.1.1.42 EC-1.1.1.41 EC-4.1.3.7 EC-4.1.3.7 EC-2.3.1.61 EC-1.2.4.2 EC-4.2.1.3	Citrate Cycle (TCA)	YLL041C and YMR118C) or (YDR178W and YLL141W and YLL041C)) (YGR244C and YOR142W) YNL0096W YLR174W (YNL037C and YOR136W)) YCR005C (YNR001C or YPR001W) (YIL125W and YDR148C and YFL018C) (YLR304C or YJL200C) YLR304C VYJL200C)	Sdh2-m) or (Sdh3-m) or (Sdh3-m) or (Sdh4-m) Lsc-m Idp3-p Idp1-m Idp2 Idh-m Idp2 (Cit1-m) or (Cit3-m) (Kgd1-m and Kgd2-m and PdE3-m) (Kgd1-m and Kgd2-m and Kgd2-m and Kgd2-m and PdE3-m) (Aco1-m) or (Aco2-m) Aco1 (Ecm17) or (Aco1-m) or (Aco1-m)
ITCOALM ICDHyp ICDHym I	Itaconate—CoA ligase (ADP-forming), mitochondrial Isocitrate dehydrogenase (NADP+), peroxisomal Isocitrate dehydrogenase (NADP+), mitochondrial isocitrate dehydrogenase (NADP) Isocitrate dehydrogenase (NADP) Isocitrate synthase, peroxisomal citrate synthase, peroxisomal citrate synthase, mitochondrial oxoglutarate dehydrogenase (dihydrolipoamide S-succinyltransferase), mitochondrial oxoglutarate dehydrogenase (lipoamide), mitochondrial Aconitate hydratase, mitochondrial aconitase sulfite reductase (NADPH2)	[m]: atp + coa + itacon <==> adp + itaccoa + pi [x]: icit + nadp> akg + co2 + nadph [m]: icit + nadp> akg + co2 + nadph [c]: icit + nadp> akg + co2 + nadph [m]: icit + nad> akg + co2 + nadph [m]: icit + nad> akg + co2 + nadph [x]: accoa + h2o + oaa> cit + coa + h [m]: accoa + h2o + oaa> cit + coa + h [m]: coa + sdhlam> dhlam + succoa [m]: akg + h + lpam <==> co2 + sdhlam [m]: cit <==> icit [c]: cit <==> icit [c]: (3) h2o + h2s + (3) nadp <==> (5) h + (3) nadph + so3	EC-6.2.1.5 EC-1.1.1.42 EC-1.1.1.42 EC-1.1.1.42 EC-1.1.1.41 EC-4.1.3.7 EC-4.1.3.7 EC-2.3.1.61 EC-1.2.4.2 EC-4.2.1.3 EC-4.2.1.3	Citrate Cycle (TCA) Cycle (TCA) Cysteine Metabolism	YLL041C and YMR118C) or (YDR178W and YJL045W and YKL141W and YLL041C)) (YGR244C and YOR142W) NL009W YDL066W YLR174W (YNL037C and YOR136W)) YCR005C (YNR001C or YPR001W) (YIL125W and YDR148C and YFL018C) (YIL25W and YDR148C and YFL018C) (YLR304C or YJL200C) YLR304C (YJR137C or YFR030W)	Sdh2-m) or (Sdh3-m) or (Sdh3-m) or (Sdh3-m) or (Sdh4-m) Lsc-m Idp3-p Idp1-m Idp2 Idh-m Cit2-p (Cit1-m) or (Cit3-m) (Cit3-m) (Kgd1-m and Kgd2-m and PdE3-m) (Kgd1-m and Rgd2-m and PdE3-m) (Aco2-m) or (Aco2-m) Aco1 (Ecm17) or (Met10)
ITCOALM ICDHyp ICDHym ICDHym ICDHy ICDHYM ICDHXM CSp CSM AKGDbm AKGDbm ACONTM ACONTM SULR SLFAT	Itaconate—CoA ligase (ADP-forming), mitochondrial Isocitrate dehydrogenase (NADP+), peroxisomal Isocitrate dehydrogenase (NADP+), mitochondrial isocitrate dehydrogenase (NADP) Isocitrate dehydrogenase (NAD+), mitochondrial citrate synthase, peroxisomal citrate synthase, mitochondrial oxoglutarate dehydrogenase (dihydrolipoamide S-succinyltransferase), mitochondrial oxoglutarate dehydrogenase (lipoamide), mitochondrial Aconitate hydratase, mitochondrial aconitase sulfite reductase (NADPH2) sulfate adenylytransferase (ADP)	[m]: atp + coa + itacon <==> adp + itaccoa + pi [x]: icit + nadp> akg + co2 + nadph [m]: icit + nadp> akg + co2 + nadph [c]: icit + nadp> akg + co2 + nadph [m]: icit + nadp> akg + co2 + nadph [m]: icit + nad> akg + co2 + nadh [x]: accoa + h2o + oaa> cit + coa + h [m]: accoa + h2o + oaa> cit + coa + h [m]: accoa + h2o + oaa> cit + coa + h [m]: accoa + h2o + oaa> cit + coa + h [m]: coa + sdhlam> dhlam + succoa [m]: akg + h + lpam <==> co2 + sdhlam [m]: cit <==> icit [c]: cit <==> icit [c]: cit <==> icit [c]: (3) h2o + h2s + (3) nadp <==> (5) h + (3) nadph + so3 [c]: adp + h + so4 <==> aps + pi	EC-6.2.1.5 EC-1.1.1.42 EC-1.1.1.42 EC-1.1.1.41 EC-4.1.3.7 EC-4.1.3.7 EC-4.1.3.7 EC-4.2.3.1.61 EC-4.2.1.3 EC-4.2.1.3 EC-4.2.1.3	Citrate Cycle (TCA) Cysteine Metabolism Cysteine Metabolism	YLL041C and YMR118C) or (YDR178W and YLL141W and YLL041C)) (YGR244C and YOR142W) YNL0096W YLR174W (YNL037C and YOR136W)) YCR005C (YNR001C or YPR001W) (YIL125W and YDR148C and YFL018C) (YLR304C or YJL200C) YLR304C VYJL200C)	Sdh2-m) or (Sdh3-m) or (Sdh3-m) or (Sdh4-m) Lsc-m Idp3-p Idp1-m Idp2 Idh-m Idp2 (Cit1-m) or (Cit3-m) (Kgd1-m and Kgd2-m and PdE3-m) (Kgd1-m and Kgd2-m and Kgd2-m and Kgd2-m and PdE3-m) (Aco1-m) or (Aco2-m) Aco1 (Ecm17) or (Aco1-m) or (Aco1-m)
ITCOALM ICDHyp ICDHym ICDHym ICDHym ICDHym ICDHxm CSp CSm AKGDbm AKGDam ACONTm ACONT	Itaconate—CoA ligase (ADP-forming), mitochondrial Isocitrate dehydrogenase (NADP+), peroxisomal Isocitrate dehydrogenase (NADP+), mitochondrial isocitrate dehydrogenase (NADP) Isocitrate dehydrogenase (NADP) Isocitrate synthase, peroxisomal citrate synthase, peroxisomal citrate synthase, mitochondrial oxoglutarate dehydrogenase (dihydrolipoamide S-succinyltransferase), mitochondrial oxoglutarate dehydrogenase (lipoamide), mitochondrial Aconitate hydratase, mitochondrial aconitase sulfite reductase (NADPH2)	[m]: atp + coa + itacon <==> adp + itaccoa + pi [x]: icit + nadp> akg + co2 + nadph [m]: icit + nadp> akg + co2 + nadph [c]: icit + nadp> akg + co2 + nadph [m]: icit + nad> akg + co2 + nadph [m]: icit + nad> akg + co2 + nadph [x]: accoa + h2o + oaa> cit + coa + h [m]: accoa + h2o + oaa> cit + coa + h [m]: coa + sdhlam> dhlam + succoa [m]: akg + h + lpam <==> co2 + sdhlam [m]: cit <==> icit [c]: cit <==> icit [c]: (3) h2o + h2s + (3) nadp <==> (5) h + (3) nadph + so3	EC-6.2.1.5 EC-1.1.1.42 EC-1.1.1.42 EC-1.1.1.41 EC-4.1.3.7 EC-4.1.3.7 EC-2.3.1.61 EC-1.2.4.2 EC-4.2.1.3 EC-4.2.1.3 EC-4.2.1.3 EC-4.2.1.3 EC-1.8.2.2 EC-2.7.7.5 EC-2.3.1.3	Citrate Cycle (TCA) Cycle (TCA) Cysteine Metabolism	YLL041C and YMR118C) or (YDR178W and YJL045W and YKL141W and YLL041C)) (YGR244C and YOR142W) NL009W YDL066W YLR174W (YNL037C and YOR136W)) YCR005C (YNR001C or YPR001W) (YIL125W and YDR148C and YFL018C) (YIL25W and YDR148C and YFL018C) (YLR304C or YJL200C) YLR304C (YJR137C or YFR030W)	Sdh2-m) or (Sdh3-m) or (Sdh3-m) or (Sdh3-m) or (Sdh4-m) Lsc-m Idp3-p Idp1-m Idp2 Idh-m Cit2-p (Cit1-m) or (Cit3-m) (Cit3-m) (Kgd1-m and Kgd2-m and PdE3-m) (Kgd1-m and Rgd2-m and PdE3-m) (Aco2-m) or (Aco2-m) Aco1 (Ecm17) or (Met10)

PAPSR	phosphoadenylyl-sulfate reductase (thioredoxin)	[c]: paps + trdrd> (2) h + pap + so3 + trdox	EC-1848	Cysteine Metabolism	YPR167C	Met16
CYSTRS						
	Cysteinyl-tRNA synthetase	[c]: atp + cys-L + trnacys> amp + cystrna + ppi	EC-6.1.1.16		YNL247W	Cyt1
CYSS	cysteine synthase	[c] : acser + h2s> ac + cys-L + h	EC-4.2.99.8		YGR012W	Csy1
BPNT	3',5'-bisphosphate nucleotidase	[c] : h2o + pap> amp + pi	EC-3.1.3.7	Cysteine Metabolism	YOL064C	Met22
ADSK	adenylyl-sulfate kinase	[c] : aps + atp> adp + h + paps	EC-2.7.1.25	Cysteine Metabolism	YKL001C	Met14
NMNAT	nicotinamide-nucleotide adenylyltransferase	[c] : atp + h + nmn> nad + ppi	EC-2.7.7.1	Fatty Acid Biosynthesis	YGR010W	Nma2
NADDPp	NAD diphosphatase, peroxisomal	[x] : h2o + nad> amp + (2) h + nmn	EC-3.6.1.22		YGL067W	Npy1-p
MCOATAm	Malonyl-CoA-ACO transacylase, mitochondrial	[m] : ACP + malcoa <==> coa + malACP		Fatty Acid Biosynthesis	YOR221C	Mct1-m
MCOATA		[c] : ACP + malcoa <==> coa + malACP				
	Malonyl-CoA-ACP transacylase			Fatty Acid Biosynthesis	(YKL182W and YPL231W	
KATp	3-ketoacyl-CoA thiolase, peroxisomal	[x] : 3oacoa + coa> accoa + acoa		Fatty Acid Biosynthesis	YIL160C	Pot1-p
HACDp	3-hydroxyacyl-CoA dehydrogenase, peroxisomal	[x] : 3hacoa + nad <==> 3oacoa + h + nadh	EC-1.1.1.35	Fatty Acid Biosynthesis	YKR009C	Fox2-p
					(YGR037C and YNR016C	(Acb1 and
1					and (YKL182W and	Acc1 and Fas
FAS80_L	fatty acid synthase (n-C8:0), lumped reaction	[c]: accoa + (8) h + (3) malcoa + (6) nadph> (3) co2 + (4) coa + (2) h2o + (6) nadp + octa	FC-2.3.1.85	Fatty Acid Biosynthesis	YPL231W)))
	(·· σου), ······	[5] - 200 (2) - (2) - (2) - (3) - (4)		200, 1000 2000, 100000		ť
					(YGR037C and YNR016C	(Acb1 and
					and (YKL182W and	Acc1 and Fas
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	EC-2.3.1.86	Fatty Acid Biosynthesis	YPL231W)))
						(Acp1-m and
					(YKL192C and YER061C	Cem1-m and
					and YOR221C and	Mct1-m and
FAS80ACPm_L	fatty acyl-ACP synthase (n-C8:0ACP), mitochondrial, lumped reaction	[m] : 20ACD + (0) h + (2) mcIACD + (6) podph > (2) ACD + (2) 202 + (2) h20 + (6) podp + 20ACD		Fatty Acid Biosynthesis	YKL055C)	Oar1-m)
		[m] : acACP + (9) h + (3) malACP + (6) nadph> (3) ACP + (3) co2 + (3) h2o + (6) nadp + ocACP	E0 0 0 4 0E			
FAS260	fatty acid synthase (n-C26:0)	[c]: (3) h + malcoa + (2) nadph + ttc> co2 + coa + h2o + hexc + (2) nadp		Fatty Acid Biosynthesis	YLR372W	Sur4
FAS240_L	fatty acid synthase (n-C24:0), lumped reaction	[c]: (9) h + (3) malcoa + (6) nadph + ocdca> (3) co2 + (3) coa + (3) h2o + (6) nadp + ttc	EC-2.3.1.85	Fatty Acid Biosynthesis	YCR034W	Fen1
1			1	I	ĺ	(Acp1-m and
1			1	I	(YKL192C and YER061C	Cem1-m and
1			1	I	and YOR221C and	Mct1-m and
FAS182ACPm	fatty-acyl-ACP synthase (n-C18:2ACP), mitochondrial	[m]: (5) h + malACP + (4) nadph + (2) o2 + palmACP> ACP + co2 + (5) h2o + (4) nadp + ocdcyaACP	1	Fatty Acid Biosynthesis	YKL055C)	Oar1-m)
	25,17.07 Synamos (17 S TO.E. 101), Illiconormalia	[1] (1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	1	. In the Brooking	1.1.20000 /	(Acp1-m and
1			1	I	(YKL192C and YER061C	
1			1	1		Cem1-m and
L.	L.,			L	and YOR221C and	Mct1-m and
FAS181ACPm	fatty-acyl-ACP synthase (n-C18:1ACP), mitochondrial	[m] : (4) h + malACP + (3) nadph + o2 + palmACP> ACP + co2 + (3) h2o + (3) nadp + octeACP		Fatty Acid Biosynthesis	YKL055C)	Oar1-m)
					(YGR037C and YNR016C	(Acb1 and
					and (YKL182W and	Acc1 and Fas
FAS180COA	fatty-acyl-CoA synthase (n-C18:0CoA)	[c]: (3) h + malcoa + (2) nadph + pmtcoa> co2 + coa + h2o + (2) nadp + stcoa	FC-2.3.1.86	Fatty Acid Biosynthesis	YPL231W)))
	,,	(2) 100 (2) 100		r any rane and your and	,,	(Acp1-m and
1					(YKL192C and YER061C	Cem1-m and
1					and YOR221C and	
						Mct1-m and
FAS180ACPm	fatty-acyl-ACP synthase (n-C18:0ACP), mitochondrial	[m]: (3) h + malACP + (2) nadph + palmACP> ACP + co2 + h2o + (2) nadp + ocdcaACP		Fatty Acid Biosynthesis	YKL055C)	Oar1-m)
					(YGR037C and YNR016C	(Acb1 and
1					and (YKL182W and	Acc1 and Fas
FAS180	fatty acid synthase (n-C18:0)	[c]: (3) h + hdca + malcoa + (2) nadph> co2 + coa + h2o + (2) nadp + ocdca	FC-2 3 1 85	Fatty Acid Biosynthesis	YPL231W)))
710100	latty and dynamics (in 6 10.0)	[6] - (6) 11 - 11464 - 1141664 - (2) 114461 - 662 - 664 - 1126 - (2) 11446 - 66464	20 2.0.1.00	r dity / told Bloody itt roote		(Acp1-m and
					()//// 4000 VED0040	
					(YKL192C and YER061C	Cem1-m and
					and YOR221C and	Mct1-m and
FAS161ACPm	fatty-acyl-ACP synthase (n-C16:1ACP), mitochondrial	[m]: (4) h + malACP + myrsACP + (3) nadph + o2> ACP + co2 + (3) h2o + hdeACP + (3) nadp		Fatty Acid Biosynthesis	YKL055C)	Oar1-m)
					(YGR037C and YNR016C	(Acb1 and
					and (YKL182W and	Acc1 and Fas
FAS160COA	fatty-acyl-CoA synthase (n-C16:0CoA)	[c]: (3) h + malcoa + (2) nadph + tdcoa> co2 + coa + h2o + (2) nadp + pmtcoa	FC-2 3 1 86	Fatty Acid Biosynthesis	YPL231W)))
17101000071	latty deyr oort synthase (if o re.ooort)	[6] . (6) II · IIIaloda · (2) IIadpii · Idood · Coz · Cod · IIzo · (2) IIadp · piiloda	LO 2.0.1.00	ratty / told Biosynthesis	11 220111))	/ Acad as and
					()//// 4000 VED0040	(Acp1-m and
					(YKL192C and YER061C	Cem1-m and
					and YOR221C and	Mct1-m and
FAS160ACPm	fatty-acyl-ACP synthase (n-C16:0ACP), mitochondrial	[m]: (3) h + malACP + myrsACP + (2) nadph> ACP + co2 + h2o + (2) nadp + palmACP		Fatty Acid Biosynthesis	YKL055C)	Oar1-m)
					(YGR037C and YNR016C	(Acb1 and
					and (YKL182W and	Acc1 and Fas
FAS160	fatty acid synthase (n-C16:0)	[c]: (3) h + malcoa + (2) nadph + ttdca> co2 + coa + h2o + hdca + (2) nadp	FC-2 3 1 85	Fatty Acid Biosynthesis	YPL231W)))
<u> </u>	,	(2) (1) (1) (1) (1) (1) (1) (1) (1) (1) (1	12 2.0.1.00		,,,	(Acp1-m and
1			1	I	(YKL192C and YER061C	
1						Cem1-m and
	L			L	and YOR221C and	Mct1-m and
FAS141ACPm	fatty-acyl-ACP synthase (n-C14:1ACP), mitochondrial	[m]: ddcaACP + (4) h + malACP + (3) nadph + o2> ACP + co2 + (3) h2o + (3) nadp + tdeACP		Fatty Acid Biosynthesis	YKL055C)	Oar1-m)
1			1	I	(YGR037C and YNR016C	(Acb1 and
1			1	I	and (YKL182W and	Acc1 and Fas
FAS140COA	fatty-acyl-CoA synthase (n-C14:0CoA)	[c]: ddcacoa + (3) h + malcoa + (2) nadph> co2 + coa + h2o + (2) nadp + tdcoa	EC-2.3.1.86	Fatty Acid Biosynthesis	YPL231W)))
	,,	(2) 1111 (2) (2) (2) (2) (2) (2) (2) (2) (2) (2)	12 2.000		,,,	(Acp1-m and
1					(YKL192C and YER061C	
1			1	I		Cem1-m and
	L		1	L	and YOR221C and	Mct1-m and
FAS140ACPm	fatty-acyl-ACP synthase (n-C14:0ACP), mitochondrial	[m]: ddcaACP + (3) h + malACP + (2) nadph> ACP + co2 + h2o + myrsACP + (2) nadp		Fatty Acid Biosynthesis	YKL055C)	Oar1-m)
				1	(YGR037C and YNR016C	(Acb1 and
					and (YKL182W and	Acc1 and Fas
FAS140	fatty acid synthase (n-C14:0)	[c]: ddca + (3) h + malcoa + (2) nadph> co2 + coa + h2o + (2) nadp + ttdca	EC 2 2 1 05	Fatty Acid Biosynthesis	YPL231W)))
1 70 140	ratty acid synthase (II-C 14.0)	[6] . duca + (6) ii + iiidicoa + (2) iiaupii> 602 + 604 + 1120 + (2) iiaup + (tuca	LO-2.3.1.03	atty Acid Diosynthesis		/
1			1	I	(YGR037C and YNR016C	(Acb1 and
			1	1	and (YKL182W and	Acc1 and Fas
FAS120COA	fatty-acyl-CoA synthase (n-C12:0CoA)	[c] : dcacoa + (3) h + malcoa + (2) nadph> co2 + coa + ddcacoa + h2o + (2) nadp	EC-2.3.1.86	Fatty Acid Biosynthesis	YPL231W)))
				<u> </u>	- '	(Acp1-m and
			1	1	(YKL192C and YER061C	Cem1-m and
	1	1	1	1		
					and VORSSIA and	
E40400465	forth and AOD and have to OAOOACC	[m] . de-AOD . (0) b . m-IAOD . (0) m-deb . AOD		Fatte Anial Discours	and YOR221C and	Mct1-m and
FAS120ACPm	fatty-acyl-ACP synthase (n-C12:0ACP), mitochondrial	[m] : dcaACP + (3) h + malACP + (2) nadph> ACP + co2 + ddcaACP + h2o + (2) nadp		Fatty Acid Biosynthesis	YKL055C)	Oar1-m)
FAS120ACPm	fatty-acyl-ACP synthase (n-C12:0ACP), mitochondrial	[m] : dcaACP + (3) h + malACP + (2) nadph> ACP + co2 + ddcaACP + h2o + (2) nadp		Fatty Acid Biosynthesis		
FAS120ACPm	fatty-acyl-ACP synthase (n-C12:0ACP), mitochondrial	[m] : dcaACP + (3) h + malACP + (2) nadph> ACP + co2 + ddcaACP + h2o + (2) nadp		Fatty Acid Biosynthesis	YKL055C)	Oar1-m)
FAS120ACPm	fatty-acyl-ACP synthase (n-C12:0ACP), mitochondrial fatty acid synthase (n-C12:0)	[m]: dcaACP + (3) h + malACP + (2) nadph> ACP + co2 + ddcaACP + h2o + (2) nadp [c]: dca + (3) h + malcoa + (2) nadph> co2 + coa + ddca + h2o + (2) nadp	EC-2.3.1.85	Fatty Acid Biosynthesis Fatty Acid Biosynthesis	YKL055C) (YGR037C and YNR016C	Oar1-m) (Acb1 and

1				1		1
					(YGR037C and YNR016C	(Acb1 and
					and (YKL182W and	Acc1 and Fas
FAS100COA	fatty acyl-CoA synthase (n-C10:0CoA)	[c]: (3) h + malcoa + (2) nadph + occoa> co2 + coa + dcacoa + h2o + (2) nadp	EC-2.3.1.86	Fatty Acid Biosynthesis	YPL231W)))
						(Acp1-m and
					(YKL192C and YER061C	Cem1-m and
					and YOR221C and	Mct1-m and
FAS100ACPm	fatty-acyl-ACP synthase (n-C10:0ACP), mitochondrial	[m]: (3) h + malACP + (2) nadph + ocACP> ACP + co2 + dcaACP + h2o + (2) nadp		Fatty Acid Biosynthesis	YKL055C)	Oar1-m)
					(YGR037C and YNR016C	(Acb1 and
					and (YKL182W and	Acc1 and Fas
FAS100	fatty acid synthase (n-C10:0)	[c]: (3) h + malcoa + (2) nadph + octa> co2 + coa + dca + h2o + (2) nadp	FC-2 3 1 85	Fatty Acid Biosynthesis	YPL231W)))
FACOAL80p	fatty-acid-CoA ligase (octanoate), peroxisomal	[x]: atp + coa + octa <==> amp + occoa + ppi		Fatty Acid Biosynthesis	YER015W	Faa2-p
FACOAL260p	fatty-acidCoA ligase (octanoale), peroxisomal	[x] : atp + coa + octa <==> amp + beccoa + ppi		Fatty Acid Biosynthesis	YBR041W	Fat1-p
FACOAL240p	fatty-acidCoA ligase (n-C24:0), peroxisomal	[x] : atp + coa + flexc <==> amp + ppi + ttccoa		Fatty Acid Biosynthesis	YBR041W	Fat1-p
FACOAL240p	Tatty-acidCoA ligase (II-C24.0), peroxisornal	[x] . atp + coa + ttc <> amp + ppi + ttccoa	EC-0.2.1.3	ratty Acid Biosynthesis	I BRU4 I W	(Faa4) or (
					(YMR246W or YIL009W	Faa3) or (
FACOAL182	fatty acid. CaA linear (actadas manto)	[a] ota Land Landau zana ann Landunana Lani	FC 6 2 4 2	Fatty Acid Biosynthesis	or YOR317W)	Faa1)
FACUAL 102	fatty-acidCoA ligase (octadecynoate)	[c] : atp + coa + ocdcya <==> amp + ocdycacoa + ppi	EC-0.2.1.3	ratty Acid Biosynthesis	or roksirw)	(Faa1) or (
					(YOR317W or YIL009W	Faa3) or (
EACOAL 404	fath, said CaA linear (astadosanasta)	[s] of the control of	FC 6 2 4 2	Fatty Acid Biosynthesis	or YMR246W)	Faa4)
FACOAL181	fatty-acidCoA ligase (octadecenoate)	[c] : atp + coa + ocdcea <==> amp + odecoa + ppi	EC-6.2.1.3	Fally Acid Biosynthesis	OI TIVIR246VV)	
					(VOD247W ex VII 000W	(Faa1) or (
E40041400	f-th!d O-A !! (t-dt-)	following a second and a second a second and	E00010	Fatte Asid Bissesthesis	(YOR317W or YIL009W	Faa3) or (
FACOAL180	fatty-acid—CoA ligase (octadecanoate)	[c] : atp + coa + ocdca <==> amp + ppi + stcoa	EC-6.2.1.3		or YMR246W)	Faa4)
FACOAL161p	fatty-acidCoA ligase (hexadecenoate), peroxisomal	[x]: atp + coa + hdcea <==> amp + hdcoa + ppi	EC-6.2.1.3	Fatty Acid Biosynthesis	YER015W	Faa2-p
			1	1	()(OD047)())(II 000)()	(Faa1) or (
	L	La de la companya del companya de la companya de la companya del companya de la c		L	(YOR317W or YIL009W	Faa3) or (
FACOAL161	fatty-acidCoA ligase (hexadecenoate)	[c] : atp + coa + hdcea <==> amp + hdcoa + ppi		Fatty Acid Biosynthesis	or YMR246W)	Faa4)
FACOAL160p	fatty-acidCoA ligase (hexadecanoate), peroxisomal	[x] : atp + coa + hdca <==> amp + pmtcoa + ppi	EC-6.2.1.3	Fatty Acid Biosynthesis	YER015W	Faa2-p
			1	1		(Faa1) or (
L			L	L	(YOR317W or YIL009W	Faa3) or (
FACOAL160	fatty-acidCoA ligase (hexadecanoate)	[c] : atp + coa + hdca <==> amp + pmtcoa + ppi		Fatty Acid Biosynthesis	or YMR246W)	Faa4)
FACOAL141p	fatty-acid-CoA ligase (tetradecenoate), peroxisomal	[x] : atp + coa + ttdcea <==> amp + ppi + tdecoa	EC-6.2.1.3	Fatty Acid Biosynthesis	YER015W	Faa2-p
						(Faa1) or (
					(YOR317W or YIL009W	Faa3) or (
FACOAL141	fatty-acid—CoA ligase (tetradecenoate)	[c] : atp + coa + ttdcea <==> amp + ppi + tdecoa		Fatty Acid Biosynthesis	or YMR246W)	Faa4)
FACOAL140p	fatty-acid—CoA ligase (tetradecanoate), peroxisomal	[x]: atp + coa + ttdca <==> amp + ppi + tdcoa	EC-6.2.1.3	Fatty Acid Biosynthesis	YER015W	Faa2-p
						(Faa1) or (
					(YOR317W or YIL009W	Faa3) or (
FACOAL140	fatty-acidCoA ligase (tetradecanoate)	[c] : atp + coa + ttdca <==> amp + ppi + tdcoa		Fatty Acid Biosynthesis	or YMR246W)	Faa4)
FACOAL120p	fatty-acidCoA ligase (dodecanoate), peroxisomal	[x]: atp + coa + ddca <==> amp + ddcacoa + ppi		Fatty Acid Biosynthesis	YER015W	Faa2-p
FACOAL100p	fatty-acidCoA ligase (decanoate), peroxisomal	[x] : atp + coa + dca <==> amp + dcacoa + ppi		Fatty Acid Biosynthesis	YER015W	Faa2-p
FA182ACPH	fatty-acyl-ACP hydrolase	[c]: h2o + ocdcyaACP <==> ACP + h + ocdcya	EC-3.1.2.14	Fatty Acid Biosynthesis	(YKL182W and YPL231W	
FA181ACPH	fatty-acyl-ACP hydrolase	[c]: h2o + octeACP <==> ACP + h + ocdcea		Fatty Acid Biosynthesis	(YKL182W and YPL231W	
FA180ACPH	fatty-acyl-ACP hydrolase	[c]: h2o + ocdcaACP <==> ACP + h + ocdca	EC-3.1.2.14	Fatty Acid Biosynthesis	(YKL182W and YPL231W	Fas
FA161ACPH	fatty-acyl-ACP hydrolase	[c] : h2o + hdeACP <==> ACP + h + hdcea	EC-3.1.2.14	Fatty Acid Biosynthesis	(YKL182W and YPL231W	Fas
FA160ACPH	fatty-acyl-ACP hydrolase	[c] : h2o + palmACP <==> ACP + h + hdca	EC-3.1.2.14	Fatty Acid Biosynthesis	(YKL182W and YPL231W	Fas
FA141ACPH	fatty-acyl-ACP hydrolase	[c]: h2o + tdeACP <==> ACP + h + ttdcea	EC-3.1.2.14	Fatty Acid Biosynthesis	(YKL182W and YPL231W	Fas
FA140ACPH	fatty-acyl-ACP hydrolase	[c] : h2o + myrsACP <==> ACP + h + ttdca	EC-3.1.2.14	Fatty Acid Biosynthesis	(YKL182W and YPL231W	Fas
FA120ACPH	fatty-acyl-ACP hydrolase	[c]: ddcaACP + h2o <==> ACP + ddca + h	EC-3.1.2.14	Fatty Acid Biosynthesis	(YKL182W and YPL231W	Fas
DESAT18_2	Oleoyl-CoA desaturase (n-C18:1CoA -> n-C18:2CoA)	[c]: h + nadph + o2 + odecoa> (2) h2o + nadp + ocdycacoa	EC-	Fatty Acid Biosynthesis		
DESAT18	stearoyl-CoA desaturase (n-C18:0CoA -> n-C18:1CoA)	[c]: h + nadph + o2 + stcoa> (2) h2o + nadp + odecoa	EC-	Fatty Acid Biosynthesis	YGL055W	Ole1
DESAT16	Palmitoyl-CoA desaturase (n-C16:0CoA -> n-C16:1CoA)	[c] : h + nadph + o2 + pmtcoa> (2) h2o + hdcoa + nadp	EC-	Fatty Acid Biosynthesis	YGL055W	Ole1
DESAT14	Myristicoyl-CoA desaturase (n-C14:0CoA -> n-C14:1CoA)	[c]: h + nadph + o2 + tdcoa> (2) h2o + nadp + tdecoa	EC-	Fatty Acid Biosynthesis		
ACOATAm	Acetyl-CoA ACP transacylase, mitochondrial	[m]: ACP + accoa <==> acACP + coa	EC-2.3.1.41	Fatty Acid Biosynthesis	YER061C	Cem1-m
ACOATA	Acetyl-CoA ACP transacylase	[c] : ACP + accoa <==> acACP + coa	EC-2.3.1.38	Fatty Acid Biosynthesis	(YKL182W and YPL231W	Fas
ACCOACr	acetyl-CoA carboxylate, reversible reaction	[c] : accoa + atp + hco3 <==> adp + h + malcoa + pi	EC-6.4.1.2	Fatty Acid Biosynthesis	YNR016C	Acc1
ACACT1m	acetyl-CoA C-acetyltransferase, mitochondrial	[m]: (2) accoa> aacoa + coa		Fatty Acid Biosynthesis	YPL028W	Erg10-m
ACACT1	acetyl-CoA C-acetyltransferase	[c]: (2) accoa> aacoa + coa		Fatty Acid Biosynthesis	YPL028W	Erg10
HACD8p	3-hydroxyacyl-CoA dehydrogenase (3-oxooctadecanoyl-CoA), peroxisomal	[x]: 3ohodcoa + h + nadh <==> 3hodcoa + nad		Fatty Acid Degradation	YKR009C	Fox2-p
HACD7p	3-hydroxyacyl-CoA dehydrogenase (3-oxohexadecanoyl-CoA), peroxisomal	[x]: 3ohdcoa + h + nadh <==> 3hhdcoa + nad		Fatty Acid Degradation	YKR009C	Fox2-p
HACD6p	3-Hydroxyacyl-CoA dehydrogenase (3-oxotetradecanoyl-CoA), peroxisomal	[x]: 3otdcoa + h + nadh <==> 3htdcoa + nad		Fatty Acid Degradation	YKR009C	Fox2-p
HACD5p	3-hydroxyacyl-CoA dehydrogenase (3-oxodecanoyl-CoA), peroxisomal	[x]: 3oddcoa + h + nadh <==> 3hddcoa + nad		Fatty Acid Degradation	YKR009C	Fox2-p
HACD4p	3-hydroxyacyl-CoA dehydrogenase (3-oxodecanoyl-CoA), peroxisomal	[x]: 3odcoa + h + nadh <==> 3hdcoa + nad		Fatty Acid Degradation	YKR009C	Fox2-p
HACD10p	3-hydroxyacyl-CoA dehydrogenase (3-oxohexacosyl-CoA), peroxisomal	[x]: 3hxccoa + nad <==> 3ohxccoa + h + nadh		Fatty Acid Degradation	YKR009C	Fox2-p
FAO80p	fatty acid oxidation (octanoyl-CoA), peroxisomal	[x]: (3) coa + (3) h2o + (3) nad + (3) o2 + occoa> (4) accoa + (3) h + (3) h2o2 + (3) nadh	1	Fatty Acid Degradation		i i
FAO240p	fatty acid oxidation (tetradecansoyl-CoA), peroxisomal	[x] : (3) coa + (3) h2o + (3) nad + (3) o2 + ttccoa> (3) accoa + (3) h + (3) h2o2 + (3) nadh + stcoa		Fatty Acid Degradation		
FAO182p_odd/odd	Fatty acid oxidation (double bonds on odd num. carbon), peroxisomal	[x]: (8) coa + (8) h2o + (8) nad + (6) o2 + ocdycacoa> (9) accoa + (8) h + (6) h2o2 + (8) nadh		Fatty Acid Degradation		
,	,, ,, ,, , ,, , , ,, , , , , , , , , , , , , , , , , , , ,	[x]: (8) coa + (8) h2o + (8) nad + nadph + (7) o2 + ocdycacoa> (9) accoa + (7) h + (7) h2o2 + (8) nadh		, , , , , , , , , , , , , , , , , , , ,		
FAO182p_even/odd	Fatty acid oxidation (double bond on even and odd num. carbon), peroxisomal	+ nadp	1	Fatty Acid Degradation		
·-		[x]: (8) coa + (8) h2o + (8) nad + (2) nadph + (8) o2 + ocdycacoa> (9) accoa + (6) h + (8) h2o2 + (8)	1	1		
FAO182p_even/even	Fatty acid oxidation (double bonds on even num. carbon), peroxisomal	nadh + (2) nadp	1	Fatty Acid Degradation	1	
FAO181p_odd	Fatty acid oxidation (double bond on odd num. carbon), peroxisomal	[x]: (8) coa + (8) h2o + (8) nad + (7) o2 + odecoa> (9) accoa + (8) h + (7) h2o2 + (8) nadh		Fatty Acid Degradation		
r=	, ([x]: (8) coa + (8) h2o + (8) nad + nadph + (8) o2 + odecoa> (9) accoa + (7) h + (8) h2o2 + (8) nadh +	1	, , , , , , , , , , , , , , , , , , , ,		
FAO181p_even	Fatty acid oxidation (double bond on even num. carbon), peroxisomal	nadp		Fatty Acid Degradation		
FAO161p_odd	Fatty acid oxidation (double bond on odd num. carbon), peroxisomal	[x]: (7) coa + (7) h2o + hdcoa + (7) nad + (6) o2> (8) accoa + (7) h + (6) h2o2 + (7) nadh		Fatty Acid Degradation		
	, peromonial	[x]: (7) coa + (7) h2c + hdcoa + (7) had + hdcoa + (7) nad + nadph + (7) o2> (8) accoa + (6) h + (7) h2c2 + (7) hadh +	1			
FAO161p_even	Fatty acid oxidation (double bond on even num. carbon), peroxisomal	Inadp	1	Fatty Acid Degradation	1	
FAO141p_odd	Fatty acid oxidation (double bond on odd num. carbon), peroxisomal	[x]: (6) coa + (6) h2o + (6) nad + (5) o2 + tdecoa> (7) accoa + (6) h + (5) h2o2 + (6) nadh	1	Fatty Acid Degradation		
. , . o 1 + 1 p_ouu	, any acid children (acabic bond on odd nam, carbon), peroxisonial	[X]: (6) coa + (6) h2o + (6) nad + nadph + (6) o2 + tdecoa> (7) accoa + (5) h + (6) h2o2 + (6) nadh +	+	. axy note Degradation	- 	1
FAO141p even	fatty acid oxidation (double bonds on even num. carbon), peroxisomal	[k] . (d) Coa + (d) 1120 + (d) 11au + 11aupii + (d) 02 + (decoa> (7) accoa + (5) 11 + (6) 11202 + (6) 11auii + 11aupii + (6) 02 + (decoa> (7) accoa + (5) 11 + (6) 11202 + (6) 11auii + (6) 02 +	1	Fatty Acid Degradation		
ECOAH8p	3-hydroxyacyl-CoA dehydratase (3-hydroxyoctadecanoyl-CoA), peroxisomal	[x]: 3hodcoa <==> h2o + od2coa	FC-4 2 1 17	Fatty Acid Degradation	YKR009C	Fox2-p
ECOAH8p ECOAH7p	3-hydroxyacyl-CoA denydratase (3-hydroxyoctadecanoyl-CoA), peroxisomal 3-hydroxyacyl-CoA dehydratase (3-hydroxyhexadecanoyl-CoA), peroxisomal	[x] : 3nodcoa <==> nzo + odzcoa [x] : 3hhdcoa <==> h2o + hdd2coa		Fatty Acid Degradation	YKR009C YKR009C	Fox2-p Fox2-p
LOUMITE	o-nyuroxyacyr-con denyuratase (o-nyuroxynexadecanoyr-con), peroxisomal					
ECOAH6p	3-hydroxyacyl-CoA dehydratase (3-hydroxytetradecanoyl-CoA), peroxisomal	[x]: 3htdcoa <==> h2o + td2coa		Fatty Acid Degradation	YKR009C	Fox2-p

I COO ALLE	10		1=0 . 0	5 " A B	hurnaan.	1= 0
ECOAH5p	3-hydroxyacyl-CoA dehydratase (3-hydroxydodecanoyl-CoA), peroxisomal	[x] : 3hddcoa <==> dd2coa + h2o		Fatty Acid Degradation	YKR009C	Fox2-p
ECOAH4p	3-hydroxyacyl-CoA dehydratase (3-hydroxydecanoyl-CoA), peroxisomal	[x]: 3hdcoa <==> dc2coa + h2o	EC-4.2.1.17	Fatty Acid Degradation	YKR009C	Fox2-p
ECOAH11p	3-hydroxyacyl-CoA dehydratase (3-hydroxyhexacosyl-CoA), peroxisomal	[x]: h2o + hxc2coa <==> 3hxccoa		Fatty Acid Degradation	YKR009C	Fox2-p
ACOAO9p	acyl-CoA oxidase (hexacanoyl-CoA), peroxisomal	[x]: hexccoa + o2> h2o2 + hxc2coa		Fatty Acid Degradation	YGL205W	Pox1-p
ACOAO8p	acyl-CoA oxidase (octadecanoyl-CoA), peroxisomal	[x]: o2 + stcoa> h2o2 + od2coa	EC-1.3.3.6	Fatty Acid Degradation	YGL205W	Pox1-p
ACOAO7p	acyl-CoA oxidase (hexadecanoyl-CoA), peroxisomal	[x]: o2 + pmtcoa> h2o2 + hdd2coa	FC-1.3.3.6	Fatty Acid Degradation	YGL205W	Pox1-p
ACOAO6p	acyl-CpA oxidase (tetradecanoyl-CoA), peroxisomal	[x] : o2 + tdcoa> h2o2 + td2coa		Fatty Acid Degradation	YGL205W	Pox1-p
ACOAO5p	acyl-CoA oxidase (dodecanoyl-CoA), peroxisomal	[x] : ddcacoa + o2> dd2coa + h2o2		Fatty Acid Degradation	YGL205W	Pox1-p
ACOAO4p	acyl-CoA oxidase (decanoyl-CoA), peroxisomal	[x]: dcacoa + o2> dc2coa + h2o2	EC-1.3.3.6	Fatty Acid Degradation	YGL205W	Pox1-p
ACACT9p	acetyl-CoA acyltransferase (tetracosanoyl-CoA), peroxisomal	[x]: 3ohxccoa + coa> accoa + ttccoa		Fatty Acid Degradation	YIL160C	Pot1-p
ACACT8p	acetyl-CoA acyltransferase (hexadecanoyl-CoA), peroxisomal	[x] : 3ohodcoa + coa> accoa + pmtcoa		Fatty Acid Degradation	YIL160C	Pot1-p
ACACT7p	acetul-CoA acyltransferase (tetradecanoyl-CoA), peroxisomal	[x]: 3ohdcoa + coa> accoa + tdcoa	EC-2.3.1.16	Fatty Acid Degradation	YIL160C	Pot1-p
ACACT6p	acetyl-CoA C-acetyltransferase (dodecanoyl), peroxisomal	[x]: 3otdcoa + coa> accoa + ddcacoa		Fatty Acid Degradation	YIL160C	Pot1-p
ACACT5p	acetyl-CoA C-acyltransferase (decanoyl-CoA), peroxisomal	[x]: 3oddcoa + coa> accoa + dcacoa		Fatty Acid Degradation	YIL160C	Pot1-p
ACACT4p	acetyl-CoA C-acetyltransferase (octanoyl-CoA), peroxisomal	[x]: 3odcoa + coa> accoa + occoa	EC-2.3.1.16	Fatty Acid Degradation	YIL160C	Pot1-p
						(Rma1) or (
					(YKL132C or YOR241W	Met7) or (
	L		 			
THFGLUS	Tetrahydrofolate:L-glutamate gamma-ligase (ADP-forming)	[c] : atp + glu-L + thf <==> adp + h + pi + thfglu	EC-6.3.2.17	Folate Metabolism	or YMR113W)	Fol3)
					(YDR019C and YMR189W	(Gcv1-m and
					and YAL044C and (Gcv2-m and
					YBR221C and YER178W)	Gcv3-m and
THFATm	tetrahydrofolate aminomethyltransferase, mitochondrial	[m] : h2o + methf> 5fthf + h	EC-2.1.2.10	Folate Metabolism)	PdE1-m)
QULNS	quinolinate synthase	[c] : dhap + iasp> h + (2) h2o + pi + quln		Folate Metabolism		
QUEINO	quinoimate synthase	[6] . driab + lasb - x ii + (2) ii 20 + pr + quiii		i olate wetabolisiii		(Motto) or (
						(Met12) or (
MTHFR3	5,10-methylenetetrahydrofolatereductase (NADPH)	[c] : h + mlthf + nadph> 5mthf + nadp		Folate Metabolism	(YPL023C or YGL125W)	Met13)
MTHFDm	methylenetetrahydrofolate dehydrogenase (NADP), mitochondrial	[m] : mlthf + nadp <==> h + methf + nadph	EC-1.5.1.5	Folate Metabolism	YBR084W	Mis1-m
MTHFD2		[c] : mlthf + nad> h + methf + nadh			YKR080W	Mtd1
	methylenetetrahydrofolate dehydrogenase (NAD)			Folate Metabolism		
MTHFD	methylenetetrahydrofolate dehydrogenase (NADP)	[c] : mlthf + nadp <==> h + methf + nadph	EC-1.5.1.5	Folate Metabolism	YGR204W	Ade3
MTHFCm	methenyltetrahydrifikate cyclohydrolase, mitochondrial	[m] : h2o + methf <==> 10fthf	EC-3.5.4.9	Folate Metabolism	YBR084W	Mis1-m
MTHFC	methenyltetrahydrofolate cyclohydrolase	[c] : h2o + methf <==> 10fthf	EC-3.5.4.9	Folate Metabolism		Ade3
					YGR204W	
HPPKm	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase,	[m] : 2ahhmp + atp> 2ahhmd + amp + h	EC-2.7.6.3	Folate Metabolism	YNL256W	Fol1-m
GTPCI	GTP cyclohydrolase I	[c] : gtp + h2o> ahdt + for	FC-3 5 4 16	Folate Metabolism	YGR267C	Fol2
FTHFLm			EC-6.3.4.3	Folate Metabolism	YBR084W	Mis1-m
	formate-tetrahydrofolate ligase, mitochondrial	[m] : atp + for + thf <==> 10fthf + adp + pi				
FTHFL	formate-tetrahydrofolate ligase	[c] : atp + for + thf <==> 10fthf + adp + pi	EC-6.3.4.3	Folate Metabolism	YGR204W	Ade3
FTHFI	5-Formyltetrahydrofolate:10-Formyltetrahydrofolate isomerase	[c] : 5fthf + atp + h2o> 10fthf + adp + pi		Folate Metabolism		
			FC 6 2 2 2			
FTHFCLm	5-formethyltetrahydrofolate cyclo-ligase, mitochondrial	[m] : 5fthf + atp> adp + methf + pi	EC-6.3.3.2	Folate Metabolism		
FTHFCL	5-formethyltetrahydrofolate cyclo-ligase	[c] : 5fthf + atp> adp + methf + pi	EC-6.3.3.2	Folate Metabolism	YER183C	Fau1
FOLDm	fold, mitochondrial	[m]: 2ahhmd + 4abz> dhpt + ppi		Folate Metabolism	YNL256W	Fol1-m
			E00400			
FMETTRSm	Methionyl-tRNA formyltransferase, mitochondrial	[m] : 10fthf + mettrna> fmettrna + h + thf	EC-2.1.2.9	Folate Metabolism	YBL013W	Fmt1-m
DNTPPA	Dihydroneopterin triphosphate pyrophosphatase	[c] : ahdt + h2o> dhpmp + h + ppi		Folate Metabolism		
DNMPPA	Dihydroneopterin monophosphate dephosphorylase	[c] : dhpmp + h2o> dhnpt + pi		Folate Metabolism	YDL100C	Arr4
			5005115			
DHPSm	dihydropteroate synthase, mitochondrial	[m] : 2ahhmp + 4abz> dhpt + h2o		Folate Metabolism	YNL256W	Fol1-m
DHNPAm	dihydroneopterin aldolase, mitochondrial	[m] : dhnpt> 2ahhmp + gcald + h	EC-4.1.2.25	Folate Metabolism	YNL256W	Fol1-m
DHFS	dihydrofolate synthase	[c] : atp + dhpt + glu-L> adp + dhf + pi	FC-6.3.2.12	Folate Metabolism		
					VOD00011	D()
DHFRim	dihydrofolate reductase, mitochondrial	[m] : dhf + h + nadph> nadp + thf	EC-1.5.1.3	Folate Metabolism	YOR236W	Dfr1-m
DHFRi	dihydrofolate reductase (irreversible)	[c] : dhf + h + nadph> nadp + thf	EC-1.5.1.3	Folate Metabolism	YOR236W	Dfr1
ASPOcm	aspartate oxidase	asp-L[c] + fad[m]> fadh2[m] + iasp[c]		Folate Metabolism		
			500101		V/DD 4040	DI 0
AKP1	alkaline phosphatase (Dihydroneopterin)	[c] : ahdt + (3) h2o> dhnpt + (2) h + (3) pi	EC-3.1.3.1	Folate Metabolism	YDR481C	Pho8
ADCS	4-amino-4-deoxychorismate synthase	[c] : chor + gln-L> 4adcho + glu-L		Folate Metabolism	YNR033W	Abz1
ADCL	4-aminobenzoate synthase	[c] : 4adcho> 4abz + h + pyr		Folate Metabolism		
PMANM			E0 E 4 0 0		VEL 0450	050
PIMANIM	phosphomannomutase	[c] : man1p <==> man6p	EC-5.4.2.8	Fructose and mannose metabolism	YFL045C	Sec53
			EC-			(Pfk26) or (
PFK26	6-phosphofructo-2-kinase	[c]: atp + f6p> adp + f26bp + h	2.7.1.105	Fructose and mannose metabolism	(YIL107C or YOL136C)	Pfk27)
MAN6PI						
	mannose-6-phosphate isomerase	[c] : man6p <==> f6p	EC-5.3.1.8	Fructose and mannose metabolism	YER003C	Pmi40
MAN1PT	mannose-1-phosphate guanylyltransferase	[c] : gtp + h + man1p> gdpmann + ppi	EC-2.7.7.13	Fructose and mannose metabolism	YDL055C	Psa1
FRUK	fructose-1-phosphate kinase	[c] : atp + f1p> adp + fdp + h		Fructose and mannose metabolism		
FBP26				Fructose and mannose metabolism	YJL155C	Ehn26
	Fructose-2,6-bisphosphate 2-phosphatase	[c] : f26bp + h2o> f6p + pi				Fbp26
UGLT	UDPglucosehexose-1-phosphate uridylyltransferase	[c] : gal1p + udpg <==> g1p + udpgal		Galactose metabolism	YBR018C	Gal7
UDPG4E	UDPglucose 4-epimerase	[c] : udpg <==> udpgal	EC-5.1.3.2	Galactose metabolism	YBR019C	Gal10
RAFGH	Raffinose galactohydrolase	[c] : h2o + raffin> gal + sucr	EC-3.2.1.22	Galactose metabolism	YBR184W	Mel1
MELTGH	Melibiitol galactohydrolase	[c] : h2o + melt <==> gal + sbt-D	EC-3.2.1.22	Galactose metabolism	YBR184W	Mel1
						(Mal32) or (
1			I		1	Mal12) or (
I			I		1	
I			I		1	Fsp2) or (
I			I		(YBR299W or YGR292W	Mal33) or (
I			I		or YJL221C or YGR287C	Mal13) or (
MALT.	alpha alugasidasa	[a] : h2a + matt > (2) ala D	EC 2 2 4 22	Galactose metabolism		
MALT	alpha-glucosidase	[c] : h2o + malt> (2) glc-D			or YIL172C or YJL216C)	Mal14)
GGLGH	Galactosylglycerol galactohydrolase	[c] : qql + h2o <==> qal + qlyc	IFC-3.2.1.22	Galactose metabolism	YBR184W	Mel1
	Calactosylgiyeerol galactoriyarolase	[c] . ggi · 1120 · · gai · giyo				(Ugp1) or (
i contract of the contract of	Calactosyngryceror galactorrytrolase	[0] . 9gr + 1120 gur + 9ry0				
CALL				Colostono motoboli	()/// 02E/M == 1// 040***	
GALU	UTP-glucose-1-phosphate uridylyltransferase	[c]: g1p + h + utp <==> ppi + udpg	EC-2.7.7.9	Galactose metabolism	(YKL035W or YHL012W)	Ugp2)
GALU GALT			EC-2.7.7.9	Galactose metabolism Galactose metabolism	(YKL035W or YHL012W) YBR018C	
GALT	UTP-glucose-1-phosphate uridylyltransferase galactose-1-phosphate uridylyltransferase	[c] : g1p + h + utp <==> ppi + udpg [c] : ga1fp + h + utp <==> ppi + udpgal	EC-2.7.7.9 EC-2.7.7.10	Galactose metabolism	YBR018C	Ugp2) Gal7
GALT GALS3	UTP-glucose-1-phosphate uridylyltransferase galactose-1-phosphate uridylyltransferase a-galactosidase (melibiose)	[c]: g1p + h + utp <==> ppi + udpg [c]: gal1p + h + utp <==> ppi + udpgal [c]: h2o + melib> gal + gic-D	EC-2.7.7.9 EC-2.7.7.10 EC-3.2.1.22	Galactose metabolism Galactose metabolism	YBR018C YBR184W	Ugp2) Gal7 Mel1
GALT GALS3 GALK	UTP-glucose-1-phosphate uridylyltransferase galactose-1-phosphate uridylyltransferase a-galactosidase (melibiose) galactokinase	[c]: g1p + h + utp <==> ppi + udpg (c]: gal1p + h + utp <==> ppi + udpgal [c]: h2o + melib -> gal + gic-D [c]: atp + gal -> adp + gal1p + h	EC-2.7.7.9 EC-2.7.7.10 EC-3.2.1.22 EC-2.7.1.6	Galactose metabolism Galactose metabolism Galactose metabolism	YBR018C YBR184W YBR020W	Ugp2) Gal7 Mel1 Gal1
GALT GALS3	UTP-glucose-1-phosphate uridylyltransferase galactose-1-phosphate uridylyltransferase a-galactosidase (melibiose) galactokinase	[c]: g1p + h + utp <==> ppi + udpg [c]: gal1p + h + utp <==> ppi + udpgal [c]: h2o + melib> gal + gic-D	EC-2.7.7.9 EC-2.7.7.10 EC-3.2.1.22 EC-2.7.1.6	Galactose metabolism Galactose metabolism	YBR018C YBR184W	Ugp2) Gal7 Mel1
GALT GALS3 GALK GALIGH	UTP-glucose-1-phosphate uridylyltransferase galactose-1-phosphate uridylyltransferase a-galactosidase (melibiose) galactokinase 1-alpha-D-Galactosyl-myo-inositol galactohydrolase	[c] : g1p + h + utp <==> ppi + udpg [c] : ga1fp + h + utp <==> ppi + udpgal [c] : h2o + melib -> gal + glc-D [c] : atp + gal -> adp + ga1fp + h [c] : 1Dgall + h2o <==> gal + inost	EC-2.7.7.9 EC-2.7.7.10 EC-3.2.1.22 EC-2.7.1.6	Galactose metabolism Galactose metabolism Galactose metabolism Galactose metabolism	YBR018C YBR184W YBR020W YBR184W	Ugp2) Gal7 Mel1 Gal1 Mel1
GALT GALS3 GALK GALIGH EPMGH	UTP-glucose-1-phosphate uridylyltransferase galactose-1-phosphate uridylyltransferase a-galactosidase (melibiose) galactokinase 1-alpha-D-Galactosyl-myo-inositol galactohydrolase Epimellibiose galactohydrolase	[c] : g1p + h + utp <==> ppi + udpg [c] : gal1p + h + utp <==> ppi + udpgal [c] : h2o + melib -> gal + gic-D [c] : atp + gal -> adp + gal1p + h [c] : 1Dgali + h2o <==> gal + inost [c] : epm + h2o <==> gal + man	EC-2.7.7.9 EC-2.7.7.10 EC-3.2.1.22 EC-2.7.1.6	Galactose metabolism Galactose metabolism Galactose metabolism Galactose metabolism Galactose metabolism	YBR018C YBR184W YBR020W YBR184W YBR184W	Ugp2) Gal7 Mel1 Gal1 Mel1 Mel1 Mel1
GALT GALS3 GALK GALIGH EPMGH DGGH	UTP-glucose-1-phosphate uridylyltransferase galactose-1-phosphate uridylyltransferase a-galactosidase (melibiose) galactosinase 1-alpha-D-Galactosyl-myo-inositol galactohydrolase Epimelibiose galactohydrolase alpha-D-glucoside glucohydrose	[c]: g1p + h + utp <==> ppi + udpg [c]: gal1p + h + utp <==> ppi + udpgal [c]: h2o + melib> gal + gic-D [c]: atp + gal> adp + gal1p + h [c]: 1Dgali + h2o <==> gal + inost [c]: epm + h2o <==> gal + man [c]: 61g + h2o> gal + gic-D	EC-2.7.7.9 EC-2.7.7.10 EC-3.2.1.22 EC-2.7.1.6 EC-3.2.1.22	Galactose metabolism	YBR018C YBR184W YBR020W YBR184W	Ugp2) Gal7 Mel1 Gal1 Mel1
GALT GALS3 GALK GALIGH EPMGH	UTP-glucose-1-phosphate uridylyltransferase galactose-1-phosphate uridylyltransferase a-galactosidase (melibiose) galactokinase 1-alpha-D-Galactosyl-myo-inositol galactohydrolase Epimellibiose galactohydrolase	[c]: g1p + h + utp <==> ppi + udpg [c]: gal1p + h + utp <==> ppi + udpgal [c]: h2o + melib> gal + gic-D [c]: atp + gal> adp + gal1p + h [c]: 1Dgali + h2o <==> gal + inost [c]: epm + h2o <==> gal + man [c]: 61g + h2o> gal + gic-D	EC-2.7.7.9 EC-2.7.7.10 EC-3.2.1.22 EC-2.7.1.6 EC-3.2.1.22	Galactose metabolism Galactose metabolism Galactose metabolism Galactose metabolism Galactose metabolism	YBR018C YBR184W YBR020W YBR184W YBR184W	Ugp2) Gal7 Mel1 Gal1 Mel1 Mel1 Mel1
GALT GALS3 GALK GALIGH EPMGH DGGH G6PDA	UTP-glucose-1-phosphate uridylyltransferase galactose-1-phosphate uridylyltransferase a-galactosidase (melibiose) galactokinase 1-alpha-D-Galactosyl-myo-inositol galactohydrolase Epimelibiose galactohydrolase alpha-D-glucoside glucohydrase glucosamine-6-phosphate deaminase	[c] : g1p + h + utp <==> ppi + udpg [c] : ga1p + h + utp <==> ppi + udpgal [c] : h2o + melib -> gal + glc-D [c] : atp + gal -> adp + ga1p + h [c] : 1Dgall + h2o <==> gal + inost [c] : epm + h2o <==> gal + man [c] : 6dg + h2o -> gal + glc-D [c] : gam6p + h2o -> 56p + nh4	EC-2.7.7.9 EC-2.7.7.10 EC-3.2.1.22 EC-2.7.1.6 EC-3.2.1.22 EC-3.5.99.6	Galactose metabolism Glucosamine Metabolism	YBR018C YBR184W YBR020W YBR184W YBR184W YJL221C	Ugp2) Gal7 Mel1 Gal1 Mel1 Mel1 Mel1 Fsp2
GALT GALS3 GALK GALIGH EPMGH DGGH G6PDA UDPACGLP	UTP-glucose-1-phosphate uridylyltransferase galactose-1-phosphate uridylyltransferase a-galactosidase (melibiose) galactokinase laipha-D-Galactosyl-myo-inositol galactohydrolase Epimelibiose galactohydrolase alpha-D-glucoside glucohydrase glucosamine-6-phosphate deaminase UDP-N-acetylglucosamine diphosphorylase	(c) : g1p + h + utp <==> ppi + udpg (c) : gal1p + h + utp <==> ppi + udpgal (c) : h2o + melib -> gal + gic-D (c) : atp + gal -> adp + gal1p + h (c) : 1Dgali + h2o <==> gal + inost (c) : epm + h2o <==> gal + man (c) : 6g + h2o -> gal + glc-D (c) : gam6p + h2o -> f6p + nh4 (c) : acgam1p + h + utp <==> ppi + udpacgal	EC-2.7.7.9 EC-2.7.7.10 EC-3.2.1.22 EC-2.7.1.6 EC-3.2.1.22 EC-3.5.99.6 EC-2.7.7.23	Galactose metabolism Glucosamine Metabolism Glutamate metabolism	YBR018C YBR184W YBR020W YBR184W YBR184W YJL221C YDL103C	Ugp2) Gal7 Mel1 Gal1 Mel1 Mel1 Mel1 Fsp2 Qri1
GALT GALS3 GALK GALIGH EPMGH DGGH G8PDA UDPACGLP SSALY	UTP-glucose-1-phosphate uridylyltransferase galactose-1-phosphate uridylyltransferase a-galactosidase (melibiose) galactokinase 1-alpha-D-Galactosyl-myo-inositol galactohydrolase Epimelibiose galactohydrolase alpha-D-glucoside glucohydrase glucosamine-6-phosphate deaminase UDP-N-acetylglucosamine diphosphorylase succinate-semialdehyde dehydrogenase (NADP)	C : g1p + h + utp <==> ppi + udpg	EC-2.7.7.9 EC-2.7.7.10 EC-3.2.1.22 EC-2.7.1.6 EC-3.2.1.22 EC-3.5.99.6 EC-2.7.7.23 EC-1.2.1.16	Galactose metabolism Glucosamine Metabolism Glutamate metabolism Glutamate metabolism	YBR018C YBR184W YBR020W YBR184W YBR184W YJL221C YDL103C YBR006W	Ugp2) Gal7 Mel1 Gal1 Mel1 Mel1 Mel1 Fsp2
GALT GALS3 GALK GALIGH EPMGH DGGH G8PDA UDPACGLP SSALY	UTP-glucose-1-phosphate uridylyltransferase galactose-1-phosphate uridylyltransferase a-galactosidase (melibiose) galactokinase 1-alpha-D-Galactosyl-myo-inositol galactohydrolase Epimelibiose galactohydrolase alpha-D-glucoside glucohydrase glucosamine-6-phosphate deaminase UDP-N-acetylglucosamine diphosphorylase succinate-semialdehyde dehydrogenase (NADP)	(c) : g1p + h + utp <==> ppi + udpg (c) : gal1p + h + utp <==> ppi + udpgal (c) : h2o + melib -> gal + gic-D (c) : atp + gal -> adp + gal1p + h (c) : 1Dgali + h2o <==> gal + inost (c) : epm + h2o <==> gal + man (c) : 6g + h2o -> gal + glc-D (c) : gam6p + h2o -> f6p + nh4 (c) : acgam1p + h + utp <==> ppi + udpacgal	EC-2.7.7.9 EC-2.7.7.10 EC-3.2.1.22 EC-2.7.1.6 EC-3.2.1.22 EC-3.5.99.6 EC-2.7.7.23 EC-1.2.1.16	Galactose metabolism Glucosamine Metabolism Glutamate metabolism	YBR018C YBR184W YBR020W YBR184W YBR184W YJL221C YDL103C	Ugp2) Gal7 Mel1 Gal1 Mel1 Mel1 Mel1 Fsp2 Qri1
GALT GALS3 GALK GALIGH EPMGH DGGH G6PDA UDPACGLP SSALY PYRSCDm	UTP-glucose-1-phosphate uridylyltransferase galactose-1-phosphate uridylyltransferase a-galactosidase (melibiose) galactokinase 1-alpha-D-Galactosyl-myo-inositol galactohydrolase Epimelibiose galactohydrolase alpha-D-glucoside glucohydrase glucosamine-6-phosphate deaminase UDP-N-acetylglucosamine diphosphorylase succinate-semialdehyde dehydrogenase (NADP) D1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	C : g1p + h + utp <==> ppi + udpg C : ga1p + h + utp <==> ppi + udpga C : h2o + melib -> gal + glc-D C : atp + gal -> adp + ga1p + h C : 10gal + h2o <==> gal + inost C : epm + h2o <==> gal + man C : 6dg + h2o -> gal + glc-D C : gam6p + h2o -> f6p + nh4 C : acgam1p + h + utp <==> ppi + udpacgal C : h2o + nadp + sucsal -> (2) h + nadph + succ M : gluSas + h2o + nadp -> glu-l + (2) h + nadph C : h2o + nadp + sucsal -> (2) h + nadph C : h2o + nadp + sucsal -> (2) h + nadph C : h2o + nadp -> glu-l + (2) h + nadph	EC-2.7.7.9 EC-2.7.7.10 EC-3.2.1.22 EC-2.7.1.6 EC-3.2.1.22 EC-3.5.99.6 EC-2.7.7.23 EC-1.2.1.16 EC-1.5.1.12	Galactose metabolism Glucosamine Metabolism Glutamate metabolism Glutamate metabolism Glutamate metabolism Glutamate metabolism	YBR018C YBR184W YBR020W YBR184W YBR184W YJL221C YDL103C YBR006W YHR037W	Ugp2) Gal7 Mel1 Gal1 Mel1 Mel1 Mel1 Mel1 Psp2 Qri1 Uga2 Put2-m
GALT GALS3 GALK GALIGH EPMGH DGGH GBPDA UDPACGLP SSALY PYRSCDm PGAMT	UTP-glucose-1-phosphate uridylyltransferase galactose-1-phosphate uridylyltransferase a-galactosidase (melibiose) galactokinase 1-alpha-D-Galactosyl-myo-inositol galactohydrolase Epimelibiose galactohydrolase alpha-D-glucoside glucohydrase glucosamine-6-phosphate deaminase UDP-N-acetylglucosamine diphosphorylase succinate-semialdehyde dehydrogenase (NADP) D1-pyrroline-5-carboxylate dehydrogenase, mitochondrial phosphoglucosamine mutase	[c]: g1p + h + utp <==> ppi + udpg [c]: gal1p + h + utp <==> ppi + udpgal [c]: h2o + melib -> gal + glc-D [c]: atp + gal -> adp + gal1p + h [c]: 1Dgali + h2o <==> gal + inost [c]: epm + h2o <==> gal + man [c]: 6dg + h2o -> gal + glc-D [c]: gam6p + h2o -> f6p + nh4 [c]: acgam1p + h + utp <==> ppi + udpacgal [c]: h2o + nadp + sucsal -> (2) h + nadph + succ [m]: glu5sa + h2o + nadp -> glu-L + (2) h + nadph [c]: gam1p <==> gam6p	EC-2.7.7.9 EC-2.7.7.10 EC-3.2.1.22 EC-2.7.1.6 EC-3.2.1.22 EC-3.5.99.6 EC-2.7.7.23 EC-1.2.1.16 EC-1.5.1.12	Galactose metabolism Glucosamine Metabolism Glutamate metabolism	YBR018C YBR184W YBR020W YBR184W YBR184W YJL221C YDL103C YBR006W	Ugp2) Gal7 Mel1 Gal1 Mel1 Mel1 Mel1 Fsp2 Ori1 Uga2
GALT GALS3 GALK GALIGH EPMGH DGGH GGPDA UDPACGLP SSALY PYR5CDm PGAMT P5CDm	UTP-glucose-1-phosphate uridylyltransferase galactose-1-phosphate uridylyltransferase a-galactosidase (melibiose) galactokinase 1-alpha-D-Galactosyl-myo-inositol galactohydrolase Epimelibiose galactohydrolase alpha-D-glucoside glucohydrase glucosamine-6-phosphate deaminase UDP-N-acetylglucosamine diphosphorylase succinate-semiladehyde dehydrogenase (NADP) D1-pyrroline-5-carboxylate dehydrogenase, mitochondrial phosphoglucosamine mutase 1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	[c] : g1p + h + utp <==> ppi + udpg [c] : ga1p + h + utp <==> ppi + udpgal [c] : l2x0 + melit -> ga1 + g1c-D [c] : atp + ga1 -> adp + ga1p + h [c] : 1Dga1l + h2o <==> ga1 + inost [c] : etp + h2o <==> ga1 + inost [c] : etp + h2o -> ga1 + glc-D [c] : gam6p + h2o -> fgh + nha [c] : acgam1p + h + utp <==> ppi + udpacgal [c] : h2o + nadp + sucsal -> (2) h + nadph + succ [m] : glu5sa + h2o + nadp -> glu-L + (2) h + nadph [c] : acgam1p <==> gam6p [m] : 1pyf5c + (2) h2o + nad -> glu-L + h + nadh	EC-2.7.7.9 EC-2.7.7.10 EC-3.2.1.22 EC-2.7.1.6 EC-3.2.1.22 EC-3.5.99.6 EC-2.7.7.23 EC-1.2.1.16 EC-5.4.2.10	Galactose metabolism Glucosamine Metabolism Glutamate metabolism	YBR018C YBR184W YBR020W YBR184W YBR184W YJL221C YDL103C YBR006W YHR037W YEL058W	Ugp2) Gal7 Mel1 Gal1 Mel1 Mel1 Fsp2 Qri1 Uga2 Put2-m Pem1
GALT GALT GALK GALIGH EPMGH DGGH GGPDA UDPACGLP SSALY PYRSCDm PGAMT	UTP-glucose-1-phosphate uridylyltransferase galactose-1-phosphate uridylyltransferase a-galactosidase (melibiose) galactokinase 1-alpha-D-Galactosyl-myo-inositol galactohydrolase Epimelibiose galactohydrolase alpha-D-glucoside glucohydrase glucosamine-6-phosphate deaminase UDP-N-acetylglucosamine diphosphorylase succinate-semialdehyde dehydrogenase (NADP) D1-pyrroline-5-carboxylate dehydrogenase, mitochondrial phosphoglucosamine mutase	[c]: g1p + h + utp <==> ppi + udpg [c]: gal1p + h + utp <==> ppi + udpgal [c]: h2o + melib -> gal + glc-D [c]: atp + gal -> adp + gal1p + h [c]: 1Dgali + h2o <==> gal + inost [c]: epm + h2o <==> gal + man [c]: 6dg + h2o -> gal + glc-D [c]: gam6p + h2o -> f6p + nh4 [c]: acgam1p + h + utp <==> ppi + udpacgal [c]: h2o + nadp + sucsal -> (2) h + nadph + succ [m]: glu5sa + h2o + nadp -> glu-L + (2) h + nadph [c]: gam1p <==> gam6p	EC-2.7.7.9 EC-2.7.7.10 EC-3.2.1.22 EC-2.7.1.6 EC-3.2.1.22 EC-3.5.99.6 EC-2.7.7.23 EC-1.2.1.16 EC-5.4.2.10	Galactose metabolism Glucosamine Metabolism Glutamate metabolism	YBR018C YBR184W YBR020W YBR184W YBR184W YJL221C YDL103C YBR006W YHR037W	Ugp2) Gal7 Mel1 Gal1 Mel1 Mel1 Mel1 Mel1 Psp2 Qri1 Uga2 Put2-m

						(Gdh3) or (
GLUDy	glutamate dehydrogenase (NADP)	[c] : glu-L + h2o + nadp <==> akg + h + nadph + nh4	EC-1.4.1.4	Glutamate metabolism	(YAL062W or YOR375C)	Gdh1)
GLUDxi	glutamate dehydrogenase (NAD)	[c] : glu-L + h2o + nad> akg + h + nadh + nh4	EC-1.4.1.2	Glutamate metabolism	YDL215C	Gdh2
GLUDC	Glutamate Decarboxylase	[c] : glu-L + h> 4abut + co2		Glutamate metabolism	YMR250W	Gad1
CSNATirp	carnitine O-acetyltransferase, rev erse direction, peroxisomal	[x]: accoa + crn> acrn + coa	EC-2.3.1.7	Glutamate metabolism	YML042W	Cat2-p
					(VNII 103W) or VDD038W	(Chs1) or (
CHTNS	chitin synthase	[c] : udpacgal> chitin + h + udp	FC-2 4 1 16	Glutamate metabolism	(YNL192W or YBR038W or YBR023C)	Chs2) or (Chs3)
ACGAMPM	phosphoacetylglucosamine mutase	[c] : acgam6p <==> acgam1p	EC-5.4.2.3		YEL058W	Pcm1
ACGAM6PS	N-acetylglucosamine-6-phosphate synthase	[c] : accoa + gam6p <==> acgam6p + coa + h	EC-2.3.1.4		YFL017C	Gna1
ABTA	4-aminobutyrate transaminase	[c] : 4abut + akg> glu-L + sucsal		Glutamate metabolism	YGR019W	Uga1
GLUTRSm	glutamyl-tRNA synthetase, mitochondrial	[m] : atp + glu-L + trnaglu> amp + glutrna + ppi	EC-6.1.1.17	Glutamine Metabolism	YOL033W	Mse1-m
GLUTRS	Glutamyl-tRNA synthetase	[c] : atp + glu-L + trnaglu> amp + glutrna + ppi		Glutamine Metabolism	YGL245W	Mse2
GLUN	glutaminase	[c] : gln-L + h2o> glu-L + nh4	EC-3.5.1.2			
GLNTRS	Glutaminyl-tRNA synthetase	[c] : atp + gln-L + trnagln> amp + glntrna + ppi		Glutamine Metabolism	YOR168W	Gln4
GLNS	glutamine synthetase	[c] : atp + glu-L + nh4> adp + gln-L + h + pi	EC-6.3.1.2	Glutamine Metabolism	YPR035W	Gln1
					(VIZI 404C as VMD004W	(Gfa1) or (
GF6PTA	glutamine-fructose-6-phosphate transaminase	[c] : f6p + gln-L> gam6p + glu-L	EC 2 6 1 16	Glutamine Metabolism	(YKL104C or YMR084W or YMR085W)	Gfa2) or (Gfa3)
GIGITA	gidtamine-nuclose-o-priospriate transaminase	[c] . lop + giii-L> gamop + gid-L	LC-2.0.1.10	Gidanine Wetabolishi	GI TIVII (OUSVV)	(Trp2) or (
ANS	anthranilate synthase	[c] : chor + gln-L> anth + glu-L + h + pyr	FC-4.1.3.27	Glutamine Metabolism	(YER090W or YKL211C)	Trp3)
7410	ditinatinate dynamics	[c]: (0.01) 12dgr_SC + (0.02) dcacoa + (0.06) ddcacoa + (0.17) hdcoa + (0.09) ocdycacoa + (0.24)	20 11110127	Ciddaninio Modabolioni	(12100011 01 11122110)	po /
TRIGS_SC	triglycerol synthesis	odecoa + (0.27) pmtcoa + (0.05) stcoa + (0.1) tdcoa> coa + (0.01) triglyc SC		Glycerolipid Metabolism		
GLYK	glycerol kinase	[c] : atp + glyc> adp + glyc3p + h	EC-2.7.1.30	Glycerolipid Metabolism	YHL032C	Gut1
						(Hor2) or (
G3PT	glycerol-3-phosphatase	[c] : glyc3p + h2o> glyc + pi		Glycerolipid Metabolism	(YER062C or YIL053W)	Rhr2)
G3PDm	glycerol-3-phosphate dehydrogenase (FAD), mitochondrial	[m] : fad + glyc3p> dhap + fadh2		Glycerolipid Metabolism	YIL155C	Gut2-m
G3PD1irm	glycerol-3-phosphate dehydrogenase (NAD), mitochondrial	[m] : dhap + h + nadh> glyc3p + nad		Glycerolipid Metabolism	YOL059W	Gpd2-m
G3PD1ir	glycerol-3-phosphate dehydrogenase (NAD)	[c] : dhap + h + nadh> glyc3p + nad	EC-1.1.1.8	Glycerolipid Metabolism	YDL022W	Gpd1
						(Dak1) or (
DHAK ALCD2m	dihydroxyacetone kinase alcohol dehydrogenase (ethanol), mitochondrial	[c] : atp + dha> adp + dhap + h		Glycerolipid Metabolism	(YML070W or YFL053W) YMR083W	Dak2)
ALCD2III ALCD19y	alcohol dehydrogenase (glycerol, NADP)	[m] : etoh + nad <==> acald + h + nadh [c] : qlyald + h + nadph> qlyc + nadp	EG-1.1.1.1	Glycerolipid Metabolism Glycerolipid Metabolism	YHR104W	Adh3-m Gre3
ALCDIBY	alconol deriyarogenase (glycerol, NADF)	[c] . giyalu + II + Haupii> giyo + Haup		Glycerolipid Metabolisiii	THR 104VV	(Ses1) or (
SERTRS	Seryl-tRNA synthetase	[c] : atp + ser-L + trnaser> amp + ppi + sertrna	EC-6 1 1 11	Glycine and Serine Metabolism	(YDR023W or YHR011W)	
OLIVINO	ociyi u u v synanciase	[o] . dip + Sci E + tindSci + timp + ppi + Sci tind	EC-	Ciyonic and conne wetabolism	(1510200 01 111101100)	Dia+)
			Undetermin			(Cha1) or (
SERD_L	L-serine deaminase	[c] : ser-L> nh4 + pyr	ed	Glycine and Serine Metabolism	(YCL064C or YIL168W)	Sdl1)
PSP_L	phosphoserine phosphatase (L-serine)	[c]: h2o + pser-L> pi + ser-L	EC-3.1.3.3	Glycine and Serine Metabolism	YGR208W	Ser2
PSERT	phosphoserine transaminase	[c]: 3php + glu-L> akg + pser-L	EC-2.6.1.52	Glycine and Serine Metabolism	YOR184W	Ser1
						(Ser3) or (
PGCD	phosphoglycerate dehydrogenase	[c] : 3pg + nad> 3php + h + nadh		Glycine and Serine Metabolism	(YER081W or YIL074C)	Ser33)
HSK	homoserine kinase	[c] : atp + hom-L> adp + h + phom		Glycine and Serine Metabolism	YHR025W	Thr1
HSDyi	homoserine dehydrogenase (NADP), irreversible	[c] : aspsa + h + nadph> hom-L + nadp		Glycine and Serine Metabolism	YJR139C	Hom6
HSDxi	homoserine dehydrogenase (NADH), irreversible	[c] : aspsa + h + nadh> hom-L + nad	EC-1.1.1.3	Glycine and Serine Metabolism	YJR139C	Hom6 (Grs1) or (
GLYTRS	Glycyl-tRNA synthetase	[c] : atp + gly + trnagly> amp + glytrna + ppi	EC-6 1 1 14	Glycine and Serine Metabolism	(YBR121C or YPR081C)	Grs2)
OLI IIIO	olys): u u u v ojnulouso	[o] - orb - gry - undgry - unip - gryund - pp.	20 0	Siyomo ana comio motaconom	(15/(1210 0/ 11/(0010)	(Gcv1-m and
					(YDR019C and YMR189W	
					and YAL044C and	Gcv3-m and
GLYCLm	glycine cleavage system, mitochondrial	[m] : gly + nad + thf> co2 + mlthf + nadh + nh4	EC-2.1.2.10	Glycine and Serine Metabolism	YFL018C)	PdE3-m)
GHMT2rm	glycine hydroxymethyltransferase, reversible, mitochondrial	[m] : ser-L + thf <==> gly + h2o + mlthf		Glycine and Serine Metabolism	YBR263W	Shm1-m
GHMT2r	glycine hydroxymethyltransferase, reversible	[c] : ser-L + thf <==> gly + h2o + mlthf	EC-2.1.2.1	Glycine and Serine Metabolism	YLR058C	Shm2
						(Gcv1-m and
					(YDR019C and YMR189W	
000	about a state of a sure of a sure of a sure of the state	full distance and a selection of a selection of the	504044	Objects and Objects Mattaballians	and YAL044C and	Gcv3-m and
GCCcm	glycine-cleavage complex (lipoylprotein), mitochondrial	[m] : dhlpro + nad <==> h + lpro + nadh	EC-1.8.1.4	Glycine and Serine Metabolism	YFL018C)	PdE3-m) (Gcv1-m and
					(YDR019C and YMR189W	
					and YAL044C and	Gcv2-III and Gcv3-m and
GCCbim	glycine-cleavage complex (lipoylprotein) irreversible, mitochondrial	[m] : alpro + thf> dhlpro + mlthf + nh4	FC-2.1.2.10	Glycine and Serine Metabolism	YFL018C)	PdE3-m)
	35,000 000000000000000000000000000000000	this table and the same and			,	(Gcv1-m and
					(YDR019C and YMR189W	
					and YAL044C and	Gcv3-m and
GCCam	glycine-cleavage complex (lipoylprotein), mitochondrial	[m] : gly + h + lpro <==> alpro + co2	EC-1.4.4.2	Glycine and Serine Metabolism	YFL018C)	PdE3-m)
						(Gcv1-m and
					(YDR019C and YMR189W	
				la	and YAL044C and	Gcv3-m and
GCC2cm	glycine-cleavage complex (lipoamide), mitochondrial	[m] : dhlam + nad <==> h + lpam + nadh	EC-1.8.1.4	Glycine and Serine Metabolism	YFL018C)	PdE3-m)
					(YDR019C and YMR189W	(Gcv1-m and
					and YAL044C and	Gcv2-m and Gcv3-m and
GCC2bim	glycine-cleavage system (lipoamide) irreversible, mitochondrial	[m] : alpam + thf> dhlam + mithf + nh4	FC-2 1 2 10	Glycine and Serine Metabolism	YFL018C)	PdE3-m)
COCLONIII	g-y-sine dicarage system (iipoamide) ineversible, milloutonulidi	paga separat and a suman a man a mar	LO 2.1.2.10	5.75.116 drid Gerine MetabolisiII		(Gcv1-m and
					(YDR019C and YMR189W	
					and YAL044C and	Gcv3-m and
GCC2am	glycine-cleavage complex (lipoamide), mitochondrial	[m] : gly + h + lpam <==> alpam + co2	EC-1.4.4.2	Glycine and Serine Metabolism	YFL018C)	PdE3-m)
CYSTS	cystathionine beta-synthase	[c] : hcys-L + ser-L> cyst-L + h2o	EC-4.2.1.22	Glycine and Serine Metabolism	YGR155W	Cys4
AGT	alanine-glyoxylate transaminase	[c] : ala-L + glx <==> gly + pyr	EC-2.6.1.44	Glycine and Serine Metabolism	YFL030W	Agt1
TPI	triose-phosphate isomerase	[c] : dhap <==> g3p	EC-5.3.1.1	Glycolysis/Gluconeogenesis	YDR050C	Tpi1
50.00						(Cdc19) or (
PYK	pyruvate kinase	[c] : adp + h + pep> atp + pyr	EC-2.7.1.40	Glycolysis/Gluconeogenesis	(YAL038W or YOR347C)	Pyk2)

					(YKL152C or YDL021W	(Gpm1) or (Gpm2) or (
PGM	phosphoglycerate mutase	[c] : 2pg <==> 3pg	EC-5.4.2.1	Glycolysis/Gluconeogenesis	or YOL056W)	Gpm3)
PGK	phosphoglycerate kinase	[c] : 3pg + atp <==> 13dpg + adp	EC-2.7.2.3	Glycolysis/Gluconeogenesis	YCR012W	Pgk1
PGI	glucose-6-phosphate isomerase	[c] : g6p <==> f6p	EC-5.3.1.9	Glycolysis/Gluconeogenesis	YBR196C	Pgi1
					(YGR240C and YMR205C	Ĭ
PFK_3	phosphofructokinase, rxn3	[c] : atp + s7p> adp + h + s17bp	EC-2.7.1.11	Glycolysis/Gluconeogenesis)	Pfk
					(YGR240C and YMR205C	
PFK_2	Phosphofructokinase	[c] : atp + tag6p-D> adp + h + tagdp-D	EC-2.7.1.11	Glycolysis/Gluconeogenesis) ()()() () () () () () () ()	Pfk
PFK	phosphofructokinase	[c] : atp + f6p> adp + fdp + h	EC-2 7 1 11	Glycolysis/Gluconeogenesis	(YGR240C and YMR205C	Pfk
FFK	priosprioriuctokinase	[c] . atp + 10p> aup + 1up + 11	EC-2.7.1.11	Glycolysis/Glucolleogerlesis	,	FIK
					((YBR221C and	(PdE1-m and
					YER178W) and YNL071W	PdE2-m and
PDHm	pyruvate dehydrogenase, mitochondrial	[m]: coa + nad + pyr> accoa + co2 + nadh	EC-1.2.4.1	Glycolysis/Gluconeogenesis	and YFL018C)	PdE3-m)
						(Kgd1-m and
					(YIL125W and YDR148C	Kgd2-m and
PDHcm	pyruvate dehydrogenase (dihydrolipoamide dehydrogenase), mitochondrial	[m] : dhlam + nad> h + lpam + nadh	EC-1.8.1.4	Glycolysis/Gluconeogenesis	and YFL018C)	PdE3-m) (Hxk1) or (
HEX7	hexokinase (D-fructose:ATP)	[c] : atp + fru> adp + f6p + h	EC-2.7.1.1	Glycolysis/Gluconeogenesis	(YFR053C or YGL253W)	Hxk2)
TIEX	nexolande (Bildeloses (Til)	loj. alp + na - z dap + lop + n	20 2.7.1.1	Ciycolysis/Ciucolicogenesis	(11110000 01 10220011)	(Hxk1) or (
HEX4	hexokinase (D-mannose:ATP)	[c] : atp + man> adp + h + man6p	EC-2.7.1.1	Glycolysis/Gluconeogenesis	(YFR053C or YGL253W)	Hxk2)
		L'A CT C C C C C C C C C C C C C C C C C C		. , ,	,	(Hxk1) or (
					(YFR053C or YGL253W	Hxk2) or (
HEX1	hexokinase (D-glucose:ATP)	[c] : atp + glc-D> adp + g6p + h	EC-2.7.1.1	Glycolysis/Gluconeogenesis	or YCL040W)	Glk1)
GLUK	Glucokinase	[c] : atp + glc-D> adp + g6p-B + h		Glycolysis/Gluconeogenesis	YCL040W	Glk1
						(Tdh1) or (
				1	(YJL052W or YJR009C or	Tdh2) or (
GAPD	glyceraldehyde-3-phosphate dehydrogenase	[c]: g3p + nad + pi <==> 13dpg + h + nadh	EC-1.2.1.12	Glycolysis/Gluconeogenesis	YGR192C)	Tdh3)
G6PI2	Glucose-6-phosphate isomerase	[c] : g6p-B <==> f6p-B	EC-5.3.1.9	Glycolysis/Gluconeogenesis	YBR196C	Pgi1
G6PI	Glucose-6-phosphate isomerase	[c] : g6p <==> g6p-B	EC-5.3.1.9	Glycolysis/Gluconeogenesis	YBR196C	Pgi1
-BA3	Sedoheptulose 1,7-bisphosphate D-glyceraldehyde-3-phosphate-lyase	[c]: s17bp <==> dhap + e4p	EC-4.1.2.13	Glycolysis/Gluconeogenesis	YKL060C	Fba1
BA2	D-Fructose 1-phosphate D-glyceraldehyde-3-phosphate-lyase	[c]: f1p <==> dhap + glyald	EC-4.1.2.13	Glycolysis/Gluconeogenesis	YKL060C	Fba1
FBA	fructose-bisphosphate aldolase	[c] : fdp <==> dhap + g3p	EC-4.1.2.13	Glycolysis/Gluconeogenesis	YKL060C	Fba1
						(Err2) or (
						Eno1) or (
					(YPL281C or YGR254W	Eno2) or (
					or YHR174W or	Err1) or (Err
ENO	enolase	[c] : 2pg <==> h2o + pep	EC-4.2.1.11	Glycolysis/Gluconeogenesis	YOR393W or YMR323W))
DPGM	Diphosphoglyceromutase	[c] : 13dpg <==> 23dpg + h		Glycolysis/Gluconeogenesis	YKL152C	Gpm1
G16MTg	Glycolipid 1,6-alpha-D-mannosyltransferase, Golgi apparatus	[g] : gdpmann + m1macchitppdol> gdp + h + m2macchitppdol		Glycoprotein Metabolism		
G13MTg	Glycolipid 1,3-alpha-D-mannosyltransferase, Golgi apparatus	[g] : gdpmann + macchitppdol> gdp + h + m1macchitppdol	EC-	Glycoprotein Metabolism		
OAOMTO			EC-	Characteris Mathelian	(YDR483W or YOR099W or YKR061W or YBR205W or YBR199W or YNL029C	Ktr1-g) or (Ktr2-g) or (Ktr3-g) or (Ktr4-g) or (Ktr5-g) or (Ktr6-g) or (
G12MT2g	Glycolipid 1,2-alpha-D-mannosyltransferase, Golgi apparatus	[g] : gdpmann + m3macchitppdol> gdp + h + m4macchitppdol	EC- 2.4.1.131	Glycoprotein Metabolism	or YKR061W or YBR205W or YBR199W or YNL029C	Ktr2-g) or (Ktr3-g) or (Ktr4-g) or (Ktr5-g) or (Ktr6-g) or (Yur1-g)
G12MT1g	Glycolipid 1,2-alpha-D-mannosyltransferase, Golgi apparatus Glycolipid 1,2-alpha-D-mannosyltransferase, Golgi apparatus Dolichyl-phosphate D-mannosyltransferase	[g] : gdpmann + m3macchitppdol> gdp + h + m4macchitppdol [g] : gdpmann + m2macchitppdol> gdp + h + m3macchitppdol dolp[c] + gdpmann[c]> dolmanp[r] + gdp[c]	2.4.1.131 EC- 2.4.1.131	Glycoprotein Metabolism Glycoprotein Metabolism Glycoprotein Metabolism	or YKR061W or YBR205W or YBR199W or YNL029C or YPL053C or YJL139C)	Ktr2-g) or (Ktr3-g) or (Ktr4-g) or (Ktr5-g) or (Ktr6-g) or (Yur1-g) (Kre2-g) or (Ktr1-g) or (Ktr1-g) or (Ktr2-g) or (Ktr2-g) or (Ktr3-g) or (Ktr4-g) or (
G12MT2g G12MT1g DOLPMTcer DOLPMMer DOLK	Glycolipid 1,2-alpha-D-mannosyltransferase, Golgi apparatus Dolichyl-phosphate D-mannosyltransferase Dolichyl-phosphate-mannose-protein mannosyltransferase, endoplasmic reticular	[g] : gdpmann + m2macchitppdol> gdp + h + m3macchitppdol dolp[c] + gdpmann[c]> dolmanp[r] + gdp[c] [r] : dolmanp> dolp + h + mannan	EC- 2.4.1.131 EC-2.4.1.83	Glycoprotein Metabolism Glycoprotein Metabolism Glycoprotein Metabolism	or YKR061W or YBR205W or YBR199W or YNL029C or YPL053C or YJL139C) (YDR483W or YOR099W or YKR061W or YBR205W or YBR199W or YNL029C or YPL053C or YJL139C) YPR183W ((YDL095W and YAL023C) or YJR143C or YDL093W or YJR143C or YJC193W or YJR143C or YDL093W or YGR199W)	ktr2-g) or (ktr3-g) or (ktr4-g) or (ktr5-g) or (ktr6-g) or (ktr6-g) or (ktr6-g) or (ktr1-g) or (ktr1-g) or (ktr2-g) or (ktr2-g) or (ktr3-g) or (ktr4-g) or (ktr4-g) or (ktr4-g) or (ktr4-g) or (ktr6-g) or (kt
G12MT1g DOLPMTcer DOLPMMer DOLK	Glycolipid 1,2-alpha-D-mannosyltransferase, Golgi apparatus Dolichyl-phosphate D-mannosyltransferase Dolichyl-phosphate-mannose-protein mannosyltransferase, endoplasmic reticular Dolichol kinase	[g] : gdpmann + m2macchitppdol> gdp + h + m3macchitppdol dolp[c] + gdpmann[c]> dolmanp[r] + gdp[c] [r] : dolmanp> dolp + h + mannan [c] : ctp + dolichol> cdp + dolp + h	EC- 2.4.1.131 EC-2.4.1.83 EC- 2.4.1.109 EC-	Glycoprotein Metabolism Glycoprotein Metabolism Glycoprotein Metabolism Glycoprotein Metabolism	or YKR061W or YBR205W or YBR199W or YNL029C or YPL053C or YJL139C) (YDR483W or YOR099W or YKR061W or YBR205W or YBR199W or YNL029C or YPL053C or YJL139C) YPR183W ((YDL095W and YAL023C) or YOR321W or YJR143C or YJL093W or YJR143C or YJR143C or YJR143C or YJR143C or YJR143C or YJR143C or YJR199W) YMR013C	ktr2-g) or (ktr3-g) or (ktr4-g) or (ktr4-g) or (ktr5-g) or (ktr5-g) or (ktr6-g) or (ktr1-g) or (ktr1-g) or (ktr2-g) or (ktr3-g) or (ktr3-g) or (ktr3-g) or (ktr3-g) or (ktr4-g) or (ktr4-g) or (ktr4-g) or (ktr4-g) or (ktr5-g) or (ktr5-g) or (ktr6-g) or (yur1-g) Dpm1 (Pmt1-er and Pmt2-er) or (Pmt3-er) or (Pmt4-er) or (Pmt5-er) or (Pmt5-er) or (Pmt6-er) or (Pmt6-er) or (Pmt6-er) or (Pmt6-er) Sec59
G12MT1g DOLPMTcer DOLPMMer DOLK	Glycolipid 1,2-alpha-D-mannosyltransferase, Golgi apparatus Dolichyl-phosphate D-mannosyltransferase Dolichyl-phosphate-mannose-protein mannosyltransferase, endoplasmic reticular	[g] : gdpmann + m2macchitppdol> gdp + h + m3macchitppdol dolp[c] + gdpmann[c]> dolmanp[r] + gdp[c] [r] : dolmanp> dolp + h + mannan	EC- 2.4.1.131 EC-2.4.1.83	Glycoprotein Metabolism Glycoprotein Metabolism Glycoprotein Metabolism Glycoprotein Metabolism	or YKR061W or YBR205W or YBR199W or YNL029C or YPL053C or YJL139C) (YDR483W or YOR099W or YKR061W or YBR205W or YBR199W or YNL029C or YPL053C or YJL139C) YPR183W ((YDL095W and YAL023C) or YJR143C or YDL093W or YJR143C or YJC193W or YJR143C or YDL093W or YGR199W)	ktr2-g) or (ktr3-g) or (ktr4-g) or (ktr4-g) or (ktr5-g) or (ktr5-g) or (ktr6-g) or (ktr1-g) or (ktr1-g) or (ktr2-g) or (ktr2-g) or (ktr2-g) or (ktr3-g) or (ktr3-g) or (ktr4-g) or (ktr6-g) or (kt
G12MT1g DOLPMTcer DOLPMMer	Glycolipid 1,2-alpha-D-mannosyltransferase, Golgi apparatus Dolichyl-phosphate D-mannosyltransferase Dolichyl-phosphate-mannose—protein mannosyltransferase, endoplasmic reticular Dolichol kinase Ureidoglycolate hydrolase	[g] : gdpmann + m2macchitppdol> gdp + h + m3macchitppdol dolp[c] + gdpmann[c]> dolmanp[r] + gdp[c] [r] : dolmanp> dolp + h + mannan [c] : ctp + dolichol> cdp + dolp + h	EC- 2.4.1.131 EC-2.4.1.83 EC- 2.4.1.109 EC-	Glycoprotein Metabolism Glycoprotein Metabolism Glycoprotein Metabolism Glycoprotein Metabolism	or YKR061W or YBR205W or YBR199W or YNL029C or YPL053C or YJL139C) (YDR483W or YOR099W or YKR061W or YBR205W or YBR199W or YNL029C or YPL053C or YJL139C) YPR183W ((YDL095W and YAL023C) or YOR321W or YJR143C or YJL093W or YJR143C or YJR143C or YJR143C or YJR143C or YJR143C or YJR143C or YJR199W) YMR013C	ktr2-g) or (ktr3-g) or (ktr4-g) or (ktr4-g) or (ktr5-g) or (ktr5-g) or (ktr6-g) or (ktr1-g) or (ktr1-g) or (ktr2-g) or (ktr3-g) or (ktr3-g) or (ktr3-g) or (ktr3-g) or (ktr4-g) or (ktr4-g) or (ktr4-g) or (ktr4-g) or (ktr5-g) or (ktr5-g) or (ktr6-g) or (yur1-g) Dpm1 (Pmt1-er and Pmt2-er) or (Pmt3-er) or (Pmt4-er) or (Pmt5-er) or (Pmt5-er) or (Pmt6-er) or (Pmt6-er) or (Pmt6-er) or (Pmt6-er) Sec59
G12MT1g DOLPMTcer DOLPMMer DOLK UGLYCHr	Glycolipid 1,2-alpha-D-mannosyltransferase, Golgi apparatus Dolichyl-phosphate D-mannosyltransferase Dolichyl-phosphate-mannose—protein mannosyltransferase, endoplasmic reticular Dolichol kinase Ureidoglycolate hydrolase phosphoribosylpyrophosphate synthetase 1-(5-phosphoribosyl)-5-{(6-phosphoribosylamino)methylideneamino)imidazole-4-	[g]: gdpmann + m2macchitppdol> gdp + h + m3macchitppdol dolp[c] + gdpmann[c]> dolmanp[r] + gdp[c] [r]: dolmanp> dolp + h + mannan [c]: ctp + dolichol> cdp + dolp + h [c]: (2) h + h2o + urdglyc <==> co2 + glx + (2) nh4 [c]: atp + r5p <==> amp + h + prpp	EC- 2.4.1.131 EC-2.4.1.83 EC- 2.4.1.109 EC- EC-3.5.3.19	Glycoprotein Metabolism Glycoprotein Metabolism Glycoprotein Metabolism Glycoprotein Metabolism Histidine Metabolism Histidine Metabolism	or YKR061W or YBR205W or YBR199W or YNL029C or YPL053C or YJL139C) (YDR483W or YOR099W or YKR061W or YBR205W or YBR205W or YBR205W or YBR199W or YNL029C or YPL053C or YJL139C) YPR183W ((YDL095W and YAL023C) or YOR321W or YJR143C or YDL093W or YJR143C or YDL093W or YGR199W) YMR013C (YOL061W or YBL068W or YER099C or YHL011C or YKL181W)	Ktr2-g) or (Ktr3-g) or (Ktr3-g) or (Ktr4-g) or (Ktr4-g) or (Ktr5-g) or (Ktr5-g) or (Ktr1-g) or (Ktr1-g) or (Ktr2-g) or (Ktr3-g) or (Ktr4-g) or (Ktr4-g) or (Ktr4-g) or (Ktr4-g) or (Ktr3-g) or (Ktr5-g) or (Ftr5-g) or (Pmt3-er) or (Pmt3-er) or (Pmt4-er) or (Pmt5-er) or (Pmt5-er) or (Pmt6-er) Sec59 Dai3 (Prs5) or (Prs4) or (Prs2) or (Prs3) or (Prs3) or (Prs1)
G12MT1g DOLPMTcer DOLPMMer DOLK UGLYCHr PRPPS	Glycolipid 1,2-alpha-D-mannosyltransferase, Golgi apparatus Dolichyl-phosphate D-mannosyltransferase Dolichyl-phosphate-mannose—protein mannosyltransferase, endoplasmic reticular Dolichol kinase Ureidoglycolate hydrolase phosphoribosylpyrophosphate synthetase 1-(5-phosphoribosyl)-5-{(5-phosphoribosylamino)methylideneamino)imidazole-4 carboxamide isomerase (irreversible)	[g] : gdpmann + m2macchitppdol> gdp + h + m3macchitppdol dolp[c] + gdpmann[c]> dolmanp[r] + gdp[c] [r] : dolmanp> dolp + h + mannan [c] : ctp + dolichol> cdp + dolp + h [c] : (2) h + h2o + urdglyc <==> co2 + glx + (2) nh4 [c] : atp + r5p <==> amp + h + prpp [c] : prfp> prlp	EC- 2.4.1.131 EC-2.4.1.83 EC- 2.4.1.109 EC- EC- EC-3.5.3.19	Glycoprotein Metabolism Glycoprotein Metabolism Glycoprotein Metabolism Glycoprotein Metabolism Histidine Metabolism Histidine Metabolism Histidine Metabolism	or YKR061W or YBR205W or YBR199W or YNL029C or YPL053C or YJL139C) (YDR483W or YOR099W or YKR061W or YBR205W or YBR205W or YNL029C or YPL053C or YJL139C) (YDL095W and YAL023C) or YOR321W or YOR199W) YMR013C (YDL095W and YAL023C) (YOL061W or YDL093W or YGR199W) YMR013C (YOL061W or YBL068W or YER099C or YHL011C or YKL181W)	ktr2-g) or (ktr3-g) or (ktr3-g) or (ktr4-g) or (ktr5-g) or (ktr5-g) or (ktr5-g) or (ktr1-g) or (ktr2-g) or (ktr3-g) or (pm13-er) or (p
G12MT1g DOLPMTcer DOLPMMer DOLK JGLYCHr PRPPS PRMICII PRATPP	Glycolipid 1,2-alpha-D-mannosyltransferase, Golgi apparatus Dolichyl-phosphate D-mannosyltransferase Dolichyl-phosphate-mannose—protein mannosyltransferase, endoplasmic reticular Dolichol kinase Ureidoglycolate hydrolase phosphoribosylpyrophosphate synthetase 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino)imidazole-4-carboxamide isomerase (irreversible) phosphoribosyl-ATP pyrophosphatase	[g] : gdpmann + m2macchitppdol> gdp + h + m3macchitppdol dolp[c] + gdpmann[c]> dolmanp[r] + gdp[c] [r] : dolmanp> dolp + h + mannan [c] : ctp + dolichol> cdp + dolp + h [c] : (2) h + h2o + urdglyc <==> co2 + glx + (2) nh4 [c] : atp + r5p <==> amp + h + prpp [c] : prfp> prlp [c] : h2o + prbatp> h + ppl + prbamp	EC- 2.4.1.131 EC-2.4.1.83 EC- 2.4.1.109 EC- EC-3.5.3.19 EC-2.7.6.1	Glycoprotein Metabolism Glycoprotein Metabolism Glycoprotein Metabolism Glycoprotein Metabolism Histidine Metabolism Histidine Metabolism Histidine Metabolism Histidine Metabolism Histidine Metabolism Histidine Metabolism	or YKR061W or YBR205W or YBR199W or YNL029C or YPL053C or YJL139C) (YDR483W or YOR099W or YKR061W or YBR205W or YBR199W or YNL029C or YPL053C or YJL139C) YPR183W ((YDL095W and YAL023C) or YOR321W or YJR143C or YDL093W or YJR032C (YOL061W or YBL068W or YER099C or YHL011C or YKL181W) YIL020C YCL030C	ktr2-g) or (ktr3-g) or (ktr4-g) or (ktr4-g) or (ktr4-g) or (ktr5-g) or (ktr5-g) or (ktr5-g) or (ktr1-g) or (ktr2-g) or (ktr2-g) or (ktr2-g) or (ktr2-g) or (ktr3-g) or (ktr3-g) or (ktr3-g) or (ktr4-g) or (ktr4-g) or (ktr4-g) or (ktr4-g) or (pr4-g) or (pm4-er) or (pm5-er) or (pr6-g) or (pr8-g) or (pr8-
G12MT1g DOLPMTcer DOLPMMer DOLK JGLYCHr PRPPS PRMICII PRATPP PRAMPC	Glycolipid 1,2-alpha-D-mannosyltransferase, Golgi apparatus Dolichyl-phosphate D-mannosyltransferase Dolichyl-phosphate-mannose—protein mannosyltransferase, endoplasmic reticular Dolichol kinase Ureidoglycolate hydrolase phosphoribosylpyrophosphate synthetase 1-(6-phosphoribosyl)-5-[(6-phosphoribosylamino)methylideneamino)imidazole-4-carboxamide isomerase (irreversible) phosphoribosyl-ATP pyrophosphatase phosphoribosyl-ATP cyclohydrolase	[g]: gdpmann + m2macchitppdol> gdp + h + m3macchitppdol dolp[c] + gdpmann[c]> dolmanp[r] + gdp[c] [r]: dolmanp> dolp + h + mannan [c]: ctp + dolichol> cdp + dolp + h [c]: (2) h + h2o + urdglyc <==> co2 + glx + (2) nh4 [c]: atp + r5p <==> amp + h + prpp [c]: prfp> prlp [c]: h2o + prbartp> h + ppi + prbamp [c]: h2o + prbartp> prfp	EC- 2.4.1.131 EC-2.4.1.83 EC-2.4.1.83 EC- 2.4.1.109 EC- EC-3.5.3.19 EC-3.5.3.19	Giycoprotein Metabolism Giycoprotein Metabolism Giycoprotein Metabolism Giycoprotein Metabolism Histidine Metabolism Histidine Metabolism Histidine Metabolism Histidine Metabolism	or YKR061W or YBR205W or YBR199W or YNL029C or YPL053C or YJL139C) (YDR483W or YOR099W or YKR061W or YBR205W or YBR199W or YNL029C or YPL053C or YJL139C) YPR183W ((YDL095W and YAL023C)) or YOR321W or YJR143C or YDL093W or YGR199W YMR013C (YOL061W or YBL068W or YER099C or YHL011C or YKL181W) YIL020C YCL030C YCL030C	ktr2-g) or (ktr3-g) or (ktr4-g) or (ktr4-g) or (ktr4-g) or (ktr5-g) or (ktr5-g) or (ktr1-g) or (ktr2-g) or (ktr3-g) or (ktr3-g) or (ktr4-g) or (ktr3-g) or (ktr3-g) or (ktr3-g) or (ktr5-g) or (ktr5-g) or (ktr5-g) or (Pmt3-er) or (Pmt3-er) or (Pmt4-er) or (Pmt4-er) or (Pmt5-er) or (Pmt5-er) or (Prs4) or (Prs2) or (Prs3) or (Prs3) or (Prs3) or (Prs3) or (Prs1)
G12MT1g DOLPMTcer DOLPMMer DOLK JGLYCHr PRPPS PRMICII PRATPP PRAMPC	Glycolipid 1,2-alpha-D-mannosyltransferase, Golgi apparatus Dolichyl-phosphate D-mannosyltransferase Dolichyl-phosphate-mannose—protein mannosyltransferase, endoplasmic reticular Dolichol kinase Ureidoglycolate hydrolase phosphoribosylpyrophosphate synthetase 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino)imidazole-4-carboxamide isomerase (irreversible) phosphoribosyl-ATP pyrophosphatase	[g] : gdpmann + m2macchitppdol> gdp + h + m3macchitppdol dolp[c] + gdpmann[c]> dolmanp[r] + gdp[c] [r] : dolmanp> dolp + h + mannan [c] : ctp + dolichol> cdp + dolp + h [c] : (2) h + h2o + urdglyc <==> co2 + glx + (2) nh4 [c] : atp + r5p <==> amp + h + prpp [c] : prfp> prlp [c] : h2o + prbatp> h + ppl + prbamp	EC- 2.4.1.131 EC-2.4.1.83 EC-2.4.1.83 EC- 2.4.1.109 EC- EC-3.5.3.19 EC-3.5.3.19	Glycoprotein Metabolism Glycoprotein Metabolism Glycoprotein Metabolism Glycoprotein Metabolism Histidine Metabolism Histidine Metabolism Histidine Metabolism Histidine Metabolism Histidine Metabolism Histidine Metabolism	or YKR061W or YBR205W or YBR199W or YNL029C or YPL053C or YJL139C) (YDR483W or YOR099W or YKR061W or YBR205W or YBR199W or YNL029C or YPL053C or YJL139C) YPR183W ((YDL095W and YAL023C) or YOR321W or YJR143C or YDL093W or YJR032C (YOL061W or YBL068W or YER099C or YHL011C or YKL181W) YIL020C YCL030C	ktr2-g) or (ktr3-g) or (ktr4-g) or (ktr4-g) or (ktr4-g) or (ktr5-g) or (ktr5-g) or (ktr1-g) or (ktr2-g) or (ktr2-g) or (ktr2-g) or (ktr2-g) or (ktr3-g) or (ktr3-g) or (ktr3-g) or (ktr4-g) or (ktr5-g) or (ktr5-g) or (pm11-er and pm12-er) or (pm14-er) or (pm15-er) or (pm15-er) or (pm15-er) or (pr15-g) or (p
G12MT1g DOLPMTcer DOLPMMer DOLK JGLYCHr PRPPS PRMICII PRATPP PRAMPC GPDH	Glycolipid 1,2-alpha-D-mannosyltransferase, Golgi apparatus Dolichyl-phosphate D-mannosyltransferase Dolichyl-phosphate-mannose—protein mannosyltransferase, endoplasmic reticular Dolichol kinase Ureidoglycolate hydrolase phosphoribosylpyrophosphate synthetase 1-(6-phosphoribosyl)-5-[(6-phosphoribosylamino)methylideneamino)imidazole-4-carboxamide isomerase (irreversible) phosphoribosyl-ATP pyrophosphatase phosphoribosyl-ATP cyclohydrolase	[g]: gdpmann + m2macchitppdol> gdp + h + m3macchitppdol dolp[c] + gdpmann[c]> dolmanp[r] + gdp[c] [r]: dolmanp> dolp + h + mannan [c]: ctp + dolichol> cdp + dolp + h [c]: (2) h + h2o + urdglyc <==> co2 + glx + (2) nh4 [c]: atp + r5p <==> amp + h + prpp [c]: prfp> prlp [c]: h2o + prbartp> h + ppi + prbamp [c]: h2o + prbartp> prfp	EC- 2.4.1.131 EC-2.4.1.83 EC-2.4.1.83 EC- 2.4.1.109 EC- EC-3.5.3.19 EC-3.5.3.19	Giycoprotein Metabolism Giycoprotein Metabolism Giycoprotein Metabolism Giycoprotein Metabolism Histidine Metabolism Histidine Metabolism Histidine Metabolism Histidine Metabolism	or YKR061W or YBR205W or YBR199W or YNL029C or YPL053C or YJL139C) (YDR483W or YOR099W or YKR061W or YBR205W or YBR199W or YNL029C or YPL053C or YJL139C) YPR183W ((YDL095W and YAL023C)) or YOR321W or YJR143C or YDL093W or YGR199W YMR013C (YOL061W or YBL068W or YER099C or YHL011C or YKL181W) YIL020C YCL030C YCL030C	Ktr2-g) or (Ktr3-g) or (Ktr3-g) or (Ktr4-g) or (Ktr4-g) or (Ktr5-g) or (Ktr5-g) or (Ktr2-g) or (Ktr2-g) or (Ktr2-g) or (Ktr2-g) or (Ktr3-g) or (Ktr3-g) or (Ktr3-g) or (Ktr3-g) or (Ktr4-g) or (Ktr4-g) or (Ktr4-g) or (Ktr3-g) or (Ktr3-g) or (Ktr3-g) or (Ktr3-g) or (Ktr5-g) or (Ftr5-g) or (Fmt3-er) or (Fmt3-er) or (Fmt5-er) or (Fmt6-er) Sec59 Dal3 (Frs5) or (Frs4) or (Frs2) or (Frs3) or (Frs3) or (Frs3) or (Frs3) or (Frs1) His6
G12MT1g DOLPMTcer DOLPMMer DOLK JGLYCHr PRPPS PRMICII PRATPP PRAMPC GPDH G3PS	Glycolipid 1,2-alpha-D-mannosyltransferase, Golgi apparatus Dolichyl-phosphate D-mannosyltransferase Dolichyl-phosphate-mannose—protein mannosyltransferase, endoplasmic reticular Dolichol kinase Ureidoglycolate hydrolase phosphoribosylpyrophosphate synthetase 1-(5-phosphoribosyl-)-5-[(5-phosphoribosylamino)methylideneamino)imidazole-4-carboxamide isomerase (irreversible) phosphoribosyl-AMP cyclohydrolase phosphoribosyl-AMP cyclohydrolase imidazole-glycerol-phosphate dehydratase Imidazole-glycerol-phosphates	[g]: gdpmann + m2macchitppdol> gdp + h + m3macchitppdol dolp[c] + gdpmann[c]> dolmanp[r] + gdp[c] [r]: dolmanp> dolp + h + mannan [c]: ctp + dolichol> cdp + dolp + h [c]: (2) h + h2o + urdglyc <==> co2 + glx + (2) nh4 [c]: atp + r5p <==> amp + h + prpp [c]: h2o + prbatp> h + ppi + prbamp [c]: h2o + prbamp> prfp [c]: ih2o + prbamp> prfp [c]: elig3p> h2o + imacp [c]: glnL+ rpfp> aicar + elig3p + glu-L + h	EC- 2.4.1.131 EC-2.4.1.131 EC-2.4.1.83 EC- 2.4.1.109 EC- EC-3.5.3.19 EC-3.5.3.19 EC-3.6.1.31 EC-3.6.1.31 EC-3.6.1.31 EC-3.6.1.31	Glycoprotein Metabolism Glycoprotein Metabolism Glycoprotein Metabolism Glycoprotein Metabolism Glycoprotein Metabolism Histidine Metabolism Histidine Metabolism Histidine Metabolism Histidine Metabolism Histidine Metabolism Histidine Metabolism	or YKR061W or YBR205W or YBR199W or YNL029C or YPL053C or YJL139C) (YDR483W or YOR099W or YKR061W or YBR205W or YBR205W or YNL029C or YPL053C or YJL139C) (YDL095W and YAL023C) or YOR321W or YGR199W) YMR013C (YDL095W and YAL023C) (YOL061W or YDL093W or YGR199W) YMR013C (YOL061W or YBL068W or YER099C or YHL011C or YKL181W) YIL020C YCL030C YCL030C YCL030C YCR202W	ktr2-g) or (ktr3-g) or (ktr3-g) or (ktr4-g) or (ktr4-g) or (ktr5-g) or (ktr5-g) or (ktr1-g) or (ktr2-g) or (ktr3-g) or (ktr3-g) or (ktr3-g) or (ktr3-g) or (ktr4-g) or (pm1-er or (pm1-er or (pm4-er) or (pm4-er) or (pm5-er) or (pm5-er) or (prs4-) or (prs5-) or (prs3-) or (prs3-) or (prs1-) his6 his4 his4 his4
G12MT1g DOLPMTcer DOLPMMer DOLK UGLYCHr PRPPS PRMICII PRATPP PRAMPC IGPDH IGG3PS HSTPT	Glycolipid 1,2-alpha-D-mannosyltransferase, Golgi apparatus Dolichyl-phosphate D-mannosyltransferase Dolichyl-phosphate-mannose—protein mannosyltransferase, endoplasmic reticular Dolichol kinase Ureidoglycolate hydrolase phosphoribosylpyrophosphate synthetase 1-(5-phosphoribosyl)-5-{(5-phosphoribosylamino)methylideneamino)imidazole-4 carboxamide isomerase (irreversible) phosphoribosyl-ATP pyrophosphatase phosphoribosyl-AMP cyclohydrolase imidazoleglycerol-phosphate dehydratase	[g] : gdpmann + m2macchitppdol> gdp + h + m3macchitppdol dolp[c] + gdpmann[c]> dolmanp[r] + gdp[c] [r] : dolmanp> dolp + h + mannan [c] : ctp + dolichol> cdp + dolp + h [c] : (2) h + h2o + urdglyc <==> co2 + glx + (2) nh4 [c] : atp + r5p <==> amp + h + prpp [c] : h2o + prbatp> h + ppi + prbamp [c] : h2o + prbamp> prfp [c] : l2o + prbamp> prfp	EC-2.4.1.131 EC-2.4.1.131 EC-2.4.1.83 EC-2.4.1.109 EC- EC-3.5.3.19 EC-3.5.3.19 EC-3.5.3.19 EC-4.2.1.19 EC-4.2.1.19 EC-2.6.1.9	Glycoprotein Metabolism Glycoprotein Metabolism Glycoprotein Metabolism Glycoprotein Metabolism Histidine Metabolism Histidine Metabolism Histidine Metabolism Histidine Metabolism Histidine Metabolism Histidine Metabolism	or YKR061W or YBR205W or YBR199W or YBR199W or YNL029C or YPL053C or YJL139C) (YDR483W or YOR099W or YKR061W or YBR205W or YBR205W or YBR199W or YNL029C or YPL053C or YJL139C) (YDL095W and YAL023C) or YOR321W or YJR143C or YDL093W or YGR199W) YMR013C (YOL061W or YBL068W or YER099C or YHL011C or YKL181W) YIL020C YCL030C YCL030C YCL030C YOR202W YBR248C	ktr2-g) or (ktr3-g) or (ktr4-g) or (ktr4-g) or (ktr4-g) or (ktr5-g) or (ktr5-g) or (ktr5-g) or (ktr1-g) or (ktr2-g) or (ktr2-g) or (ktr2-g) or (ktr2-g) or (ktr3-g) or (ktr3-g) or (ktr3-g) or (ktr4-g) or (ktr4-g) or (ktr4-g) or (ktr4-g) or (pm1-er and pm12-er) or (pm15-er) or (pm4-er) or (pm5-er) or (pm5-er) or (pm5-er) or (pr84) or (pr84) or (pr85) or (pr87) or (pr81) or (pr83) or (pr81) or (pr81) or (pr83) or (pr81) or (p
G12MT1g DOLPMTcer DOLPMMer DOLK UGLYCHr PRPPS PRMICII PRATPP PRAMPC	Glycolipid 1,2-alpha-D-mannosyltransferase, Golgi apparatus Dolichyl-phosphate D-mannosyltransferase Dolichyl-phosphate-mannose—protein mannosyltransferase, endoplasmic reticular Dolichol kinase Ureidoglycolate hydrolase phosphoribosylpyrophosphate synthetase 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino)imidazole-4 carboxamide isomerase (irreversible) phosphoribosyl-ATP pyrophosphatase phosphoribosyl-ATP pyrophosphatase phosphoribosyl-ATP pyrophosphatase phosphoribosyl-ATP pyrophosphatase imidazoleglycerol-phosphate dehydratase Imidazoleglycerol-3-phosphate synthase limidazoleglycerol-3-phosphate synthase limidazole-phosphate transaminase	[g]: gdpmann + m2macchitppdol> gdp + h + m3macchitppdol dolp[c] + gdpmann[c]> dolmanp[r] + gdp[c] [r]: dolmanp> dolp + h + mannan [c]: ctp + dolichol> cdp + dolp + h [c]: (2) h + h2o + urdglyc <==> co2 + glx + (2) nh4 [c]: atp + r5p <==> amp + h + prpp [c]: prfp> prlp [c]: h2o + prbatp> h + ppi + prbamp [c]: h2o + prbamp> prfp [c]: eig3p> h2o + imacp [c]: gln-L + prlp> aicar + eig3p + glu-L + h [c]: gln-L + prlp> aicar + eig3p + gln-L + h [c]: gln-L + prlp> aicar + eig3p + gln-L + h [c]: gln-L + prlp> aicar + eig3p + gln-L + h [c]: gln-L + prlp> aicar + eig3p + gln-L + h [c]: gln-L + prlp> aicar + eig3p + gln-L + h [c]: gln-L + prlp> aicar + eig3p + gln-L + h [c]: gln-L + prlp> aicar + eig3p + gln-L + h [c]: gln-L + prlp> aicar + eig3p + gln-L + h [c]: gln-L + prlp> aicar + eig3p + gln-L + h [c]: gln-L + prlp> aicar + eig3p + gln-L + h [c]: gln-L + prlp> aicar + eig3p + gln-L + h [c]: gln-L + prlp> aicar + eig3	EC- 2.4.1.131 EC-2.4.1.83 EC-2.4.1.83 EC-2.4.1.109 EC- EC-3.5.3.19 EC-3.5.3.19 EC-3.5.3.16 EC-3.6.1.31 EC-3.6.1.31 EC-3.6.1.31 EC-3.6.1.31 EC-3.6.1.9	Glycoprotein Metabolism Glycoprotein Metabolism Glycoprotein Metabolism Glycoprotein Metabolism Glycoprotein Metabolism Histidine Metabolism	or YKR061W or YBR205W or YBR199W or YNL029C or YPL053C or YJL139C) (YDR483W or YOR099W or YKR061W or YBR205W or YBR199W or YNL029C or YPL053C or YJL139C) YPR183W ((YDL095W and YAL023C)) or YOR321W or YJR143C or YJL139C) YMR013C (YOL061W or YBL068W or YER099C or YHL011C or YKL181W) YIL020C YCL030C YCL030C YCR0202W YBR248C YIL116W	Ktr2-g) or (Ktr3-g) or (Ktr4-g) or (Ktr4-g) or (Ktr4-g) or (Ktr5-g) or (Ktr5-g) or (Ktr2-g) or (Ktr3-g) or (Ktr3-g) or (Ktr4-g) or (Ktr3-g) or (Ktr3-g) or (Ktr5-g) or (Ftr4-g) or (Fr4-g) or (Fr5-g)

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HISTD	histidinol dehydrogenase	[c]: h2o + histd + (2) nad> (3) h + his-L + (2) nadh		Histidine Metabolism	YCL030C	His4
ATPPRT	ATP phosphoribosyltransferase	[c] : atp + prpp> ppi + prbatp	EC-2.4.2.17	Histidine Metabolism	YER055C	His1
ARMT	hnRNP arginine N-methyltransferase	[c] : amet + his-L> NPmehis + ahcys + h		Histidine Metabolism	YBR034C	Hmt1
ALLTNr	allantoinase, reversible reaction	[c] : alltn + h2o <==> alltt + h	EC-3.5.2.5	Histidine Metabolism	YIR027C	Dal1
ALLTAHr	Allantoate aminohydrolase, reversible	[c] : alltt + h2o <==> urdglyc + urea	EC-3.5.3.4	Histidine Metabolism	YIR029W	Dal2
M1PD	mannitol-1-phosphate 5-dehydrogenase	[c]: mnl1p + nad <==> f6p + h + nadh	EC-1.1.1.17	Mannitol Metabolism		
SFGTH	S-Formylglutathione hydralase	[c] : Sfglutth + h2o <==> for + gthrd + h		Methane Metabolism	YJL068C	Sfgh
0. 0	e i omijigaaamene njaraace	[o] : organia + nizo + + nor + garra + n	20 0: 1:2: 12	motifació motabolioni	1020000	(Fdh1) or (
					(VOD0000 VDI 075W	
				L	(YOR388C or YPL275W	Fdh2) or (
FDH	formate dehydrogenase	[c] : for + nad> co2 + nadh		Methane Metabolism	or YPL276W)	Fdh3)
SHSL4r	O-succinylhomoserine lyase (elimination), reversible	[c]: h2o + suchms <==> 2obut + h + nh4 + succ	EC-4.2.99.9	Methionine Metabolism	YML082W	Cgs1
SHSL1	O-succinylhomoserine lyase (L-cysteine)	[c] : cys-L + suchms> cyst-L + h + succ	FC-4.2.99.9	Methionine Metabolism		
MHPGLUT	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase	[c] : hcys-L + mhpglu> hpglu + met-L		Methionine Metabolism	YER091C	Met6
METTRSm	methionyl-tRNA synthetase, mitochondrial	[m] : atp + met-L + trnamet> amp + mettrna + ppi		Methionine Metabolism	YGR171C	Msm1-m
METTRS	Methionyl-tRNA synthetase	[c] : atp + met-L + trnamet> amp + mettrna + ppi	EC-6.1.1.10	Methionine Metabolism	YGR264C	Mes1
METS	methionine synthase	[c] : 5mthf + hcys-L> met-L + thf	EC-2.1.1.13	Methionine Metabolism	YER091C	Met6
METB1	metb1	[c] : achms + cys-L> ac + cyst-L + h		Methionine Metabolism	YJR130C	Str2
III.C.I.D.I	motor :	[6] Lasimo - Go E - Las - Got E - H		Wicking in the Wickerson	10111000	(Sam2) or (
METAT	mothics in a colonical disconfigures	fall of the 1 h2a I mat I as a mat I million	FC 2 F 4 6	Mathianina Matabalian	(VDDE02C as VLD400W)	
	methionine adenosyltransferase	[c] : atp + h2o + met-L> amet + pi + ppi	EC-2.5.1.6	Methionine Metabolism	(YDR502C or YLR180W)	Sam1)
HSERTA	homoserine O-trans-acetylase	[c]: accoa + hom-L <==> achms + coa		Methionine Metabolism	YNL277W	Met2
DIPS	diphthine synthase	[c]: amet + caphis> ahcys + cmaphis + h	EC-2.1.1.98	Methionine Metabolism	YLR172C	Dph5
CYSTLp	cystathione b-lyase, peroxisomal	[x] : cyst-L + h2o> hcys-L + nh4 + pyr	EC-4.4.1.8	Methionine Metabolism	YGL184C	Str3-p
CYSTL			EC-4.4.1.8		YFR055W	
	cystathionine b-lyase	[c] : cyst-L + h2o> hcys-L + nh4 + pyr				Cys1
CYSTGL	cystathionine g-lyase	[c] : cyst-L + h2o> 2obut + cys-L + nh4	EC-4.4.1.1	Methionine Metabolism	YAL012W	Cys3
AHSERL2	O-acetylhomoserine (thiol)-lyase	[c] : achms + h2s> ac + h + hcys-L		Methionine Metabolism	YLR303W	Met17
			EC-			
AHSERL	O-acetylhomoserine (thiol)-lyase	[c] : achms + ch4s> ac + h + met-L	4.2.99.10	Methionine Metabolism	YLR303W	Met17
AHCi				Methionine Metabolism		
	adenosylhomocysteinase	[c] : ahcys + h2o> adn + hcys-L			YER043C	Sah1
PUNP3m	purine-nucleoside phosphorylase (Guanosine), mitochondrial	[m] : gsn + pi <==> gua + r1p		NAD Biosynthesis	YLR209C	Pnp1-m
PUNP1m	purine-nucleoside phosphorylase (Adenosine), mitochondrial	[m] : adn + pi <==> ade + r1p	EC-2.4.2.1	NAD Biosynthesis	YLR209C	Pnp1-m
NNDPRm	nicotinate-nucleotide diphosphorylase (carboxylating), mitochondrial	[m]: (2) h + prpp + quln> co2 + nicrnt + ppi		NAD Biosynthesis	YFR047C	Bna6-m
NNDPR				NAD Biosynthesis	YFR047C	Bna6
	nicotinate-nucleotide diphosphorylase (carboxylating)	[c]: (2) h + prpp + quln> co2 + nicrnt + ppi				
NNATm	nicotinate-nucleotide adenylyltransferase, mitochondrial	[m] : atp + h + nicrnt> dnad + ppi	EC-2.7.7.18	NAD Biosynthesis	YLR328W	Nma1-m
NNAT	nicotinate-nucleotide adenylyltransferase	[c]: atp + h + nicrnt> dnad + ppi	EC-2.7.7.18	NAD Biosynthesis	YLR328W	Nma1
NNAMrm	nicotinamidase, reversible, mitochondrial	[m] : h2o + ncam <==> nac + nh4		NAD Biosynthesis	YGL037C	Pnc1-m
NNAMr				NAD Biosynthesis	YGL037C	Pnc1
	nicotinamidase, reversible	[c] : h2o + ncam <==> nac + nh4				
NMNATm	nicotinamide-nucleotide adenylyltransferase, mitochondrial	[m] : atp + h + nmn> nad + ppi		NAD Biosynthesis	YLR328W	Nma1-m
NAPRTm	NAPRTase, mitochondrial	[m]: h + nac + prpp> nicrnt + ppi	EC-2.4.2.11	NAD Biosynthesis	YOR209C	Npt1-m
NAPRT	NAPRTase	[c]: h + nac + prpp> nicrnt + ppi		NAD Biosynthesis	YOR209C	Npt1
NADS1m	NAD synthase (nh3), mitochondrial	[m] : atp + dnad + nh4> amp + h + nad + ppi		NAD Biosynthesis	YHR074W	Qns1-m
NADS1	NAD synthase (nh3)	[c] : atp + dnad + nh4> amp + h + nad + ppi	EC-6.3.1.5	NAD Biosynthesis	YHR074W	Qns1
NADPPPSm	NADP phosphatase	[m] : h2o + nadp> nad + pi		NAD Biosynthesis		
NADPPPS	NADP phosphatase	[c] : h2o + nadp> nad + pi		NAD Biosynthesis		
NADNm	NAD nucleosidase, mitochondrial	[m] : h2o + nad> adprib + h + ncam	FC-3 2 2 5	NAD Biosynthesis		
NADN	NAD nucleosidase			NAD Biosynthesis		
NADN	NAD nucleosidase	[c] : h2o + nad> adprib + h + ncam	EU-3.2.2.5	NAD Biosynthesis		
						(Utr1-m) or (
					(YJR049C or YPL188W or	r Pos5-m) or (
NADKm	NAD kinase, mitochondrial	[m] : atp + nad> adp + h + nadp	FC-2.7.1.23	NAD Biosynthesis	YEL041W)	Utr2-m)
		[rij tag				(Utr1) or (
					() (D0 400) VEL 0441W	
					(YJR049C or YEL041W or	
NADK	NAD kinase	[c] : atp + nad> adp + h + nadp	EC-2.7.1.23	NAD Biosynthesis	YPL188W)	Pos5)
UREASE	urea carboxylase	[c]: atp + hco3 + urea <==> adp + allphn + h + pi	EC-6.3.4.6	Nitrogen Metabolism	YBR208C	Dur1
	,		=======	J		(Nit3) or (
NITDI ACE	nitrilaco	[a] : (2) h2a + ind2aan > ind2aa + nh4	FC 2.5.4	Nitrogon Motabolism	(VI B251C V II 426'4')	
NTRLASE	nitrilase	[c] : (2) h2o + ind3acnl> ind3ac + nh4		Nitrogen Metabolism	(YLR351C or YJL126W)	Nit2)
ALPHNH	allophanate hydrolase	[c] : allphn + (3) h + h2o> (2) co2 + (2) nh4		Nitrogen Metabolism	YBR208C	Dur1
XPPT	xanthine phosphoribosyltransferase	[c] : prpp + xan> ppi + xmp	EC-2.4.2.22	Nucleotide Salvage Pathways	YJR133W	Xpt1
URIDK2rn	uridylate kinase (dUMP), nuclear	[n] : atp + dump <==> adp + dudp		Nucleotide Salvage Pathways	YKL024C	Ura6-n
URIDK2r	uridylate kinase (dUMP)	[c] : atp + dump <==> adp + dudp		Nucleotide Salvage Pathways	YKL024C	Ura6
UMPKn	UMP kinase, nuclear	[n] : atp + ump <==> adp + udp		Nucleotide Salvage Pathways	YKL024C	Ura6-n
UMPK	UMP kinase	[c] : atp + ump <==> adp + udp		Nucleotide Salvage Pathways	YKL024C	Ura6
RNTR4	ribonucleoside-triphosphate reductase (UTP)	[c]: trdrd + utp> dutp + h2o + trdox	EC-1.17.4.2	Nucleotide Salvage Pathways		
RNTR3	ribonucleoside-triphosphate reductase (CTP)	[c] : ctp + trdrd> dctp + h2o + trdox		Nucleotide Salvage Pathways		1
				Nucleotide Salvage Pathways		+
RNTR2	ribonucleoside-triphosphate reductase (GTP)	[c] : gtp + trdrd> dgtp + h2o + trdox				
RNTR1	ribonucleoside-triphosphate reductase (ATP)	[c] : atp + trdrd> datp + h2o + trdox	EC-1.17.4.2	Nucleotide Salvage Pathways		
					(YER070W and YGR180C	
RNDR4n	ribonucleoside-diphosphate reductase (UDP), nuclear	[n]: trdrd + udp> dudp + h2o + trdox	FC-1 17 4 1	Nucleotide Salvage Pathways	b	Rnr14-n
h	, and the second		25	The state of the s	(YER070W and YJL026W	
DNDD4	sibanuslaasida dinkaankata radustaas (LIDD)	followed at the section of the section of	FC 1 17 1 1	Nucleatide Caluses Dethurs:	LICOTOVV and TJEOZOVV	
RNDR4	ribonucleoside-diphosphate reductase (UDP)	[c] : trdrd + udp> dudp + h2o + trdox	EC-1.17.4.1	Nucleotide Salvage Pathways)	Rnr12
					(YER070W and YGR180C	
RNDR3n	ribonucleoside-diphosphate reductase (CDP), nuclear	[n] : cdp + trdrd> dcdp + h2o + trdox	EC-1.17.4.1	Nucleotide Salvage Pathways	b	Rnr14-n
	() , , , , , , , , , , , , , , , , , ,			1	(YER070W and YJL026W	
DNIDDS	ribonuelessida dinhaanhata radustass (CDD)	[a] : ada + trdrd > dada + b2a + trday	FC 4 47 4 4	Nucleatide Calvage Dethingur	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	
RNDR3	ribonucleoside-diphosphate reductase (CDP)	[c] : cdp + trdrd> dcdp + h2o + trdox	EC-1.17.4.1	Nucleotide Salvage Pathways	,	Rnr12
				1	(YER070W and YGR180C	, I
RNDR2n	ribonucleoside-diphosphate reductase (GDP), nuclear	[n] : gdp + trdrd> dgdp + h2o + trdox	EC-1.17.4.1	Nucleotide Salvage Pathways	b	Rnr14-n
					(YER070W and YJL026W	
RNDR2	ribonucleoside-diphosphate reductase (GDP)	[c] : gdp + trdrd> dgdp + h2o + trdox	EC 1 17 4 4	Nucleotide Salvage Pathways	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	Rnr12
ININURA	moonucleoside-dipriospriate reductase (GDP)	[6] . gap + data> agap + 1120 + daox	EC-1.17.4.1	inucieotiue Salvage Patriways		INII IZ
l	1		l			
			l		((YER070W and	1
					((YER070W and YGR180C) or (YGR180C	(Rnr14-n) or
RNDR1n	ribonucleoside-diphosphate reductase, nuclear	[n] : adp + trdrd> dadp + h2o + trdox	E0 4 47 4 4	Nucleotide Salvage Pathways		(Rnr14-n) or (Rnr34-n)

]
					((YIL066C and YJL026W) or (YER070W and) (Rnr32) or (
RNDR1	ribonucleoside-diphosphate reductase (ADP)	[c] : adp + trdrd> dadp + h2o + trdox	EC-1.17.4.1	Nucleotide Salvage Pathways	YJL026W))	Rnr12)
PYNP2r	pyrimidine-nucleoside phosphorylase (uracil)	[c] : pi + uri <==> r1p + ura	EC-2.4.2.2	Nucleotide Salvage Pathways	,,	
PUNP7	purine-nucleoside phosphorylase (Xanthosine)	[c] : pi + xtsn <==> r1p + xan		Nucleotide Salvage Pathways	YLR209C	Pnp1
PUNP6	purine-nucleoside phosphorylase (Deoxyinosine)	[c]: din + pi <==> 2dr1p + hxan		Nucleotide Salvage Pathways	YLR209C	Pnp1
PUNP5 PUNP4	purine-nucleoside phosphorylase (Inosine) purine-nucleoside phosphorylase (Deoxyguanosine)	[c] : ins + pi <==> hxan + r1p [c] : dgsn + pi <==> 2dr1p + gua		Nucleotide Salvage Pathways Nucleotide Salvage Pathways	YLR209C YLR209C	Pnp1 Pnp1
PUNP3	purine-nucleoside phosphorylase (Deoxyguanosine) purine-nucleoside phosphorylase (Guanosine)	[c] : gsn + pi <==> gua + r1p		Nucleotide Salvage Pathways	YLR209C	Pnp1
PUNP2	purine-nucleoside phosphorylase (Counsaine)	[c] : dad-2 + pi <==> 2dr1p + ade		Nucleotide Salvage Pathways	YLR209C	Pnp1
PUNP1	purine-nucleoside phosphorylase (Adenosine)	[c] : adn + pi <==> ade + r1p		Nucleotide Salvage Pathways	YLR209C	Pnp1
NTP4	nucleoside-triphosphatase (dGTP)	[c] : dgtp + h2o> dgdp + h + pi		Nucleotide Salvage Pathways		
NTP3	nucleoside-triphosphatase (GTP)	[c] : gtp + h2o> gdp + h + pi		Nucleotide Salvage Pathways		
NTD9	5'-nucleotidase (GMP)	[c] : gmp + h2o> gsn + pi		Nucleotide Salvage Pathways		
NTD8 NTD7	5'-nucleotidase (dGMP) 5'-nucleotidase (AMP)	[c] : dgmp + h2o> dgsn + pi [c] : amp + h2o> adn + pi		Nucleotide Salvage Pathways Nucleotide Salvage Pathways		-
NTD6	5'-nucleotidase (AMP)	[c] : damp + h2o> dad-2 + pi		Nucleotide Salvage Pathways		+
NTD5	5'-nucleotidase (dTMP)	[c] : dtmp + h2o> pi + thymd		Nucleotide Salvage Pathways		1
NTD4	5'-nucleotidase (CMP)	[c] : cmp + h2o> cytd + pi		Nucleotide Salvage Pathways		
NTD3	5'-nucleotidase (dCMP)	[c] : dcmp + h2o> dcyt + pi		Nucleotide Salvage Pathways		1
NTD2	5'-nucleotidase (UMP)	[c] : h2o + ump> pi + uri		Nucleotide Salvage Pathways		
NTD11	5'-nucleotidase (IMP)	[c] : h2o + imp> ins + pi		Nucleotide Salvage Pathways		
NTD10	5'-nucleotidase (XMP)	[c] : h2o + xmp> pi + xtsn		Nucleotide Salvage Pathways		
NTD1 NDPK9	5'-nucleotidase (dUMP) nucleoside-diphophate kinase (ATP:IDP)	[c] : dump + h2o> duri + pi [c] : atp + idp <==> adp + itp		Nucleotide Salvage Pathways Nucleotide Salvage Pathways	YKL067W	Ynk1
NDPK9	nucleoside-diphosphate kinase (ATP:IDP) nucleoside-diphosphate kinase (ATP:dADP)	[c] : atp + idp <==> adp + itp [c] : atp + dadp <==> adp + datp		Nucleotide Salvage Pathways	YKL067W YKL067W	Ynk1
NDPK7	nucleoside-diphosphate kinase (ATP:dADP)	[c] : atp + dadp <==> adp + datp [c] : atp + dcdp <==> adp + dctp		Nucleotide Salvage Pathways	YKL067W	Ynk1
NDPK6	nucleoside-diphosphate kinase (ATT:dcbr)	[c] : atp + dcdp <==> adp + dctp		Nucleotide Salvage Pathways	YKL067W	Ynk1
NDPK5	nucleoside-diphosphate kinase (ATP:dGDP)	[c] : atp + dgdp <==> adp + dgtp		Nucleotide Salvage Pathways	YKL067W	Ynk1
NDPK4	nucleoside-diphosphate kinase (ATP:dTDP)	[c] : atp + dtdp <==> adp + dttp	EC-2.7.4.6	Nucleotide Salvage Pathways	YKL067W	Ynk1
NDPK3	nucleoside-diphosphate kinase (ATP:CDP)	[c] : atp + cdp <==> adp + ctp		Nucleotide Salvage Pathways	YKL067W	Ynk1
NDPK2	nucleoside-diphosphate kinase (ATP:UDP)	[c] : atp + udp <==> adp + utp		Nucleotide Salvage Pathways	YKL067W	Ynk1
NDPK1	nucleoside-diphosphate kinase (ATP:GDP)	[c] : atp + gdp <==> adp + gtp		Nucleotide Salvage Pathways	YKL067W	Ynk1
NDP4 NDP3q	nucleoside-diphosphatase (dGDP)	[c] : dgdp + h2o> dgmp + h + pi		Nucleotide Salvage Pathways	YEL042W	Cda1 a
NDP3g	nucleoside-diphosphatase (GDP), Golgi apparatus nucleoside-diphosphatase (GDP)	[g] : gdp + h2o> gmp + h + pi [c] : gdp + h2o> gmp + h + pi		Nucleotide Salvage Pathways Nucleotide Salvage Pathways	TELU42VV	Gda1-g
INSK	insosine kinase	[c] : atp + ins> adp + h + imp		Nucleotide Salvage Pathways		
HXPRT	hypoxanthine phosphoribosyltransferase (Hypoxanthine)	[c] : hxan + prpp> imp + ppi		Nucleotide Salvage Pathways	YDR399W	Hpt1
GSNK	guanosine kinase	[c] : atp + gsn> adp + gmp + h		Nucleotide Salvage Pathways		1
GNNUC	gnnuc	[c] : gsn + h2o> gua + rib-D		Nucleotide Salvage Pathways	YDR400W	Urh1
DTMPK	dTMP kinase	[c] : atp + dtmp <==> adp + dtdp		Nucleotide Salvage Pathways	YJR057W	Cdc8
DCYTD	deoxycytidine deaminase	[c] : dcyt + h + h2o> duri + nh4		Nucleotide Salvage Pathways	YLR245C	Cdd1
DCTPD	dCTP deaminase	[c] : dctp + h + h2o> dutp + nh4		Nucleotide Salvage Pathways	YHR144C	Dcd1
DADK DADA	deoxyadenylate kinase Deoxyadenosine deaminase	[c] : atp + damp <==> adp + dadp [cl : dad-2 + h + h2o> din + nh4	EC-2.7.4.11	Nucleotide Salvage Pathways Nucleotide Salvage Pathways	YNL141W	Aah1
CYTK2	cytidylate kinase (dCMP)	[c] : atp + dcmp <==> adp + dcdp	FC-2 7 4 14	Nucleotide Salvage Pathways	TINE 141VV	Adiii
CYTK1	cytidylate kinase (CMP)	[c] : atp + comp <==> adp + cdp		Nucleotide Salvage Pathways		+
CYTDK2	cytidine kinase (GTP)	[c] : cytd + gtp> cmp + gdp + h		Nucleotide Salvage Pathways	YNR012W	Urk1
CMPN	CMP nucleosidase	[c] : cmp + h2o> csn + r5p	EC-3.2.2.10	Nucleotide Salvage Pathways		
ATPM	ATP maintenance requirement	[c] : atp + h2o> adp + h + pi		Nucleotide Salvage Pathways		
AMPN	AMP nucleosidase	[c] : amp + h2o> ade + r5p	EC-3.2.2.4	Nucleotide Salvage Pathways	(YML035C or YBR284W or YJL070C)	(Amd1) or (Amd5) or (Amd3)
ADPT	adanina phambaribas/transforasa	[a] : ada + aran > ama + ani	EC-2.4.2.7	Nucleotide Salvage Pathways	(YML022W or YDR441C)	(Apt1) or (Apt2)
ADNUC	adenine phosphoribosyltransferase adnuc	[c] : ade + prpp> amp + ppi [c] : adn + h2o> ade + rib-D	EG-2.4.2.1	Nucleotide Salvage Pathways	YDR400W	Urh1
ADNK1	adenosine kinase	[c] : adn + atp> adp + amp + h	EC-2.7.1.20	Nucleotide Salvage Pathways	YJR105W	Ado1
ADK4m	adentylate kinase (ITP), mitochondrial	[m] : amp + itp <==> adp + idp		Nucleotide Salvage Pathways	YER170W	Adk2-m
ADK4	adentylate kinase (ITP)	[c] : amp + itp <==> adp + idp		Nucleotide Salvage Pathways	YDR226W	Adk1
ADK3m	adentylate kinase (GTP)	[m] : amp + gtp <==> adp + gdp		Nucleotide Salvage Pathways	YER170W	Adk2-m
ADK3	adentylate kinase (GTP)	[c] : amp + gtp <==> adp + gdp		Nucleotide Salvage Pathways	YDR226W	Adk1
ADK1m	adenylate kinase, mitochondrial	[m] : amp + atp <==> (2) adp		Nucleotide Salvage Pathways	YER170W	Adk2-m
ADK1 ADD	adenylate kinase adenine deaminase	[c] : amp + atp <==> (2) adp [c] : ade + h + h2o> hxan + nh4	EC-2.7.4.3 EC-3.5.4.2	Nucleotide Salvage Pathways Nucleotide Salvage Pathways	YDR226W YNL141W	Adk1 Aah1
ADD ADA	Adenosine deaminase Adenosine deaminase	[c] : ade + n + n2o> nxan + nn4 [c] : adn + h + h2o> ins + nh4		Nucleotide Salvage Pathways	YNL141W YNL141W	Aan1 Aah1
GUAPRT	quanine phosphoribosyltransferase	[c] : gua + prpp> gmp + ppi	LC-3.5.4.4	Nucleotide Savage Pathway	YDR399W	Hpt1
PEPAT	Peptide alpha-N-acetyltransferase	[c] : accoa + pepd> apep + coa + h	EC-2.3.1.88	Other Amino Acid Metabolism	(YDL040C or YGR147C)	(Nat1) or (Nat2)
NTRLASE3	nitrilase	[c] : acybut + (2) h2o> glu-L + nh4	EC-3.5.5.1	Other Amino Acid Metabolism	(YLR351C or YJL126W)	(Nit3) or (Nit2)
NTDI ACEC	nikilose	followers (2) has a plat to his	50055	Other Amine Aniel Material	(VII 406W 3/1 B0540)	(Nit2) or (
NTRLASE2 NABTNO	nitrilase N4-Acetylaminobutanal:NAD+ oxidoreductase	[c] : aprop + (2) h2o> ala-L + nh4 [c] : h2o + n4abutn + nad> 4aabutn + (2) h + nadh		Other Amino Acid Metabolism Other Amino Acid Metabolism	(YJL126W or YLR351C)	Nit3)
LCADm	lactaldehyde dehydrogenase, mitochondrial	[m]: h2o + lald-L + nad <==> (2) h + lac-L + nadh		Other Amino Acid Metabolism	YER073W	Ald5-m
GTMLT	g-glutamyltransferase	[c] : ala-L + qthrd> cgly + qluala		Other Amino Acid Metabolism	YLR299W	Ecm38
GTHS	glutathione synthetase	[c] : atp + glucys + gly> adp + gthrd + h + pi		Other Amino Acid Metabolism	YOL049W	Gsh2
					(YBR244W or YIR037W	(Gpx2) or (Hyr1) or (
GTHP	glutathione peridoxase	[c] : (2) gthrd + h2o2 <==> gthox + (2) h2o		Other Amino Acid Metabolism	or YKL026C)	Gpx1)
GTHO	glutathione oxidoreductase	[c] : gthox + h + nadph> (2) gthrd + nadp		Other Amino Acid Metabolism	YPL091W	Glr1
GLUCYS GLPT	gamma-glutamylcysteine synthetase	[c] : atp + cys-L + glu-L> adp + glucys + h + pi		Other Amino Acid Metabolism	YJL101C YLR195C	Gsh1
OLF I	glycylpeptide N-tetradecanoyltransferase	[c]: glp + tdcoa> coa + tglp	EC-2.3.1.97	Other Amino Acid Metabolism	I FL I BOC	Nmt1

APRTO2	N-acetylputrescine: oxygen oxireductase (deaminating)	[c]: aprut + h2o + o2> h2o2 + n4abutn + nh4	EC-1.4.3.4	Other Amino Acid Metabolism		
. D. ITD					()/00000000	(Ald4-m) or (
ABUTDm	Aminobutyraldehyde dehydrogenase, mitochondrial	[m]: 4abutn + h2o + nad> 4abut + (2) h + nadh		Other Amino Acid Metabolism	(YOR374W or YER073W)	Ald5-m)
AABTN	4-acetamidobutyrate deacetylase	[c] : 4aabutn + h2o> 4abut + ac	EC-3.5.1.63	Other Amino Acid Metabolism		
SUCD3-u6m	succinate dehydrogenase (ubiquinone-6), mitochondrial	[m] : fadh2 + q6 <==> fad + q6h2	EC-1.3.5.1	Oxidative phosphorylation	((YDR178W and YKL141W and YKL148C and YLL041C) or (YKL141W and YKL148C and YLL041C and YLR164W) or (YDR178W and YKL148C and YLL041C and YMR118C) or (YDR178W and YJL045W and YKL141W and YLL041C))	(Sdh-m) or (Sdh2-m) or (Sdh3-m) or (Sdh4-m)
1	7				1 1 1 1	ĺ í
					((YDR178W and YKL141W and YKL141W and YKL148C and YLL041C) or (YKL141W and YKL148C and YLL041C and YLR164W) or (YDR178W and YKL148C and YMKL148C or (YDR178W and YJL041C and YMK118C) or (YDR178W and YJL045W and YKL141W	(Sdh-m) or (Sdh2-m) or (Sdh3-m) or (
SUCD1m	succinate dehydrogenase, mitochondrial	[m] : fad + succ <==> fadh2 + fum		Oxidative phosphorylation	and YLL041C))	Sdh4-m)
PPAm	inorganic diphosphatase, mitochondrial	[m] : h2o + ppi> h + (2) pi	EC-3.6.1.1		YMR267W	Ppa2-m
PPA	inorganic diphosphatase	[c]: h2o + ppi> h + (2) pi	EC-3.6.1.1	Oxidative phosphorylation	YBR011C	lpp1
NADH2-u6m	NADH dehydrogenase, mitochondrial	[m] : h + nadh + q6> nad + q6h2	EC-1.6.99.3	Oxidative phosphorylation	(YML120C or YKL192C)	(Ndi1-m) or (Acp1-m) (Nde1-m) or (
NADH2-u6cm	NADH dehydrogenase, cytosolic/mitochondrial	h[c] + nadh[c] + q6[m]> nad[c] + q6h2[m]	FC-1 6 99 3	Oxidative phosphorylation	(YMR145C or YDL085W)	Nde2-m)
MDHp	malate dehydrogenase, peroxisomal	[x] : mal-L + nad <==> h + nadh + oaa		Oxidative phosphorylation	YDL078C	Mdh3-p
MDHm	malate dehydrogenase, mitochondrial	[m] : mal-L + nad <==> h + nadh + oaa		Oxidative phosphorylation	YKL085W	Mdh1-m
MDH	malate dehydrogenase	[c] : mal-L + nad <==> h + nadh + oaa		Oxidative phosphorylation	YOL126C	Mdh2
FUMm	fumarase, mitochondrial	[m] : fum + h2o <==> mal-L	EC-4.2.1.2		YPL262W	Fum1-m
FUM	fumarase	[c] : fum + h2o <==> mai-L	EC-4.2.1.2		YPL262W	Fum1
FRDm	fumarate reductase, mitochondrial	[m] : fadh2 + fum> fad + succ	EC-1.3.99.1		YJR051W	Osm1-m
FDNG			EC-1.3.99.1		TJRUSTW	OSIII I-III
CYOR_u6m	formate dehydrogenase, cytosolic/mitochondrial ubiquinol-6 cytochrome c reductase	for[c] + h[c] + q6[m]> co2[c] + q6h2[m] (2) ficytc[m] + (1.5) h[m] + q6h2[m]> (2) focytc[m] + (1.5) h[c] + q6[m]		Oxidative phosphorylation	(Q0105 and YBL045C and YDR529C and YDR529C and YEL024W and YFR033C and YGR183C and YHR001W-A and YJL166W and YOR065W and YPR191W)	Cbc1-m
					((Q0045 and Q0250 and Q0275 and YDL067C and YGL187C and YGL191W and YHR051W and YHR038C and YHR395C and YMR256C and YMR052W) or (Q0045 and Q0250 and Q0275 and YDL067C and	
CYOOm	cytochrome c oxidase, mitochondrial	(4) focytc[m] + (6) h[m] + o2[m]> (4) ficytc[m] + (6) h[c] + (2) h2o[m]	EC-1.9.3.1	Oxidative phosphorylation	YGL187C and YGL191W and YHR051W and YIL111W and YLR038C and YLR395C and YMR256C))	(Cco1-m) or (Cco2-m)
CYOOm ATPS3v	cytochrome c oxidase, mitochondrial ATP synthase, vacuole	(4) focytc[m] + (6) h[m] + o2[m]> (4) ficytc[m] + (6) h[c] + (2) h2o[m] adp[v] + (3) h[c] + pi[v]> atp[v] + (2) h[v] + h2o[v]		Oxidative phosphorylation Oxidative phosphorylation	and YHR051W and YIL111W and YLR038C and YLR395C and	Cco2-m)

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					(/ O0000 and O000E and	
					((Q0080 and Q0085 and	
					Q0130 and YBL099W and	
					YBR039W and YDL004W	
					and YDL181W and	
					YDR298C and YDR322C-A	
					and YDR377W and	
					YJR121W and YKL016C	
					and YLR295C and	
					YML081C-A and YOL077W	
					A and YPL078C and	
					YPL271W and YPR020W)	
					or (Q0080 and Q0085	
					and Q0130 and YBL099W	
					and YBR039W and	
					YDL004W and YDL181W	
					and YDR298C and	
					YDR377W and YJR121W	
					and YKL016C and	
					YLR295C and YML081C-A	
			1	1	and YPL078C and	(Atps2-m) or
ATPS3m	ATP synthase, mitochondrial	adp[m] + (3) h[c] + pi[m]> atp[m] + (2) h[m] + h2o[m]	EC-3.6.3.14	Oxidative phosphorylation	YPL271W))	(Atps1-m)
				, ,		1 1
1					(YBR127C and YDL185W	
			1	1	and YEL027W and	
			1	1	YEL051W and YGR020C	
			1	1		
			1	1	and YHR026W and	1
			1	1	YHR039C-A and YKL080W	
					and YLR447C and	
					YMR054W and YOR332W	
					and YPL234C and	
ATPS3g	ATP synthase, Golgi Apparatus	adp[g] + (3) h[c] + pi[g]> atp[g] + (2) h[g] + h2o[g]		Oxidative phosphorylation	YPR036W)	Hatp-g
PTPATim	panthetheine-phosphate adenylyltransferase	[m] : atp + h + pan4p> dpcoa + ppi		Pantothenate and CoA Biosynthesis		
PTPATi	pantetheine-phosphate adenylyltransferase	[c] : atp + h + pan4p> dpcoa + ppi		Pantothenate and CoA Biosynthesis		
PPNCL2	phosphopantothenate-cysteine ligase	[c]: 4ppan + ctp + cys-L> 4ppcys + cmp + h + ppi		Pantothenate and CoA Biosynthesis		
PPCDC	phosphopantothenoylcysteine decarboxylase	[c]: 4ppcys + h> co2 + pan4p		Pantothenate and CoA Biosynthesis		
PNTK	pantothenate kinase	[c] : atp + pnto-R> 4ppan + adp + h	EC-2.7.1.33	Pantothenate and CoA Biosynthesis	YDR531W	Pnk1
PANTS	pantothenate synthase	[c] : ala-B + atp + pant-R> amp + h + pnto-R + ppi	EC-6.3.2.1	Pantothenate and CoA Biosynthesis	YIL145C	Pan6
MOHMT	3-methyl-2-oxobutanoate hydroxymethyltransferase	[c] : 3mob + h2o + mlthf> 2dhp + thf	EC-2.1.2.11	Pantothenate and CoA Biosynthesis	YBR176W	Ecm31
DPRm	2-dehydropantoate 2-reductase, mitochondrial	[m] : 2dhp + h + nadph> nadp + pant-R	EC-	Pantothenate and CoA Biosynthesis	YLR355C	llv5-m
DPR	2-dehydropantoate 2-reductase	[c]: 2dhp + h + nadph> nadp + pant-R	EC-	Pantothenate and CoA Biosynthesis	YHR063C	Pan5
DPCOAKm	dephospho-CoA kinase, mitochondrial	[m]: atp + dpcoa> adp + coa + h		Pantothenate and CoA Biosynthesis		
DPCOAK	dephospho-CoA kinase	[c] : atp + dpcoa> adp + coa + h		Pantothenate and CoA Biosynthesis		
DBTSr	dethiobiotin synthase	[c] : atp + co2 + dann <==> adp + dtbt + (3) h + pi		Pantothenate and CoA Biosynthesis	YNR057C	Bio4
	biotin synthase	[c] : dtbt + s <==> btn + (2) h		Pantothenate and CoA Biosynthesis	YGR286C	Bio2
IBISC		[6] . 4.6.4 . 6		Pantothenate and CoA Biosynthesis	1.0.12000	5.02
BTSr ASP1DC		[c] : asp-l + h> ala-B + co2				
ASP1DC	aspartate 1-decarboxylase adenosylmethionine-8-amino-7-oxononanoate transaminase	[c] : asp-L + h> ala-B + co2	EC-4.1.1.11		YNR058W	Bio3
ASP1DC AMAOTr	adenosylmethionine-8-amino-7-oxononanoate transaminase	[c]: 8aonn + amet <==> amob + dann	EC-4.1.1.11	Pantothenate and CoA Biosynthesis	YNR058W	Bio3
ASP1DC			EC-4.1.1.11		YNR058W YPL148C	Ppt2-m
ASP1DC AMAOTr ACPSm	adenosylmethionine-8-amino-7-oxononanoate transaminase acyl carrier protein synthase, mitochondrial	[c] : 8aonn + amet <==> amob + dann [m] : coa + h2o -> (2) h + pan4p + pap	EC-4.1.1.11 EC-2.6.1.62	Pantothenate and CoA Biosynthesis Pantothenate and CoA Biosynthesis	YPL148C	Ppt2-m (Tkl1) or (
ASP1DC AMAOTr	adenosylmethionine-8-amino-7-oxononanoate transaminase	[c]: 8aonn + amet <==> amob + dann	EC-4.1.1.11 EC-2.6.1.62	Pantothenate and CoA Biosynthesis		Ppt2-m (Tkl1) or (Tkl2)
ASP1DC AMAOTr ACPSm TKT2	adenosylmethionine-8-amino-7-oxononanoate transaminase acyl carrier protein synthase, mitochondrial transketolase	[c]: 8aonn + amet <==> amob + dann [m]: coa + h2o -> (2) h + pan4p + pap [c]: e4p + xu5p-D <==> f6p + g3p	EC-2.6.1.62 EC-2.2.1.1	Pantothenate and CoA Biosynthesis Pantothenate and CoA Biosynthesis Pentose Phosphate Cycle	YPL148C (YPR074C or YBR117C)	Ppt2-m (Tkl1) or (Tkl2) (Tkl2) or (
ASP1DC AMAOTr ACPSm	adenosylmethionine-8-amino-7-oxononanoate transaminase acyl carrier protein synthase, mitochondrial	[c] : 8aonn + amet <==> amob + dann [m] : coa + h2o -> (2) h + pan4p + pap	EC-2.6.1.62 EC-2.2.1.1	Pantothenate and CoA Biosynthesis Pantothenate and CoA Biosynthesis	YPL148C	Ppt2-m (Tkl1) or (Tkl2) (Tkl2) or (Tkl1)
ASP1DC AMAOTr ACPSm TKT2	adenosylmethionine-8-amino-7-oxononanoate transaminase acyl carrier protein synthase, mitochondrial transketolase transketolase	[c]: 8aonn + amet <==> amob + dann [m]: coa + h2o -> (2) h + pan4p + pap [c]: e4p + xu5p-D <==> f6p + g3p [c]: r5p + xu5p-D <==> g3p + s7p	EC-4.1.1.11 EC-2.6.1.62 EC-2.2.1.1	Pantothenate and CoA Biosynthesis Pantothenate and CoA Biosynthesis Pentose Phosphate Cycle Pentose Phosphate Cycle	YPL148C (YPR074C or YBR117C) (YBR117C or YPR074C)	Ppt2-m (Tkl1) or (Tkl2) (Tkl2) or (Tkl1) (Tal1) or (
ASP1DC AMAOTr ACPSm TKT2 TKT1	adenosylmethionine-8-amino-7-oxononanoate transaminase acyl carrier protein synthase, mitochondrial transketolase transketolase transaldolase	[c]: 8aonn + amet <==> amob + dann [m]: coa + h2o -> (2) h + pan4p + pap [c]: e4p + xu5p-D <==> f6p + g3p [c]: r5p + xu5p-D <==> g3p + s7p [c]: g3p + s7p <==> e4p + f6p	EC-4.1.1.11 EC-2.6.1.62 EC-2.2.1.1 EC-2.2.1.1	Pantothenate and CoA Biosynthesis Pantothenate and CoA Biosynthesis Pentose Phosphate Cycle Pentose Phosphate Cycle Pentose Phosphate Cycle	YPL148C (YPR074C or YBR117C) (YBR117C or YPR074C) (YLR354C or YGR043C)	Ppt2-m (Tkl1) or (Tkl2) (Tkl2) or (Tkl1) (Tal1) or (Tal2)
ASP1DC AMAOTr ACPSm TKT2 TKT1 TALA RPI	adenosylmethionine-8-amino-7-oxononanoate transaminase acyl carrier protein synthase, mitochondrial transketolase transketolase transketolase transaldolase ribose-5-phosphate isomerase	[c]: 8aonn + amet <==> amob + dann [m]: coa + h2o -> (2) h + pan4p + pap [c]: e4p + xu5p-D <==> f6p + g3p [c]: r5p + xu5p-D <==> g3p + s7p [c]: g3p + s7p <==> e4p + f6p [c]: r5p <==> ru5p-D	EC-4.1.1.11 EC-2.6.1.62 EC-2.2.1.1 EC-2.2.1.1 EC-2.2.1.2 EC-5.3.1.6	Pantothenate and CoA Biosynthesis Pantothenate and CoA Biosynthesis Pentose Phosphate Cycle	YPL148C (YPR074C or YBR117C) (YBR117C or YPR074C) (YLR354C or YGR043C) YOR095C	Ppt2-m (Tkl1) or (Tkl2) (Tkl2) or (Tkl1) (Tal1) or (Tal2) Rki1
ASPIDC AMAOTr ACPSm TKT2 TKT1 TALA RPI RPI RPE	adenosylmethionine-8-amino-7-oxononanoate transaminase acyl carrier protein synthase, mitochondrial transketolase transketolase transketolase ribose-5-phosphate isomerase ribulose 5-phosphate 3-epimerase	[c]: 8aonn + amet <==> amob + dann [m]: coa + h2o -> (2) h + pan4p + pap [c]: e4p + xu5p-D <==> f6p + g3p [c]: f5p + xu5p-D <==> g3p + s7p [c]: g3p + s7p <==> e4p + f6p [c]: ru5p-D <==> ru5p-D [c]: ru5p-D <==> xu5p-D	EC-4.1.1.11 EC-2.6.1.62 EC-2.2.1.1 EC-2.2.1.1 EC-2.2.1.2 EC-5.3.1.6 EC-5.1.3.1	Pantothenate and CoA Biosynthesis Pantothenate and CoA Biosynthesis Pentose Phosphate Cycle	YPL148C (YPR074C or YBR117C) (YBR117C or YPR074C) (YLR354C or YGR043C) YOR095C YJL121C	Ppt2-m (Tkl1) or (Tkl2) (Tkl2) or (Tkl1) (Tkl1) or (Tal1) or (Tal2) Rki1
ASP1DC AMAOTr ACPSm TKT2 TKT1 TALA RPI	adenosylmethionine-8-amino-7-oxononanoate transaminase acyl carrier protein synthase, mitochondrial transketolase transketolase transketolase transaldolase ribose-5-phosphate isomerase	[c]: 8aonn + amet <==> amob + dann [m]: coa + h2o -> (2) h + pan4p + pap [c]: e4p + xu5p-D <==> f6p + g3p [c]: r5p + xu5p-D <==> g3p + s7p [c]: g3p + s7p <==> e4p + f6p [c]: r5p <==> ru5p-D	EC-4.1.1.11 EC-2.6.1.62 EC-2.2.1.1 EC-2.2.1.1 EC-2.2.1.2 EC-5.3.1.6 EC-5.1.3.1	Pantothenate and CoA Biosynthesis Pantothenate and CoA Biosynthesis Pentose Phosphate Cycle	YPL148C (YPR074C or YBR117C) (YBR117C or YPR074C) (YLR354C or YGR043C) YOR095C	Ppt2-m (Tkl1) or (Tkl2) (Tkl2) or (Tkl1) (Tal1) or (Tal2) Rki1 Rpe1
ASPIDC AMAOTr ACPSm TKT2 TKT1 TALA RPI RPE RBK	adenosylmethionine-8-amino-7-oxononanoate transaminase acyl carrier protein synthase, mitochondrial transketolase transketolase transaldolase ribose-5-phosphate isomerase ribulose 5-phosphate 3-epimerase ribokinase	[c]: 8aonn + amet <==> amob + dann [m]: coa + h2o -> (2) h + pan4p + pap [c]: e4p + xu5p-D <==> f6p + g3p [c]: r5p + xu5p-D <==> g3p + s7p [c]: g3p + s7p <==> e4p + f6p [c]: r5p <==> ru5p-D [c]: ru5p-D <==> xu5p-D [c]: atp + rib-D -> adp + h + r5p	EC-2.1.1 EC-2.2.1.1 EC-2.2.1.1 EC-2.2.1.2 EC-5.3.1.6 EC-5.1.3.1 EC-2.7.1.15	Pantothenate and CoA Biosynthesis Pantothenate and CoA Biosynthesis Pentose Phosphate Cycle	YPL148C (YPR074C or YBR117C) (YBR117C or YPR074C) (YLR354C or YGR043C) YOR095C YJL121C YCR036W	Ppt2-m (Tkl1) or (Tkl2) (Tkl2) or (Tkl1) (Tal1) or (Tal2) Rki1 Rpe1 Rbk1 (Pgm1) or (
ASPIDC AMAOTr ACPSm TKT2 TKT1 TALA RPI RPI RPE	adenosylmethionine-8-amino-7-oxononanoate transaminase acyl carrier protein synthase, mitochondrial transketolase transketolase transketolase ribose-5-phosphate isomerase ribulose 5-phosphate 3-epimerase	[c]: 8aonn + amet <==> amob + dann [m]: coa + h2o -> (2) h + pan4p + pap [c]: e4p + xu5p-D <==> f6p + g3p [c]: f5p + xu5p-D <==> g3p + s7p [c]: g3p + s7p <==> e4p + f6p [c]: ru5p-D <==> ru5p-D [c]: ru5p-D <==> xu5p-D	EC-4.1.1.11 EC-2.6.1.62 EC-2.2.1.1 EC-2.2.1.1 EC-2.2.1.2 EC-5.3.1.6 EC-5.1.3.1	Pantothenate and CoA Biosynthesis Pantothenate and CoA Biosynthesis Pentose Phosphate Cycle	YPL148C (YPR074C or YBR117C) (YBR117C or YPR074C) (YLR354C or YGR043C) YOR095C YJL121C	Ppt2-m (Tkl1) or (Tkl2) or (Tkl2) or (Tkl1) (Tal1) or (Tal2) Rki1 Rpe1 Rbk1 (Pgm1) or (Pgm2)
ASPIDC AMAOTr ACPSm TKT2 TKT1 TALA RPI RPE RBE RBK	adenosylmethionine-8-amino-7-oxononanoate transaminase acyl carrier protein synthase, mitochondrial transketolase transketolase transaldolase ribose-5-phosphate isomerase ribose-5-phosphate 3-epimerase ribokinase phosphopentomutase	[c]: 8aonn + amet <==> amob + dann [m]: coa + h2o -> (2) h + pan4p + pap [c]: e4p + xu5p-D <==> f6p + g3p [c]: r5p + xu5p-D <==> g3p + s7p [c]: g3p + s7p <==> e4p + f6p [c]: r5p <==> ru5p-D [c]: ru5p-D <==> xu5p-D [c]: xu5p-D <==> xu5p-D [c]: tp + rib-D -> adp + h + r5p [c]: r1p <==> r5p	EC-2.2.1.1 EC-2.2.1.1 EC-2.2.1.2 EC-2.2.1.2 EC-5.3.1.6 EC-5.1.3.1 EC-2.7.1.15	Pantothenate and CoA Biosynthesis Pantothenate and CoA Biosynthesis Pentose Phosphate Cycle	YPL148C (YPR074C or YBR117C) (YBR117C or YPR074C) (YLR354C or YGR043C) YOR095C YJL121C YCR036W (YKL127W or YMR105C)	Ppt2-m (Tkt1) or (Tkt1) or (Tkt2) or (Tkt1) (Tat1) or (Tat2) Rki1 Rpe1 Rbk1 (Pgm1) or (Pgm2) (Pgm1) or (
ASPIDC AMAOTr ACPSm TKT2 TKT1 TALA RPI RPE RBK	adenosylmethionine-8-amino-7-oxononanoate transaminase acyl carrier protein synthase, mitochondrial transketolase transketolase transaldolase ribose-5-phosphate isomerase ribulose 5-phosphate 3-epimerase ribokinase	[c]: 8aonn + amet <==> amob + dann [m]: coa + h2o -> (2) h + pan4p + pap [c]: e4p + xu5p-D <==> f6p + g3p [c]: r5p + xu5p-D <==> g3p + s7p [c]: g3p + s7p <==> e4p + f6p [c]: r5p <==> ru5p-D [c]: ru5p-D <==> xu5p-D [c]: atp + rib-D -> adp + h + r5p	EC-2.2.1.1 EC-2.2.1.1 EC-2.2.1.2 EC-2.2.1.2 EC-5.3.1.6 EC-5.1.3.1 EC-2.7.1.15	Pantothenate and CoA Biosynthesis Pantothenate and CoA Biosynthesis Pentose Phosphate Cycle	YPL148C (YPR074C or YBR117C) (YBR117C or YPR074C) (YLR354C or YGR043C) YOR095C YJL121C YCR036W	Ppt2-m (Tkl1) or (Tkl2) or (Tkl2) or (Tkl1) (Tkl2) or (Tkl1) (Tal1) or (Tal2) Rkl1 Rpe1 Rkkl1 (Pgm1) or (Pgm2) (Pgm1) or (Pgm2)
ASPIDC AMAOTr ACPSm TKT2 TKT1 TALA RPI RPE RBK PPM	adenosylmethionine-8-amino-7-oxononanoate transaminase acyl carrier protein synthase, mitochondrial transketolase transketolase transaldolase ribose-5-phosphate isomerase ribose-5-phosphate 3-epimerase ribokinase phosphopentomutase	[c]: 8aonn + amet <==> amob + dann [m]: coa + h2o -> (2) h + pan4p + pap [c]: e4p + xu5p-D <==> f6p + g3p [c]: r5p + xu5p-D <==> g3p + s7p [c]: g3p + s7p <==> e4p + f6p [c]: r5p <==> ru5p-D [c]: ru5p-D <==> xu5p-D [c]: xu5p-D <==> xu5p-D [c]: tp + rib-D -> adp + h + r5p [c]: r1p <==> r5p	EC-2.2.1.1 EC-2.2.1.1 EC-2.2.1.2 EC-2.2.1.2 EC-5.3.1.6 EC-5.1.3.1 EC-2.7.1.15	Pantothenate and CoA Biosynthesis Pantothenate and CoA Biosynthesis Pentose Phosphate Cycle	YPL148C (YPR074C or YBR117C) (YBR117C or YPR074C) (YLR354C or YGR043C) YOR095C YJL121C YCR036W (YKL127W or YMR105C)	Ppt2-m (Tki1) or (Tki2) (Tki2) or (Tki1) (Tki2) or (Tal2) (Tki1) or (Tal2) (Tki1) (Tal2) (Tki1) (Tal2) (Tki1) (Tal2) (Tki1) (Tal2) (Tki1) (Tal2) (Tki1) (Tki
ASPIDC AMAOTr ACPSm TKT2 TKT1 TALA RPI RPE RBK PPM	adenosylmethionine-8-amino-7-oxononanoate transaminase acyl carrier protein synthase, mitochondrial transketolase transketolase transaldolase ribose-5-phosphate isomerase ribose-5-phosphate 3-epimerase ribokinase phosphopentomutase	[c]: 8aonn + amet <==> amob + dann [m]: coa + h2o -> (2) h + pan4p + pap [c]: e4p + xu5p-D <==> f6p + g3p [c]: r5p + xu5p-D <==> g3p + s7p [c]: g3p + s7p <==> e4p + f6p [c]: r5p <==> ru5p-D [c]: ru5p-D <==> xu5p-D [c]: xu5p-D <==> xu5p-D [c]: tp + rib-D -> adp + h + r5p [c]: r1p <==> r5p	EC-2.2.1.1 EC-2.2.1.1 EC-2.2.1.2 EC-2.2.1.2 EC-5.3.1.6 EC-5.1.3.1 EC-2.7.1.15	Pantothenate and CoA Biosynthesis Pantothenate and CoA Biosynthesis Pentose Phosphate Cycle	YPL148C (YPR074C or YBR117C) (YBR117C or YPR074C) (YLR354C or YGR043C) YOR095C YJL121C YCR036W (YKL127W or YMR105C) (YKL127W or YMR105C) (YNR034W or YHR163W	Ppt2-m (Tkl1) or (Tkl2) or (Tkl2) or (Tkl1) (Tkl2) or (Tkl1) (Tkl2) or (Tal2) Rki1 Rpe1 Rbk1 (Pgm1) or (Pgm2) (Pgm1) or (Pgm2) (Sol1) or (Sol3) or (Sol3) or (
ASPIDC AMAOTr ACPSm TKT2 TKT1 TALA RPI RPE RBK PPM PGMT	adenosylmethionine-8-amino-7-oxononanoate transaminase acyl carrier protein synthase, mitochondrial transketolase transketolase transaldolase ribose-5-phosphate isomerase ribose-5-phosphate 3-epimerase ribokinase phosphopentomutase	[c]: 8aonn + amet <==> amob + dann [m]: coa + h2o -> (2) h + pan4p + pap [c]: e4p + xu5p-D <==> f6p + g3p [c]: r5p + xu5p-D <==> g3p + s7p [c]: g3p + s7p <==> e4p + f6p [c]: r5p <==> ru5p-D [c]: ru5p-D <==> xu5p-D [c]: atp + rib-D -> adp + h + r5p [c]: r1p <==> r5p [c]: r1p <==> r5p [c]: r1p <==> r6p [c]: g1p <==> g6p	EC-4.1.1.11 EC-2.6.1.62 EC-2.2.1.1 EC-2.2.1.2 EC-5.3.1.6 EC-5.1.3.1 EC-2.7.1.15 EC-5.4.2.7	Pantothenate and CoA Biosynthesis Pantothenate and CoA Biosynthesis Pentose Phosphate Cycle	YPL148C (YPR074C or YBR117C) (YBR117C or YPR074C) (YLR354C or YGR043C) YOR095C YJL121C YCR036W (YKL127W or YMR105C) (YKL127W or YMR105C) (YNR034W or YHR163W or YGR248W or	Ppt2-m (Tk1) or (Tk1)
ASPIDC AMAOTr ACPSm TKT2 TKT1 TALA RPI RPE RBK PPM PGMT	adenosylmethionine-8-amino-7-oxononanoate transaminase acyl carrier protein synthase, mitochondrial transketolase transketolase transaldolase ribose-5-phosphate isomerase ribose-5-phosphate 3-epimerase ribokinase phosphopentomutase	[c]: 8aonn + amet <==> amob + dann [m]: coa + h2o -> (2) h + pan4p + pap [c]: e4p + xu5p-D <==> f6p + g3p [c]: r5p + xu5p-D <==> g3p + s7p [c]: g3p + s7p <==> e4p + f6p [c]: r5p <==> ru5p-D [c]: ru5p-D <==> xu5p-D [c]: xu5p-D <==> xu5p-D [c]: tp + rib-D -> adp + h + r5p [c]: r1p <==> r5p	EC-4.1.1.11 EC-2.6.1.62 EC-2.2.1.1 EC-2.2.1.2 EC-5.3.1.6 EC-5.1.3.1 EC-2.7.1.15 EC-5.4.2.7	Pantothenate and CoA Biosynthesis Pantothenate and CoA Biosynthesis Pentose Phosphate Cycle	YPL148C (YPR074C or YBR117C) (YBR117C or YPR074C) (YLR354C or YGR043C) YOR095C YJL121C YCR036W (YKL127W or YMR105C) (YKL127W or YMR105C) (YNR034W or YHR163W	Ppt2-m (Tkl1) or (Tkl2) or (Tkl2) or (Tkl2) or (Tkl1) or (Tal2) Rki1 Rpe1 Rbk1 (Pgm1) or (Pgm2) (Pgm1) or (Pgm2) (Sol1) or (Sol3) or (Sol4) or (Sol2)
ASPIDC AMAOTr ACPSm TKT2 TKT1 TALA RPI RPE RBK PPM PGMT	adenosylmethionine-8-amino-7-oxononanoate transaminase acyl carrier protein synthase, mitochondrial transketolase transketolase transaldolase ribose-5-phosphate isomerase ribulose 5-phosphate 3-epimerase ribokinase phosphopentomutase phosphoglucomutase	[c]: 8aonn + amet <==> amob + dann [m]: coa + h2o -> (2) h + pan4p + pap [c]: e4p + xu5p-D <==> f6p + g3p [c]: r5p + xu5p-D <==> g3p + s7p [c]: g3p + s7p <==> e4p + f6p [c]: r5p <==> ru5p-D [c]: ru5p-D <==> xu5p-D [c]: atp + rib-D -> adp + h + r5p [c]: r1p <==> r5p [c]: r1p <==> r5p [c]: r1p <==> r6p [c]: g1p <==> g6p	EC-4.1.1.11 EC-2.6.1.62 EC-2.2.1.1 EC-2.2.1.2 EC-5.1.3.1 EC-5.1.3.1 EC-5.1.3.1 EC-5.4.2.7 EC-5.4.2.7	Pantothenate and CoA Biosynthesis Pantothenate and CoA Biosynthesis Pentose Phosphate Cycle	YPL148C (YPR074C or YBR117C) (YBR117C or YPR074C) (YLR354C or YGR043C) YOR095C YJL121C YCR036W (YKL127W or YMR105C) (YKL127W or YMR105C) (YNR034W or YHR163W or YGR248W or YCR073W-A)	Ppt2-m (Tkt1) or (Tkt2) or (Tkt2) or (Tkt2) or (Tkt3) (Tkt2) or (Tkt3)
ASPIDC AMAOTr ACPSm TKT2 TKT1 TALA RPI RPE RBK PPM PGMT	adenosylmethionine-8-amino-7-oxononanoate transaminase acyl carrier protein synthase, mitochondrial transketolase transaketolase transaldolase transaldolase ribose-5-phosphate isomerase riboulose 5-phosphate 3-epimerase riboulose 5-phosphate 3-epimerase riboulose 5-phosphate 3-epimerase riboulose 5-phosphopentomutase phosphopentomutase phosphoglucomutase 6-phosphogluconolactonase phosphogluconate dehydrogenase	[c]: 8aonn + amet <==> amob + dann [m]: coa + h2o -> (2) h + pan4p + pap [c]: e4p + xu5p-D <==> f6p + g3p [c]: r5p + xu5p-D <==> g3p + s7p [c]: g3p + s7p <==> e4p + f6p [c]: r6p <==> ru5p-D [c]: ru5p-D <==> xu5p-D [c]: atp + rib-D -> adp + h + r5p [c]: r1p <==> r6p [c]: g1p <==> g6p	EC-4.1.1.11 EC-2.6.1.62 EC-2.2.1.1 EC-2.2.1.2 EC-5.1.3.1 EC-5.1.3.1 EC-5.1.3.1 EC-5.4.2.7 EC-5.4.2.7	Pantothenate and CoA Biosynthesis Pantothenate and CoA Biosynthesis Pentose Phosphate Cycle	YPL148C (YPR074C or YBR117C) (YBR117C or YPR074C) (YLR354C or YGR043C) YOR095C YJL121C YCR036W (YKL127W or YMR105C) (YKL127W or YMR105C) (YNR034W or YHR163W or YGR248W or	Ppt2-m (Tkl1) or (Tkl2) or (Tkl2) or (Tkl2) or (Tkl1) or (Tal2) Rki1 Rpe1 Rbk1 (Pgm1) or (Pgm2) (Pgm1) or (Pgm2) (Sol1) or (Sol3) or (Sol4) or (Sol2)
ASPIDC AMAOTr ACPSm TKT2 TKT1 TALA RPI RPE RBK PPM PGMT G6PDH2er	adenosylmethionine-8-amino-7-oxononanoate transaminase acyl carrier protein synthase, mitochondrial transketolase transketolase transaldolase ribose-5-phosphate isomerase ribulose 5-phosphate 3-epimerase ribulose 5-phosphate 3-epimerase ribosphopentomutase phosphopentomutase phosphoglucomutase 6-phosphogluconolactonase	[c]: 8aonn + amet <==> amob + dann [m]: coa + h2o -> (2) h + pan4p + pap [c]: e4p + xu5p-D <==> f6p + g3p [c]: r5p + xu5p-D <==> g3p + s7p [c]: g3p + s7p <==> e4p + f6p [c]: r5p <==> ru5p-D [c]: nu5p-D <==> xu5p-D [c]: atp + rib-D -> adp + h + r5p [c]: r1p <==> r5p [c]: g1p <==> g6p	EC-4.1.1.11 EC-2.6.1.62 EC-2.2.1.1 EC-2.2.1.2 EC-5.1.3.1 EC-5.1.3.1 EC-5.1.3.1 EC-5.4.2.7 EC-5.4.2.7	Pantothenate and CoA Biosynthesis Pantothenate and CoA Biosynthesis Pentose Phosphate Cycle	YPL148C (YPR074C or YBR117C) (YBR117C or YPR074C) (YLR354C or YGR043C) YOR095C YJL121C YCR036W (YKL127W or YMR105C) (YKL127W or YMR105C) (YNR034W or YHR163W or YGR248W or YCR073W-A)	Ppt2-m (Tk11) or (Tk12) or (Tk12) or (Tk12) or (Tk11) (Tk11) or (Tal2) (Tk12) (Tk12) (Tk12) (Tk12) (Tk12) (Tk12) (Tk12) (Tk12) (Tk12) or (Pgm1) or (Pgm2) (Sol1) or (Sol4) or (Sol4) or (Sol2) (Gnd2) or (Gnd1)
ASPIDC AMAOTr ACPSm TKT2 TKT1 TALA RPI RPE RBK PPM PGMT	adenosylmethionine-8-amino-7-oxononanoate transaminase acyl carrier protein synthase, mitochondrial transketolase transaketolase transaldolase transaldolase ribose-5-phosphate isomerase riboulose 5-phosphate 3-epimerase riboulose 5-phosphate 3-epimerase riboulose 5-phosphate 3-epimerase riboulose 5-phosphopentomutase phosphopentomutase phosphoglucomutase 6-phosphogluconolactonase phosphogluconate dehydrogenase	[c]: 8aonn + amet <==> amob + dann [m]: coa + h2o -> (2) h + pan4p + pap [c]: e4p + xu5p-D <==> f6p + g3p [c]: r5p + xu5p-D <==> g3p + s7p [c]: g3p + s7p <==> e4p + f6p [c]: r6p <==> ru5p-D [c]: ru5p-D <==> xu5p-D [c]: atp + rib-D -> adp + h + r5p [c]: r1p <==> r6p [c]: g1p <==> g6p	EC-4.1.1.11 EC-2.6.1.62 EC-2.2.1.1 EC-2.2.1.2 EC-5.3.1.6 EC-5.1.3.1 EC-2.7.1.15 EC-5.4.2.7 EC-5.4.2.2 EC-3.1.1.31	Pantothenate and CoA Biosynthesis Pantothenate and CoA Biosynthesis Pentose Phosphate Cycle	YPL148C (YPR074C or YBR117C) (YBR117C or YPR074C) (YLR354C or YGR043C) YOR095C YJL121C YCR036W (YKL127W or YMR105C) (YKL127W or YMR105C) (YNR034W or YHR163W or YGR248W or YCR073W-A)	Ppt2-m (Tkt1) or (Tkt2) or (Tkt2) or (Tkt2) or (Tkt3) (Tkt2) or (Tkt3)
ASPIDC AMAOTr ACPSm TKT2 TKT1 TALA RPI RPE RBK PPM PGMT G6PDH2er	adenosylmethionine-8-amino-7-oxononanoate transaminase acyl carrier protein synthase, mitochondrial transketolase transketolase transaldolase ribose-5-phosphate isomerase ribulose 5-phosphate 3-epimerase ribulose 5-phosphate 3-epimerase ribokinase phosphoglucomutase 6-phosphoglucomoutase phosphogluconolactonase phosphogluconate dehydrogenase glucose 6-phosphate dehydrogenase, endoplasmic reticular	[c]: 8aonn + amet <==> amob + dann [m]: coa + h2o -> (2) h + pan4p + pap [c]: e4p + xu5p-D <==> f6p + g3p [c]: r5p + xu5p-D <==> g3p + s7p [c]: g3p + s7p <==> e4p + f6p [c]: r5p <==> ru5p-D [c]: xu5p-D <==> xu5p-D [c]: xu5p-D <==> xu5p-D [c]: xu1p-D <==> xu5p-D [c]: r1p <==> r5p [c]: g1p <==> g6p [c]: g1p <==> g6p [c]: 6pgl + h2o> 6pgc + h [c]: 6pgc + nadp> co2 + nadph + ru5p-D [f]: g6p + nadp> 6pgl + h + nadph	EC-4.1.1.11 EC-2.6.1.62 EC-2.2.1.1 EC-2.2.1.2 EC-5.3.1.6 EC-5.1.3.1 EC-2.7.1.15 EC-5.4.2.7 EC-5.4.2.2 EC-3.1.1.31 EC-1.1.1.44	Pantothenate and CoA Biosynthesis Pantothenate and CoA Biosynthesis Pentose Phosphate Cycle	YPL148C (YPR074C or YBR117C) (YBR117C or YPR074C) (YLR354C or YGR043C) YOR095C YJL121C YCR036W (YKL127W or YMR105C) (YKL127W or YMR105C) (YNR034W or YHR163W or YGR043W-A) (YGR256W or YHR183W)	Ppt2-m (Tk11) or (Tk12) or (Tk12) or (Tk12) or (Tk11) (Tk11) or (Tal2) (Tk12) (Tk12) (Tk12) (Tk12) (Tk12) (Tk12) (Tk12) (Tk12) (Tk12) or (Pgm1) or (Pgm2) (Sol1) or (Sol4) or (Sol4) or (Sol2) (Gnd2) or (Gnd1)
ASPIDC AMAOTr ACPSm TKT2 TKT1 TALA RPI RPE RBK PPM PGMT G6PDH2er G6PDH2 DRBK	adenosylmethionine-8-amino-7-oxononanoate transaminase acyl carrier protein synthase, mitochondrial transketolase transketolase transaldolase ribose-5-phosphate isomerase ribulose 5-phosphate 3-epimerase ribulose 5-phosphate 3-epimerase ribosphopentomutase phosphopentomutase phosphoglucomutase 6-phosphogluconolactonase phosphogluconate dehydrogenase glucose 6-phosphate dehydrogenase, endoplasmic reticular glucose 6-phosphate dehydrogenase	[c]: 8aonn + amet <==> amob + dann [m]: coa + h2o -> (2) h + pan4p + pap [c]: e4p + xu5p-D <==> f6p + g3p [c]: r5p + xu5p-D <==> g3p + s7p [c]: g3p + s7p <==> e4p + f6p [c]: r5p <==> ru5p-D [c]: ru5p-D <==> xu5p-D [c]: atp + rib-D -> adp + h + r5p [c]: r1p <==> r5p [c]: r1p <==> r6p [c]: g1p <==> g6p [c]: g1p <=> p6p [c]: g1p <=> p6p [c]: 6pg + nadp -> 6pg + h + nadph [c]: g6p + nadp -> 6pg + h + nadph [c]: g6p + nadp -> 6pg + h + nadph [c]: g6p + nadp -> 6pg + h + nadph	EC-4.1.1.11 EC-2.6.1.62 EC-2.2.1.1 EC-2.2.1.2 EC-5.3.1.6 EC-5.1.3.1 EC-2.7.1.15 EC-5.4.2.7 EC-5.4.2.2 EC-3.1.1.31 EC-1.1.1.44 EC-1.1.1.49 EC-2.7.1.15	Pantothenate and CoA Biosynthesis Pantothenate and CoA Biosynthesis Pentose Phosphate Cycle	YPL148C (YPR074C or YBR117C) (YBR117C or YPR074C) (YLR354C or YGR043C) YOR095C YJL121C YCR036W (YKL127W or YMR105C) (YKL127W or YMR105C) (YNR034W or YHR163W or YGR248W or YCR073W-A) (YGR256W or YHR183W) YNL241C YCR036W	Ppt2-m (Tki1) or (Tki2) or (Tki2) or (Tki2) or (Tki1) or (Tal2) expending for the first period for the first perio
ASPIDC AMAOTr ACPSm TKT2 TKT1 TALA RPI RPE RBK PPM PGMT G6PDH2er G6PDH2 DRBK DRBK PSERSm_SC	adenosylmethionine-8-amino-7-oxononanoate transaminase acyl carrier protein synthase, mitochondrial transketolase transaketolase transaketolase transaketolase transaketolase ribose-5-phosphate isomerase riboise 5-phosphate 3-epimerase riboise 5-phosphate 3-epimerase ribokinase phosphopentomutase phosphoglucomutase 6-phosphoglucomolactonase phosphogluconate dehydrogenase glucose 6-phosphate dehydrogenase, endoplasmic reticular glucose 6-phosphate dehydrogenase Deoxyribokinase Deoxyribokinase Deoxyribokinase	[c]: 8aonn + amet <==> amob + dann [m]: coa + h2o -> (2) h + pan4p + pap [c]: e4p + xu5p-D <==> f6p + g3p [c]: r5p + xu5p-D <==> g3p + s7p [c]: g3p + s7p <==> e4p + f6p [c]: r5p <==> ru5p-D [c]: nu5p-D <==> xu5p-D [c]: nu5p-D <==> xu5p-D [c]: atp + rib-D -> adp + h + r5p [c]: r1p <==> r5p [c]: r1p <==> r5p [c]: g1p <==> g6p [c]: g1p <=> p6p [c]: g6pg + nadp -> 6pgg + h [c]: g6pg + nadp -> 6pgl + h + nadph [c]: g6p + nadp -> 6pgl + h + nadph [c]: g6p + nadp -> 6pgl + h + nadph [c]: g6p + nadp -> 6pgl + h + nadph [c]: atp + dilb -> 2dr5p + adp + h [m]: (0.01) cdpdagSC + ser_L <==> cmp + h + (0.01) ps_SC	EC-4.1.1.11 EC-2.6.1.62 EC-2.2.1.1 EC-2.2.1.2 EC-5.3.1.6 EC-5.1.3.1 EC-2.7.1.15 EC-5.4.2.7 EC-5.4.2.2 EC-3.1.1.31 EC-1.1.1.44 EC-1.1.1.49 EC-2.7.1.15 EC-2.7.1.15 EC-2.7.1.89	Pantothenate and CoA Biosynthesis Pantothenate and CoA Biosynthesis Pentose Phosphate Cycle	YPL148C (YPR074C or YBR117C) (YBR117C or YPR074C) (YLR354C or YGR043C) YOR095C YJL121C YCR036W (YKL127W or YMR105C) (YKL127W or YMR105C) (YNR034W or YHR163W or YGR248W or YCR073W-A) (YGR256W or YHR183W) YNL241C YCR036W YCR036W YCR036W YCR036W	Ppt2-m (Tkt1) or (Tkt2) or (Tkt2) or (Tkt2) or (Tkt1) (Tkt1) (Tal1) or (Tal2) (Tkt1) (Tgm1) or (Pgm2) (Pgm1) or (Pgm2) (Sol1) or (Sol4) or (Sol4) or (Sol2) (Gnd2) or (Gnd1) Zwf1 (Rbt1) (Cho1-m (Rbt1) or (Sol4) or (Sol4) or (Sol4) or (Sol5) (Sol7) (Sol6) (Sol7) (Sol7
ASPIDC AMAOTr ACPSm TKT2 TKT1 TALA RPI RPE RBK PPM PGMT PGL GRPDH2er GRPDH2er GRPDH2 DRBK PSERS_SC	adenosylmethionine-8-amino-7-oxononanoate transaminase acyl carrier protein synthase, mitochondrial transketolase transketolase transaldolase ribose-5-phosphate isomerase ribulose 5-phosphate 3-epimerase ribulose 5-phosphate 3-epimerase ribulose 5-phosphate 3-epimerase ribosphopentomutase phosphoplucomutase 6-phosphoglucomolactonase phosphogluconate dehydrogenase glucose 6-phosphate dehydrogenase, endoplasmic reticular glucose 6-phosphate dehydrogenase Deoxyribokinase phosphatidylserine synthase, yeast-specific, mitochondrial phosphatidylserine synthase, yeast-specific	[c]: 8aonn + amet <==> amob + dann [m]: coa + h2o -> (2) h + pan4p + pap [c]: e4p + xu5p-D <==> f6p + g3p [c]: r5p + xu5p-D <==> g3p + s7p [c]: g3p + s7p <==> e4p + f6p [c]: r6p <==> ru5p-D [c]: ru5p-D <==> xu5p-D [c]: atp + rib-D -> adp + h + r5p [c]: r1p <==> r5p [c]: r1p <==> r5p [c]: g1p <==> g6p [c]: g1p <==> g6p [c]: g1p <=>> g6p [c]: g1p <=>> g6p [c]: 6pg + nadp -> 6pg + h + nadph [c]: g6p + nadp -> 6pg + h + nadph [c]: g1p + nadp -> 6pg + h + nadph [c]: g1p + nadp -> 6pg + h + nadph [c]: g1p + nadp -> 6pg + h + nadph [c]: g1p + nadp -> 6pg + h + nadph [c]: g1p + nadp -> 6pg + h + nadph [c]: g1p + nadp -> 6pg + h + nadph [c]: g1p + nadp -> 6pg + h + nadph [c]: g1p + nadp -> 6pg + nadp -> 6pg + h + nadph [c]: g1p + nadp -> 6pg + nadp -> 6pg + h + nadph [c]: g1p + nadp -> 6pg + nadp -> 6pg + h + nadph [c]: g1p + nadp -> 6pg + nadp -> 6pg + h + nadph [c]: g1p + nadp -> 6pg + nadp -> 6pg + h + nadph [c]: g1p + nadp -> 6pg + nadp -> 6pg + h + nadph [c]: g1p + nadp -> 6pg + nadp -> 6pg + h + nadph [c]: g1p + nadp -> 6pg + nadp -> 6pg + h + nadph [c]: g1p + nadp -> 6pg + nadp -> 6pg + h + nadph [c]: g1p + nadp -> 6pg + nadp -> 6pg + h + nadph [c]: g1p + nadp -> 6pg + nadp -> 6pg + h + nadph [c]: g1p + nadp -> 6pg + nadp -> 6pg + h + nadph [c]: g1p + nadp -> 6pg + nadp -> 6pg + h + nadph	EC-4.1.1.11 EC-2.6.1.62 EC-2.2.1.1 EC-2.2.1.2 EC-5.3.1.6 EC-5.1.3.1 EC-2.7.1.15 EC-5.4.2.7 EC-5.4.2.2 EC-3.1.1.44 EC-1.1.1.49 EC-2.7.1.15 EC-2.7.8.8	Pantothenate and CoA Biosynthesis Pantothenate and CoA Biosynthesis Pentose Phosphate Cycle Phospholipid Biosynthesis Phospholipid Biosynthesis	YPL148C (YPR074C or YBR117C) (YBR117C or YPR074C) (YLR354C or YGR043C) YOR095C YJL121C YCR036W (YKL127W or YMR105C) (YKL127W or YMR105C) (YNR034W or YHR163W or YGR248W or YGR248W or YCR073W-A) (YGR256W or YHR183W) YNL241C YCR036W YER026C	Ppt2-m (Tki1) or (Tki2) (Tki2) or (Tki2) or (Tki2) or (Tai2) (Tki2) or (Tai2) (Tki2) or (Tai2) (Tki2) or (Tki2) (Tki2) or
ASPIDC AMAOTr ACPSm TKT2 TKT1 TALA RPI RPE RBK PPM PGMT G6PDH2er G6PDH2er G6PDH2D DRBK PSERS_SC PSERS_SC PSERS_SC PSERS_SC	adenosylmethionine-8-amino-7-oxononanoate transaminase acyl carrier protein synthase, mitochondrial transketolase transaldolase transaldolase transaldolase ribose-5-phosphate isomerase ribose-5-phosphate 3-epimerase ribulose 5-phosphate 3-epimerase ribulose 5-phosphate 3-epimerase phosphopentomutase phosphoglucomutase 6-phosphoglucomutase phosphogluconate dehydrogenase glucose 6-phosphate dehydrogenase, endoplasmic reticular glucose 6-phosphate dehydrogenase Deoxyribokinase phosphatidylserine synthase, yeast-specific, mitochondrial phosphatidylserine decarboxylase, yeast-specific phosphatidylserine decarboxylase, yeast-specific, vacuolar	[c]: 8aonn + amet <==> amob + dann [m]: coa + h2o -> (2) h + pan4p + pap [c]: e4p + xu5p-D <==> f6p + g3p [c]: r5p + xu5p-D <==> g3p + s7p [c]: g3p + s7p <==> e4p + f6p [c]: r5p <==> ru5p-D [c]: nu5p-D <==> xu5p-D [c]: nu5p-D <==> xu5p-D [c]: atp + rib-D -> adp + h + r5p [c]: r1p <==> r5p [c]: g1p <==> r5p [c]: g1p <==> r5p [c]: g1p <==> g6p [c]: 6pgl + h2o -> 6pgc + h [c]: 6pgc + nadp -> 6pgl + h + nadph [c]: g6p + nadp -> 6pgl + h + nadph [c]: g1p >=> dr5p + dap + h [c]: atp + drib ->> 2dr5p + adp + h [c]: atp + drib ->> 2dr5p + adp + h [c]: atp + drib ->> 2dr5p + adp + h [m]: (0.01) cdpdag_ SC + ser-L <==> cmp + h + (0.01) ps_ SC [c]: (0.01) cdpdag_ SC + ser-L <==> cmp + h + (0.01) ps_ SC [c]: (0.01) cdpdag_ SC + ser-L <==> cmp + h + (0.01) ps_ SC [c]: (0.01) cdpdag_ SC + ser-L <==> cmp + h + (0.01) ps_ SC [c]: (0.01) cdpdag_ SC + ser-L <==> cmp + h + (0.01) ps_ SC	EC-4.1.1.11 EC-2.6.1.62 EC-2.2.1.1 EC-2.2.1.2 EC-5.3.1.6 EC-5.3.1.6 EC-5.1.3.1 EC-2.7.1.15 EC-5.4.2.7 EC-5.4.2.2 EC-3.1.1.31 EC-1.1.1.44 EC-1.1.1.49 EC-2.7.8.8 EC-2.7.8.8 EC-2.7.8.8	Pantothenate and CoA Biosynthesis Pantothenate and CoA Biosynthesis Pentose Phosphate Cycle Phospholipid Biosynthesis Phospholipid Biosynthesis Phospholipid Biosynthesis	YPL148C (YPR074C or YBR117C) (YBR117C or YPR074C) (YLR354C or YGR043C) YOR095C YJL121C YCR036W (YKL127W or YMR105C) (YKL127W or YMR105C) (YNR034W or YHR163W or YGR248W or YCR073W-A) (YGR256W or YHR183W) YNL241C YCR036W YER026C YER026C YGR170W	Ppt2-m (Tki1) or (Tki2) (Tki2) or (Tki1) (Tki2) or (Tki1) (Tki2) or (Tal2) (Rki1) (Rpe1 (Rki1) (Rpe1) (Ryen1) or (Pgm2) (Sol1) or (Sol3) or (Sol3) or (Sol4) or (Gnd1) Zwf1 (Rki1) Zwf1 (Cho1-m (Cho1
ASPIDC AMAOTr ACPSm TKT2 TKT1 TALA RPI RPE RBK PPM PGMT PGL GND G6PDH2er G6PDH2 DRBK PSERSm SC PSERS_SC PSERS_SC PSERS_SC PSERD_SC	adenosylmethionine-8-amino-7-oxononanoate transaminase acyl carrier protein synthase, mitochondrial transketolase transketolase transaldolase ribose-5-phosphate isomerase ribolose 5-phosphate 3-epimerase ribolose 5-phosphate 3-epimerase ribokinase phosphopentomutase 6-phosphoglucomutase 6-phosphoglucomolactonase phosphogluconate dehydrogenase glucose 6-phosphate dehydrogenase, endoplasmic reticular glucose 6-phosphate dehydrogenase Deoxyribokinase phosphatidylserine synthase, yeast-specific, mitochondrial phosphatidylserine decarboxylase, yeast-specific, vacuolar phosphatidylserine decarboxylase, yeast-specific, mitochondrial	[c]: 8aonn + amet <==> amob + dann [m]: coa + h2o -> (2) h + pan4p + pap [c]: e4p + xu5p-D <==> f6p + g3p [c]: r5p + xu5p-D <==> g3p + s7p [c]: g3p + s7p <==> e4p + f6p [c]: r5p <==> ru5p-D [c]: ru5p-D <==> xu5p-D [c]: g1p <==> r5p [c]: r1p <==> r5p [c]: g1p <==> g6p [c]: g1p <==> g6p [c]: g6pg + nadp> 6pgl + h + nadph [c]: g6pg + nadp> 6pgl + h + nadph [c]: g6p + nadp> 6pgl + h + nadph [c]: g6p + nadp> 6pgl + h + nadph [c]: atp + drib> 2dri5p + adp + h [m]: (0.01) cdpdag _SC + ser-L <==> cmp + h + (0.01) ps _SC [c]: (0.01) cdpdag _SC + ser-L <==> cmp + h + (0.01) ps _SC [c]: (0.01) cdpdag _SC -> co2 + (0.01) ps _SC [m]: h + (0.01) ps _SC> co2 + (0.01) ps _SC [m]: h + (0.01) ps _SC> co2 + (0.01) ps _SC	EC-4.1.1.11 EC-2.6.1.62 EC-2.2.1.1 EC-2.2.1.2 EC-5.3.1.6 EC-5.1.3.1 EC-2.7.1.15 EC-5.4.2.7 EC-5.4.2.2 EC-3.1.1.31 EC-1.1.1.44 EC-1.1.1.49 EC-2.7.1.15 EC-2.7.1.8 EC-2.7.1.8 EC-2.7.1.8 EC-2.7.8.8 EC-4.1.1.65	Pantothenate and CoA Biosynthesis Pantothenate and CoA Biosynthesis Pentose Phosphate Cycle Pentose Phosphate Sycle Phospholipid Biosynthesis Phospholipid Biosynthesis Phospholipid Biosynthesis Phospholipid Biosynthesis	YPL148C (YPR074C or YBR117C) (YBR117C or YPR074C) (YLR354C or YGR043C) YOR095C YJL121C YCR036W (YKL127W or YMR105C) (YKL127W or YMR105C) (YNR034W or YHR163W or YGR248W or YGR248W or YGR248W or YGR246W or YGR036W YYCR073W-A) (YGR256W or YHR183W) YNL241C YCR036W YER026C YER026C YER026C YER026C YER026C YRN1169C	Ppt2-m
ASPIDC AMAOTr ACPSm TKT2 TKT1 TALA RPI RPI RPE RBK PPM PGMT PGL GND G6PDH2er G6PDH2er G6PDH2 DRBK PSERSm_SC PSERDy_SC PSERDy_SC PSERDy_SC PSERDy_SC PSERDy_SC	adenosylmethionine-8-amino-7-oxononanoate transaminase acyl carrier protein synthase, mitochondrial transketolase transaketolase transaldolase phosphate 3-epimerase tribulose 5-phosphate 3-epimerase phosphopentomutase phosphopentomutase phosphoglucomutase 6-phosphoglucomutase phosphogluconate dehydrogenase glucose 6-phosphate dehydrogenase, endoplasmic reticular glucose 6-phosphate dehydrogenase Deoxyribokinase phosphatidylserine synthase, yeast-specific, mitochondrial phosphatidylserine decarboxylase, yeast-specific, oligi apparatus	[c]: 8aonn + amet <==> amob + dann [m]: coa + h2c -> (2) h + pan4p + pap [c]: e4p + xu5p-D <==> f6p + g3p [c]: r5p + xu5p-D <==> g3p + s7p [c]: g3p + s7p <==> e4p + f6p [c]: r5p <==> ru5p-D [c]: ru5p-D <==> xu5p-D [c]: ru5p-D <==> xu5p-D [c]: ru5p-D <==> xu5p-D [c]: atp + rib-D -> adp + h + r5p [c]: g1p <==> r5p [c]: g1p <==> g6p [c]: 6pgl + h2c -> 6pgc + h [c]: 6pgc + nadp -> co2 + nadph + ru5p-D [r]: g6p + nadp -> 6pgl + h + nadph [r]: g1p <=> b6pl + h2c -> 6pgl + h + nadph [r]: g1p <=> co2 + ru5p + h + ru5p	EC-4.1.1.11 EC-2.6.1.62 EC-2.2.1.1 EC-2.2.1.2 EC-5.3.1.6 EC-5.1.3.1 EC-2.7.1.15 EC-5.4.2.7 EC-5.4.2.2 EC-3.1.1.44 EC-1.1.1.49 EC-2.7.1.15 EC-2.7.8.8 EC-4.1.1.65 EC-4.1.1.65 EC-4.1.1.65 EC-4.1.1.65 EC-4.1.1.65	Pantothenate and CoA Biosynthesis Pantothenate and CoA Biosynthesis Pentose Phosphate Cycle Phospholipid Biosynthesis Phospholipid Biosynthesis Phospholipid Biosynthesis Phospholipid Biosynthesis Phospholipid Biosynthesis Phospholipid Biosynthesis	YPL148C (YPR074C or YBR117C) (YBR117C or YPR074C) (YLR354C or YGR043C) YOR095C YJL121C YCR036W (YKL127W or YMR105C) (YKL127W or YMR105C) (YNR034W or YHR163W or YGR248W or YGR248W or YGR246W YCR073W-A) (YGR256W or YHR183W) YNL241C YCR036W YER026C YGR170W YNL169C YGR170W	Ppt2-m (Tki1) or (Tki2) (Tki2) or (Tki2) or (Tki2) or (Tal2) or (Tal2) (Tki2) or (Tal2) (Tki2) or (Pgm2) (Pgm1) or (Pgm2) (Pgm1) or (Sol3) or (Sol3) or (Sol3) or (Sol4) or (Gnd1) (Sol4) or (Gnd2) or (Tki2) (Sol4) or (Tki2)
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ASPIDC AMAOTr ACPSm TKT2 TKT1 TALA RPI RPE RBK PPM PGMT PGL GND G6PDH2er G6PDH2er G6PDH2 DRBK PSERSm SC PSERSD SC PSERDV_SC PSERDV_SC PSERDU_SC PSERDU_SC	adenosylmethionine-8-amino-7-oxononanoate transaminase acyl carrier protein synthase, mitochondrial transketolase transketolase transaldolase ribose-5-phosphate isomerase ribulose 5-phosphate 3-epimerase ribulose 5-phosphate 3-epimerase ribulosinase phosphopentomutase 6-phosphoglucomutase 6-phosphoglucomate dehydrogenase glucose 6-phosphate dehydrogenase, endoplasmic reticular glucose 6-phosphate dehydrogenase Deoxyribokinase phosphatidylserine synthase, yeast-specific, mitochondrial phosphatidylserine decarboxylase, yeast-specific, vacuolar phosphatidylserine decarboxylase, yeast-specific, oliqi apparatus Phosphatidylserine decarboxylase, yeast-specific, Golgi apparatus Phosphatidyls-methylethanolamine N-methyltransferase, yeast-specific phosphatidylinositol synthase, yeast-specific	[c]: 8aonn + amet <==> amob + dann [m]: coa + h2o -> (2) h + pan4p + pap [c]: e4p + xu5p-D <==> f6p + g3p [c]: r5p + xu5p-D <==> g3p + s7p [c]: g3p + s7p <==> e4p + f6p [c]: r5p <==> ru5p-D [c]: ru5p-D <==> xu5p-D [c]: ru5p-D <==> xu5p-D [c]: ru5p-D <==> xu5p-D [c]: atp + rib-D -> adp + h + r5p [c]: r1p <==> r5p [c]: g1p <==> r6p [c]: g1p <==> g6p [c]: g1p <==> g6p [c]: g1p <=>> g6p [c]: g6p + nadp -> 6pgl + h + nadph [c]: g6p + nadp -> 6pgl + h + nadph [c]: g6p + nadp -> 6pgl + h + nadph [c]: atp + drib -> 2dri5p + adp + h [m]: (0.01) cdpdag SC + ser-L <==> cmp + h + (0.01) ps SC [c]: (0.01) cdpdag SC + ser-L <==> cmp + h + (0.01) ps SC [c]: (0.01) ru5p SC -> co2 + (0.01) pe SC [m]: h + (0.01) ps SC -> co2 + (0.01) pe SC [c]: (0.01) ru5drag SC -> co2 + (0.01) pe SC [c]: (0.01) ru5drag SC -> co2 + (0.01) pe SC [c]: (0.01) ru5drage SC -> co2 + (0.01) pe SC [c]: (0.01) ru5drage SC -> co2 + (0.01) pe SC [c]: (0.01) ru5drage SC -> co2 + (0.01) pe SC [c]: (0.01) ru5drage SC -> co2 + (0.01) pe SC [c]: (0.01) ru5drage SC -> co2 + (0.01) pe SC [c]: (0.01) ru5drage SC -> co2 + (0.01) pe SC [c]: (0.01) ru5drage SC -> co2 + (0.01) pe SC [c]: (0.01) ru5drage SC -> co2 + (0.01) pe SC [c]: (0.01) ru5drage SC -> co2 + (0.01) pe SC [c]: (0.01) ru5drage SC -> co2 + (0.01) pe SC [c]: (0.01) ru5drage SC -> co2 + (0.01) pe SC [c]: (0.01) ru5drage SC -> co2 -> co2 + (0.01) pe SC [c]: (0.01) ru5drage SC -> co2 -> co2 + (0.01) pe SC [c]: (0.01) ru5drage SC -> co2 -> co2 -> co2 +> (0.01) pe SC [c]: (0.01) ru5drage SC -> co2 -> co2 -> co2 -> co2 +> (0.01) pe SC [c]: (0.01) ru5drage SC -> co2 -> c	EC-4.1.1.11 EC-2.6.1.62 EC-2.2.1.1 EC-2.2.1.2 EC-5.3.1.6 EC-5.1.3.1 EC-2.7.1.15 EC-5.4.2.7 EC-5.4.2.2 EC-3.1.1.31 EC-1.1.1.44 EC-1.1.1.49 EC-2.7.1.15 EC-2.7.1.85 EC-2.7.8.8 EC-4.1.1.65 EC-4.1.1.65 EC-4.1.1.65 EC-2.1.1.16	Pantothenate and CoA Biosynthesis Pantothenate and CoA Biosynthesis Pentose Phosphate Cycle Pentose Phosphate Sycle Phospholipid Biosynthesis	YPL148C (YPR074C or YBR117C) (YBR117C or YPR074C) (YLR354C or YGR043C) YOR095C YJL121C YCR036W (YKL127W or YMR105C) (YKL127W or YMR105C) (YNR034W or YHR163W or YGR248W or YGR248W or YGR248W or YGR246W or YGR256W or YHR183W) YNL241C YCR036W YER026C YER026C YGR170W YNL169C YGR170W YJR073C YPR113W	Ppt2-m
ASPIDC AMAOTr ACPSm TKT2 TKT1 TALA RPI RPE RBK PPM PGMT G6PDH2er G6PDH2er G6PDH2er G6PDH2 DRBK PSERS_SC PSERS_SC PSERD_SC PMETM_SC	adenosylmethionine-8-amino-7-oxononanoate transaminase acyl carrier protein synthase, mitochondrial transketolase transketolase transaldolase ribose-5-phosphate isomerase ribulose 5-phosphate 3-epimerase ribulose 5-phosphate 3-epimerase ribulose 6-phosphate 3-epimerase phosphopentomutase 6-phosphoglucomutase 6-phosphoglucomutase phosphogluconate dehydrogenase glucose 6-phosphate dehydrogenase, endoplasmic reticular glucose 6-phosphate dehydrogenase Deoxyribokinase phosphatidylserine synthase, yeast-specific, mitochondrial phosphatidylserine decarboxylase, yeast-specific, reticondrial phosphatidylserine decarboxylase, yeast-specific, mitochondrial phosphatidylserine decarboxylase, yeast-specific, mitochondrial phosphatidylserine decarboxylase, yeast-specific, mitochondrial phosphatidylserine decarboxylase, yeast-specific, mitochondrial phosphatidylserine decarboxylase, yeast-specific, oligi apparatus Phosphatidyl-N-methylterlansferase, yeast-specific	[c]: 8aonn + amet <==> amob + dann [m]: coa + h2o -> (2) h + pan4p + pap [c]: e4p + xu5p-D <==> f6p + g3p [c]: r5p + xu5p-D <==> g3p + s7p [c]: g3p + s7p <==> e4p + f6p [c]: r15p <==> ru5p-D [c]: nu5p-D <==> xu5p-D [c]: nu5p-D <==> xu5p-D [c]: r1p <==> r5p [c]: r1p <==> r5p [c]: g1p <==> r5p [c]: g1p <==> g6p [c]: 6pgl + h2o -> 6pgc + h [c]: 6pgc + nadp -> 6pgl + h + nadph [c]: g6p + nadp -> 6pgl + h + nadph [c]: g1p + rib-D -> 6pgl + h + nadph [c]: g1p <=> s6p [c]: a1p + d1b -> 2dr5p + adp + h [c]: a1p + d1b -> 2dr5p + adp + h [m]: (0.01) cdpdag_ SC + ser-L <==> cmp + h + (0.01) ps_SC (c): (0.01) cdpdag_ SC + ser-L <==> cmp + h + (0.01) ps_SC (c): (0.01) cdpdag_ SC -> co2 + (0.01) pe_SC (m): h + (0.01) ps_SC -> co2 + (0.01) pe_SC (m): h + (0.01) ps_SC -> co2 + (0.01) pe_SC (c): ame + (0.01) ps_SC -> co2 + (0.01) pe_SC (c): ame + (0.01) ps_SC -> co2 + (0.01) pe_SC (c): ame + (0.01) ps_SC -> co2 + (0.01) pe_SC (c): ame + (0.01) ps_SC -> co2 + (0.01) pe_SC (c): ame + (0.01) ps_SC -> co2 + (0.01) pe_SC (c): ame + (0.01) ps_SC -> co2 + (0.01) pe_SC (c): ame + (0.01) ps_SC -> co2 + co3 + ps_0 + h + (0.01) ps_SC -> co2 + (0.01) pe_SC (c): ame + (0.01) ps_SC -> co2 + (0.01) pe_SC (c): ame + (0.01) ps_SC -> co2 + (0.01) pe_SC (c): ame + (0.01) ps_SC -> co2 + (0.01) pe_SC (c): ame + (0.01) ps_SC -> co2 + (0.01) pe_SC (c): ame + (0.01) ps_SC -> co2 + (0.01) pe_SC (c): ame + (0.01) ps_SC -> co2 + (0.01) pe_SC (c): ame + (0.01) ps_SC -> co2 + (0.01) pe_SC (c): ame + (0.01) ps_SC -> co2 + (0.01) pe_SC (c): ame + (0.01) ps_SC -> co2 + (0.01) pe_SC (c): ame + (0.01) ps_SC -> co2 + (0.01) pe_SC (c): ame + (0.01) ps_SC -> co2 + (0.01) pe_SC (c): ame + (0.01) ps_SC -> co2 + (0.01) pe_SC (c): ame + (0.01) ps_SC -> co2 + (0.01) pe_SC (c): ame + (0.01) ps_SC -> co2 + (0.01) pe_SC (c): ame + (0.01) ps_SC -> co2 + (0.01) pe_SC (c): ame + (0.01) ps_SC -> co2 + (0.01) pe_SC (c): ame + (0.01) ps_SC	EC-4.1.1.11 EC-2.6.1.62 EC-2.2.1.1 EC-2.2.1.2 EC-5.3.1.6 EC-5.1.3.1 EC-2.7.1.15 EC-5.4.2.7 EC-5.4.2.2 EC-3.1.1.31 EC-1.1.1.44 EC-1.1.1.49 EC-2.7.1.15 EC-2.7.1.85 EC-2.7.8.8 EC-4.1.1.65 EC-4.1.1.65 EC-4.1.1.65 EC-2.1.1.16	Pantothenate and CoA Biosynthesis Pantothenate and CoA Biosynthesis Pantothenate and CoA Biosynthesis Pentose Phosphate Cycle Pentose Phosphate Sycle Pentose Phosphate Sycle Pentose Phosphate Sycle Phospholipid Biosynthesis	YPL148C (YPR074C or YBR117C) (YBR117C or YPR074C) (YLR354C or YGR043C) YOR095C YJL121C YCR036W (YKL127W or YMR105C) (YKL127W or YMR105C) (YNR034W or YHR163W or YGR248W or YGR248W or YGR246W or YGR073W-A) (YGR256W or YHR183W) YNL241C YCR036W YER026C YER026C YER026C YGR170W YNL169C YGR170W YJR073C	Ppt2-m (Tki1) or (Tki2) (Tki2) or (Tki2) or (Tki2) or (Tal2) or (Tal2) (Tki2) or (Tal2) (Tki2) or (Pgm2) (Pgm1) or (Pgm2) (Pgm1) or (Sol3) or (Sol3) or (Sol3) or (Sol4) or (Gnd2) or (Gnd1) (Zwf1 Rbk1 (Zwf1 (Zwf1 Rbk1 (Zwf1 (Zwf1 Rbk1 (Zwf1 (Zwf1 Rbk1 (Zwf1 (Zwf1 Rbk1 (Zwf1 (Zwf1 Rbk1 (Zwf1 (Zwf1 Rbk1 (Zwf1 (Zwf1 Rbk1 (Zwf1 (Zwf1 Rbk1 (Zwf1 R
ASPIDC AMAOTr ACPSm TKT2 TKT1 TALA RPI RPE RBK PPM PGMT PGL G6PDH2er G6PDH2er G6PDH2er G6PDH2 DRBK PSERS_SC PSERS_SC PSERS_SC PSERD_SC PINOS_SC PINOS_SC	adenosylmethionine-8-amino-7-oxononanoate transaminase acyl carrier protein synthase, mitochondrial transketolase transketolase transaldolase ribose-5-phosphate isomerase ribulose 5-phosphate 3-epimerase ribulose 5-phosphate 3-epimerase ribulosinase phosphopentomutase 6-phosphoglucomutase 6-phosphoglucomate dehydrogenase glucose 6-phosphate dehydrogenase, endoplasmic reticular glucose 6-phosphate dehydrogenase Deoxyribokinase phosphatidylserine synthase, yeast-specific, mitochondrial phosphatidylserine decarboxylase, yeast-specific, vacuolar phosphatidylserine decarboxylase, yeast-specific, oliqi apparatus Phosphatidylserine decarboxylase, yeast-specific, Golgi apparatus Phosphatidyls-methylethanolamine N-methyltransferase, yeast-specific phosphatidylinositol synthase, yeast-specific	[c]: 8aonn + amet <==> amob + dann [m]: coa + h2o -> (2) h + pan4p + pap [c]: e4p + xu5p-D <==> f6p + g3p [c]: r5p + xu5p-D <==> g3p + s7p [c]: g3p + s7p <==> e4p + f6p [c]: r5p <==> ru5p-D [c]: ru5p-D <==> xu5p-D [c]: ru5p-D <==> xu5p-D [c]: ru5p-D <==> xu5p-D [c]: atp + rib-D -> adp + h + r5p [c]: r1p <==> r5p [c]: g1p <==> r6p [c]: g1p <==> g6p [c]: g1p <==> g6p [c]: g1p <=>> g6p [c]: g6p + nadp -> 6pgl + h + nadph [c]: g6p + nadp -> 6pgl + h + nadph [c]: g6p + nadp -> 6pgl + h + nadph [c]: atp + drib -> 2dri5p + adp + h [m]: (0.01) cdpdag SC + ser-L <==> cmp + h + (0.01) ps SC [c]: (0.01) cdpdag SC + ser-L <==> cmp + h + (0.01) ps SC [c]: (0.01) ru5p SC -> co2 + (0.01) pe SC [m]: h + (0.01) ps SC -> co2 + (0.01) pe SC [c]: (0.01) ru5drag SC -> co2 + (0.01) pe SC [c]: (0.01) ru5drag SC -> co2 + (0.01) pe SC [c]: (0.01) ru5drage SC -> co2 + (0.01) pe SC [c]: (0.01) ru5drage SC -> co2 + (0.01) pe SC [c]: (0.01) ru5drage SC -> co2 + (0.01) pe SC [c]: (0.01) ru5drage SC -> co2 + (0.01) pe SC [c]: (0.01) ru5drage SC -> co2 + (0.01) pe SC [c]: (0.01) ru5drage SC -> co2 + (0.01) pe SC [c]: (0.01) ru5drage SC -> co2 + (0.01) pe SC [c]: (0.01) ru5drage SC -> co2 + (0.01) pe SC [c]: (0.01) ru5drage SC -> co2 + (0.01) pe SC [c]: (0.01) ru5drage SC -> co2 + (0.01) pe SC [c]: (0.01) ru5drage SC -> co2 + (0.01) pe SC [c]: (0.01) ru5drage SC -> co2 -> co2 + (0.01) pe SC [c]: (0.01) ru5drage SC -> co2 -> co2 + (0.01) pe SC [c]: (0.01) ru5drage SC -> co2 -> co2 -> co2 +> (0.01) pe SC [c]: (0.01) ru5drage SC -> co2 -> co2 -> co2 -> co2 +> (0.01) pe SC [c]: (0.01) ru5drage SC -> co2 -> c	EC-4.1.1.11 EC-2.6.1.62 EC-2.2.1.1 EC-2.2.1.2 EC-2.2.1.2 EC-5.3.1.6 EC-5.1.3.1 EC-2.7.1.15 EC-5.4.2.7 EC-5.4.2.2 EC-3.1.1.31 EC-1.1.1.44 EC-1.1.1.49 EC-2.7.1.8 EC-2.7.8.8	Pantothenate and CoA Biosynthesis Pantothenate and CoA Biosynthesis Pentose Phosphate Cycle Pentose Phosphate Sycle Phospholipid Biosynthesis	YPL148C (YPR074C or YBR117C) (YBR117C or YPR074C) (YLR354C or YGR043C) YOR095C YJL121C YCR036W (YKL127W or YMR105C) (YKL127W or YMR105C) (YNR034W or YHR163W or YGR248W or YGR248W or YGR248W or YGR246W or YGR256W or YHR183W) YNL241C YCR036W YER026C YER026C YGR170W YNL169C YGR170W YJR073C YPR113W	Ppt2-m

Page 19 Page			T				(Tor2) or (
Application				EC-			
	PIN3K_SC	1-phosphatidylinositol 3-kinase, yeast-specific	[c] : atp + (0.01) ptd1ino_SC> adp + h + (0.01) ptd3ino_SC	2.7.1.137	Phospholipid Biosynthesis	or YJR066W)	
150 150	DIADEK CC	phoophotish disposited 4 phoophoto 5 kinggo yearst appetin	[6] . etc. 1 (0.04) etd disc. CC. 2 edg. 1 b. 1 (0.04) etd 4 4 5 b. CC.	FC 2 7 4 60	Dheanhalinid Discunthesis	(VDD200M ex VED040M)	
Proc. Comparison Comparis							
Compared Systems of Proceedings of Processing Compared Systems of Processing Compared Syste			[c] : atp + (0.01) ptd3ino SC> adp + h + (0.01) ptd134bp SC	LO 0.1.4.11		11 220044	1101
### FTOM 50	PGPPAm_SC			EC-3.1.3.27			
Was before the production of	PETOHM_SC	phosphatidylethanolamine N-methyltransferase, yeast-specific		EC-2.1.1.17	Phospholipid Biosynthesis	YGR157W	Cho2
Proc. Proc	PETHCT		[c] : ctp + ethamp + h> cdpea + ppi	EC-2.7.7.14		YGR007W	Muq1
1979 Park							
Page 19							
10.000 10.000 10.0000 10.00000 10.000000 10.00000000 10.0000000 10.0000000 10.00000000 10.00000000 10.0000000 10.0000000000							
Proc. Pair Security Americans positioned from the process of t	WFAPS_SC	metrylene-ratty-acyr-priospriolipid synthase, yeast-specific	[c] . amet + (0.01) ptomeeta_SC> ancys + n + (0.01) ptozmeeta_SC	EC-2.1.1.16	Priospriolipia Biosynthesis	TJRU/3C	
Angle	LPP_SC	lipid phosphate phosphatase, yeast-specific			Phospholipid Biosynthesis	(YDR284C or YDR503C)	
April 20	GAT2_SC	glycerol 3-phosphate acyltransferase (glycerone phosphate), yeast-specific	pmtcoa + (0.05) stcoa + (0.1) tdcoa> (0.01) 1agly3p_SC + coa		Phospholipid Biosynthesis		
The Process Comment	0.74 00						
Comparison private product p			(0.27) pmtcoa + (0.05) stcoa + (0.1) tdcoa> (0.01) 1ag3p_SC + coa	E00704		VIIDAOOM	E-14
2007Pts COP Daspfyleroe symbols as passed minoteners 1	ETHAPI_SC				Phospholipid Biosynthesis		
250m							
### Section of the process of the pr							
Section Sect	DASTN_SC	CDF-Diacyigiyceror synthetase, yeast-specific	[6] . CLP + 11 + (0.01) pa_3C <> (0.01) Cupuag_3C + ppi	EC-2.7.7.41	Priospriolipia Biosynthesis	1 BR029C	
ACCPT SC Storoglopyrolar characteropsychological productions C C C C C C C C C	DAGPYP_SC	diacylglycerol pyrophosphate phosphatase, yeast-specific	[c]: h2o + (0.01) pa_SC> (0.01) 12dgr_SC + pi	EC-3.1.3.4	Phospholipid Biosynthesis	(YDR284C or YDR503C)	Lpp1)
2 PROS Completing symbols, year-specific, mitochondrial [ii] (0.01) rights, SC + (0.01) gs, SC - (0.01	DACCET SC	disculative and shall nonhoon het ranafarana, venat, anacifia	[a] - (0.01) 12dar SC + adaphal > amp + b + (0.01) pa SC	EC 2702	Dhoopholinid Riccunthooin	(VNII 120C or VHD122M)	
			[c] . (0.01) 120g1_SC + capcilot> crip + 11 + (0.01) pc_SC				
Combine ploughate opision/files registed/files re							
CPD-Supply service - propognization interface - propognization - propognizatio							
2000 Popular	CHEI CID		Calony + Cup + 11> Cupcilion + ppi	LC-2.7.7.13	Tiospriolipia biosyntitesis	161(2020	1 001
MGAT_BC 1-Ap-(-piperot-) principative and principative specific property principal (0.05) stock + (0.7) princip a (0.05) stock + (0.7) princip a (0.5) stock + (0.7) princip a (0.7) (0.7)	CDPDGPm_SC			EC-2.7.8.8	Phospholipid Biosynthesis	YCL004W	Pgs1-m
	AGAT SC	1-Acyl-glycerol-3-phosphate acyltraneferase, yeast-specific		FC-2 3 1 51	Phospholipid Riosynthesis	VDI 052C	Slc1
PPDC1				LO-2.3.1.31		TDE032C	OIC I
PPSS Unsportlyrinogen III synthase [] : Impli -> 120 + uppg3 EC 4.2.1.72 Porphyrin and Chlorophyl Metabolism VOR278W Hern4	7.D.1.7.1.1.C_00	asylamyarskyassishisphissishiais readstass, yeast opesine	[b] : (b.o.) haggsp_oo + n + haapn + (b.o.) hagop_oo + haap		Thoophishipia Biodynaticole		
PPSMT uncoophylmogen methyltransferase S (2) amert + uppg3 > (2) ahoys + h + shd 2.1.1.107 Pophyrin and Chlorophyll Metabolism VRR066W Met1	UPPDC1	uroporphyrinogen decarboxylase (uroporphyrinogen III)	[c]: (4) h + uppg3> (4) co2 + cpppg3	EC-4.1.1.37	Porphyrin and Chlorophyll Metabolism	YDR047W	Hem12
PPSMT unpophylmogen methylmaneferase C (2) amet + uppg3 - 2(2) ahorys + n + shd 2,1,1107 unphylm and Chiorophyll Metabolism VRR069W Met1	UPP3S	uroporphyrinogen-III synthase	[c] : hmbil> h2o + uppg3		Porphyrin and Chlorophyll Metabolism	YOR278W	Hem4
PBNGS porpholilinogen synthase ([: 2 Saop → h + 2 h20 + ppbng	UPP3MT	uroporphyrinogen methyltransferase	[c] : (2) amet + uppg3 -> (2) ahcys + h + shcl		Porphyrin and Chlorophyll Metabolism	YKR069W	Met1
MBS hydroxymethyblane synthase [c]: n2o + (4) pplmg → hmbl + (4) nh4	PPPGOm	protoporphyrinogen oxidase, mitochondrial	[m]: (3) o2 + (2) pppg9> (6) h2o + (2) ppp9	EC-1.3.3.4	Porphyrin and Chlorophyll Metabolism	YER014W	Hem14-m
MBS hydroxymethyblane synthase [c]: n2o + (4) pplmg → hmbl + (4) nh4	PPBNGS	porphobilinogen synthase	[c]: (2) 5aop> h + (2) h2o + ppbng	EC-4.2.1.24	Porphyrin and Chlorophyll Metabolism	YGL040C	Hem2
Ferrochelatase, mitochondrial m :fe2 + pp69 -> (2) h + pheme EC.4.99.11 Porphyrin and Chlorophyll Metabolism VOR176W Hem15-m Porphyrin							
Comport Composition Comp							
ALASM S-aminolevulinate synthase, milochondrial m]; gly + h + succoa -> 5aop + co2 + coa EC.2.3.1.37 Porphyrin and Chlorophyll Metabolism CP.23.1.37 Porphyrin and Pyrimidine Biosynthesis CP.23.1.37 Purine and Pyrimidine Biosynthesis CP.23.1.38 Purine and Pyrimidine Biosynthesis CP.23.1.39 Purine and Pyrimidine	FCLTm	Ferrochelatase, mitochondrial	[m] : fe2 + ppp9> (2) h + pheme	EC-4.99.1.1	Porphyrin and Chlorophyll Metabolism	YOR176W	Hem15-m
Company Com	CPPPGO	coproporphyrinogen oxidase (O2 required)	[c] : cpppg3 + (2) h + o2> (2) co2 + (2) h2o + pppg9	EC-1.3.3.3	Porphyrin and Chlorophyll Metabolism	YDR044W	Hem13
VILDORS VIMP synthetase (2) : f5p + ura <==> h2o + psd5p EC 4.2.1.70 Purine and Pyrimidine Biosynthesis VILOSW or YPL212C or Pbu32 or (YCLOSW or YPL212C or Pbu32) or (YCLOSW or YPL212C or YPL32W OR YPL212C or Pbu32) or (YCLOSW or YPL212C or Pbu32) or (YCLOSW or YPL212C or Pbu32) or (YCLOSW or YPL212C or YPL32W OR YPL212C or Pbu32) or (YCLOSW or YPL212C or YPL32W OR Y	ALASm	5-aminolevulinate synthase, mitochondrial	[m] : gly + h + succoa> 5aop + co2 + coa	EC-2.3.1.37	Porphyrin and Chlorophyll Metabolism	YDR232W	Hem1-m
VJMP synthetase C : fsp + ura <==> h2o + psd5p EC- 42.170 Purine and Pyrimidine Biosynthesis VGL063W or YNL292W Pus4 JRIK2 uridine kinase (GTP-Uridine) C : atp + uri → 2dp + h + ump EC- 27.148 Purine and Pyrimidine Biosynthesis VR012W Urk1 JRIK1 uridine kinase (ATP-Uridine) C : atp + uri → 2dp + h + ump EC- 27.148 Purine and Pyrimidine Biosynthesis VR012W Urk1 JRIK1 uridine kinase (ATP-Uridine) C : atp + uri → 2dp + h + ump EC- 27.148 Purine and Pyrimidine Biosynthesis VR012W Urk1 JRIK1 Uridine kinase (ATP-Uridine) C : atp + uri → 2dp + trid → 2dp + 2d							
URIK2				I			
Uridine kinase (ATP-Uridine) (c) : atp + uri → adp + th ump EC.2.71.48 Purine and Pyrimidine Biosynthesis VNR012W Urk1	YUMPS						
	URIK2						
TRDR							
FIDER thioredoxin reductase (NADPH) C : h + nadph + trdox -> nadp + trdrd EC.1.8.1.9 Purine and Pyrimidine Biosynthesis VOR353W Trd							
ITMDS thymidylate synthase C 3 dump + mlthf -> dhf + dtmp EC.2.1.1.45 Purine and Pyrimidine Biosynthesis YCR074C Cdc21			[m]: n + nadpn + trdox> nadp + trdrd				
TMDPP							
TMDK1 thymidine kinase (ATP:thymidine)							
PRFGS phosphoribosylformylglycinamidine synthase [c] : atp + fgam + gln-L + h 2c) -> adp + fpram + glu-L + h p i EC-6.3.6.3. Purine and Pyrimidine Biosynthesis YAR015W Ade for the phosphoribosylamino imidazole synthase (c) : 5aizc + asp-L + atp <==> 25aisc + adp + h p i EC-6.3.6. EC-6.3.6. Purine and Pyrimidine Biosynthesis YAR015W Ade for the phosphoribosylamino imidazole synthase (c) : atp + fpram -> adp + air + (2) h + p i EC-6.3.3. Purine and Pyrimidine Biosynthesis YGL234W Ade for the phosphoribosylgycinamide synthase (c) : atp + gly + pram <==> adp + gar + h + p i EC-6.3.4.13 Purine and Pyrimidine Biosynthesis YGL234W Ade for the phosphoribosylgycinamide synthase (c) : 35ccmp + h2o -> cmp + h EC-6.3.4.17 Purine and Pyrimidine Biosynthesis YGL234W Ade for the phosphoribosylgycinamide synthase (c) : 35ccmp + h2o -> cmp + h EC-3.1.4.17 Purine and Pyrimidine Biosynthesis YGR360C Pde for the phosphoribosylgycinamide synthase (c) : 35cgmp + h2o -> gmp + h EC-3.1.4.17 Purine and Pyrimidine Biosynthesis YGR360C Pde for the phosphoribosylgycinamide phosphodiesterase (c) : 35cgmp + h2o -> damp + h EC-3.1.4.17 Purine and Pyrimidine Biosynthesis YGR360C Pde for the phosphoribosylgycinamide phosphodiesterase (c) : 35cdmp + h2o -> damp + h EC-3.1.4.17 Purine and Pyrimidine Biosynthesis YGR360C Pde for the phosphoribosylgycinamide phosphodiesterase (c) : 35cdmp + h2o -> damp + h EC-3.1.4.17 Purine and Pyrimidine Biosynthesis YGR360C Pde for the phosphoribosylgycinamide phosphodiesterase (c) : 35cdmp + h2o -> damp + h EC-3.1.4.17 Purine and Pyrimidine Biosynthesis YGR360C Pde for the phosphoribosylgycinamide phos			[c] : etn + thymd -> edn + dtmn + h			I LRZUYC	Lub I
PRASCS phosphoribosylaminolimidazolesuccinocarboxamide synthase [c] : 5sizc + asp-L + atp <==> 25aics + adp + h + pi EC-6.3.2.6 Purine and Pyrimidine Biosynthesis YAR015W Ade1 PRAIS phosphoribosylaminolimidazole synthase [c] : atp + fpram → adp + air + (2) h + pi EC-6.3.3.1 Purine and Pyrimidine Biosynthesis YGL234W Ade5,7 PRAGSr phosphoribosylglycinamide synthase [c] : atp + fg/r pram <==> adp + gar + h + pi EC-6.3.4.13 Purine and Pyrimidine Biosynthesis YGL234W Ade5,7 PDE5 3',5'-cyclic-nucleotide phosphodiesterase [c] : 35ccmp + h2o →> cmp + h EC-3.1.4.17 Purine and Pyrimidine Biosynthesis YOR360C Pde2 PDE4 3',5'-cyclic-nucleotide phosphodiesterase [c] : 35cimp + h2o →> mp + h EC-3.1.4.17 Purine and Pyrimidine Biosynthesis YOR360C Pde2 PDE3 3',5'-cyclic-nucleotide phosphodiesterase [c] : 35cimp + h2o →> h + imp EC-3.1.4.17 Purine and Pyrimidine Biosynthesis YOR360C Pde2 PDE2 3',5'-cyclic-nucleotide phosphodiesterase [c] : 35cdmp + h2o →> damp + h EC-3.1.4.17 Purine and Pyrimidine Biosynthesis YOR360C Pde2 PDE1 3',5'-cycli			[c] : atp + fram + cln-l + h2o> adp + foram + cln-l + h + pi			YGR061C	Ade6
PRAIS phosphoribosylaminoimidazole synthase C 3 tp + fpram → 3 dp + air + (2) h + pi EC-6.3.3.1 Purine and Pyrimidine Biosynthesis YGL234W Ade5,7 PRAGSr phosphoribosylgycinamide synthase C 3 tp + gly + pram <==> adp + gar + h + pi EC-6.3.4.13 Purine and Pyrimidine Biosynthesis YGL234W Ade5,7 PRAGSr phosphoribosylgycinamide synthase C 3 tp + gly + pram <==> adp + gar + h + pi EC-6.3.4.17 Purine and Pyrimidine Biosynthesis YGR36W Ade5,7 PRAGSr phosphoribosylgycinamide synthase C 3 tp + gly + pram <==> adp + gar + h + pi EC-6.3.4.17 Purine and Pyrimidine Biosynthesis YGR36W Ade5,7 PRAGSr phosphoribosylgycinamide synthase C 3 tp + gly + pram <==> adp + gar + h + pi EC-6.3.4.17 Purine and Pyrimidine Biosynthesis YGR36W Ade5,7 PRAGSr phosphoribosylgycinamide synthase C 3 tp + gly + pram <==> adp + gar + h + pi EC-6.3.4.17 Purine and Pyrimidine Biosynthesis YGR36W Pde2 PDE4 3',5'-cyclic-nucleotide phosphodiesterase C 3 tp + pram + pi EC-3.1.4.17 Purine and Pyrimidine Biosynthesis YGR36W Pde2 PDE2 3',5'-cyclic-nucleotide phosphodiesterase C 3 tp + pram + pi EC-3.1.4.17 Purine and Pyrimidine Biosynthesis YGR36W Pde2 PDE4 3',5'-cyclic-nucleotide phosphodiesterase C 3 tp + pram + pi EC-3.1.4.17 Purine and Pyrimidine Biosynthesis YGR36W Pde2 PDE4 3',5'-cyclic-nucleotide phosphodiesterase C 3 tp + pram + pra							
PRAGSr phosphoribosylglycinamide synthase [c] : atp + gly + pram <=⇒ adp + gar + h + pi EC-6.3.4.13 Purine and Pyrimidine Biosynthesis YGL234W Ade5,7 PDE5 3;5-cyclic-nucleotide phosphodiesterase (c] : 35ccmp + h2o → cmp + h EC-3.1.4.17 Purine and Pyrimidine Biosynthesis YGR360C Pde2 PDE4 3;5-cyclic-nucleotide phosphodiesterase (c] : 35cgmp + h2o → gmp + h EC-3.1.4.17 Purine and Pyrimidine Biosynthesis YGR360C Pde2 PDE3 3;5-cyclic-nucleotide phosphodiesterase (c] : 35cdmp + h2o → h + imp EC-3.1.4.17 Purine and Pyrimidine Biosynthesis YGR360C Pde2 PDE4 3;5-cyclic-nucleotide phosphodiesterase (c] : 35cdmp + h2o → damp + h EC-3.1.4.17 Purine and Pyrimidine Biosynthesis YGR360C Pde2 PDE5 3;5-cyclic-nucleotide phosphodiesterase (c] : 35cdmp + h2o → damp + h EC-3.1.4.17 Purine and Pyrimidine Biosynthesis YGR360C Pde2 PDE6 3;5-cyclic-nucleotide phosphodiesterase (c] : camp + h2o → amp + h EC-3.1.4.17 Purine and Pyrimidine Biosynthesis YGR360C Pde2 PDE6 3;5-cyclic-nucleotide phosphodiesterase (c] : camp + h2o → amp + h EC-3.1.4.17 Purine and Pyrimidine Biosynthesis YGR360C Pde2 PDE7 0rotate phosphoribosyltransferase (c] : crot5p + ppi <=⇒ orot + prpp EC-2.4.2.10 Purine and Pyrimidine Biosynthesis YGR360C YMR271C Ura10 YMR271							
DE5 3',5'-cyclic-nucleotide phosphodiesterase G :35ccmp + h2o →> cmp + h EC.3.1.4.17 Purine and Pyrimidine Biosynthesis VOR360C Pde2							
2006 31,5°-cyclic-nucleotide phosphodiesterase C 35cgmp + h2o → gmp + h EC-3.1.4.17 Purine and Pyrimidine Biosynthesis YOR360C Pde2		3',5'-cyclic-nucleotide phosphodiesterase					
2023 3/.5-cyclic-nucleotide phosphodiesterase [c] : 35cimp + h2o -> h + imp EC-3.1.4.17 Purine and Pyrimidine Biosynthesis YOR360C Pde2	PDE4	3',5'-cyclic-nucleotide phosphodiesterase		EC-3.1.4.17	Purine and Pyrimidine Biosynthesis		
PDE2 3',5'-cyclic-nucleotide phosphodiesterase [c] : 35cdamp + h2o -> damp + h PDE3 3',5'-cyclic-nucleotide phosphodiesterase [c] : camp + h2o -> damp + h PDE4 3',5'-cyclic-nucleotide phosphodiesterase [c] : camp + h2o -> amp + h PDE5 3',5'-cyclic-nucleotide phosphodiesterase [c] : camp + h2o -> amp + h PDE6 3',5'-cyclic-nucleotide phosphodiesterase [c] : camp + h2o -> amp + h PDE7 0rotate phosphoribosyltransferase [c] : crot5p + ppi <==> orot + prpp PDE7 0rotate phosphoribosyltransferase [c] : crot5p + ppi <==> orot + prpp PDE8 3',5'-cyclic-nucleotide phosphodiesterase (YOR360C or YGL248W) (YOR360C or Y	PDE3	3',5'-cyclic-nucleotide phosphodiesterase	[c] : 35cimp + h2o> h + imp	EC-3.1.4.17	Purine and Pyrimidine Biosynthesis		Pde2
PDE1 3;5'-cyclic-nucleotide phosphodiesterase [c] : camp + h2o -> amp + h	PDE2						
(Ura5) or (ORPT orotate phosphoribosyltransferase [c]: orot5p + ppi <==> orot + prpp (C]: orot5p + ppi <==> orot + prpp (VML106W or YMR271C) (VmL106W or YM	PDE1						
						,	(Ura5) or (
	OMPDC						

IMPD	IMP dehydrogenase	[cl : h2o + imp + nad> h + nadh + xmp	EC- 1.1.1.205	Purine and Pyrimidine Biosynthesis	(YAR073W or YHR216W or YML056C or YLR432W or YAR075W)	(Imd1) or (Imd2) or (Imd4) or (Imd3) or (Imd5)
					,	(Ade16) or (
IMPC	IMP cyclohydrolase	[c] : h2o + imp <==> fprica		Purine and Pyrimidine Biosynthesis	(YLR028C or YMR120C)	Ade17)
GMPS2	GMP synthase	[c] : atp + gln-L + h2o + xmp> amp + glu-L + gmp + (2) h + ppi		Purine and Pyrimidine Biosynthesis	YMR217W	Gua1
GLUPRT GK2	glutamine phosphoribosyldiphosphate amidotransferase	[c] : gln-L + h2o + prpp> glu-L + ppi + pram [c] : datp + qmp <==> dadp + qdp		Purine and Pyrimidine Biosynthesis	YMR300C YDR454C	Ade4 Guk1
GK1	guanylate kinase (GMP:dATP) guanylate kinase (GMP:ATP)	[c] : atp + gmp <==> adp + gdp		Purine and Pyrimidine Biosynthesis Purine and Pyrimidine Biosynthesis	YDR454C	Guk1
GARFTI	phosphoribosylglycinamide formyltransferase, irreversible	[c] : 10fthf + gar> fgam + h + thf		Purine and Pyrimidine Biosynthesis	YDR408C	Ade8
DUTPDP	dUTP diphosphatase	[c] : dutp + h2o> dump + h + ppi		Purine and Pyrimidine Biosynthesis	YBR252W	Dut1
DURIPP	deoxyuridine phosphorylase	[c] : duri + pi <==> 2dr1p + ura	20 0.0.1.20	Purine and Pyrimidine Biosynthesis	YLR209C	Pnp1
DURIK1	deoxyuridine kinase (ATP:Deoxyuridine)	[c] : atp + duri> adp + dump + h		Purine and Pyrimidine Biosynthesis		·
DHORTSn	dihydroorotase, nuclear	[n] : dhor-S + h2o <==> cbasp + h	EC-3.5.2.3	Purine and Pyrimidine Biosynthesis	YJL130C	Ura2-n
DHORTS	dihydroorotase	[c] : dhor-S + h2o <==> cbasp + h	EC-3.5.2.3	Purine and Pyrimidine Biosynthesis	YLR420W	Ura4
DHORD4	dihydoorotic acid (ubiquinone-6)	dhor-S[c] + q6[m] <==> orot[c] + q6h2[m]		Purine and Pyrimidine Biosynthesis	YKL216W	Ura1
DHORD	dihydoorotic acid dehydrogenase	[c] : dhor-S + o2 <==> h2o2 + orot		Purine and Pyrimidine Biosynthesis	YKL216W	Ura1
DGK1	deoxyguanylate kinase (dGMP:ATP)	[c] : atp + dgmp <==> adp + dgdp		Purine and Pyrimidine Biosynthesis	YDR454C	Guk1
DCMPDA	dCMP deaminase	[c] : dcmp + h + h2o <==> dump + nh4		Purine and Pyrimidine Biosynthesis	YHR144C	Dcd1
CYTD CTPS2	cytidine deaminase CTP synthase (qlutamine)	[c] : cytd + h + h2o> nh4 + uri c : atp + gln-L + h2o + utp> adp + ctp + glu-L + (2) h + pi	EC-3.5.4.5 EC-6.3.4.2	Purine and Pyrimidine Biosynthesis Purine and Pyrimidine Biosynthesis	YLR245C (YBL039C or YJR103W)	Cdd1 (Ura7) or (Ura8)
	, , ,					(Ura7) or (
CTPS1 CSND	CTP synthase (NH3)	[c] : atp + nh4 + utp> adp + ctp + (2) h + pi		Purine and Pyrimidine Biosynthesis	(YBL039C or YJR103W) YPR062W	Ura8)
ATPATF3	Cytosine deaminase ATP adenylyltransferase	[c] : csn + h + h2o> nh4 + ura [c] : gdp + gtp + h> gp4g + pi		Purine and Pyrimidine Biosynthesis Purine and Pyrimidine Biosynthesis	YPR062W YCL050C	Fcy1 Apa1
ATPATF2	ATP adenylytransferase	[c] : adp + gtp + h> ap4g + pi		Purine and Pyrimidine Biosynthesis	YCL050C	Apa1
ATPATF1	ATP adenylytransferase	[c] : adp + gtp + n> ap4g + pi		Purine and Pyrimidine Biosynthesis	YDR530C	Apa2
ASPCTn	aspartate carbamoyltransferase, nuclear	[n] : asp-L + cbp> cbasp + h + pi		Purine and Pyrimidine Biosynthesis	YJL130C	Ura2-n
AP4AHr	Ap4A hydrolase, reversible	[c] : ap4a + h2o <==> (2) adp + (2) h		Purine and Pyrimidine Biosynthesis	YDR305C	Hnt2
AMPDA	Adenosine monophosphate deaminase	[c]: amp + h + h2o> imp + nh4		Purine and Pyrimidine Biosynthesis	YML035C	Amd1
AIRCr	phosphoribosylaminoimidazole carboxylase	[c] : air + co2 <==> 5aizc + h	EC-4.1.1.21	Purine and Pyrimidine Biosynthesis	YOR128C	Ade2
AICART	phosphoribosylaminoimidazolecarboxamide formyltransferase	[c] : 10fthf + aicar <==> fprica + thf	EC-2.1.2.3	Purine and Pyrimidine Biosynthesis	(YLR028C or YMR120C)	(Ade16) or (Ade17)
ADSS	adenylosuccinate synthase	[c]: asp-L + gtp + imp> dcamp + gdp + (2) h + pi		Purine and Pyrimidine Biosynthesis	YNL220W	Ade12
ADSL2r	adenylosuccinate lyase	[c] : 25aics <==> aicar + fum	EC-4.3.2.2	Purine and Pyrimidine Biosynthesis	YLR359W	Ade13
ADSL1r	adenylsuccinate lyase	[c] : dcamp <==> amp + fum		Purine and Pyrimidine Biosynthesis	YLR359W	Ade13
ADNCYC	adenylate cyclase	[c] : atp> camp + ppi		Purine and Pyrimidine Biosynthesis	YJL005W	Cyr1
PYDXO	pyridoxal oxidase	[c]: (2) h2o + nh4 + (0.5) o2 + pydx <==> (2) h2o2 + pydam		Pyridoxine Metabolism	YBR035C	Pdx3
PYDXNO	pyridoxine oxidase	[c] : o2 + pydxn <==> h2o2 + pydx	EC-1.4.3.5	Pyridoxine Metabolism	YBR035C	Pdx3
PYDXNK PYDXK	pyridoxine kinase	[c] : atp + pydxn> adp + h + pdx5p	EC-2.7.1.35	Pyridoxine Metabolism Pyridoxine Metabolism		
PYDAK	pyridoxal kinase	[c] : atp + pydx> adp + h + pydx5p		Pyridoxine Metabolism Pyridoxine Metabolism		
PYAM5PO	pyridoxamine kinase pyridoxamine 5'-phosphate oxidase	[c] : atp + pydam> adp + h + pyam5p [c] : h2o + o2 + pyam5p> h2o2 + nh4 + pydx5p	EC-2.7.1.35 EC-1.4.3.5	Pyridoxine Metabolism	YBR035C	Pdx3
PDX5PO	pyridoxinii e 5-priospriate oxidase pyridoxine 5'-phosphate oxidase	[c] : 02 + pdx5p <==> h2o2 + pydx5p	EC-1.4.3.5	Pyridoxine Metabolism	YBR035C	Pdx3
OHPBAT	O-Phospho-4-hydroxy-L-threonine:2-oxoglutarate aminotransferase	[c] : glu-L + ohpb <==> akg + phthr		Pyridoxine Metabolism	YOR184W	Ser1
HYPOE	hypothetical enyme	[c] : h2o + pyam5p> pi + pydam	20 2:0:1:02	Pyridoxine Metabolism	101110111	
PYRDC	pyruvate decarboxylase	[c]: h + pyr> acald + co2	EC-4.1.1.1	Pyruvate metabolism	(YGR087C or YLR134W or YLR044C)	(Pdc6) or (Pdc5) or (Pdc1)
HCITSn	homocitrate synthase, nuclear	[n] : accoa + akg + h2o> coa + h + hcit	EC-4.1.3.21	Pyruvate metabolism	(YDL131W or YDL182W)	(Lys21-n) or (Lys20-n)
HCITSm	homocitrate synthase, mitochondrial	[m] : accoa + akg + h2o> coa + h + hcit	EC-4.1.3.21	Pyruvate metabolism		
FALDH	formaldehyde dehydrogenase	[c] : fald + gthrd + nad <==> Sfglutth + h + nadh	EC-1.2.1.1	Pyruvate metabolism	YDL168W	Sfa1
ALCD2x	alcohol dehydrogenase (ethanol)	[c] : etoh + nad <==> acald + h + nadh		Pyruvate metabolism	(YGL256W or YBR145W or YDL168W or YOL086C or YMR303C)	(Adh4) or (Adh5) or (Sfa1) or (Adh1) or (Adh2)
ACSp	acetyl-CoA synthetase	[x] : ac + atp + coa> accoa + amp + ppi		Pyruvate metabolism	YAL054C	Acs1-p
ACSm	acetyl-CoA synthetase, mitochondrial	[m] : ac + atp + coa> accoa + amp + ppi		Pyruvate metabolism	YAL054C	Acs1-m
ACS	acetyl-CoA synthetase	[c] : ac + atp + coa> accoa + amp + ppi		Pyruvate metabolism	YLR153C	Acs2
ACOAH	acetyl-CoA hydrolase	[c] : ac + coa + h> accoa + h2o	EC-3.1.2.1	Pyruvate metabolism	YBL015W	Ach1
OPHHX6	2-Octaprenylphenol hydroxylase	[c] : 2oph_5 + (0.5) o2> 2oph_5	1	Quinone Biosynthesis	VDDE20W	Dodd
OPHBDC6 OMPHHX6m	Octaprenyl-hydroxybenzoate decarboxylase 2-octaprenyl-6-methoxyphenol hydroxylase, mitochondrial	[c] : 3ophb_5 + h> 2oph_5 + co2 [m] : 2omph_5 + (0.5) o2> 2ombzl_5	1	Quinone Biosynthesis Quinone Biosynthesis	YDR538W	Pad1
OMPHEX6m OMMBLHX6m			1	0 1 81 / // 1	YGR255C	Coa6-m
OMBZLM6m	2-Octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase, mitochodnrial 2-Octaprenyl-6-methoxy-benzoquinol methylase, mitochodnrial	[m] : 2ommbl_5 + (0.5) o2> 2omnmbl_5 [m] : 2ombzl_5 + amet> 2ommbl_5 + ahcys + h	1	Quinone Biosynthesis Quinone Biosynthesis	YML110C	Coq6-m Coq5-m
OHPHM6n	2-octaprenyl-6-hydroxyphenol methylase, nuclear	[n] : 20hbb1_5 + amet> 20hhbb_5 + ahcys + h	1	Quinone Biosynthesis	YPL266W	Dim1-n
HBZOPT6m	Hydroxybenzoate octaprenyltransferase, mitochondrial	[m] : 4hbz + octdp_5> 3ophb_5 + ppi		Quinone Biosynthesis	(YPL172C or YNR041C or YBR003W)	(Cox10-m) or
					YKL019W) or (YJL031C and YPR176C) or YMR101C or (YDL090C and YKL019W) or	(Ggt1) or (Bet24) or (Srt1) or (Ram12) or (
HBZOPT6	Hydroxybenzoate octaprenyltransferase	[c] : 4hbz + octdp_5> 3ophb_5 + ppi	1	Quinone Biosynthesis	YBR002C)	Rer2)
DMQMT6m CHRPL	3-Dimethylubiquinonol 3-methyltransferase, mitochondrial Chorismate pyruvate lyase	[m] : 2omhmbl_5 + amet> ahcys + h + q6h2		Quinone Biosynthesis Quinone Biosynthesis	YOL096C (YKL211C or YER090W)	Coq3-m (Trp3) or (Trp2)
OFFICE	Ononomate pyruvate tyase	[c] : chor> 4hbz + pyr		Quinone biosynthesis	(INLETTO OF TEROSON)	1165)

RBFSb	riboflavin synthase	[c] : (2) dmlz> 4r5au + ribflv	EC-2.5.1.9	Riboflavin Metabolism	YBR256C	Rib5
RBFSa	riboflavin synthase	[c] : 4r5au + db4p> dmlz + (2) h2o + pi	EC-2.5.1.9	Riboflavin Metabolism	YOL143C	Rib4
RBFKm	riboflavin kinase, mitochondrial	[m] : atp + ribflv> adp + fmn + h		Riboflavin Metabolism	YDR236C	Fmn1-m
RBFK	riboflavin kinase	[c] : atp + ribflv> adp + fmn + h		Riboflavin Metabolism	YDR236C	Fmn1
PMDPHT	pyrimidine phosphatase	[c] : 5aprbu + h2o> 4r5au + pi	20 2.7.11.20	Riboflavin Metabolism	12.12000	
GTPCII	GTP cyclohydrolase II	[c] : gtp + (3) h2o> 25dhpp + for + (2) h + ppi	EC 3 5 4 25	Riboflavin Metabolism	YBL033C	Rib1
FMNATm				Riboflavin Metabolism	T BLUSSC	KIDT
	FMN adenylyltransferase, mitochondrial	[m] : atp + fmn + h> fad + ppi			VDL0450	E - 14
FMNAT	FMN adenylyltransferase	[c] : atp + fmn + h> fad + ppi	EC-2.7.7.2		YDL045C	Fad1
DHPPDA	diaminohydroxyphosphoribosylaminopyrimidine deaminase	[c] : 25dhpp + h + h2o> 5apru + nh4	EC-3.5.4.26	Riboflavin Metabolism	YBR153W	Rib7
DB4PS	3,4-Dihydroxy-2-butanone-4-phosphate	[c] : ru5p-D> db4p + for + h		Riboflavin Metabolism		
APRAUR	5-amino-6-(5-phosphoribosylamino)uracil reductase	[c] : 5apru + h + nadph> 5aprbu + nadp	EC-	Riboflavin Metabolism	YBR153W	Rib7
ACP1e	acid phosphatase, extracellular (secreted)	[e] : fmn + h2o> pi + ribflv	EC-3.1.3.2	Riboflavin Metabolism	YAR071W	Pho11-e
SPHPL	sphinganine phosphate lyase	[c] : sph1p> ethamp + hxdcal		Sphingolipid Metabolism	YDR294C	Dpl1
						(Lcb4) or (
SLCBK2	sphingolipid long chain base kinase (phytosphingosine)	[c]: atp + psphings> adp + h + psph1p		Sphingolipid Metabolism	(YOR171C or YLR260W)	Lcb5)
	in the second se	fall and beliands and a beliant		Springer production	(,	(Lcb5) or (
SLCBK1	sphingolipid long chain base kinase (sphinganine)	[c]: atp + sphqn> adp + h + sph1p		Sphingolipid Metabolism	(YLR260W or YOR171C)	Lcb4)
SEOBILI	Spriingolipid long chain base kinase (spriinganine)	[c] ap + spiign> aup + ii + spiirp		Ophingolipia Wetabolisin	(YDR062W and YMR296C	LCD4)
SERPT	serine C-palmitovltransferase	[c]: h + pmtcoa + ser-L> 3dsphgn + co2 + coa	EC 221 E0	Sphingolipid Metabolism	(TDIXOOZVV and TWIX290C	Lcb
SERF I	Serille G-pairiiloyittarisierase	[c] . II + pilitoa + Sei-L> Susprigii + Co2 + Coa	EC-2.3.1.50	Spriingolipiu wetabolism	,	
00000					()((0.01)	(Lcb3) or (
SBPP2	sphingoid base-phosphate phosphatase (phytosphingosine 1-phosphate)	[c]: h2o + psph1p> pi + psphings		Sphingolipid Metabolism	(YJL134W or YKR053C)	Ysr3)
						(Lcb3) or (
SBPP1	sphingoid base-phosphate phosphatase (sphinganine 1-phosphatase)	[c] : h2o + sph1p> pi + sphgn		Sphingolipid Metabolism	(YJL134W or YKR053C)	Ysr3)
PSPHS	Phytosphingosine synthesis	[c]: h + nadph + o2 + sphgn> h2o + nadp + psphings		Sphingolipid Metabolism	YDR297W	Sur2
PSPHPL	phytosphingosine phosphate lyase	[c] : psph1p> 2hhxdal + ethamp		Sphingolipid Metabolism	YDR294C	Dpl1
	mannose-inositol phosphorylceramide synthase (ceramide-3, 26C), yeast-					(Csg2) or (
MIPCS326_SC	specific	[c]: gdpmann + (0.01) ipc326_SC> gdp + h + (0.01) mipc326_SC	1	Sphingolipid Metabolism	(YBR036C or YPL057C)	Sur1)
30020_00	mannose-inositol phosphorylceramide synthase (ceramide-3, 24C), yeast-	[-] - 3		ganpia motaboliom	((Csg2) or (
MIPCS324_SC	specific	[c]: gdpmann + (0.01) ipc324_SC> gdp + h + (0.01) mipc324_SC	1	Sphingolipid Metabolism	(YBR036C or YPL057C)	Sur1)
IVIII 00027_00		[0] . gapmam - (0.01) ipooz=_00 gup + ii + (0.01) iiiipooz=_00	+	Oprimigoripiu ivietabolisiii	(IBNOSCO OF TELOS/C)	
MIDODOO CC	mannose-inositol phosphorylceramide synthase (ceramide-2, 26C), yeast-	[1]	1	Onblood Bold Matel 12	()/DD0000 1/5: 0===	(Csg2) or (
MIPCS226_SC	specific	[c] : gdpmann + (0.01) ipc226_SC> gdp + h + (0.01) mipc226_SC		Sphingolipid Metabolism	(YBR036C or YPL057C)	Sur1)
	mannose-inositol phosphorylceramide synthase (ceramide-2, 24C), yeast-					(Csg2) or (
MIPCS224_SC	specific	[c] : gdpmann + (0.01) ipc224_SC> gdp + h + (0.01) mipc224_SC		Sphingolipid Metabolism	(YBR036C or YPL057C)	Sur1)
	mannose-inositol phosphorylceramide synthase (ceramide-1, 26C), yeast-					(Csg2) or (
MIPCS126_SC	specific	[c] : gdpmann + (0.01) ipc126_SC> gdp + h + (0.01) mipc126_SC		Sphingolipid Metabolism	(YBR036C or YPL057C)	Sur1)
_						(Csg2) or (
MIPCS124_SC	mannose-inositiol phophorylceramide synthase (ceramide-1, 24C), yeast-specific	[c]: gdpmann + (0.01) ipc124_SC> gdp + h + (0.01) mipc124_SC		Sphingolipid Metabolism	(YBR036C or YPL057C)	Sur1)
MIP2CS326_SC	mannose-(inositol-P)2-ceramide synthase (ceramide-3, 26C), yeast-specific	[c] : (0.01) mipc326_SC + (0.01) ptd1ino_SC> (0.01) 12dgr_SC + (0.01) mip2c326_SC		Sphingolipid Metabolism	YDR072C	lpt1
MIP2CS324 SC	mannose-(inositol-P)2-ceramide synthase (ceramide 3, 24C), yeast specific	[c] : (0.01) mipc324_SC + (0.01) ptd1ino_SC> (0.01) 12dgr_SC + (0.01) mip2c324_SC		Sphingolipid Metabolism	YDR072C	lpt1
MIP2CS226_SC	mannose-(inositol-P)2-ceramide synthase (ceramide-3, 24C), yeast-specific	[c]: (0.01) mipc234_3C + (0.01) ptd find_3C => (0.01) 12dgr_3C + (0.01) mip2c324_3C		Sphingolipid Metabolism	YDR072C	lpt1
MIP2CS224 SC		[c] : (0.01) mipc225_3C + (0.01) ptd fino_3C> (0.01) 12dgr_3C + (0.01) mip2c226_3C				·
	mannose-(inositol-P)2-ceramide synthase (ceramide-2, 26C), yeast specific			Sphingolipid Metabolism	YDR072C	lpt1
MIP2CS126_SC	mannose-(inositol-P)2-ceramide synthase (ceramide-1, 26C), yeast-specific	[c]: (0.01) mipc126_SC + (0.01) ptd1ino_SC> (0.01) 12dgr_SC + (0.01) mip2c126_SC		Sphingolipid Metabolism	YDR072C	lpt1
MIP2CS124_SC	mannose-(inositol-P)2-ceramide synthase (ceramide-1, 24C), yeast-specific	[c]: (0.01) mipc124_SC + (0.01) ptd1ino_SC> (0.01) 12dgr_SC + (0.01) mip2c124_SC		Sphingolipid Metabolism	YDR072C	lpt1
IPCS326_SC	Inositol phosphorylceramide synthase (ceramide-3, 26C), yeast-specific	[c] : cer3_26 + (0.01) ptd1ino_SC> (0.01) 12dgr_SC + (0.01) ipc326_SC		Sphingolipid Metabolism	YKL004W	Aur1
IPCS324_SC	Inositol phosphorylceramide synthase (ceramide-3, 24C), yeast-specific	[c] : cer3_24 + (0.01) ptd1ino_SC> (0.01) 12dgr_SC + (0.01) ipc324_SC		Sphingolipid Metabolism	YKL004W	Aur1
IPCS226_SC	Inositol phosphoryceramide synthase (ceramide-2, 26C), yeast-specific	[c] : cer2_26 + (0.01) ptd1ino_SC> (0.01) 12dgr_SC + (0.01) ipc226_SC		Sphingolipid Metabolism	YKL004W	Aur1
IPCS224_SC	Inositol phosphorylceramide synthase (ceramide-2, 24C), yeast-specific	[c] : cer2_24 + (0.01) ptd1ino_SC> (0.01) 12dgr_SC + (0.01) ipc224_SC		Sphingolipid Metabolism	YKL004W	Aur1
IPCS126 SC	Inositol phosphorylceramide synthase (ceramide-1, 26C), yeast-specific	[c]: cer1_26 + (0.01) ptd1ino_SC> (0.01) 12dgr_SC + (0.01) ipc126_SC		Sphingolipid Metabolism	YKL004W	Aur1
IPCS124_SC	Inositol phosphorylceramide synthase (ceramide-1, 24C), yeast-specific	[c] : cer1_24 + (0.01) ptd1ino_SC> (0.01) 12dgr_SC + (0.01) ipc124_SC		Sphingolipid Metabolism	YKL004W	Aur1
CERS326	Ceramide-3 synthase (26C)	[c] : cer2_26 + h + nadph + o2> cer3_26 + h2o + nadp		Sphingolipid Metabolism	YMR272C	Scs7
CERS324	Ceramide-3 synthase (24C)	[c] : cer2_24 + h + nadph + o2> cer3_24 + h2o + nadp		Sphingolipid Metabolism	YMR272C	Scs7
CERS226	Ceramide-2 synthase (26C)	[c] : hexccoa + psphings> cer2_26 + coa + h		Sphingolipid Metabolism	TWITETEG	0001
			_			
CERS224	Ceramide-2 synthase (24C)	[c] : psphings + ttccoa> cer2_24 + coa + h		Sphingolipid Metabolism	VA IDORGO	0 =
CERS2'26	Ceramide-2' synthase (26C)	[c] : cer1_26 + h + nadph + o2> cer2'_26 + h2o + nadp		Sphingolipid Metabolism	YMR272C	Scs7
CERS2'24	Ceramide-2' synthase (24C)	[c] : cer1_24 + h + nadph + o2> cer2'_24 + h2o + nadp		Sphingolipid Metabolism	YMR272C	Scs7
CERS126	Ceramide-1 synthase (26C)	[c]: hexccoa + sphgn> cer1_26 + coa + h		Sphingolipid Metabolism		<u> </u>
CERS124	Ceramide-1 synthase (24C)	[c]: sphgn + ttccoa> cer1_24 + coa + h		Sphingolipid Metabolism		
CERH126	Ceramide-1 hydroxylase (26C)	[c] : cer1_26 + h + nadph + o2> cer2_26 + h2o + nadp		Sphingolipid Metabolism	YDR297W	Sur2
CERH124	Ceramide-1 hydroxylase (24C)	[c] : cer1_24 + h + nadph + o2> cer2_24 + h2o + nadp		Sphingolipid Metabolism	YDR297W	Sur2
3DSPHR	3-Dehydrosphinganine reductase	[c]: 3dsphgn + h + nadph> nadp + sphgn	EC-	Sphingolipid Metabolism	YBR265W	Tsc10
						(Spr1-e) or (
			1		(YOR190W or YDR261C	Exg2-e) or (
13BGHe	Exo-1,3-beta-glucan glucohydrase, extracellular	[e]: 13BDglcn + h2o> glc-D	EC-3 2 1 58	Starch and sucrose metabolism	or YLR300W)	Exg1-e)
13BGH	Endo-1,3-beta-glucan glucohydrase	[c] : 13BDglcn + h2o> glc-D		Starch and sucrose metabolism	YGR282C	Bgl2
SQLS	Squalene synthase	[c] : (2) frdp + h + nadph> nadp + (2) ppi + sql		Sterol Biosynthesis	YHR190W	Erg9
SQLEer		[r] : h + nadph + o2 + sql> Ssq23epx + h2o + nadp	EC-2.5.1.21	Sterol Biosynthesis	YGR175C	
	Squalene epoxidase, endoplasmic reticular	[r] : n + nadpn + oz + sqi> Ssqz3epx + nzo + nadp [c] : amet + zvmst> ahcvs + fecost + h		Sterol Biosynthesis		Erg1-er
SAM24MT	S-adenosyl-methionine delta-24-sterol-c-methyltransferase				YML008C	Erg6
PMEVK	phosphomevalonate kinase	[c] : 5pmev + atp> 5dpmev + adp		Sterol Biosynthesis	YMR220W	Erg8
MEVK4	mevalonate kinase (utp)	[c] : mev-R + utp> 5pmev + h + udp		Sterol Biosynthesis	YMR208W	Erg12
	mevalonate kinase (gtp)	[c] : gtp + mev-R> 5pmev + gdp + h		Sterol Biosynthesis	YMR208W	Erg12
MEVK3		[c] : ctp + mev-R> 5pmev + cdp + h		Sterol Biosynthesis	YMR208W	Erg12
MEVK2	mevalonate kinase (ctp)			Internal Discountly and	YMR208W	Erg12
MEVK2 MEVK1	mevalonate kinase (ctp) mevalonate kinase (atp)	[c] : atp + mev-R> 5pmev + adp + h		Sterol Biosynthesis	TIVITAZOOVV	
MEVK2	mevalonate kinase (atp) lanosterol synthase	[c] : atp + mev-R> 5pmev + adp + h [c] : Ssq23epx> lanost		Sterol Biosynthesis	YHR072W	Erg7
MEVK2 MEVK1	mevalonate kinase (atp) lanosterol synthase			Sterol Biosynthesis		Erg7 Erg11
MEVK2 MEVK1 LNSTLS LNS14DM	mevalonate kinase (atp) lanosterol synthase cytochrome P450 lanosterol 14-alpha-demethylase	[c] : Ssq23epx> lanost [c] : (2) h + lanost + (3) nadph + (3) o2> 44mctr + for + (4) h2o + (3) nadp	EC-5.4.99.7 EC-	Sterol Biosynthesis Sterol Biosynthesis	YHR072W YHR007C	Erg11
MEVK2 MEVK1 LNSTLS LNS14DM IPDDI	mevalonate kinase (atp) lanosterol synthase cytochrome P450 lanosterol 14-alpha-demethylase isopentenyl-diphosphate D-isomerase	[c] : Ssq23epx -> lanost [g] : (2) h + lanost + (3) nadph + (3) o2 -> 44mctr + for + (4) h2o + (3) nadp [c] : jpdp <==> dmpp	EC-5.4.99.7 EC- EC-5.3.3.2	Sterol Biosynthesis Sterol Biosynthesis Sterol Biosynthesis	YHR072W YHR007C YPL117C	Erg11 Idi1
MEVK2 MEVK1 LNSTLS LNS14DM IPDDI HMGCOASm	mevalonate kinase (atp) lanosterol synthase cytochrome P450 lanosterol 14-alpha-demethylase isopentenyl-diphosphate D-isomerase Hydroxymethylglutaryl CoA synthase, mitochondrial	[c] : Ssq23epx -> lanost [c] : (2) h + lanost + (3) nadph + (3) o2 -> 44mctr + for + (4) h2o + (3) nadp [c] : ipdp <==> dmpp [m] : coa + h + hmgcoa <==> aacoa + accoa + h2o	EC-5.4.99.7 EC- EC-5.3.3.2 EC-4.1.3.5	Sterol Biosynthesis Sterol Biosynthesis Sterol Biosynthesis Sterol Biosynthesis	YHR072W YHR007C YPL117C YML126C	Erg11 Idi1 Erg13-m
MEVK2 MEVK1 LNSTLS LNS14DM IPDDI HMGCOASm	mevalonate kinase (atp) lanosterol synthase cytochrome P450 lanosterol 14-alpha-demethylase isopentenyl-diphosphate D-isomerase	[c] : Ssq23epx -> lanost [g] : (2) h + lanost + (3) nadph + (3) o2 -> 44mctr + for + (4) h2o + (3) nadp [c] : jpdp <==> dmpp	EC-5.4.99.7 EC- EC-5.3.3.2 EC-4.1.3.5	Sterol Biosynthesis Sterol Biosynthesis Sterol Biosynthesis	YHR072W YHR007C YPL117C	Erg11 Idi1 Erg13-m Erg13
MEVK2 MEVK1 LNSTLS LNS14DM IPDDI HMGCOASM HMGCOAS	mevalonate kinase (atp) lanosterol synthase cytochrome P450 lanosterol 14-alpha-demethylase isopentenyl-diphosphate D-isomerase Hydroxymethylglutaryl CoA synthase, mitochondrial Hydroxymethylglutaryl CoA synthase	[c]: Ssq23epx -> lanost [g]: (2) h + lanost + (3) nadph + (3) o2 -> 44mctr + for + (4) h2o + (3) nadp [g]: jpdp <==> dmpp [m]: coa + h + hmgcoa <==> aacoa + accoa + h2o [c]: coa + h + hmgcoa <==> aacoa + accoa + h2o	EC-5.4.99.7 EC- EC-5.3.3.2 EC-4.1.3.5 EC-4.1.3.5	Sterol Biosynthesis Sterol Biosynthesis Sterol Biosynthesis Sterol Biosynthesis Sterol Biosynthesis	YHR072W YHR007C YPL117C YML126C YML126C	Erg11 Idi1 Erg13-m Erg13 (Hmg2) or (
MEVK2 MEVK1 LNSTLS LNS14DM IPDDI HMGCOASM HMGCOAS	mevalonate kinase (atp) lanosterol synthase cytochrome P450 lanosterol 14-alpha-demethylase isopentenyl-diphosphate D-isomerase Hydroxymethylglutaryl CoA synthase, mitochondrial Hydroxymethylglutaryl CoA synthase Hydroxymethylglutaryl CoA reductase	[c]: Ssq23epx -> lanost [c]: (2) h + lanost + (3) nadph + (3) o2 -> 44mctr + for + (4) h2o + (3) nadp [c]: jpdy ===> dmpp [m]: coa + h + hmgcoa <==> aacoa + accoa + h2o [c]: coa + h + hmgcoa <==> aacoa + accoa + h2o [c]: coa + mev-R + (2) nadp <==> (2) h + hmgcoa + (2) nadph	EC-5.4.99.7 EC- EC-5.3.3.2 EC-4.1.3.5 EC-4.1.3.5	Sterol Biosynthesis Sterol Biosynthesis Sterol Biosynthesis Sterol Biosynthesis Sterol Biosynthesis Sterol Biosynthesis	YHR072W YHR007C YPL117C YML126C YML126C (YLR450W or YML075C)	Erg11 Idi1 Erg13-m Erg13 (Hmg2) or (Hmg1)
MEVK2 MEVK1 LNSTLS LNS14DM IPDDI HMGCOASM HMGCOAS HMGCOAR GRTT	mevalonate kinase (atp) lanosterol synthase cytochrome P450 lanosterol 14-alpha-demethylase isopentenyl-diphosphate D-isomerase Hydroxymethylglutaryl CoA synthase, mitochondrial Hydroxymethylglutaryl CoA synthase Hydroxymethylglutaryl CoA reductase geranyltranstransferase	[c]: Ssq23epx -> lanost [c]: (2) h + lanost + (3) nadph + (3) o2 -> 44mctr + for + (4) h2o + (3) nadp [c]: ipdp <==> dmpp [m]: coa + h + hmgcoa <==> aacoa + accoa + h2o [c]: coa + h + hmgcoa <==> aacoa + accoa + h2o [c]: coa + mev-R + (2) nadp <==> (2) h + hmgcoa + (2) nadph [c]: grdp + ipdp -> frdp + ppi	EC-5.4.99.7 EC- EC-5.3.3.2 EC-4.1.3.5 EC-4.1.3.5 EC-1.1.1.34 EC-2.5.1.10	Sterol Biosynthesis	YHR072W YHR007C YPL117C YML126C YML126C (YLR450W or YML075C) YJL167W	Erg11 Idi1 Erg13-m Erg13 (Hmg2) or (Hmg1) Erg20
MEVK2 MEVK1 LNSTLS LNSTLS LNS14DM IPPDI HMGCOASM HMGCOAS HMGCOAR GRTT DPMVD	mevalonate kinase (atp) lanosterol synthase cytochrome P450 lanosterol 14-alpha-demethylase isopentenyl-diphosphate D-isomerase Hydroxymethylglutaryl CoA synthase, mitochondrial Hydroxymethylglutaryl CoA synthase Hydroxymethylglutaryl CoA reductase	[c]: Ssq23epx -> lanost [c]: (2) h + lanost + (3) nadph + (3) o2 -> 44mctr + for + (4) h2o + (3) nadp [c]: jpdy ===> dmpp [m]: coa + h + hmgcoa <==> aacoa + accoa + h2o [c]: coa + h + hmgcoa <==> aacoa + accoa + h2o [c]: coa + mev-R + (2) nadp <==> (2) h + hmgcoa + (2) nadph	EC-5.4.99.7 EC- EC-5.3.3.2 EC-4.1.3.5 EC-4.1.3.5 EC-1.1.1.34 EC-2.5.1.10 EC-4.1.1.33	Sterol Biosynthesis	YHR072W YHR007C YPL117C YML126C YML126C (YLR450W or YML075C) YJL167W YNR043W	Erg11 Idi1 Erg13-m Erg13 (Hmg2) or (Hmg1)
MEVK2 MEVK1 LNSTLS LNS14DM IPDDI HMGCOASM HMGCOAR GRTT	mevalonate kinase (atp) lanosterol synthase cytochrome P450 lanosterol 14-alpha-demethylase isopentenyl-diphosphate D-isomerase Hydroxymethylglutaryl CoA synthase, mitochondrial Hydroxymethylglutaryl CoA synthase Hydroxymethylglutaryl CoA reductase geranyltranstransferase	[c]: Ssq23epx -> lanost [c]: (2) h + lanost + (3) nadph + (3) o2 -> 44mctr + for + (4) h2o + (3) nadp [c]: ipdp <==> dmpp [m]: coa + h + hmgcoa <==> aacoa + accoa + h2o [c]: coa + h + hmgcoa <==> aacoa + accoa + h2o [c]: coa + mev-R + (2) nadp <==> (2) h + hmgcoa + (2) nadph [c]: grdp + ipdp -> frdp + ppi	EC-5.4.99.7 EC- EC-5.3.3.2 EC-4.1.3.5 EC-4.1.3.5 EC-1.1.1.34 EC-2.5.1.10 EC-4.1.1.33 EC-2.5.1.1	Sterol Biosynthesis	YHR072W YHR007C YPL117C YML126C YML126C (YLR450W or YML075C) YJL167W	Erg11 Idi1 Erg13-m Erg13 (Hmg2) or (Hmg1) Erg20

C8STI	C-8 sterol isomerase	[c] : fecost> epist		Sterol Biosynthesis	YMR202W	IEra?
C5STDS					YLR056W	Erg2
	C-5 sterol desaturase	[c] : epist + h + nadph + o2> ergtrol + (2) h2o + nadp		Sterol Biosynthesis		Erg3
C4STMO2	C-4 sterol methyl oxidase (4-methylzymosterol)	[c]: 4mzym + (3) h + (3) nadph + (3) o2> (4) h2o + (3) nadp + zym_int1		Sterol Biosynthesis	YGR060W	Erg25
C4STMO1	C-4 sterol methyl oxidase (4,4-dimethylzymosterol)	[c]: 44mzym + (3) h + (3) nadph + (3) o2> 4mzym_int1 + (4) h2o + (3) nadp		Sterol Biosynthesis	YGR060W	Erg25
C3STKR2	C-3 sterol keto reductase (zymosterol)	[c] : h + nadph + zym_int2> nadp + zymst		Sterol Biosynthesis	YLR100W	Erg27
C3STKR1	C-3 sterol keto reductase (4-methylzymosterol)	[c] : 4mzym_int2 + h + nadph> 4mzym + nadp		Sterol Biosynthesis	YLR100W	Erg27
C3STDH2	C-3 sterol dehydrogenase (zymosterol)	[c] : nad + zym_int1> co2 + h + nadh + zym_int2	EC-5.3.3.1	Sterol Biosynthesis	YGL001C	Erg26
C3STDH1	C-3 sterol dehydrogenase (4-methylzymosterol)	[c]: 4mzym_int1 + nad> 4mzym_int2 + co2 + h + nadh	EC-5.3.3.1	Sterol Biosynthesis	YGL001C	Erg26
C24STRer	C-s24 sterol reductase, endoplamic reticular	[r]: ergtetrol + h + nadph> ergst + nadp		Sterol Biosynthesis	YGL012W	Erg4-er
C22STDS	C-22 sterol desaturase	[c]: ergtrol + h + nadph + o2> ergtetrol + (2) h2o + nadp		Sterol Biosynthesis	YMR015C	Erg5
C14STR	C-14 sterol reductase	[c] : 44mctr + h + nadph> 44mzym + nadp		Sterol Biosynthesis	YNL280C	Erg24
TMPPP	thiamine-phosphate diphosphorylase	[c] : 2mahmp + 4mpetz + h> ppi + thmmp	EC-2.5.1.3	Thiamine Metabolism	YPL214C	Thi6
TMPKr	thiamine-phosphate kinase	[c] : atp + thmmp <==> adp + thmpp		Thiamine Metabolism	11 12140	11110
TMN						
	thiaminase	[c] : h2o + thm> 4ahmmp + 4mhetz + h		Thiamine Metabolism	V0D4400	Thion
TMDPPK	thiamine-diphosphate kinase	[c] : atp + thmpp> adp + thmtp		Thiamine Metabolism	YOR143C	Thi80
TMDPK	thiamine diphosphokinase	[c] : atp + thm> amp + h + thmpp	EC-2.7.6.2	Thiamine Metabolism	YOR143C	Thi80
THZPSN2_SC	thiazole phosphate synthesis (ribose 5-phosphate), yeast-specifc	[c] : achms + cys-L + gly + h + r5p> 4abut + 4mpetz + ac + co2 + (3) h2o + nh4 + pyr		Thiamine Metabolism		
THZPSN1_SC	thiazole phosphate synthesis (xylulose 5-phosphate), yeast-specific	[c] : achms + cys-L + gly + h + xu5p-D> 4abut + 4mpetz + ac + co2 + (3) h2o + nh4 + pyr		Thiamine Metabolism		
THMPe	thiamin phosphatase, extracellular	[e] : h2o + thmmp> pi + thm	EC-3.1.3.2	Thiamine Metabolism	YBR092C	Pho3-e
THMP	thiamin phosphatase	[c] : h2o + thmmp> pi + thm		Thiamine Metabolism		1
THMDPe	thiamin diphosphatase, extracellular	[e] : (2) h2o + thmpp> h + (2) pi + thm	EC-3.1.3.2	Thiamine Metabolism	YBR092C	Pho3-e
	anariii alprioopriataoo, oxtaoonalar	[6] (2) (126 · 4 m)p · 11 · (2) p · 4 m	20 0.1.0.2	Triadrinio Metaboliciii	15110020	(Thi20) or (
PMPK	phosphomethylpyrimidine kinase	[c] : 4ampm + atp> 2mahmp + adp	EC-2.7.4.7	Thiamine Metabolism	(YOL055C or YPL258C)	Thi21) or (
i				1	(YOL055C or YPL258C or	Thi21) or (
HMPK1	hydroxymethylpyrimidine kinase (ATP)	[c]: 4ahmmp + atp> 4ampm + adp + h	EC-2.7.1.49	Thiamine Metabolism	YPR121W)	Thi22)
HETZK	hydroxyethylthiazole kinase	[c] : 4mhetz + atp> 4mpetz + adp + h		Thiamine Metabolism	YPL214C	Thi6
AHMMPS		[c] : 4ffffetz + atp> 4fffpetz + atp + ff	LU 2.7.1.50	Thiamine Metabolism	1 [2.170	
	4-amino-5-hydroxymethyl-2-methylpyrimidine synthetase		EC 6 4 4 0		VKI 104C	Mot1 m
THRTRSm	threonyl-tRNA synthetase, mitochondrial	[m] : atp + thr-L + trnathr> amp + ppi + thrtrna	EC-6.1.1.3	Threonine and Lysine Metabolism	YKL194C	Mst1-m
THRTRS	Threonyl-tRNA synthetase	[c] : atp + thr-L + trnathr> amp + ppi + thrtrna	EC-6.1.1.3	Threonine and Lysine Metabolism	YIL078W	Ths1
THRS	threonine synthase	[c] : h2o + phom> pi + thr-L	EC-4.2.3.1	Threonine and Lysine Metabolism	YCR053W	Thr4
THRD_Lm	L-threonine deaminase, mitochondrial	[m] : thr-L> 2obut + nh4		Threonine and Lysine Metabolism	YER086W	llv1-m
				, , , , , , , , , , , , , , , , , , , ,		(Cha1) or (
THRD L	L-threonine deaminase	[c] : thr-L> 2obut + nh4		Throoning and Lyging Matcheliam	(YCL064C or YKL218C)	, , ,
THRA	Threonine aldolase		EC-4.1.2.5	Threonine and Lysine Metabolism Threonine and Lysine Metabolism	YEL046C	Sry1)
		[c] : acald + gly> thr-L				Gly1
SACCD2	saccharopine dehydrogenase (NAD, L-lysine forming)	[c]: h2o + nad + saccrp-L <==> akg + h + lys-L + nadh	EC-1.5.1.7	Threonine and Lysine Metabolism	YIR034C	Lys1
SACCD1	saccharopine dehydrogenase (NADP, L-glutamate forming)	[c]: L2aadp6sa + glu-L + h + nadph <==> h2o + nadp + saccrp-L	EC-1.5.1.10	Threonine and Lysine Metabolism	YNR050C	Lys9
OXAGm	non-enzymatic reaction, mitochondrial	[m]: h + oxag <==> 2oxoadp + co2		Threonine and Lysine Metabolism		
MCITDm	2-methylcitrate dehydratase, mitochondrial	[m] : hcit <==> b124tc + h2o	EC-4.2.1.79	Threonine and Lysine Metabolism		1
LYSTRSm	Lysyl-tRNA synthetase, mitochondrial	[m] : atp + lys-L + trnalys> amp + lystrna + ppi	EC-6.1.1.6	Threonine and Lysine Metabolism	YNL073W	Msk1-m
LYSTRS	Lysyl-tRNA synthetase	[c] : atp + lys-L + trnalys> amp + lystma + ppi	EC-6.1.1.6	Threonine and Lysine Metabolism	YDR037W	Krs1
HICITDm	homoisocitrate dehydrogenase, mitochondrial	[m] : hicit + nad <==> h + nadh + oxaq	EC-0.1.1.0	Threonine and Lysine Metabolism	YIL094C	Lys12-m
HACNHm	homoacontinate hydratase, mitochondrial	[m]: b124tc + h2o <==> hicit		Threonine and Lysine Metabolism	YDR234W	Lys4-m
AATA	2-aminoadipate transaminase	[c] : 2oxoadp + glu-L <==> L2aadp + akg	EC-2.6.1.39	Threonine and Lysine Metabolism		
AASAD2	L-aminoadipate-semialdehyde dehydrogenase (NADH)	[c]: L2aadp + atp + h + nadh> L2aadp6sa + amp + nad + ppi	EC-1.2.1.31	Threonine and Lysine Metabolism	(YBR115C and YGL154C	Lys25
AASAD1	L-aminoadipate-semialdehyde dehydrogenase (NADPH)	[c]: L2aadp + atp + h + nadph> L2aadp6sa + amp + nadp + ppi	EC-1.2.1.31	Threonine and Lysine Metabolism	(YBR115C and YGL154C	Lys25
4HTHRS	4-Hydroxy-L-threonine synthase	[c] : h2o + phthr> 4hthr + pi		Threonine and Lysine Metabolism	YCR053W	Thr4
SQLter	squalene endoplamic reticular transport	sql[c] <==> sql[r]		Transport, Endoplasmic Reticular		
SQ23EPXter	Squalene-2,3-epoxide endoplamic reticular transport	Ssq23epx[r] <==> Ssq23epx[c]		Transport, Endoplasmic Reticular		-
O2ter	O2 endoplamic reticulum transport	o2[c] <==> o2[r]		Transport, Endoplasmic Reticular		
MANNANter	mannan endoplasmic reticulum transport via diffusion	mannan[c] <==> mannan[r]		Transport, Endoplasmic Reticular		
H2Oter	H2O endoplasmic reticulum transport	h2o[c] <==> h2o[r]		Transport, Endoplasmic Reticular		
G6Pter	glucose 6-phosphate endoplasmic reticular transport via diffusion	g6p[c] <==> g6p[r]		Transport, Endoplasmic Reticular		
ERGTETROLter	Ergosta-5,6,22,24,(28)-tetraen-3beta-ol endoplamic reticular transport	ergtetrol[c] <==> ergtetrol[r]		Transport, Endoplasmic Reticular		1
ERGSTter	ergosterol endoplasmic reticular transport	ergst[r] <==> ergst[c]		Transport, Endoplasmic Reticular		1
DOLPt2er	dolichol phosphate endoplasmic reticular transport via proton symport			Transport, Endoplasmic Reticular	+	
DOLFIZEI	uononoi priospriate endopiasmic reticular transport via proton sympott	dolp[c] + h[c] <==> dolp[r] + h[r]	_	manaport, Endoprasmic Relicular	+	+
00014	Only the District of Electron and Control of the Co	On alfal a secondaria		Toward Fodoric 1 B # 1	1	1
6PGLter	6-phospho-D-glucono-1,5-lactone endoplasmic reticular transport via diffusion	6pgl[c] <==> 6pgl[r]		Transport, Endoplasmic Reticular		
ZYMSTt	zymosterol reversible transport	zymst[e] <==> zymst[c]		Transport, Extracellular	YOR011W	Aus1
XYLt	D-xylose reversible transport	xyl-D[e] <==> xyl-D[c]		Transport, Extracellular		
XYLTt	Xylitol transport via passive diffusion	xylt[e] <==> xylt[c]		Transport, Extracellular		
XTSNt2	xanthosine transport in via proton symport	h[e] + xtsn[e]> h[c] + xtsn[c]		Transport, Extracellular		i .
XANt	xanthine reversible transport	xan[e] <==> xan[c]		Transport, Extracellular	1	†
AAN	Administration transport	Adilej Adilej		Transport, Extracellular		(Contlar)
NA 140-				Toward Edwards	(YKR039W or YCL025C or YDR046C or YBR069C	(Gap1) or (Agp1) or (Bap3) or (Tat1) or (
VALt2r	L-valine reversible transport via proton symport	h[e] + val-L[e] <==> h[c] + val-L[c]		Transport, Extracellular	or YBR068C)	Bap2)
URIt2	uridine transport in via proton symport	h[e] + uri[e]> h[c] + uri[c]		Transport, Extracellular	YBL042C	Fui1
UREA2t2	urea reversible transport via proton symport (2 H+)	(2) h[e] + urea[e] <==> (2) h[c] + urea[c]		Transport, Extracellular	YHL016C	Dur3
URAt2	uracil transport in via proton symport	h[e] + ura[e]> h[c] + ura[c]		Transport, Extracellular	YBR021W	Fur4
TYRt2r	L-tyrosine reversible transport via proton symport	h[e] + tyr-L[e] <==> h[c] + tyr-L[c]		Transport, Extracellular	(YBR069C or YKR039W or YCL025C or YBR068C or YOL020W or YDR046C	(Tat1) or (Gap1) or (Agp1) or (Bap2) or (Tat2) or (Bap3)
	Tetradecancate (n.C14:0) transport in vio unicort				1	Dapo)
TTDCAt	Tetradecanoate (n-C14:0) transport in via uniport	ttdca[e]> ttdca[c]		Transport, Extracellular		l
					(YBR069C or YKR039W	(Tat1) or (Gap1) or (Tat2) or (
1				1	or YOL020W or YBR068C	

TREt2	trehalose transport in via proton symporter	h[e] + tre[e]> h[c] + tre[c]	Transport, Extracellular		1
THYMt3r					
ITTIVILOI	thymine reversible transport via proton antiport	h[e] + thym[c] <==> h[c] + thym[e]	Transport, Extracellular		(T-44) (
					(Tat1) or (
					Agp1) or (
				(YBR069C or YCL025C or	Gap1) or (
THRt2r	L-threonine reversible transport via proton symport	h[e] + thr-L[e] <==> h[c] + thr-L[c]	Transport, Extracellular	YKR039W or YDR508C)	Gnp1)
				·	(Thi7) or (
				(YLR237W or YOR071C	Thm1) or (
THMt2	Thiamine transport in via proton symport	h[e] + thm[e]> h[c] + thm[c]	Transport, Extracellular	or YOR192C)	Thm2)
THMDt2		h[e] + thymd[e]> h[c] + thymd[c]		or rorriszo)	111112)
	thymidine transport in via proton symport		Transport, Extracellular		
SUCRt2	sucrose transport in via proton symport	h[e] + sucr[e]> h[c] + sucr[c]	Transport, Extracellular		
SUCCt2r	succinate transport via proton symport	h[e] + succ[e] <==> h[c] + succ[c]	Transport, Extracellular		
SRB_Lt	L-sorbose reversible transport	srb-L[e] <==> srb-L[c]	Transport, Extracellular		
SPRMti	spermine irreversible uniport	sprm[e]> sprm[c]	Transport, Extracellular		
SPMDt2	spermidine transport in via proton symport	h[e] + spmd[e]> h[c] + spmd[c]	Transport, Extracellular		
					(Sul1) or (
				(YBR294W or YLR092W	Sul2) or (
SO4ti	sulfate irreversible uniport	so4[e]> so4[c]	Transport, Extracellular	or YGR125W)	Sul3)
0040	Suitate irreversible uniport	304[0] 7 304[0]	Transport, Extracellular	01 101(12011)	
					(Agp3) or (
					Agp1) or (
				(YFL055W or YCL025C or	
I				YDR508C or YKR039W or	Gap1) or (
SERt2r	L-serine reversible transport via proton symport	h[e] + ser-L[e] <==> h[c] + ser-L[c]	Transport, Extracellular	YPL265W)	Dip5)
SBT_Lt	L-sorbitol transport via passive diffusion		Transport, Extracellular	,	1
SBT_Dt	D-sorbitol transport via passive diffusion	sbt-D[e] <==> sbt-D[c]	Transport, Extracellular		
RIBt2	ribose transport in via proton symporter	h[e] + rib-D[e]> h[c] + rib-D[c]	Transport, Extracellular		
RIBFLVt2	riboflavin transport in via proton symport	h[e] + ribflv[e]> h[c] + ribflv[c]	Transport, Extracellular		
PYRt2	pyruvate transport in via proton symport	h[e] + pyr[e]> h[c] + pyr[c]	Transport, Extracellular	YKL217W	Jen1
PTRCt2	putrescine transport in via proton symport	h[e] + ptrc[e]> h[c] + ptrc[c]	Transport, Extracellular		
	a special process of the control of	12 1 34 14 F: 34			(Gap1) or (
PROt2r	L proline reversible transport via proton compart	h[e] + pro-L[e] <==> h[c] + pro-L[c]	Transport, Extracellular	(YKR039W or YOR348C)	Put4)
	L-proline reversible transport via proton symport				
PNTOt2	Pantothenate reversible transport via proton symport	h[e] + pnto-R[e] <==> h[c] + pnto-R[c]	Transport, Extracellular	YCR028C	Fen2
					(Pho84) or (
					Pho87) or (
				(YML123C or YCR037C	Pho89) or (
				or YBR296C or YJL198W	Pho90) or (
			L	or YNR013C or YCR098C	Pho91) or (
Plt2r	phosphate reversible transport via symport	h[e] + pi[e] <==> h[c] + pi[c]	Transport, Extracellular)	Git1)
					(Gap1) or (
					Agp1) or (
				(YKR039W or YCL025C	Tat2) or (
				or YOL020W or YBR068C	
BUE!					Bap2) or (
PHEt2r	L-phenylalanine reversible transport via proton symport	h[e] + phe-L[e] <==> h[c] + phe-L[c]	Transport, Extracellular	or YDR046C)	Bap3)
PEPDt3	peptide transport in via proton symport	h[e] + pepd[e]> h[c] + pepd[c]	Transport, Extracellular	YKR093W	Ptr2
PAPt	PAP reversible uniport	pap[e] <==> pap[c]	Transport, Extracellular		
					(Gap1) or (
ORNt2r	orntithine reversible transport in via proton symport	h[e] + orn[e] <==> h[c] + orn[c]	Transport, Extracellular	(YKR039W or YEL063C)	Can1)
OCDCYAt			Transport, Extracellular	(114,00011 01 1220000)	Jun 7
	Octadecynoate (n-C18:2) transport in via uniport	ocdcya[e]> ocdcya[c]			
OCDCEAt	Octadecenoate (n-C18:1) transport in via uniport	ocdcea[e]> ocdcea[c]	Transport, Extracellular		
OCDCAt	Octadecanoate (n-C18:0) transport in via uniport	ocdca[e]> ocdca[c]	Transport, Extracellular		
O2t	o2 transport (diffusion)	o2[e] <==> o2[c]	Transport, Extracellular		
NMNTP	nmntp	h[e] + nmn[e]> h[c] + nmn[c]	Transport, Extracellular		
	T	(-)(-)(-)	Transport, Extraconditi		(Mep1) or (
I				(VCD121C or VNII 140M	
L				(YGR121C or YNL142W	Mep2) or (
NH4t	ammonia reversible transport	nh4[e] <==> nh4[c]	Transport, Extracellular	or YPR138C)	Mep3)
NAt3_1	sodium proton antiporter (H:NA is 1:1)	h[e] + na1[c] <==> h[c] + na1[e]	Transport, Extracellular	YLR138W	Nha1
MMETt2	S-methylmethionine permease	h[e] + mmet[e]> h[c] + mmet[c]	Transport, Extracellular	YLL061W	Mmp1
					(Gap1) or (
1					Agp1) or (
				(V/KD020W VOL0052	Gnp1) or (
				(YKR039W or YCL025C	Bap2) or (
I				or YDR508C or YBR068C	Bap3) or (
1				or YDR046C or YGR055W	
METt2r	L-methionine reversible transport via proton symport	h[e] + met-L[e] <==> h[c] + met-L[c]	Transport, Extracellular	or YHL036W)	Mup3)
MELIBt2	melibiose transport in via symport	h[e] + melib[e]> h[c] + melib[c]	Transport, Extracellular		/
	monologe transport in via sympoti	neg - menejej - njej - menejej	Transport, Extracellular		(Lluid) on (
					(Hxt1) or (
					Hxt10) or (
1					Hxt11) or (
1					Hxt13) or (
					Hxt15) or (
					Hxt16) or (
					Hxt17) or (
				(YHR094C or YFL011W	Hxt2) or (
1				or YOL156W or YEL069C	Hxt3) or (
1				or YDL245C or YJR158W	Hxt4) or (
				or YNR072W or	
					Hxt5) or (
				YMR011W or YDR345C or	
				YHR092C or YHR096C or	
				YDR343C or YDR342C or	
MANt2	D-mannose transport in via proton symport	h[e] + man[e]> h[c] + man[c]	Transport, Extracellular	YJL214W or YJL219W)	Hxt9)
MALt2r	L-malate reversible transport via proton symport	h[e] + mal-L[e] <==> h[c] + mal-L[c]	Transport, Extracellular	1022 31 10221017)	,
171/7LLG1	E marate reversible transport via proton symport	niel i martiel niel i martiel	Transport, Extracential		

					/ Mal11 \ a= /
				(YGR289C or YBR298C	(Mal11) or (Mal31) or (
				or YDL247W or YJR160C	Mph2) or (
MALTt2	maltose transport in via proton symport	h[e] + malt[e]> h[c] + malt[c]	Transport, Extracellular)	Mph3)
LYSt2r	L-lysine reversible transport via proton symport	h[e] + lys-L[e] <==> h[c] + lys-L[c]	Transport, Extracellular	(YNL268W or YKR039W)	(Lyp1) or (Gap1)
LTOIZI	L-iysine reversible transport via proton symport		Transport, Extracellular	(TINEZOSVV OI TRROSSVV)	(Tat1) or (
					Gap1) or (
				(YBR069C or YKR039W	Agp1) or (
				or YCL025C or YBR068C	Bap2) or (
I EL HO	La coine recordible transport de preter acresort	biol , lovel fol serve biol , lovel fol	Transport Futrocallular	or YDR046C or YDR508C	Bap3) or (
LEUt2r L-LACt2r	L-leucine reversible transport via proton symport L-lactate reversible transport via proton symport	h[e] + leu-L[e] <==> h[c] + leu-L[c] h[e] + lac-L[e] <==> h[c] + lac-L[c]	Transport, Extracellular Transport, Extracellular	YKL217W	Gnp1) Jen1
Kt2r	potassium reversible transport via proton symport	h[e] + k[e] <==> h[c] + k[c]	Transport, Extracellular	TREZITYV	Jenn
INSt2	inosine transport in via proton symport	h[e] + ins[e]> h[c] + ins[c]	Transport, Extracellular		
					(ltr1) or (ltr
INSTt2	inositol transport in via proton symport	h[e] + inost[e]> h[c] + inost[c]	Transport, Extracellular	(YDR497C or YOL103W)) (T-14) (
					(Tat1) or (Gap1) or (
				(YBR069C or YKR039W	Agp1) or (
				or YCL025C or YBR068C	Bap2) or (
ILEt2r	L-isoleucine reversible transport via proton symport	h[e] + ile-L[e] <==> h[c] + ile-L[c]	Transport, Extracellular	or YDR046C)	Bap3)
HXANt2r	hypoxanthine reversible transport via proton symport	h[e] + hxan[e] <==> h[c] + hxan[c]	Transport, Extracellular		
					(Hip1) or (
				()(OD404)N)((D000)N	Gap1) or (
HISt2r	I histidina varrasible transport via protes armout	hfal , his I fal a> hfal , his I fal	Transport Futroscillular	(YGR191W or YKR039W or YCL025C or YBR069C)	Agp1) or (
HDCEAt	L-histidine reversible transport via proton symport hexadecenoate (n-C16:1) transport in via uniport	h[e] + his-L[e] <==> h[c] + his-L[c] hdcea[e]> hdcea[c]	Transport, Extracellular Transport, Extracellular	OF TOLUZSO OF TERUSSO	Tati)
HDCAt	Hexadecanoate (n-C16:0) transport in via uniport	hdca[e]> hdca[c]	Transport, Extracellular		
H2Ot	H2O transport via diffusion	h2o[e] <==> h2o[c]	Transport, Extracellular		
	·				(Fcy2) or (
				(YER056C or YER060W	Fcy21) or (
		******		or YER060W-A or	Fcy22) or (
GUAt2r GTHOXti	guanine reversible transport via proton symport	gua[e] + h[e] <==> gua[c] + h[c]	Transport, Extracellular	YGL186C)	Fcy23)
GSNt2	oxidized glutathione irreversible uniport guanosine transport in via proton symport	gthox[e]> gthox[c] gsn[e] + h[e]> gsn[c] + h[c]	Transport, Extracellular Transport, Extracellular		
GGIVIZ	guanosine transport in via proton symport	gantej i ntej> gantoj i ntoj	Transport, Extracential		(Gap1) or (
				(YKR039W or YOL020W	Tat2) or (
				or YPL265W or YOR348C	Dip5) or (
GLYt2r	glycine reversible transport via proton symport	gly[e] + h[e] <==> gly[c] + h[c]	Transport, Extracellular)	Put4)
GLYCt	glycerol transport via channel	glyc[c] <==> glyc[e]	Transport, Extracellular	YLL043W	Fps1
					(Agp3) or (Stl1) or (
				(YFL055W or YDR536W	Gap1) or (
				or YKR039W or YCL025C	Agp1) or (
GLUt2r	L-glutamate transport via proton symport, reversible	glu-L[e] + h[e] <==> glu-L[c] + h[c]	Transport, Extracellular	or YPL265W)	Dip5)
					(Gap1) or (
				(YKR039W or YCL025C	Agp1) or (
			L	or YDR508C or YPL265W	Gnp1) or (
GLNt2r	L-glutamine reversible transport via proton symport	gln-L[e] + h[e] <==> gln-L[c] + h[c]	Transport, Extracellular)	Dip5)
					(Hxt4) or (
					Gal2) or (
					Hxt11) or (
					Stl1) or (Hx
) or (Hxt13
					or (Hxt15)
					(Hxt16) or
				(YHR092C or YLR081W	Hxt10) or (
				or YOL156W or YDR536W	
				or YHR094C or YEL069C	Hxt2) or (
				or YDL245C or YJR158W	Hxt3) or (
				or YFL011W or YNR072W or YMR011W or YDR345C	
				or YHR096C or YDR343C	Hxto) or (Hxt7) or (
				or YDR342C or YJL214W	Hxt8) or (
GLCt1	glucose transport (uniport)	glc-D[e]> glc-D[c]	Transport, Extracellular	or YJL219W)	Hxt9)
GCALDt	Glycoaldehydye reversible transport	gcald[e] <==> gcald[c]	Transport, Extracellular	, , , , ,	,
GAM6Pt	D-glucosamine 6-phosphate reversible uniport	gam6p[e] <==> gam6p[c]	Transport, Extracellular		
					(Gal2) or (
				()// D004///	Hxt10) or (
				(YLR081W or YFL011W	Hxt11) or (
				or YOL156W or YNL318C or YJL219W or YDR536W	Hxt14) or (Hxt9) or (S
GALt2	D-galactose transport in via proton symport	gal[e] + h[e]> gal[c] + h[c]	Transport, Extracellular)) (8)
FUMt2r	fumarate reversible transport via symport	fum[e] + h[e] <==> fum[c] + h[c]	Transport, Extracellular	<u> </u>	
	· · · · · · · · · · · · · · · · · · ·	p 10 10 10 10 10			

						(Hxt1) or (
						Hxt10) or (
						Hxt11) or (
						Hxt13) or (
						Hxt15) or (
						Hxt16) or (
						Hxt17) or (
					(YHR094C or YFL011W	Hxt2) or (
					or YOL156W or YEL069C	Hxt3) or (
					or YDL245C or YJR158W	Hxt4) or (
					or YNR072W or	Hxt5) or (
					YMR011W or YDR345C or	
					YHR092C or YHR096C or	
					YDR343C or YDR342C or	Hxt8) or (
FRUt2	D-fructose transport in via proton symport	fru[e] + h[e]> fru[c] + h[c]		Transport, Extracellular	YJL214W or YJL219W)	Hxt9)
FORt		for[e] <==> for[c]		Transport, Extracellular		, ,
	formate transport via diffusion					-
ETOHt	ethanol reversible transport	etoh[e] <==> etoh[c]		Transport, Extracellular		
ERGSTt	ergosterol reversible transport	ergst[e] <==> ergst[c]		Transport, Extracellular	YOR011W	Aus1
DURIt2	deoxyuridine transport in via proton symport	duri[e] + h[e]> duri[c] + h[c]		Transport, Extracellular		1
DTTPt	dTTP reversible uniport			Transport, Extracellular		<u> </u>
		dttp[e] <==> dttp[c]				
DINSt2	deoxyinosine transport in via proton symport	din[e] + h[e]> din[c] + h[c]		Transport, Extracellular		
DGSNt2	deoxyguanosine transport in via proton symport	dgsn[e] + h[e]> dgsn[c] + h[c]		Transport, Extracellular		
DCYTt2	deoxycytidine transport in via proton symport	dcyt[e] + h[e]> dcyt[c] + h[c]		Transport, Extracellular		
DANNt2		dann[e] + h[e] <==> dann[c] + h[c]	 			1
	7,8-Diaminononanoate reversible transport via proton symport	ded Otal - htgl ded Otal - htgl		Transport, Extracellular		
DADNt2	deoxyadenosine transport in via proton symport	dad-2[e] + h[e]> dad-2[c] + h[c]		Transport, Extracellular		
CYTDt2	cytidine transport in via proton symport	cytd[e] + h[e]> cytd[c] + h[c]		Transport, Extracellular		1
						(Gap1) or (
			1			Gnp1) or (
			1		()((D000)***	
			1		(YKR039W or YDR508C	Bap2) or (
					or YBR068C or YDR046C	Bap3) or (
			1			Tat1) or (
CVCtO	L sustaine reversible transport via proton summert	and I fall third arms and I fall third		Transport Eutropoliulas	1 1510030 01 10102000	
CYSt2r	L-cysteine reversible transport via proton symport	cys-L[e] + h[e] <==> cys-L[c] + h[c]		Transport, Extracellular)	Tat2)
						(Fcy2) or (
					(YER056C or YER060W	Fcy21) or (
					or YER060W-A or	Fcy22) or (
001110						
CSNt2	cytosine transport in via proton symport	csn[e] + h[e]> csn[c] + h[c]		Transport, Extracellular	YGL186C)	Fcy23)
CRNt	L-carnitine reversible transport	crn[e] <==> crn[c]		Transport, Extracellular	YBR132C	Agp2
CO2t	CO2 transporter via diffusion	co2[e] <==> co2[c]		Transport, Extracellular		1 "
CITt2r		oif(a) + b(a) <==> oif(a) + b(a)				<u> </u>
CITIZI	citrate reversible transport via symport	cit[e] + h[e] <==> cit[c] + h[c]		Transport, Extracellular		Į.,
CHLt2	choline transport via proton symport	chol[e] + h[e]> chol[c] + h[c]		Transport, Extracellular	YGL077C	Hnm1
						(Vht1) or (
BTNt2i	Biotin uptake	htn[e] + h[e]> htn[c] + h[c]		Transport, Extracellular	(YGR065C or YNR056C)	Bio5)
DTINIZI	Diotiii uptake	btn[e] + h[e]> btn[c] + h[c]		Transport, Extracellular	(1010030 01 11410300)	DI03)
					((YCR024C-A and	
					YEL017C-A and YGL008C	
) or (YCR024C-A and	
					YEL017C-A and YPL036W	(Pma1) or (
ATPS	ATPase, cytosolic	atp[c] + h2o[c]> adp[c] + h[e] + pi[c]	EC-3.6.3.6	Transport, Extracellular))	Pma2)
						(Agp3) or (
					(YFL055W or YKR039W	
				L		Gap1) or (
				Transport, Extracellular	or YPL265W)	Dip5)
ASPt2r	L-aspartate reversible transport via proton symport	asp-L[e] + h[e] <==> asp-L[c] + h[c]				
ASPt2r	L-aspartate reversible transport via proton symport	asp-L[e] + h[e] <==> asp-L[c] + h[c]				(Gap1) or (
ASPt2r	L-aspartate reversible transport via proton symport	asp-L[e] + h[e] <==> asp-L[c] + h[c]			(YKR039W or YCL025C	(Gap1) or (
ASPt2r	L-aspartate reversible transport via proton symport	asp-L[e] + h[e] <==> asp-L[c] + h[c]			(YKR039W or YCL025C	Agp1) or (
					(YKR039W or YCL025C or YDR508C or YPL265W	Agp1) or (Gnp1) or (
ASPt2r ASNt2r	L-aspartate reversible transport via proton symport L-asparagine reversible transport via proton symport	asp-L[e] + h[e] <==> asp-L[c] + h[c] asn-L[e] + h[e] <==> asn-L[c] + h[c]		Transport, Extracellular		Agp1) or (
				Transport, Extracellular		Agp1) or (Gnp1) or (Dip5)
				Transport, Extracellular	or YDR508C or YPL265W	Agp1) or (Gnp1) or (Dip5) (Gap1) or (
ASNt2r	L-asparagine reversible transport via proton symport	asn-L[e] + h[e] <==> asn-L[c] + h[c]			or YDR508C or YPL265W) (YKR039W or YEL063C	Agp1) or (Gnp1) or (Dip5) (Gap1) or (Can1) or (
ASNt2r ARGt2r	L-asparagine reversible transport via proton symport L-arganine reversible transport via proton symport	asn-L[e] + h[e] <==> asn-L[c] + h[c] arg-L[e] + h[e] <==> arg-L[c] + h[c]		Transport, Extracellular	or YDR508C or YPL265W	Agp1) or (Gnp1) or (Dip5) (Gap1) or (
ASNt2r ARGt2r ARAB-Lt	L-asparagine reversible transport via proton symport L-arganine reversible transport via proton symport L-arabinoase extracellular transport	asn-L[e] + h[e] <==> asn-L[c] + h[c] arg-L[e] + h[e] <==> arg-L[c] + h[c] arab-L[e] <==> arab-L[c]		Transport, Extracellular Transport, Extracellular	or YDR508C or YPL265W) (YKR039W or YEL063C	Agp1) or (Gnp1) or (Dip5) (Gap1) or (Can1) or (
ASNt2r ARGt2r	L-asparagine reversible transport via proton symport L-arganine reversible transport via proton symport L-arabinoase extracellular transport	asn-L[e] + h[e] <==> asn-L[c] + h[c] arg-L[e] + h[e] <==> arg-L[c] + h[c]		Transport, Extracellular	or YDR508C or YPL265W) (YKR039W or YEL063C	Agp1) or (Gnp1) or (Dip5) (Gap1) or (Can1) or (
ASNt2r ARGt2r ARAB-Lt ARAB-Dt	L-asparagine reversible transport via proton symport L-arganine reversible transport via proton symport L-arabinoase extracellular transport D-arabinose reversible transport	asn-L[e] + h[e] <==> asn-L[c] + h[c] arg-L[e] + h[e] <==> arg-L[c] + h[c] arab-L[e] <==> arab-D[c] arab-D[e] <==> arab-D[c]		Transport, Extracellular Transport, Extracellular Transport, Extracellular	or YDR508C or YPL265W) (YKR039W or YEL063C or YNL270C)	Agp1) or (Gnp1) or (Dip5) (Gap1) or (Can1) or (Alp1)
ASNt2r ARGt2r ARAB-Lt ARAB-Dt AMETt2	L-asparagine reversible transport via proton symport L-arganine reversible transport via proton symport L-arabinoase extracellular transport D-arabinoase reversible transport S-adenosyl-L-methionine transport in via proton symport	asn-L[e] + h[e] <==> asn-L[c] + h[c] arg-L[e] + h[e] <==> arg-L[c] + h[c] arab-L[e] <==> arab-L[c] arab-D[e] <==> arab-D[c] amet[e] + h[e] -> amet[c] + h[c]		Transport, Extracellular Transport, Extracellular Transport, Extracellular Transport, Extracellular	or YDR508C or YPL265W) (YKR039W or YEL063C or YNL270C) YPL274W	Agp1) or (Gnp1) or (Dip5) (Gap1) or (Can1) or (Alp1) Sam3
ASNt2r ARGt2r ARAB-Lt ARAB-Dt ARAB-Dt ARAB-Tt2 ALLTTti	L-asparagine reversible transport via proton symport L-arganine reversible transport via proton symport L-arabinoase extracellular transport D-arabinose reversible transport S-adenosyl-L-methionine transport in via proton symport allantoate irreversible uniport	asn-L[e] + h[e] <==> asn-L[c] + h[c] arg-L[e] + h[e] <==> arg-L[c] + h[c] arab-L[e] <==> arab-L[c] arab-D[e] <==> arab-D[c] amet[e] + h[e] -> amet[c] + h[c] alitt[e] -> alitt[c]		Transport, Extracellular Transport, Extracellular Transport, Extracellular Transport, Extracellular Transport, Extracellular	or YDR508C or YPL265W) (YKR039W or YEL063C or YNL270C) YPL274W YJR152W	Agp1) or (Gnp1) or (Dip5) (Gap1) or (Can1) or (Alp1) Sam3 Dal5
ASNt2r ARGt2r ARAB-Lt ARAB-Dt AMETt2	L-asparagine reversible transport via proton symport L-arganine reversible transport via proton symport L-arabinoase extracellular transport D-arabinoase reversible transport S-adenosyl-L-methionine transport in via proton symport	asn-L[e] + h[e] <==> asn-L[c] + h[c] arg-L[e] + h[e] <==> arg-L[c] + h[c] arab-L[e] <==> arab-L[c] arab-D[e] <==> arab-D[c] amet[e] + h[e] -> amet[c] + h[c]		Transport, Extracellular Transport, Extracellular Transport, Extracellular Transport, Extracellular	or YDR508C or YPL265W) (YKR039W or YEL063C or YNL270C) YPL274W	Agp1) or (Gnp1) or (Dip5) (Gap1) or (Can1) or (Alp1) Sam3 Dal5 Dal4
ASNt2r ARGt2r ARAB-Lt ARAB-Dt ARAB-Dt ARAB-Tt2 ALLTTti	L-asparagine reversible transport via proton symport L-arganine reversible transport via proton symport L-arabinoase extracellular transport D-arabinose reversible transport S-adenosyl-L-methionine transport in via proton symport allantoate irreversible uniport	asn-L[e] + h[e] <==> asn-L[c] + h[c] arg-L[e] + h[e] <==> arg-L[c] + h[c] arab-L[e] <==> arab-L[c] arab-D[e] <==> arab-D[c] amet[e] + h[e] -> amet[c] + h[c] alitt[e] -> alitt[c]		Transport, Extracellular Transport, Extracellular Transport, Extracellular Transport, Extracellular Transport, Extracellular	or YDR508C or YPL265W) (YKR039W or YEL063C or YNL270C) YPL274W YJR152W	Agp1) or (Gnp1) or (Dip5) (Gap1) or (Can1) or (Alp1) Sam3 Dal5
ASNt2r ARGt2r ARAB-Lt ARAB-Dt ARAB-Dt ARAB-Tt2 ALLTTti	L-asparagine reversible transport via proton symport L-arganine reversible transport via proton symport L-arabinoase extracellular transport D-arabinose reversible transport S-adenosyl-L-methionine transport in via proton symport allantoate irreversible uniport	asn-L[e] + h[e] <==> asn-L[c] + h[c] arg-L[e] + h[e] <==> arg-L[c] + h[c] arab-L[e] <==> arab-L[c] arab-D[e] <==> arab-D[c] amet[e] + h[e] -> amet[c] + h[c] alitt[e] -> alitt[c]		Transport, Extracellular Transport, Extracellular Transport, Extracellular Transport, Extracellular Transport, Extracellular	or YDR508C or YPL265W) (YKR039W or YEL063C or YNL270C) YPL274W YJR152W	Agp1) or (Gnp1) or (Gnp1) or (Dip5) (Gap1) or (Can1) or (Alp1) Sam3 Dal5 Dal4 (Gap1) or (
ASNt2r ARGt2r ARAB-Lt ARAB-Dt ARAB-Dt ARAB-Tt2 ALLTTti	L-asparagine reversible transport via proton symport L-arganine reversible transport via proton symport L-arabinoase extracellular transport D-arabinose reversible transport S-adenosyl-L-methionine transport in via proton symport allantoate irreversible uniport	asn-L[e] + h[e] <==> asn-L[c] + h[c] arg-L[e] + h[e] <==> arg-L[c] + h[c] arab-L[e] <==> arab-L[c] arab-D[e] <==> arab-D[c] amet[e] + h[e] -> amet[c] + h[c] alitt[e] -> alitt[c]		Transport, Extracellular Transport, Extracellular Transport, Extracellular Transport, Extracellular Transport, Extracellular	or YDR508C or YPL265W) (YKR039W or YEL063C or YNL270C) YPL274W YJR152W YIR028W	Agp1) or (Gnp1) or (Gnp1) or (Dip5) (Gap1) or (Can1) or (Alp1) Sam3 Dal5 Dal4 (Gap1) or (Gap1) or (
ASNt2r ARGt2r ARAB-Lt ARAB-Dt ARAB-Tt2 ALLTTi	L-asparagine reversible transport via proton symport L-arganine reversible transport via proton symport L-arabinoase extracellular transport D-arabinose reversible transport S-adenosyl-L-methionine transport in via proton symport allantoate irreversible uniport	asn-L[e] + h[e] <==> asn-L[c] + h[c] arg-L[e] + h[e] <==> arg-L[c] + h[c] arab-L[e] <==> arab-L[c] arab-D[e] <==> arab-D[c] amet[e] + h[e] -> amet[c] + h[c] alitt[e] -> alitt[c]		Transport, Extracellular Transport, Extracellular Transport, Extracellular Transport, Extracellular Transport, Extracellular	or YDR508C or YPL265W) (YKR039W or YEL063C or YNL270C) YPL274W YJR152W YJR028W (YKR039W or YPL265W	Agp1) or (Gnp1) or (Dip5) (Gap1) or (Can1) or (Alp1) Sam3 Dal5 Dal4 (Gap1) or (Agp1) or (
ASNI2r ARGI2r ARAB-Lt ARAB-Dt AMETI2 ALLTTII ALLTNII	L-asparagine reversible transport via proton symport L-arganine reversible transport via proton symport L-arabinoase extracellular transport D-arabinose reversible transport S-adenosyl-L-methionine transport in via proton symport allantoate irreversible uniport allantoate irreversible uniport	asn-L[e] + h[e] <==> asn-L[c] + h[c] arg-L[e] + h[e] <==> arg-L[c] + h[c] arab-L[e] <==> arab-L[c] arab-D[e] <==> arab-D[c] amet[e] + h[e] -> amet[c] + h[c] alltt[e] -> alltt[c] alltn[e]> alltn[c]		Transport, Extracellular Transport, Extracellular Transport, Extracellular Transport, Extracellular Transport, Extracellular Transport, Extracellular	or YDR508C or YPL265W) (YKR039W or YEL063C or YNL270C) YPL274W YJR152W YIR028W (YKR039W or YPL265W or YCL025C or YOL020W	Agp1) or (Gnp1) or (Gnp1) or (Dip5) (Gap1) or (Can1) or (Alp1) Sam3 Dal5 Dal4 (Gap1) or (Dip5) or (Agp1) or (Tat2) or (
ASNt2r ARGt2r ARAB-Lt ARAB-Dt ARAB-Tt2 ALLTTi	L-asparagine reversible transport via proton symport L-arganine reversible transport via proton symport L-arabinoase extracellular transport D-arabinose reversible transport S-adenosyl-L-methionine transport in via proton symport allantoate irreversible uniport	asn-L[e] + h[e] <==> asn-L[c] + h[c] arg-L[e] + h[e] <==> arg-L[c] + h[c] arab-L[e] <==> arab-L[c] arab-D[e] <==> arab-D[c] amet[e] + h[e] -> amet[c] + h[c] alitt[e] -> alitt[c]		Transport, Extracellular Transport, Extracellular Transport, Extracellular Transport, Extracellular Transport, Extracellular	or YDR508C or YPL265W) (YKR039W or YEL063C or YNL270C) YPL274W YJR152W YJR028W (YKR039W or YPL265W	Agp1) or (Gnp1) or (Dip5) (Gap1) or (Can1) or (Alp1) Sam3 Dal5 Dal4 (Gap1) or (Agp1) or (
ASNI2r ARGI2r ARAB-Lt ARAB-Dt AMETI2 ALLTTII ALLTNII ALAI2r	L-asparagine reversible transport via proton symport L-arganine reversible transport via proton symport L-arabinoase extracellular transport D-arabinose reversible transport S-adenosylmethionine transport in via proton symport allantotae irreversible uniport allantoin irreversible uniport L-alanine reversible transport via proton symport	asn-L[e] + h[e] <==> asn-L[c] + h[c] arg-L[e] + h[e] <==> arg-L[c] + h[c] arab-L[e] <==> arab-L[c] arab-D[e] <==> arab-D[c] amet[e] + h[e] -> amet[c] + h[c] alitt[e] -> alitt[c] alitn[e] -> alittn[c]		Transport, Extracellular	or YDR508C or YPL265W) (YKR039W or YEL063C or YNL270C) YPL274W YJR152W YIR028W (YKR039W or YPL265W or YCL025C or YOL020W	Agp1) or (Gnp1) or (Gnp1) or (Dip5) (Gap1) or (Can1) or (Alp1) Sam3 Dal5 Dal4 (Gap1) or (Dip5) or (Agp1) or (Tat2) or (
ASNt2r ARGt2r ARAB-Lt ARAB-Dt AMETt2 ALLTTNI ALLTNII ALAt2r AKGt2r	L-asparagine reversible transport via proton symport L-arganine reversible transport via proton symport L-arabinoase extracellular transport D-arabinose reversible transport S-adenosyl-L-methionine transport in via proton symport allantoate irreversible uniport allantoin irreversible uniport L-alanine reversible transport via proton symport 2-oxoglutarate reversible transport via symport	asn-L[e] + h[e] <==> asn-L[c] + h[c] arg-L[e] + h[e] <==> arg-L[c] + h[c] arab-L[e] <==> arab-D[c] arab-D[e] <==> arab-D[c] amet[e] + h[e] -> amet[c] + h[c] alltt[e] -> alltt[c] alltn[e] -> alltn[c] ala-L[e] + h[e] <==> ala-L[c] + h[c] akg[e] + h[e] <==> akg[c] + h[c]		Transport, Extracellular	or YDR508C or YPL265W) (YKR039W or YEL063C or YNL270C) YPL274W YJR152W YIR028W (YKR039W or YPL265W or YCL025C or YOL020W	Agp1) or (Gnp1) or (Gnp1) or (Dip5) (Gap1) or (Can1) or (Alp1) Sam3 Dal5 Dal4 (Gap1) or (Dip5) or (Agp1) or (Tat2) or (
ASNI2r ARGI2r ARAB-Lt ARAB-Dt AMETI2 ALLTTNII ALLTNII ALAI2r AKGI2r AKGMAL	L-asparagine reversible transport via proton symport L-arganine reversible transport via proton symport L-arabinoase extracellular transport D-arabinose reversible transport S-adenosyl-L-methionine transport in via proton symport allantoate irreversible uniport allantoate irreversible uniport L-alanine reversible transport via proton symport 2-oxoglutarate reversible transport via symport alpha-ketoglutarate/malate transporter	asn-L[e] + h[e] <==> asn-L[c] + h[c] arg-L[e] + h[e] <==> arg-L[c] + h[c] arab-L[e] <==> arab-L[c] arab-D[e] <==> arab-D[c] amet[e] + h[e] -> amet[c] + h[c] alitt[e] -> alitt[c] alitn[e] -> alitn[c] ala-L[e] + h[e] <==> ala-L[c] + h[c] akg[e] + h[e] <==> akg[c] + h[c] akg[c] + mal-L[e] <==> akg[c] + mal-L[c]		Transport, Extracellular	or YDR508C or YPL265W) (YKR039W or YEL063C or YNL270C) YPL274W YJR152W YIR028W (YKR039W or YPL265W or YCL025C or YOL020W	Agp1) or (Gnp1) or (Gnp1) or (Dip5) (Gap1) or (Can1) or (Alp1) Sam3 Dal5 Dal4 (Gap1) or (Dip5) or (Agp1) or (Tat2) or (
ASNt2r ARGt2r ARAB-Lt ARAB-Dt AMETt2 ALLTTNI ALLTNII ALAt2r AKGt2r	L-asparagine reversible transport via proton symport L-arganine reversible transport via proton symport L-arabinoase extracellular transport D-arabinose reversible transport S-adenosyl-L-methionine transport in via proton symport allantoate irreversible uniport allantoin irreversible uniport L-alanine reversible transport via proton symport 2-oxoglutarate reversible transport via symport	asn-L[e] + h[e] <==> asn-L[c] + h[c] arg-L[e] + h[e] <==> arg-L[c] + h[c] arab-L[e] <==> arab-D[c] arab-D[e] <==> arab-D[c] amet[e] + h[e] -> amet[c] + h[c] alltt[e] -> alltt[c] alltn[e] -> alltn[c] ala-L[e] + h[e] <==> ala-L[c] + h[c] akg[e] + h[e] <==> akg[c] + h[c]		Transport, Extracellular	or YDR508C or YPL265W) (YKR039W or YEL063C or YNL270C) YPL274W YJR152W YIR028W (YKR039W or YPL265W or YCL025C or YOL020W	Agp1) or (Gnp1) or (Dip5) (Gap1) or (Can1) or (Alp1) Sam3 Dal5 Dal4 (Gap1) or (Agp1) or (
ASNI2r ARGI2r ARAB-LI ARAB-DI AMETI2 ALLTNII ALLTNII ALAI2r AKGI2r AKGMAL	L-asparagine reversible transport via proton symport L-arganine reversible transport via proton symport L-arabinoase extracellular transport D-arabinose reversible transport S-adenosyl-L-methionine transport in via proton symport allantoate irreversible uniport allantoate irreversible uniport L-alanine reversible transport via proton symport 2-oxoglutarate reversible transport via symport alpha-ketoglutarate/malate transporter	asn-L[e] + h[e] <==> asn-L[c] + h[c] arg-L[e] + h[e] <==> arg-L[c] + h[c] arab-L[e] <==> arab-L[c] arab-D[e] <==> arab-D[c] amet[e] + h[e] -> amet[c] + h[c] alitt[e] -> alitt[c] alitn[e] -> alitn[c] ala-L[e] + h[e] <==> ala-L[c] + h[c] akg[e] + h[e] <==> akg[c] + h[c] akg[c] + mal-L[e] <==> akg[c] + mal-L[c]		Transport, Extracellular	or YDR508C or YPL265W) (YKR039W or YEL063C or YNL270C) YPL274W YJR152W YIR028W (YKR039W or YPL265W or YCL025C or YOL020W	Agp1) or (Gnp1) or (Gnp1) or (Dip5) (Gap1) or (Can1) or (Alp1) Sam3 Dal5 Dal4 (Gap1) or (Dip5) or (Agp1) or (Tat2) or (
ASNI2r ARGI2r ARAB-LI ARAB-DI AMETI2 ALLTNII ALLTNII ALAI2r AKGI2r AKGMAL	L-asparagine reversible transport via proton symport L-arganine reversible transport via proton symport L-arabinoase extracellular transport D-arabinose reversible transport S-adenosyl-L-methionine transport in via proton symport allantoate irreversible uniport allantoate irreversible uniport L-alanine reversible transport via proton symport 2-oxoglutarate reversible transport via symport alpha-ketoglutarate/malate transporter	asn-L[e] + h[e] <==> asn-L[c] + h[c] arg-L[e] + h[e] <==> arg-L[c] + h[c] arab-L[e] <==> arab-L[c] arab-D[e] <==> arab-D[c] amet[e] + h[e] -> amet[c] + h[c] alitt[e] -> alitt[c] alitn[e] -> alitn[c] ala-L[e] + h[e] <==> ala-L[c] + h[c] akg[e] + h[e] <==> akg[c] + h[c] akg[c] + mal-L[e] <==> akg[c] + mal-L[c]		Transport, Extracellular	or YDR508C or YPL265W) (YKR039W or YEL063C or YNL270C) YPL274W YJR152W YIR028W (YKR039W or YPL265W or YCL025C or YOL020W or YOR348C)	Agp1) or (Gnp1) or (Gnp1) or (Dip5) (Gap1) or (Can1) or (Alp1) Sam3 Dal5 Dal4 (Gap1) or (Dal4 (Gap1) or (Put4) (Fcy2) or (
ASNI2r ARGI2r ARAB-LI ARAB-DI AMETI2 ALLTNII ALLTNII ALAI2r AKGI2r AKGMAL	L-asparagine reversible transport via proton symport L-arganine reversible transport via proton symport L-arabinoase extracellular transport D-arabinose reversible transport S-adenosyl-L-methionine transport in via proton symport allantoate irreversible uniport allantoate irreversible uniport L-alanine reversible transport via proton symport 2-oxoglutarate reversible transport via symport alpha-ketoglutarate/malate transporter	asn-L[e] + h[e] <==> asn-L[c] + h[c] arg-L[e] + h[e] <==> arg-L[c] + h[c] arab-L[e] <==> arab-L[c] arab-D[e] <==> arab-D[c] amet[e] + h[e] -> amet[c] + h[c] alitt[e] -> alitt[c] alitn[e] -> alltn[c] ala-L[e] + h[e] <==> ala-L[c] + h[c] akg[e] + h[e] <==> akg[c] + h[c] akg[c] + mal-L[e] <==> akg[c] + mal-L[c]		Transport, Extracellular	or YDR508C or YPL265W) (YKR039W or YEL063C or YNL270C) YPL274W YJR152W YIR028W (YKR039W or YPL265W or YCL025C or YOL020W or YOR348C)	Agp1) or (Gnp1) or (Gnp1) or (Dip5) (Gap1) or (Can1) or (Alp1) Sam3 Dal6 Dal4 ((Gap1) or (Agp1) or (Agp1) or (Agp1) or (Agp1) or (Fcy2) or (Fcy21) or (Fcy21) or (
ASNt2r ARG12r ARAB-Lt ARAB-Dt AMET12 ALLTTNI ALLTNII ALLTNII ALA12r AKG12r AKGMAL ADNt2	L-asparagine reversible transport via proton symport L-arganine reversible transport via proton symport L-arabinoase extracellular transport D-arabinose reversible transport S-adenosyl-L-methionine transport in via proton symport allantoale irreversible uniport allantoin irreversible uniport L-alanine reversible transport via proton symport 2-oxoglutarate reversible transport via symport alpha-ketoglutarate/malate transporter adenosine transport in via proton symport	asn-L[e] + h[e] <==> asn-L[c] + h[c] arg-L[e] + h[e] <==> arg-L[c] + h[c] arab-L[e] <==> arab-L[c] arab-D[e] <==> arab-D[c] amet[e] + h[e] -> amet[c] + h[c] alltt[e] -> alltt[c] alltn[e] -> alltn[c] alla-L[e] + h[e] <==> ala-L[c] + h[c] akg[e] + h[e] <==> akg[c] + h[c] akg[e] + h[e] <==> akg[e] + mal-L[c] adn[e] + h[e] -> adn[c] + h[c]		Transport, Extracellular	or YDR508C or YPL265W) (YKR039W or YEL063C or YNL270C) YPL274W YJR152W YIR028W (YKR039W or YPL265W or YCL025C or YOL020W or YOR348C) (YER056C or YER060W or YER060W or YER060W-A or	Agp1) or (Gnp1) or (Gnp1) or (Gnp1) or (Gap1) or (Can1) or (Alp1) Sam3 Dal5 Dal4 (Gap1) or (Dip5) or (Agp1) or (Tat2) or (Put4) [Fcy2] or (Fcy21) or (Fcy21) or (Fcy22) or (
ASNI2r ARGI2r ARAB-Lt ARAB-Dt AMETI2 ALLTTNI ALLTNII ALAI2r AKGI2r AKGMAL ADNI2 ADEI2	L-asparagine reversible transport via proton symport L-arabinoase extracellular transport D-arabinose reversible transport S-adenosyl-L-methionine transport in via proton symport allantoate irreversible uniport L-alanine reversible uniport L-alanine reversible transport via proton symport allantosis irreversible uniport L-alanine reversible transport via proton symport 2-oxoglutarate reversible transport via symport alpha-ketoglutarate/malate transporter adenosine transport in via proton symport	asn-L[e] + h[e] <==> asn-L[c] + h[c] arg-L[e] + h[e] <==> arg-L[c] + h[c] arab-L[e] <==> arab-L[c] arab-D[e] <==> arab-D[c] amet(e] + h[e] -> amet(c] + h[c] alitt[e] -> alitt[c] alitt[e] -> alltn[c] ala-L[e] + h[e] <==> ala-L[c] + h[c] akg[e] + h[e] <==> akg[e] + h[c] akg[e] + h[e] <==> akg[e] + mal-L[c] adn[e] + h[e] -> adn[c] + h[c] ade[e] + h[e] -> ade[c] + h[c]		Transport, Extracellular	or YDR508C or YPL265W) (YKR039W or YEL063C or YNL270C) YPL274W YJR152W YIR028W (YKR039W or YPL265W or YCL025C or YOL020W or YOR348C) (YER056C or YER060W or YER060W-A or YGL186C)	Agp1) or (Gnp1) or (Gnp1) or (Dip5) (Gap1) or (Can1) or (Alp1) Sam3 Dal5 Dal4 (Gap1) or (Dal4 (Gap1) or (Tat2) or (Put4) (Fcy2) or (Fcy21) or (Fcy22) or (Fcy22) or (Fcy22) or (Fcy23)
ASNI2r ARGI2r ARAB-Lt ARAB-Dt AMETI2 ALLTTII ALLTNII ALLTONII ALAI2r AKGI2r AKGMAL ADNI2	L-asparagine reversible transport via proton symport L-arabinoase extracellular transport D-arabinose reversible transport S-adenosyl-L-methionine transport in via proton symport allantoate irreversible uniport L-alanine reversible uniport L-alanine reversible transport via proton symport allantosis irreversible uniport L-alanine reversible transport via proton symport 2-oxoglutarate reversible transport via symport alpha-ketoglutarate/malate transporter adenosine transport in via proton symport	asn-L[e] + h[e] <==> asn-L[c] + h[c] arg-L[e] + h[e] <==> arg-L[c] + h[c] arab-L[e] <==> arab-L[c] arab-D[e] <==> arab-D[c] amet(e] + h[e] -> amet(c] + h[c] alitt[e] -> alitt[c] alitt[e] -> alltn[c] ala-L[e] + h[e] <==> ala-L[c] + h[c] akg[e] + h[e] <==> akg[e] + h[c] akg[e] + h[e] <==> akg[e] + mal-L[c] adn[e] + h[e] -> adn[c] + h[c] ade[e] + h[e] -> ade[c] + h[c]		Transport, Extracellular	or YDR508C or YPL265W) (YKR039W or YEL063C or YNL270C) YPL274W YJR152W YIR028W (YKR039W or YPL265W or YCL025C or YOL020W or YOR348C) (YER056C or YER060W or YER060W or YER060W-A or	Agp1) or (Gnp1) or (Gnp1) or (Gnp1) or (Gap1) or (Can1) or (Alp1) Sam3 Dal5 Dal4 (Gap1) or (Dip5) or (Agp1) or (Tat2) or (Put4) [Fcy2] or (Fcy21) or (Fcy21) or (Fcy22) or (
ASNI2r ARGI2r ARAB-Lt ARAB-Dt AMETI2 ALLTTII ALLTNtII ALAI2r AKGI2r AKGI2r AKGMAL ADNI2 ADEI2 ACI2r	L-asparagine reversible transport via proton symport L-arganine reversible transport via proton symport L-arabinoase extracellular transport D-arabinose reversible transport S-adenosylmethionine transport in via proton symport allantote irreversible uniport allantoin irreversible uniport L-alanine reversible transport via proton symport 2-oxoglutarate reversible transport via symport alpha-ketoglutarate/malate transporter adenosine transport in via proton symport adenine transport in via proton symport adenine transport in via proton symport acetate reversible transport via proton symport	asn-L[e] + h[e] <==> asn-L[c] + h[c] arg-L[e] + h[e] <==> arg-L[c] + h[c] arab-L[e] <==> arab-L[c] arab-D[e] <==> arab-D[c] amet[e] + h[e] -> amet[c] + h[c] alitt[e] -> alitt[c] alitn[e] -> alitn[c] alia-L[e] + h[e] <==> ala-L[c] + h[c] akg[e] + h[e] <==> akg[c] + h[c] akg[e] + mal-L[e] <==> akg[e] + mal-L[c] adn[e] + h[e] -> adn[c] + h[c] ade[e] + h[e] -> ade[c] + h[c] ade[e] + h[e] -> ade[c] + h[c] ade[e] + h[e] -> ade[c] + h[c]		Transport, Extracellular	or YDR508C or YPL265W) (YKR039W or YEL063C or YNL270C) YPL274W YJR152W YIR028W (YKR039W or YPL265W or YCL025C or YOL020W or YOR348C) (YER056C or YER060W or YER060W-A or YGL186C)	Agp1) or (Gnp1) or (Gnp1) or (Dip5) (Gap1) or (Can1) or (Alp1) Sam3 Dal5 Dal4 (Gap1) or (Dal4 (Gap1) or (Tat2) or (Put4) (Fcy2) or (Fcy21) or (Fcy22) or (Fcy22) or (Fcy22) or (Fcy23)
ASNI2r ARGI2r ARAB-Lt ARAB-Dt AMETI2 ALLTTNI ALLTNII ALAI2r AKGI2r AKGMAL ADNI2 ADEI2	L-asparagine reversible transport via proton symport L-arabinoase extracellular transport D-arabinose reversible transport S-adenosyl-L-methionine transport in via proton symport allantoate irreversible uniport L-alanine reversible uniport L-alanine reversible transport via proton symport allantosis irreversible uniport L-alanine reversible transport via proton symport 2-oxoglutarate reversible transport via symport alpha-ketoglutarate/malate transporter adenosine transport in via proton symport	asn-L[e] + h[e] <==> asn-L[c] + h[c] arg-L[e] + h[e] <==> arg-L[c] + h[c] arab-L[e] <==> arab-L[c] arab-D[e] <==> arab-D[c] amet(e] + h[e] -> amet(c] + h[c] alitt[e] -> alitt[c] alitt[e] -> alltn[c] ala-L[e] + h[e] <==> ala-L[c] + h[c] akg[e] + h[e] <==> akg[e] + h[c] akg[e] + h[e] <==> akg[e] + mal-L[c] adn[e] + h[e] -> adn[c] + h[c] ade[e] + h[e] -> ade[c] + h[c]		Transport, Extracellular	or YDR508C or YPL265W) (YKR039W or YEL063C or YNL270C) YPL274W YJR152W YIR028W (YKR039W or YPL265W or YCL025C or YOL020W or YOR348C) (YER056C or YER060W or YER060W-A or YGL186C)	Agp1) or (Gnp1) or (Gnp1) or (Gnp1) or (Can1) or (Can1) or (Alp1) Sam3 Dal5 Dal4 (Gap1) or (Dip5) or (Agp1) or (Tat2) or (Put4) (Fcy2) or (Fcy21) or (Fcy22) or (Fcy22) or (Fcy23) Bph1
ASNI2r ARG12r ARAB-Lt ARAB-Dt AMET12 ALLTTNI ALLTNII ALAI2r AKG12r AKGMAL ADN12 ADE12 ACI2r ACGALDt	L-asparagine reversible transport via proton symport L-arganine reversible transport via proton symport L-arabinoase extracellular transport D-arabinose reversible transport S-adenosyl-L-methionine transport in via proton symport allantoate irreversible uniport allantoate irreversible uniport L-alanine reversible transport via proton symport L-alanine reversible transport via proton symport 2-oxoglutarate reversible transport via symport alpha-ketoglutarate/malate transporter adenosine transport in via proton symport adenine transport in via proton symport acetate reversible transport via proton symport acetate reversible transport via proton symport	asn-L[e] + h[e] <==> asn-L[c] + h[c] arg-L[e] + h[e] <==> arg-L[c] + h[c] arab-L[e] <==> arab-L[c] arab-D[e] <==> arab-D[c] amet[e] + h[e] -> amet[c] + h[c] alitt[e] -> alitt[c] alitt[e] -> allttn[c] ala-L[e] + h[e] <==> ala-L[c] + h[c] akg[e] + h[e] <==> akg[c] + h[c] akg[c] + mal-L[e] <==> akg[e] + mal-L[c] adn[e] + h[e] -> adn[c] + h[c] ade[e] + h[e] -> ade[c] + h[c] ade[e] + h[e] -> ade[c] + h[c] acald[e] <==> acald[c]		Transport, Extracellular	or YDR508C or YPL265W) (YKR039W or YEL063C or YNL270C) YPL274W YJR152W YIR028W (YKR039W or YPL265W or YCL025C or YOL020W or YOR348C) (YER056C or YER060W or YER060W-A or YGL186C) YCR032W	Agp1) or (Gnp1) or (Gnp1) or (Can1) or (Can1) or (Can1) or (Alp1) Sam3 Dal5 Dal4 (Gap1) or (Dal4 (Gap1) or (Tat2) or (Fut4) (Fcy2) or (Fcy21) or (Fcy22) or (Fcy22) or (Fcy22) or (Fcy23) Bph1 (Put4) or (
ASNI2r ARGI2r ARAB-Lt ARAB-Dt AMETI2 ALLTTNI ALLTNI ALAI2r AKGIZI AKGMAL ADNI2 ADEt2 ACI2r ACALDt ABUTI2	L-asparagine reversible transport via proton symport L-arganine reversible transport via proton symport L-arabinoase extracellular transport D-arabinose reversible transport S-adenosylmethionine transport in via proton symport allantote irreversible uniport allantoin irreversible uniport L-alanine reversible transport via proton symport 2-oxoglutarate reversible transport via symport alpha-ketoglutarate/malate transporter adenosine transport in via proton symport adenine transport in via proton symport adenine transport in via proton symport acetate reversible transport via proton symport	asn-L[e] + h[e] <==> asn-L[c] + h[c] arg-L[e] + h[e] <==> arg-L[c] + h[c] arab-L[e] <==> arab-L[c] arab-D[e] <==> arab-D[c] amet[e] + h[e] -> amet[c] + h[c] alitt[e] -> alitt[c] alitn[e] -> alitn[c] alia-L[e] + h[e] <==> ala-L[c] + h[c] akg[e] + h[e] <==> akg[c] + h[c] akg[e] + mal-L[e] <==> akg[e] + mal-L[c] adn[e] + h[e] -> adn[c] + h[c] ade[e] + h[e] -> ade[c] + h[c] ade[e] + h[e] -> ade[c] + h[c] ade[e] + h[e] -> ade[c] + h[c]		Transport, Extracellular	or YDR508C or YPL265W) (YKR039W or YEL063C or YNL270C) YPL274W YJR152W YIR028W (YKR039W or YPL265W or YCL025C or YOL020W or YOR348C) (YER056C or YER060W or YER060W-A or YGL186C)	Agp1) or (Gnp1) or (Gnp1) or (Gnp1) or (Can1) or (Can1) or (Alp1) Sam3 Dal5 Dal4 (Gap1) or (Dip5) or (Agp1) or (Tat2) or (Put4) (Fcy2) or (Fcy21) or (Fcy22) or (Fcy22) or (Fcy23) Bph1
ASNI2r ARGI2r ARAB-Lt ARAB-Dt AMETI2 ALLTTNI ALLTNII ALLTNII ALAI2r AKGIZI AKGMAL ADNI2 ADEt2 ACI2r ACALDt ABUTI2	L-asparagine reversible transport via proton symport L-arganine reversible transport via proton symport L-arabinoase extracellular transport D-arabinose reversible transport S-adenosylmethionine transport in via proton symport allantote irreversible uniport allantoin irreversible uniport L-alanine reversible transport via proton symport 2-oxoglutarate reversible transport via symport alpha-ketoglutarate/malate transporter adenosine transport in via proton symport adenine transport in via proton symport acetate reversible transport via proton symport acetate reversible transport via proton symport acetate reversible transport via proton symport 4-aminobutyrate transport in via proton symport	asn-L[e] + h[e] <==> asn-L[c] + h[c] arg-L[e] + h[e] <==> arg-L[c] + h[c] arab-L[e] <==> arab-L[c] arab-D[e] <==> arab-D[c] amet[e] + h[e] -> amet[c] + h[c] alitt[e] -> alitt[c] alitn[e] -> alitn[c] alia-L[e] + h[e] <==> ala-L[c] + h[c] akg[e] + h[e] <==> akg[c] + h[c] akg[e] + mal-L[e] <==> akg[e] + mal-L[c] adn[e] + h[e] -> adn[c] + h[c] ade[e] + h[e] -> ade[c] + h[c] ac[e] + h[e] <==> ac[c] + h[c] acaid[e] <==> acaid[c] 4abut[e] + h[e]> 4abut[c] + h[c]		Transport, Extracellular	or YDR508C or YPL265W) (YKR039W or YEL063C or YNL270C) YPL274W YJR152W YIR028W (YKR039W or YPL265W or YCL025C or YOL020W or YOR348C) (YER056C or YER060W or YER060W-A or YGL186C) YCR032W	Agp1) or (Gnp1) or (Gnp1) or (Can1) or (Can1) or (Can1) or (Alp1) Sam3 Dal5 Dal4 (Gap1) or (Dal4 (Gap1) or (Tat2) or (Fut4) (Fcy2) or (Fcy21) or (Fcy22) or (Fcy22) or (Fcy22) or (Fcy23) Bph1 (Put4) or (
ASNI2r ARGI2r ARAB-LI ARAB-DI ARAB-DI ALLTNI ALLTNI ALLTNI ALAI2r AKGI2r AKGI2r AKGMAL ADNI2 ADEI2 ACI2r ACALDI ABUTI2 ABUTI2	L-asparagine reversible transport via proton symport L-arabinoase extracellular transport D-arabinose reversible transport S-adenoyl-L-methionine transport in via proton symport allantoate irreversible uniport allantoate irreversible uniport L-alanine reversible uniport L-alanine reversible transport via proton symport 2-oxoglutarate reversible transport via symport alpha-ketoglutarate/malate transporter adenosine transport in via proton symport adenine transport in via proton symport acetate reversible transport via proton symport acetate reversible transport via proton symport acetate reversible transport via proton symport acetatedehyde reversible transport 4-aminobutyrate transport via proton symport L-arabinitol transport via passive diffusion	asn-L[e] + h[e] <==> asn-L[c] + h[c] arg-L[e] + h[e] <==> arg-L[c] + h[c] arab-L[e] <==> arab-L[c] arab-D[e] <==> arab-D[c] amet[e] + h[e] >= amet[c] + h[c] alltt[e] -> alltt[c] alltt[e] -> alltn[c] ala-L[e] + h[e] <==> ala-L[c] + h[c] ala[e] + h[e] <==> ala-L[c] + h[c] akg[e] + h[e] <==> akg[e] + h[c] akg[c] + mal-L[e] <==> akg[e] + mal-L[c] adn[e] + h[e] -> adn[c] + h[c] ade[e] + h[e] -> ade[c] + h[c] acald[e] <==> acald[c] 4abut[e] + h[e] -> 4abut[c] + h[c] abt[e] <==> abt[c]		Transport, Extracellular	or YDR508C or YPL265W) (YKR039W or YEL063C or YNL270C) YPL274W YJR152W YIR028W (YKR039W or YPL265W or YCL025C or YOL020W or YOR348C) (YER056C or YER060W or YER060W-A or YGL186C) YCR032W	Agp1) or (Gnp1) or (Gnp1) or (Can1) or (Can1) or (Can1) or (Alp1) Sam3 Dal5 Dal4 (Gap1) or (Dal4 (Gap1) or (Tat2) or (Tat2) or (Fcy2) or (Fcy21) or (Fcy22) or (Fcy22) or (Fcy22) or (Fcy23) Bph1 (Put4) or (
ASNI2r ARGI2r ARAB-LI ARAB-DI AMETI2 ALLTTII ALLTNII ALAI2r AKGI2r AKGMAL ADNI2 ADEI2 ACI2r ACALDI ABUTI2 ABUTI2 ABUTI2 ABUTI2 ABUTI2 ABUTI2 ABUTI2 ABUTI2 ABUTI3 BAONNI2	L-asparagine reversible transport via proton symport L-arganine reversible transport via proton symport L-arabinoase extracellular transport D-arabinose reversible transport S-adenosyl-L-methionine transport in via proton symport allantoate irreversible uniport allantoate irreversible uniport L-alanine reversible uniport L-alanine reversible transport via proton symport 2-oxoglutarate reversible transport via symport alpha-ketoglutarate/malate transporter adenosine transport in via proton symport adenine transport in via proton symport acetate reversible transport via proton symport acetate reversible transport via proton symport acetate reversible transport via proton symport acetatelehyde reversible transport 4-aminobutyrate transport via passive diffusion 8-Amino-7-oxononanoate reversible transport via proton symport	asn-L[e] + h[e] <==> asn-L[c] + h[c] arg-L[e] + h[e] <==> arg-L[c] + h[c] arab-L[e] <==> arab-L[c] arab-D[e] <==> arab-D[c] amet[e] + h[e] -> amet[c] + h[c] alitt[e] -> alitt[c] alitt[e] -> allttn[c] ala-L[e] + h[e] <==> ala-L[c] + h[c] akg[e] + h[e] <==> akg[c] + h[c] akg[e] + mal-L[e] <==> akg[e] + mal-L[c] adn[e] + h[e] -> adn[c] + h[c] ade[e] + h[e] -> adn[c] + h[c] ace[e] + h[e] -> adc[c] + h[c] acald[e] <==> acald[c] 4abut[e] + h[e] -> 4abut[c] + h[c] abt[e] <=>> abt[c] 8aonn[e] + h[e] <=>> 8aonn[c] + h[c]		Transport, Extracellular	or YDR508C or YPL265W) (YKR039W or YEL063C or YNL270C) YPL274W YJR152W YIR028W (YKR039W or YPL265W or YCL025C or YOL020W or YOR348C) (YER056C or YER060W or YER060W-A or YGL186C) YCR032W (YOR348C or YDL210W)	Agp1) or (Gnp1) or (Gnp1) or (Dip5) (Gap1) or (Can1) or (Alp1) Sam3 Dal5 Dal4 ((Gap1) or (Agp1) or (Tat2) or (Put4) ((Fcy2) or (Fcy21) or (Fcy22) or (Fcy23) Bph1 (Put4) or (Uga4)
ASNI2r ARGI2r ARAB-Lt ARAB-Lt ARAB-Dt AMETI2 ALLTNII ALLTNII ALLTNII ALAI2r AKGI2r AKGMAL ADNI2 ADEI2 ACI2r ACI	L-asparagine reversible transport via proton symport L-arabinoase extracellular transport D-arabinose reversible transport S-adenoyl-L-methionine transport in via proton symport allantoate irreversible uniport allantoate irreversible uniport L-alanine reversible uniport L-alanine reversible transport via proton symport 2-oxoglutarate reversible transport via symport alpha-ketoglutarate/malate transporter adenosine transport in via proton symport adenine transport in via proton symport acetate reversible transport via proton symport acetate reversible transport via proton symport acetate reversible transport via proton symport acetatedehyde reversible transport 4-aminobutyrate transport via proton symport L-arabinitol transport via passive diffusion	asn-L[e] + h[e] <==> asn-L[c] + h[c] arg-L[e] + h[e] <==> arg-L[c] + h[c] arab-L[e] <==> arab-L[c] arab-D[e] <==> arab-D[c] amet[e] + h[e] >= amet[c] + h[c] alltt[e] -> alltt[c] alltt[e] -> alltn[c] ala-L[e] + h[e] <==> ala-L[c] + h[c] ala[e] + h[e] <==> ala-L[c] + h[c] akg[e] + h[e] <==> akg[e] + h[c] akg[c] + mal-L[e] <==> akg[e] + mal-L[c] adn[e] + h[e] -> adn[c] + h[c] ade[e] + h[e] -> ade[c] + h[c] acald[e] <==> acald[c] 4abut[e] + h[e] -> 4abut[c] + h[c] abt[e] <==> abt[c]		Transport, Extracellular	or YDR508C or YPL265W) (YKR039W or YEL063C or YNL270C) YPL274W YJR152W YIR028W (YKR039W or YPL265W or YCL025C or YOL020W or YOR348C) (YER056C or YER060W or YER060W-A or YGL186C) YCR032W	Agp1) or (Gnp1) or (Gnp1) or (Can1) or (Can1) or (Can1) or (Alp1) Sam3 Dal5 Dal4 (Gap1) or (Dal4 (Gap1) or (Tat2) or (Tat2) or (Fcy2) or (Fcy21) or (Fcy22) or (Fcy22) or (Fcy22) or (Fcy23) Bph1 (Put4) or (

PEtg_SC	phosphatidylethanolamine Golgi transport, yeast-specific	pe_SC[c] <==> pe_SC[g]	1	Transport, Golgi Apparatus		1
GDPt3g	GDP Golgi transport via proton anitport	gdp[g] + h[c] <==> gdp[c] + h[g]		Transport, Golgi Apparatus	+	
CO2tg	CO2 Golgi transport	co2[c] <==> co2[g]		Transport, Golgi Apparatus	1	
VALt2m	Valine reversible mitochondrial transport via proton symport	h[c] + val-L[c] <==> h[m] + val-L[m]		Transport, Mitochondrial		
TYRt2m	tyrosine mitochondrial transport via proton symport	h[c] + tyr-L[c] <==> h[m] + tyr-L[m]		Transport, Mitochondrial		
TRPt2m	tryptophan mitochondrial transport via proton symport	h[c] + trp-L[c] <==> h[m] + trp-L[m]		Transport, Mitochondrial		
THRt2m	threonine mitochondrial transport via proton symport	h[c] + thr-L[c] <==> h[m] + thr-L[m]		Transport, Mitochondrial		
THFtm	5,6,7,8-Tetrahydrofolate transport, diffusion, mitochondrial	thf[c] <==> thf[m]		Transport, Mitochondrial		
SUCFUMtm	succinate-fumarate transport, mitochondrial	fum[m] + succ[c]> fum[c] + succ[m]		Transport, Mitochondrial	YJR095W	Sfc1-m
SUCCtm	succinate transport, mitochondrial	pi[m] + succ[c]> pi[c] + succ[m]		Transport, Mitochondrial	YLR348C	Dic1-m
SERt2m	serine mitochondrial transport via proton symport	h[c] + ser-L[c] <==> h[m] + ser-L[m]		Transport, Mitochondrial		
RIBFLVtm	Riboflavin reversible mitochondrial transport	ribflv[c] <==> ribflv[m]		Transport, Mitochondrial		
QULNtm	Quinolinate reversible mitochondrial transport	quin[c] <==> quin[m]		Transport, Mitochondrial		
PYRt2m	pyruvate mitochondrial transport via proton symport	h[c] + pyr[c] <==> h[m] + pyr[m]		Transport, Mitochondrial		
PStm_SC	phosphatidylserine mitochondrial transport, yeast-specific	ps_SC[c] <==> ps_SC[m]		Transport, Mitochondrial		
PRPPtm	PRPP reversible transport, mitochondrial	prpp[c] <==> prpp[m]		Transport, Mitochondrial		
PROtm	L-proline transport, diffusion, mitochondrial	pro-L[c] <==> pro-L[m]	_	Transport, Mitochondrial	+	
PPPG9tm PIt5m	protoporphyrinogen IX mitochondrial transport	pppg9[c] <==> pppg9[m]	_	Transport, Mitochondrial	YER053C	Phc1-m
Plt2m	phosphate transport via hydroxide ion symport, mitochondrial	oh1[m] + pi[c] <==> oh1[c] + pi[m]		Transport, Mitochondrial	YJR077C	Mir1-m
PHEt2m	phosphate transporter, mitochondrial Phenylalanine mitochondrial transport via proton symport	h[c] + pi[c] <==> h[m] + pin [n]		Transport, Mitochondrial	TJROTTC	IVIII 1-III
PEtm_SC	phosphatidylethanolamine mitochondrial transport, yeast-specific	h[m] + phe-L[m] <==> h[c] + phe-L[c] pe_SC[c] <==> pe_SC[m]		Transport, Mitochondrial		
PAtm_SC				Transport, Mitochondrial		
PAPtm	phosphatidate reversible transport, mitochondrial, yeast-specific Adenosine 3',5'-bisphosphate mitochondrial transport	pa_SC[c] <==> pa_SC[m] pap(c] <==> pap[m]	+	Transport, Mitochondrial Transport, Mitochondrial	+	1
PANTtm	pantothenate mitochondrial transport	pant-R[c] <==> pant-R[m]	+	Transport, Mitochondrial	+	1
PAN4Ptm	pantotheriate milochondrial transport panthetheine 4'-phosphate reversible mitochondrial transport	pan4p[c] <==> pan4p[m]	+	Transport, Mitochondrial	+	+
	pararotrono - priopriate reversible initocrionaria transport	beauthfol, beauthfuil	+	Transport, Mitoonondiana	+	(Odc1-m) or (
OXO2Ctm	2-oxodicarboylate transporter, mitochondrial	akg[m] + oxag[c] <==> akg[c] + oxag[m]		Transport, Mitochondrial	(YPL134C or YOR222W)	Odc2-m)
ORNt3m	ornithine mitochondrial transport via proton antiport	h[c] + orn[m] <==> h[m] + orn[c]	+	Transport, Mitochondrial	YOR130C	Ort1-m
OCTDP_5tm	all-trans-Octaprenyl diphosphate	octdp_5[c] <==> octdp_5[m]	+	Transport, Mitochondrial	1.51(1000	OILI III
OAAt2m	oxaloacetate transport, mitochondrial	h[c] + oaa[c] <==> h[m] + oaa[m]	+	Transport, Mitochondrial	YKL120W	Oac1-m
O2tm	O2 transport (diffusion)	o2[c] <==> o2[m]		Transport, Mitochondrial		Oder III
NMNt2m	NMN mitochondrial transport via proton symport	h[c] + nmn[c] <==> h[m] + nmn[m]	_	Transport, Mitochondrial	+	
NH4tm	NH3 mitochondrial transport	nh4[c] <==> nh4[m]		Transport, Mitochondrial	+	
MLTHFtm	5,10-Methylenetetrahydrofolate transport, diffusion, mitochondrial	mlthf[c] <==> mlthf[m]		Transport, Mitochondrial	+	
METt2m	methionine mitochondrial transport via proton symport	h[m] + met-L[m] <==> h[c] + met-L[c]		Transport, Mitochondrial	+	
MALtm	malate transport, mitochondrial	mal-L[c] + pi[m] <==> mal-L[m] + pi[c]		Transport, Mitochondrial	YLR348C	Dic1-m
LYSt2m	Lysine mitochondrial transport via proton symport	h[c] + lys-L[c] <==> h[m] + lys-L[m]		Transport, Mitochondrial	112.10.100	5.01
IND3ACtm	indole-3-acetate mitochondrial transport via diffusion	ind3ac[c] <==> ind3ac[m]		Transport, Mitochondrial	_	
ID3ACALDtm	indole-3-acetaldehyde mitochondrial transport via diffusion	id3acald[c] <==> id3acald[m]		Transport, Mitochondrial	+	
HMGCOAtm	Hydroxymethylglutaryl-CoA reversible mitochondrial transport	hmgcoa[c] <==> hmgcoa[m]		Transport, Mitochondrial	+	
HISt2m	histidine mitochondrial transport via proton symport	h[m] + his-L[m] <==> h[c] + his-L[c]		Transport, Mitochondrial	_	
H2Otm	H2O transport, mitochondrial	h2o[c] <==> h2o[m]		Transport, Mitochondrial		
GUAtm	guanine mitochondrial transport via diffusion	gua[c] <==> gua[m]		Transport, Mitochondrial		
GSNt2m	guanosine mitochondrial transport via proton symport	gsn[c] + h[c] <==> gsn[m] + h[m]		Transport, Mitochondrial	1	
GLYt2m	glycine mitochondrial transport via proton symport	gly[c] + h[c] <==> gly[m] + h[m]		Transport, Mitochondrial	1	
GLYC3Ptm	glycerol-3-phosphate shuttle	glyc3p[c]> glyc3p[m]		Transport, Mitochondrial		
GLUt5m	L-glutamate transport into mitochondria via hydroxide ion antiport	glu-L[c] + oh1[m]> glu-L[m] + oh1[c]		Transport, Mitochondrial	1	
GLUt2m	L-glutamate reversible transport via proton symport, mitochondrial	glu-L[c] + h[c] <==> glu-L[m] + h[m]		Transport, Mitochondrial	1	
GCALDtm	glycoaldehyde mitochondrial transport	gcald[c] <==> gcald[m]		Transport, Mitochondrial		
FRDcm	fumarate reductase, cytosolic/mitochondrial	fadh2[m] + fum[c]> fad[m] + succ[c]	EC-1.3.99.1	Transport, Mitochondrial	YEL047C	Frds1
FORtm	formate mitochondrial transport	for[m]> for[c]		Transport, Mitochondrial		
FADFMNtm	FAD/FMN antiport	fad[c] + fmn[m]> fad[m] + fmn[c]		Transport, Mitochondrial	YIL134W	Flx1-m
FA182ACPtm	fatty-acyl-ACP mitochondrial transport	ocdcyaACP[m]> ocdcyaACP[c]		Transport, Mitochondrial		
FA181ACPtm	fatty-acyl-ACP mitochondrial transport	octeACP[m]> octeACP[c]		Transport, Mitochondrial		
FA180ACPtm	fatty-acyl-ACP mitochondrial transport	ocdcaACP[m]> ocdcaACP[c]		Transport, Mitochondrial		
FA161ACPtm	fatty-acyl-ACP mitochondrial transport	hdeACP[m]> hdeACP[c]		Transport, Mitochondrial		
FA160ACPtm	fatty-acyl-ACP mitochondrial transport	palmACP[m]> palmACP[c]		Transport, Mitochondrial		
FA141ACPtm	fatty-acyl-ACP mitochondrial transport	tdeACP[m]> tdeACP[c]		Transport, Mitochondrial		
FA140ACPtm	fatty-acyl-ACP mitochondrial transport	myrsACP[m]> myrsACP[c]		Transport, Mitochondrial		
FA120ACPtm	fatty-acyl-ACP mitochondrial transport	ddcaACP[m]> ddcaACP[c]		Transport, Mitochondrial		
ETOHtm	ethanol transport to mitochondria (diffusion)	etoh[c] <==> etoh[m]		Transport, Mitochondrial		1
E4Ptm	D-erythrose 4-phosphate mtiochondrial transport via diffusion	e4p[c] <==> e4p[m]		Transport, Mitochondrial	+	
E4HGLUtm	L-erythro-4-hydroxyglutamate mitochondrial transport via diffusion	e4hglu[c] <==> e4hglu[m]		Transport, Mitochondrial	-	5: 4
DICtm	dicarboxylate transport, mitochondrial	mal-L[c] + succ[m] <==> mal-L[m] + succ[c]		Transport, Mitochondrial	YLR348C	Dic1-m
DHPTtm	Dihydropteroate mitochondrial transport via diffusion	dhpt[c] <==> dhpt[m]		Transport, Mitochondrial	+	1
DHNPTtm	dhnpt mitochondrial transport	dhnpt[c] <==> dhnpt[m]		Transport, Mitochondrial	+	1
DHFtm	dihydrofolate reversible mitochondrial transport	dhf[c] <==> dhf[m]		Transport, Mitochondrial	+	1
DHAPtm	dihydroxyacetone phosphate transport, mitochondrial	dhap[m]> dhap[c]		Transport, Mitochondrial	+	1
D-LACtm	D-lactate transport, mitochondrial	h[c] + lac-D[c] <==> h[m] + lac-D[m]	-	Transport, Mitochondrial	+	1
CRNtim CRNCARtm	L-carnitine transport out of mitochondria via diffusion	crn[m] -> crn[c]	+	Transport, Mitochondrial	VOR100C	Cro1 m
CRNCARtm	carnithine-acetylcarnithine carrier, mitochondrial	acrn[c] + crn[m]> acrn[m] + crn[c]	-	Transport, Mitochondrial	YOR100C	Crc1-m
CO2tm	CO2 transport (diffusion), mitochondrial	co2[c] <==> co2[m]	+	Transport, Mitochondrial	+	+
CMPtm	CMP transport, diffusion, mitochondrial	cmp[c] <==> cmp[m]	+	Transport, Mitochondrial	YBR291C	Ctn1 m
CITtcm CITtbm	citrate transport, mitochondrial citrate transport, mitochondrial	cit[c] + icit[m] <==> cit[m] + icit[c]	+	Transport, Mitochondrial	YBR291C YBR291C	Ctp1-m Ctp1-m
		cit[c] + pep[m] <==> cit[m] + pep[c]	+	Transport, Mitochondrial		
CITtam	citrate transport, mitochondrial	cit[c] + mai-L[m] <==> cit[m] + mai-L[c]	+	Transport, Mitochondrial	YBR291C	Ctp1-m
			I		(VDD005W) == VDL0222	(Aac3-m) or (
ATPtm-H	ADDIATD transporter miteakandrial		I	Transport Mitagles - delet	(YBR085W or YBL030C	Pet9-m) or (
	ADP/ATP transporter, mitochondrial	adp[c] + atp[m] + h[c]> adp[m] + atp[c] + h[m]		Transport, Mitochondrial	or YMR056C)	Aac1-m)
	concrete mitochondrial transport via meter assessed	oon [o] + b[o] <==> con [m] + b[m]		Transport Mitashandrial		
ASPt2m	aspartate mitochondrial transport via proton symport	asp-L[c] + h[c] <==> asp-L[m] + h[m]		Transport, Mitochondrial		
	aspartate mitochondrial transport via proton symport asparagine mitochondrial transport via proton transport arginine mitochondrial transport via proton symport	asp-L(c) + h(c) <==> asp-L(m) + h(m) asn-L(c) + h(c) <==> asn-L(m) + h(m) arg-L(c) + h(c) <==> arg-L(m) + h(m)		Transport, Mitochondrial Transport, Mitochondrial Transport, Mitochondrial		

***	10.4.1				
AMETtm	S-Adenosyl-L-methionine reversible transport, mitochondrial	amet[c] <==> amet[m]	Transport, Mitochondrial		
AHCYStm	S-adenosyl-L-homocysteine reversible transport, mitochondrial	ahcys[c] <==> ahcys[m]	Transport, Mitochondrial		
ADEtm	adenine reversible transport, mitochondria	ade[c] <==> ade[m]	Transport, Mitochondrial		
ACtm	acetate transport, mitochondrial	ac[c] <==> ac[m]	Transport, Mitochondrial	1	
ACRNtim	O-acetylcarnintine transport into mitochondria via diffusion	acrn[c]> acrn[m]	Transport, Mitochondrial		
5MTHFtm	5-Methyltetrahydrofolate mitochondrial transport via diffusion	5mthf[c] <==> 5mthf[m]	Transport, Mitochondrial		
5AOPtm	5-Amino-4-oxopentanoate mitochondrial transport	5aop[c] <==> 5aop[m]	Transport, Mitochondrial		
4HPRO-LTtm	trans-4-hydroxy-L-proline mitochondrial transport via diffusion	4hpro-LT[c] <==> 4hpro-LT[m]	Transport, Mitochondrial		
4HBZtm	4-Hydroxybenzoate mitochondrial transport	4hbz[c] <==> 4hbz[m]	Transport, Mitochondrial		
4H2OGLTtm	4-hydroxy-2-oxoglutarate mitochondrial transport via diffusion	4h2oglt[c] <==> 4h2oglt[m]	Transport, Mitochondrial		
4ABZtm	4-Aminobenzoate mitochondrial transport via diffusion	4abz[c] <==> 4abz[m]	Transport, Mitochondrial	1	
4ABUTtm	4-aminobutanoate mitochondrial transport via diffusion	4abut[c] <==> 4abut[m]	Transport, Mitochondrial	—	
4ABUTNtm	4-aminobutanal mitochondrial transport via diffusion	4abutn[c] <==> 4abutn[m]	Transport, Mitochondrial	+	
3OPHB 5tm	3-Octaprenyl-4-hydroxybenzoate mitochondrial transport	3ophb_5[c] <==> 3ophb_5[m]	Transport, Mitochondrial	+	
3MOPtm	3-Methyl-2-oxopentanoate transport, diffusion, mitochondrial	3mop[c] <==> 3mop[m]	Transport, Mitochondrial		
3MOBtm					
	3-methyl-2-oxobutanoate transport, diffusion, mitochondrial	3mob[c] <==> 3mob[m]	Transport, Mitochondrial	-	-
3C4MOPtm	3-Carboxy-4-methyl-2-oxopentanoate transport, diffusion, mitochondrial	3c4mop[c] <==> 3c4mop[m]	Transport, Mitochondrial		
3C3HMPtm	2-Isopropylmalate transport, diffusion, mitochondrial	3c3hmp[c] <==> 3c3hmp[m]	Transport, Mitochondrial		
34HPPt2m	3-(4-hydroxyphenyl)pyruvate mitochondrial transport via proton symport	34hpp[c] + h[c] <==> 34hpp[m] + h[m]	Transport, Mitochondrial		
2OXOADPtim	2-oxoadipate transport out of mitochondria via diffusion	2oxoadp[m]> 2oxoadp[c]	Transport, Mitochondrial		
2OMPH_5tm	2-Octaprenyl-6-methoxyprenol mitochondrial transport	2omph_5[c] <==> 2omph_5[m]	Transport, Mitochondrial		
2MCITtm	2-methylcitrate mitochondrial transport via diffusion	2mcit[c] <==> 2mcit[m]	Transport, Mitochondrial		
2DHPtm	2-Dehydropantoate mitochondrial transport	2dhp[c] <==> 2dhp[m]	Transport, Mitochondrial		
	2-Dehydro-3-deoxy-D-arabino-heptonate7-phohsphate mitochondrial transport				
2DDA7Ptm	via diffusion	2dda7p[c] <==> 2dda7p[m]	Transport, Mitochondrial	<u> </u>	
UMPtn	UMP nuclear transport	ump[c] <==> ump[n]	Transport, Nuclear		
PTD4INOtn_SC	phosphatidyl-1D-myo-4-inositol nuclear transport, yeast-specific	ptd4ino_SC[c] <==> ptd4ino_SC[n]	Transport, Nuclear		
PTD1INOtn_SC	phosphatidyl-1D-myo-insoitol nuclear transport, yeast-specific	ptd1ino_SC[c] <==> ptd1ino_SC[n]	Transport, Nuclear		
Plt2n	phosphate nuclear transport via proton symport	h[c] + p[c] <==> h[n] + p[n]	Transport, Nuclear	1	
H2Otn	H2O transport, nuclear	h2o[n] <==> h2o[c]	Transport, Nuclear	+	
GLUt2n	glutamate nuclear transport via proton symport	glu-L[c] + h[c] <==> glu-L[n] + h[n]	Transport, Nuclear	+	1
GLNt2n	glutamine nuclear transport via proton symport	gin-L[c] + h[c] <==> gin-L[n] + h[n]	Transport, Nuclear	+	
GDPtn	GDP nuclear transport		Transport, Nuclear		
DUMPtn		gdp[c] <==> gdp[n]		-	
DHORtn	dUMP nuclear transport	dump[c] <==> dump[n]	Transport, Nuclear		-
	(S)-Dihydrooroate nuclear transport	dhor-S[c] <==> dhor-S[n]	Transport, Nuclear		-
DGDPtn	dGDP nuclear transport	dgdp[c] <==> dgdp[n]	Transport, Nuclear		
DCDPtn	dCDP nuclear transport	dcdp[c] <==> dcdp[n]	Transport, Nuclear		
DADPtn	DADP nuclear transport	dadp[c] <==> dadp[n]	Transport, Nuclear		
CO2tn	CO2 nuclear transport via diffusion	co2[n] <==> co2[c]	Transport, Nuclear		
CDPtn	CDP nuclear transport	cdp[c] <==> cdp[n]	Transport, Nuclear		
CBPtn	carbamoyl phosphate nuclear transport via diffusion	cbp[c] <==> cbp[n]	Transport, Nuclear		
CBASPtn	N-carbomoyl-L-aspartate transport, diffusion	cbasp[n] <==> cbasp[c]	Transport, Nuclear		
ASPt2n	aspartate nuclear transport via proton symport	asp-L[c] + h[c] <==> asp-L[n] + h[n]	Transport, Nuclear		
AMETtn	S-adenosyl-L-methionine nuclear transport	amet[c] <==> amet[n]	Transport, Nuclear		
AKGt2n	2-oxoglutarate nuclear transport via proton symport	akg[c] + h[c] <==> akg[n] + h[n]	Transport, Nuclear		
AHCYStn	S-adenosyl-L-homocysteine nuclear transport	ahcys[c] <==> ahcys[n]	Transport, Nuclear		
2OMPH_5tn	2-Octaprenyl-6-methoxyprenol nuclear transport	2omph_5[c] <==> 2omph_5[n]	Transport, Nuclear		
2OHPH_5tn	2-Octaprenyl-6-hydroxyphenol nuclear transport	2ohph_5[c] <==> 2ohph_5[n]	Transport, Nuclear	+	
TYRt2p	tyrosine peroxisomal transport via proton symport	h[c] + tyr-L[c] <==> h[x] + tyr-L[x]	Transport, Peroxisomal	+	
PYRt2p	pyruvate peroxisomal transport via proton symport	h[c] + pyr[c] <==> h[x] + pyr[x]	Transport, Peroxisomal	+	
Plt2p	phosphate peroxisomal transport via proton symport	h[c] + pi[c] <==> h[x] + pi[x]	Transport, Peroxisomal		
NMNt2p					
	NMN peroxisomal transport via proton symport	h[c] + nmn[c] <==> h[x] + nmn[x]	Transport, Peroxisomal		
NH4tp	ammonia peroxisomal transport		Transport Development		
MALOAAtp		nh4[c] <==> nh4[x]	Transport, Peroxisomal		
LICVC40*	malate/oxaloacetate shuttle	mal-L[x] + oaa[c] <==> mal-L[c] + oaa[x]	Transport, Peroxisomal		
HCYSt2p	Homocysteine peroxisomal transport via proton symport	mal-L[x] + oaa[c] <==> mal-L[c] + oaa[x] h[c] + hcys-L[c] <==> h[x] + hcys-L[x]	Transport, Peroxisomal Transport, Peroxisomal		
H2Otp	Homocysteine peroxisomal transport via proton symport water transport by diffusion, peroxisomal	mal-L[x] + oaa[c] <==> mal-L[c] + oaa[x] h[c] + hcys-L[c] <==> h[x] + hcys-L[x] h2o[c] <==> h2o[x]	Transport, Peroxisomal Transport, Peroxisomal Transport, Peroxisomal		
H2Otp GLXtp	Homocysteine peroxisomal transport via proton symport water transport by diffusion, peroxisomal glyoxylate transport, peroxisomal	mal-L(x) + oaa(c) <==> mal-L(c) + oaa(x) h(c) + hcys-L(c) <==> h(x) + hcys-L(x) h2o(c) <==> Pa(x) glx(c) <==> glx(x)	Transport, Peroxisomal Transport, Peroxisomal Transport, Peroxisomal Transport, Peroxisomal		
H2Otp GLXtp FA80tp	Homocysteine peroxisomal transport via proton symport water transport by diffusion, peroxisomal glyoxylate transport, peroxisomal fatty acid peroxisomal transport	mal-L[x] + oaa[c] <==> mal-L[c] + oaa[x] h[c] + hcys-L[c] <==> h[x] + hcys-L[x] h2o[c] <==> h2o[x] gMc] <==> gMxI octa[c] -> octa[x]	Transport, Peroxisomal Transport, Peroxisomal Transport, Peroxisomal Transport, Peroxisomal Transport, Peroxisomal		
H2Otp GLXtp FA80tp FA260tp	Homocysteine peroxisomal transport via proton symport water transport by diffusion, peroxisomal glyoxylate transport, peroxisomal fatty acid peroxisomal transport fatty acid peroxisomal transport	mal-L[x] + oaa[c] <==> mal-L[c] + oaa[x] h[c] + hcys-L[c] <==> h[x] + hcys-L[x] h2c[c] <==> h2c[x] g[x] <==> g[x]x octa[c] -> octa[x] hexc[c] -> hexc[x]	Transport, Peroxisomal	YBR041W	Fat1-p
H2Otp GLXtp FA80tp	Homocysteine peroxisomal transport via proton symport water transport by diffusion, peroxisomal glyoxylate transport, peroxisomal fatty acid peroxisomal transport	mal-L[x] + oaa[c] <==> mal-L[c] + oaa[x] h[c] + hcys-L[c] <==> h[x] + hcys-L[x] h2o[c] <==> h2o[x] gMc] <==> gMxI octa[c] -> octa[x]	Transport, Peroxisomal Transport, Peroxisomal Transport, Peroxisomal Transport, Peroxisomal Transport, Peroxisomal	YBR041W YBR041W	Fat1-p
H2Otp GLXtp FA80tp FA260tp FA240tp	Homocysteine peroxisomal transport via proton symport water transport by diffusion, peroxisomal glyoxylate transport, peroxisomal fatty acid peroxisomal transport fatty acid peroxisomal transport	mal-L[x] + oaa[c] <==> mal-L[c] + oaa[x] h[c] + hcys-L[c] <==> h[x] + hcys-L[x] h2c[c] <==> h2c[x] g[x] <==> g[x]x octa[c] -> octa[x] hexc[c] -> hexc[x]	Transport, Peroxisomal		
H2Otp GLXtp FA80tp FA260tp	Homocysteine peroxisomal transport via proton symport water transport by diffusion, peroxisomal glyoxylate transport, peroxisomal fatty acid peroxisomal transport	mal-L[x] + oaa[c] <==> mal-L[c] + oaa[x] h[c] + hcys-L[c] <==> h[x] + hcys-L[x] h2c[c] <==> h2c[x] g[x] <==> g[x]x octa[c] -> octa[x] hexc[c] -> hexc[x]	Transport, Peroxisomal		Fat1-p
H2Otp GLXtp FA80tp FA260tp FA240tp	Homocysteine peroxisomal transport via proton symport water transport by diffusion, peroxisomal glyoxylate transport, peroxisomal fatty acid peroxisomal transport fatty acid peroxisomal transport	mal-L[x] + oaa[c] <==> mal-L[c] + oaa[x] h[c] + hcys-L[c] <==> h[x] + hcys-L[x] h2c0[c] <==> Pac[x] gk[c] <==> glx[x] octa[c] -> octa[x] hexc[c] -> hexc[x] ttc[c] -> hcx[x]	Transport, Peroxisomal	YBR041W	Fat1-p (Pxa1-p and Pxa2-p) (Pxa1-p and
H2Otp GLXtp FA80tp FA260tp FA240tp	Homocysteine peroxisomal transport via proton symport water transport by diffusion, peroxisomal glyoxylate transport, peroxisomal fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acyl-CoA peroxisomal transport via ABC system	mal-L[x] + oaa[c] <==> mal-L[c] + oaa[x] h[c] + hcys-L[c] <==> h[x] + hcys-L[x] h2o[c] <==> h2o[x] glx[c] <==> glx[x] octa[c] -> octa[x] hexc[c] -> hexc[x] ttc[c] -> ttc[x] atp[x] + h2o[x] + ocdycacoa[c]> adp[x] + h[x] + ocdycacoa[x] + pi[x]	Transport, Peroxisomal	YBR041W	Fat1-p (Pxa1-p and Pxa2-p) (Pxa1-p and
H2Otp GLXtp FA80tp FA260tp FA240tp FA182COAabcp	Homocysteine peroxisomal transport via proton symport water transport by diffusion, peroxisomal glyoxylate transport, peroxisomal fatty acid peroxisomal transport	mal-L[x] + oaa[c] <==> mal-L[c] + oaa[x] h[c] + hcys-L[c] <==> h[x] + hcys-L[x] h2c0[c] <==> Pac[x] gk[c] <==> glx[x] octa[c] -> octa[x] hexc[c] -> hexc[x] ttc[c] -> hcx[x]	Transport, Peroxisomal	YBR041W (YPL147W and YKL188C)	Fat1-p (Pxa1-p and Pxa2-p)
H2Otp GLXtp FA80tp FA80tp FA260tp FA240tp FA182COAabcp FA181COAabcp	Homocysteine peroxisomal transport via proton symport water transport by diffusion, peroxisomal glyoxylate transport, peroxisomal fatty acid peroxisomal ransport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acyl-CoA peroxisomal transport via ABC system	mal-L[x] + oaa[c] <==> mal-L[c] + oaa[x] h[c] + hcys-L[c] <==> h[x] + hcys-L[x] h2c[c] <==> h[x] + hcys-L[x] g[x]c] <==> g[x]x octa[c] -> octa[x] hexc[c] -> hexc[x] ttc[c] -> ttc[x] atp[x] + h2o[x] + ocdycacoa[c]> adp[x] + h[x] + ocdycacoa[x] + pi[x] atp[x] + h2o[x] + odecoa[c]> adp[x] + h[x] + odecoa[x] + pi[x]	Transport, Peroxisomal	YBR041W (YPL147W and YKL188C)	Fat1-p (Pxa1-p and Pxa2-p) (Pxa1-p and Pxa2-p) (Pxa1-p and
H2Otp GLXtp FA80tp FA260tp FA240tp FA182COAabcp FA181COAabcp FA180COAabcp	Homocysteine peroxisomal transport via proton symport water transport by diffusion, peroxisomal glyoxylate transport, peroxisomal fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acyl-CoA peroxisomal transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system fatty acyl-CoA transport via ABC system	mal-L[x] + oaa[c] <==> mal-L[c] + oaa[x] h[c] + hcys-L[c] <==> h[x] + hcys-L[x] h2o[c] <==> h2o[x] gk[c] <==> gk[x] octa[c] -> octa[x] hexc[c] -> hexc[x] tt[cc] -> tt[x] atp[x] + h2o[x] + ocdycacoa[c]> adp[x] + h[x] + ocdycacoa[x] + pi[x] atp[x] + h2o[x] + odecoa[c]> adp[x] + h[x] + odecoa[x] + pi[x] atp[x] + h2o[x] + stcoa[c]> adp[x] + h[x] + pi[x] + stcoa[x]	Transport, Peroxisomal	(YPL147W and YKL188C) (YPL147W and YKL188C)	Fat1-p (Pxa1-p and Pxa2-p) (Pxa1-p and Pxa2-p)
H2Otp GLXtp FA80tp FA80tp FA260tp FA240tp FA182COAabcp FA181COAabcp	Homocysteine peroxisomal transport via proton symport water transport by diffusion, peroxisomal glyoxylate transport, peroxisomal fatty acid peroxisomal ransport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acyl-CoA peroxisomal transport via ABC system	mal-L[x] + oaa[c] <==> mal-L[c] + oaa[x] h[c] + hcys-L[c] <==> h[x] + hcys-L[x] h2c[c] <==> h[x] + hcys-L[x] g[x]c] <==> g[x]x octa[c] -> octa[x] hexc[c] -> hexc[x] ttc[c] -> ttc[x] atp[x] + h2o[x] + ocdycacoa[c]> adp[x] + h[x] + ocdycacoa[x] + pi[x] atp[x] + h2o[x] + odecoa[c]> adp[x] + h[x] + odecoa[x] + pi[x]	Transport, Peroxisomal	(YPL147W and YKL188C) (YPL147W and YKL188C)	Fat1-p (Pxa1-p and Pxa2-p) (Pxa1-p and Pxa2-p) (Pxa1-p and Pxa2-p)
H2Otp GLXtp FA80tp FA80tp FA260tp FA240tp FA182COAabcp FA181COAabcp FA180COAabcp FA161tp	Homocysteine peroxisomal transport via proton symport water transport by diffusion, peroxisomal glyoxylate transport, peroxisomal fatty acid peroxisomal ransport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acid peroxisomal transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system fatty acyl-CoA transport via ABC system	mal-L[x] + oaa[c] <==> mal-L[c] + oaa[x] h[c] + hcys-L[c] <==> h[x] + hcys-L[x] h2c[c] <==> h[x] + hcys-L[x] g]x[c] <==> g[x]x octa[c] -> octa[x] hexc[c] -> hexc[x] ttc[c] -> ttc[x] atp[x] + h2c[x] + ocdycacoa[c]> adp[x] + h[x] + ocdycacoa[x] + pi[x] atp[x] + h2c[x] + odecoa[c]> adp[x] + h[x] + odecoa[x] + pi[x] atp[x] + h2c[x] + stcoa[c]> adp[x] + h[x] + stcoa[x] hdcea[c]> hdcea[x]	Transport, Peroxisomal	YBR041W (YPL147W and YKL188C) (YPL147W and YKL188C) (YPL147W and YKL188C)	Fat1-p (Pxa1-p and Pxa2-p) (Pxa1-p and Pxa2-p) (Pxa1-p and Pxa2-p) (Pxa1-p and
H2Otp GLXtp FA80tp FA80tp FA260tp FA240tp FA182COAabcp FA181COAabcp FA180COAabcp FA161tp FA161COAabcp	Homocysteine peroxisomal transport via proton symport water transport by diffusion, peroxisomal glyoxylate transport, peroxisomal fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acyl-CoA peroxisomal transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system fatty acyl-CoA transport via ABC system fatty acyl-CoA transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system	mal-L[x] + oaa[c] <==> mal-L[c] + oaa[x] h[c] + hcys-L[c] <==> h[x] + hcys-L[x] h2o[c] <==> h[x] + hcys-L[x] g[x] <==> g[x]x octa[c] -> octa[x] hexc[c] -> hexc[x] tttc[c] -> ttt[x] atp[x] + h2o[x] + ocdycacoa[c]> adp[x] + h[x] + ocdycacoa[x] + pi[x] atp[x] + h2o[x] + odecoa[c]> adp[x] + h[x] + odecoa[x] + pi[x] atp[x] + h2o[x] + stcoa[c]> adp[x] + h[x] + stcoa[x] hdcea[c]> hdcea[x] atp[x] + h2o[x] + hdcoa[c]> adp[x] + h[x] + hdcoa[x] + pi[x]	Transport, Peroxisomal	(YPL147W and YKL188C) (YPL147W and YKL188C)	Fat1-p (Pxa1-p and Pxa2-p) (Pxa1-p and Pxa2-p) (Pxa1-p and Pxa2-p) (Pxa1-p and
H2Otp GLXtp FA80tp FA80tp FA260tp FA240tp FA182COAabcp FA181COAabcp FA180COAabcp FA161tp	Homocysteine peroxisomal transport via proton symport water transport by diffusion, peroxisomal glyoxylate transport, peroxisomal fatty acid peroxisomal ransport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acid peroxisomal transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system fatty acyl-CoA transport via ABC system	mal-L[x] + oaa[c] <==> mal-L[c] + oaa[x] h[c] + hcys-L[c] <==> h[x] + hcys-L[x] h2c[c] <==> h[x] + hcys-L[x] g]x[c] <==> g[x]x octa[c] -> octa[x] hexc[c] -> hexc[x] ttc[c] -> ttc[x] atp[x] + h2c[x] + ocdycacoa[c]> adp[x] + h[x] + ocdycacoa[x] + pi[x] atp[x] + h2c[x] + odecoa[c]> adp[x] + h[x] + odecoa[x] + pi[x] atp[x] + h2c[x] + stcoa[c]> adp[x] + h[x] + stcoa[x] hdcea[c]> hdcea[x]	Transport, Peroxisomal	YBR041W (YPL147W and YKL188C) (YPL147W and YKL188C) (YPL147W and YKL188C)	Fat1-p (Pxa1-p and Pxa2-p)
H2Ctp GLXtp FA80tp FA80tp FA260tp FA240tp FA181COAabcp FA181COAabcp FA180COAabcp FA161tp FA161COAabcp FA161COAabcp FA161COAabcp	Homocysteine peroxisomal transport via proton symport water transport by diffusion, peroxisomal glyoxylate transport, peroxisomal fatty acid peroxisomal ransport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acyl-CoA peroxisomal transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system fatty acyl-CoA transport via ABC system fatty acyl-CoA transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system fatty acid peroxisomal transport via ABC system	mal-L[x] + oaa[c] <==> mal-L[c] + oaa[x] h[c] + hcys-L[c] <==> h[x] + hcys-L[x] h[c] c] <==> h[x] + hcys-L[x] h[c] c] <==> h[x] + hcys-L[x] g x[c] <==> g x x octa[c] -> ota[x] hexc[c] -> hexc[x] ttc[c] -> ttc[x] atp[x] + h2o[x] + ocdycacoa[c]> adp[x] + h[x] + ocdycacoa[x] + pi[x] atp[x] + h2o[x] + odecoa[c]> adp[x] + h[x] + odecoa[x] + pi[x] atp[x] + h2o[x] + stcoa[c]> adp[x] + h[x] + stcoa[x] hdcea[c]> hdcea[x] atp[x] + h2o[x] + hdcoa[c]> adp[x] + h[x] + hdcoa[x] + pi[x] hdca[c]> hdca[x]	Transport, Peroxisomal	YBR041W (YPL147W and YKL188C) (YPL147W and YKL188C) (YPL147W and YKL188C) (YPL147W and YKL188C)	Fat1-p (Pxa1-p and Pxa2-p)
H2Cltp GLXtp FA80tp FA80tp FA260tp FA240tp FA182COAabcp FA181COAabcp FA180COAabcp FA161tp FA161COAabcp FA1610COAabcp FA160tp FA160COAabcp	Homocysteine peroxisomal transport via proton symport water transport by diffusion, peroxisomal glyoxylate transport, peroxisomal fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acyl-CoA peroxisomal transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system fatty acyl-CoA transport via ABC system fatty acyl-CoA transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system	mal-L[x] + oaa[c] <==> mal-L[c] + oaa[x] h[c] + hcys-L[c] <==> h[x] + hcys-L[x] h2c[c] <==> h[x] + hcys-L[x] g[x] <==> g[x]x octa[x] hexc[c] -> hexc[x] ttc[c] -> hexc[x] ttc[c] -> htc[x] atp[x] + h2o[x] + ocdycacoa[c] -> adp[x] + h[x] + ocdycacoa[x] + pi[x] atp[x] + h2o[x] + odecoa[c] -> adp[x] + h[x] + odecoa[x] + pi[x] atp[x] + h2o[x] + stcoa[c] -> adp[x] + h[x] + pi[x] + stcoa[x] hdcea[c] -> hdcea[x] atp[x] + h2o[x] + hdcoa[c] -> adp[x] + h[x] + hdcoa[x] + pi[x] atp[x] + h2o[x] + hdcoa[c] -> adp[x] + h[x] + hdcoa[x] + pi[x] hdca[c] -> hdca[x] atp[x] + h2o[x] + pmtcoa[c] -> adp[x] + h[x] + pi[x] + pmtcoa[x]	Transport, Peroxisomal	YBR041W (YPL147W and YKL188C) (YPL147W and YKL188C) (YPL147W and YKL188C)	Fat1-p (Pxa1-p and Pxa2-p)
H2Ctp GLXtp FA80tp FA80tp FA260tp FA240tp FA181COAabcp FA181COAabcp FA180COAabcp FA161tp FA161COAabcp FA161COAabcp FA161COAabcp	Homocysteine peroxisomal transport via proton symport water transport by diffusion, peroxisomal glyoxylate transport, peroxisomal fatty acid peroxisomal ransport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acyl-CoA peroxisomal transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system fatty acyl-CoA transport via ABC system fatty acyl-CoA transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system fatty acid peroxisomal transport via ABC system	mal-L[x] + oaa[c] <==> mal-L[c] + oaa[x] h[c] + hcys-L[c] <==> h[x] + hcys-L[x] h[c] c] <==> h[x] + hcys-L[x] h[c] c] <==> h[x] + hcys-L[x] g x[c] <==> g x x octa[c] -> ota[x] hexc[c] -> hexc[x] ttc[c] -> ttc[x] atp[x] + h2o[x] + ocdycacoa[c]> adp[x] + h[x] + ocdycacoa[x] + pi[x] atp[x] + h2o[x] + odecoa[c]> adp[x] + h[x] + odecoa[x] + pi[x] atp[x] + h2o[x] + stcoa[c]> adp[x] + h[x] + stcoa[x] hdcea[c]> hdcea[x] atp[x] + h2o[x] + hdcoa[c]> adp[x] + h[x] + hdcoa[x] + pi[x] hdca[c]> hdca[x]	Transport, Peroxisomal	YBR041W (YPL147W and YKL188C) (YPL147W and YKL188C) (YPL147W and YKL188C) (YPL147W and YKL188C)	Fat1-p (Pxa1-p and Pxa2-p)
H2Otp GLXtp FA80tp FA80tp FA260tp FA240tp FA182COAabcp FA181COAabcp FA180COAabcp FA161tp FA161COAabcp FA161tOAabcp FA161tOAabcp FA161tOAabcp FA161tOAabcp FA161tOAabcp FA161tOAabcp FA161tOAabcp FA161tOAabcp	Homocysteine peroxisomal transport via proton symport water transport by diffusion, peroxisomal glyoxylate transport, peroxisomal fatty acid peroxisomal ransport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acyl-CoA peroxisomal transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system fatty acyl-CoA transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system fatty acid peroxisomal transport via ABC system fatty acid peroxisomal transport via ABC system	mal-L[x] + oaa[c] <==> mal-L[c] + oaa[x] h[c] + hcys-L[c] <==> h[x] + hcys-L[x] h2o[c] <==> h[x] + hcys-L[x] g[x] <==> g[x]x octa[c] -> octa[x] hexc[c] -> hexc[x] ttc[c] -> htc[x] atp[x] + h2o[x] + ocdycacoa[c]> adp[x] + h[x] + ocdycacoa[x] + pi[x] atp[x] + h2o[x] + odecoa[c]> adp[x] + h[x] + odecoa[x] + pi[x] atp[x] + h2o[x] + stcoa[c]> adp[x] + h[x] + stcoa[x] hdcea[c]> hdcea[x] atp[x] + h2o[x] + hdcoa[c]> adp[x] + h[x] + hdcoa[x] + pi[x] atp[x] + h2o[x] + hdcoa[c]> adp[x] + h[x] + hdcoa[x] + pi[x] atp[x] + h2o[x] + hdcoa[c]> adp[x] + h[x] + pi[x] + pi[x] atp[x] + h2o[x] + pmtcoa[c]> adp[x] + h[x] + pi[x] + pmtcoa[x] atp[x] + h2o[x] + pmtcoa[c]> adp[x] + h[x] + pi[x] + pmtcoa[x] ttdcea[c]> ttdcea[x]	Transport, Peroxisomal	YBR041W (YPL147W and YKL188C)	Fat1-p (Pxa1-p and Pxa2-p) (Pxa1-p and Pxa2-p) (Pxa1-p and Pxa2-p) (Pxa1-p and Pxa2-p) (Pxa1-p and Pxa2-p) (Pxa1-p and Pxa2-p)
H2CIp GLXtp FA80tp FA80tp FA260tp FA260tp FA181COAabcp FA181COAabcp FA181COAabcp FA161tp FA161COAabcp FA160tOAabcp FA161tp FA161COAabcp FA160tOAabcp FA160tOAabcp FA160tOAabcp FA160tOAabcp FA161tp FA161COAabcp	Homocysteine peroxisomal transport via proton symport water transport by diffusion, peroxisomal glyoxylate transport, peroxisomal fatty acid peroxisomal ransport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acid peroxisomal transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system fatty acid peroxisomal transport via ABC system	mal-L[x] + oaa[c] <==> mal-L[c] + oaa[x] h[c] + hcys-L[c] <==> h[x] + hcys-L[x] h2c[c] <==> h[x] + hcys-L[x] glx[c] <==> glx[x] octa[c] -> octa[x] hexc[c] -> hexc[x] ttc[c] -> hcx[x] atp[x] + h2o[x] + ocdycacoa[c] -> adp[x] + h[x] + ocdycacoa[x] + pi[x] atp[x] + h2o[x] + odecoa[c]> adp[x] + h[x] + odecoa[x] + pi[x] atp[x] + h2o[x] + stcoa[c]> adp[x] + h[x] + pi[x] + stcoa[x] hdcea[c]> hdcea[x] atp[x] + h2o[x] + hdcoa[c]> adp[x] + h[x] + hdcoa[x] + pi[x] atp[x] + h2o[x] + hdcoa[c]> adp[x] + h[x] + pi[x] + stcoa[x] hdcea[c]> hdcea[x] atp[x] + h2o[x] + pmtcoa[c]> adp[x] + h[x] + pi[x] + pmtcoa[x] ttdcea[c]> ttdcea[x] atp[x] + h2o[x] + pmtcoa[c]> adp[x] + h[x] + pi[x] + pmtcoa[x] ttdcea[c]> ttdcea[x] atp[x] + h2o[x] + tdecoa[c]> adp[x] + h[x] + pi[x] + tdecoa[x]	Transport, Peroxisomal	YBR041W (YPL147W and YKL188C)	Fat1-p (Pxa1-p and Pxa2-p)
H2Otp GLXtp FA80tp FA80tp FA260tp FA240tp FA182COAabcp FA181COAabcp FA180COAabcp FA161tp FA161COAabcp FA161tOAabcp FA161tOAabcp FA161tOAabcp FA161tOAabcp FA161tOAabcp FA161tOAabcp FA161tOAabcp FA161tOAabcp	Homocysteine peroxisomal transport via proton symport water transport by diffusion, peroxisomal glyoxylate transport, peroxisomal fatty acid peroxisomal ransport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acyl-CoA peroxisomal transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system fatty acyl-CoA transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system fatty acid peroxisomal transport via ABC system fatty acid peroxisomal transport via ABC system	mal-L[x] + oaa[c] <==> mal-L[c] + oaa[x] h[c] + hcys-L[c] <==> h[x] + hcys-L[x] h2o[c] <==> h[x] + hcys-L[x] g[x] <==> g[x]x octa[c] -> octa[x] hexc[c] -> hexc[x] ttc[c] -> htc[x] atp[x] + h2o[x] + ocdycacoa[c]> adp[x] + h[x] + ocdycacoa[x] + pi[x] atp[x] + h2o[x] + odecoa[c]> adp[x] + h[x] + odecoa[x] + pi[x] atp[x] + h2o[x] + stcoa[c]> adp[x] + h[x] + stcoa[x] hdcea[c]> hdcea[x] atp[x] + h2o[x] + hdcoa[c]> adp[x] + h[x] + hdcoa[x] + pi[x] atp[x] + h2o[x] + hdcoa[c]> adp[x] + h[x] + hdcoa[x] + pi[x] atp[x] + h2o[x] + hdcoa[c]> adp[x] + h[x] + pi[x] + pi[x] atp[x] + h2o[x] + pmtcoa[c]> adp[x] + h[x] + pi[x] + pmtcoa[x] atp[x] + h2o[x] + pmtcoa[c]> adp[x] + h[x] + pi[x] + pmtcoa[x] ttdcea[c]> ttdcea[x]	Transport, Peroxisomal	YBR041W (YPL147W and YKL188C)	Fat1-p (Pxa1-p and Pxa2-p)
H2Otp GLXtp FA80tp FA80tp FA260tp FA240tp FA181COAabcp FA180COAabcp FA180COAabcp FA161tD FA161COAabcp FA161tOAabcp FA161COAabcp FA160COAabcp FA160COAabcp FA141tp FA141COAabcp FA141tp	Homocysteine peroxisomal transport via proton symport water transport by diffusion, peroxisomal glyoxylate transport, peroxisomal fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acyl-CoA peroxisomal transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system fatty acyl-CoA transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system fatty acid peroxisomal transport	mal-L[x] + oaa[c] <==> mal-L[c] + oaa[x] h[c] + hcys-L[c] <==> h[x] + hcys-L[x] h2c[c] <==> h[x] + hcys-L[x] glx[c] <==> glx[x] octa[c] -> octa[x] hexc[c]> hcxc[x] tttc[c]> ttc[x] atp[x] + h2o[x] + ocdycacoa[c]> adp[x] + h[x] + ocdycacoa[x] + pi[x] atp[x] + h2o[x] + odecoa[c]> adp[x] + h[x] + odecoa[x] + pi[x] atp[x] + h2o[x] + stcoa[c]> adp[x] + h[x] + pi[x] + stcoa[x] hdcea[c]> hdcea[x] atp[x] + h2o[x] + hdcoa[c]> adp[x] + h[x] + hdcoa[x] + pi[x] atp[x] + h2o[x] + hdcoa[c]> adp[x] + h[x] + pi[x] + stcoa[x] hdcea[c]> hdcea[x] atp[x] + h2o[x] + pmtcoa[c]> adp[x] + h[x] + pi[x] + pmtcoa[x] ttdcea[c]> ttdcea[x] atp[x] + h2o[x] + tdecoa[c]> adp[x] + h[x] + pi[x] + tdecoa[x] ttdcea[c]> ttdcea[x]	Transport, Peroxisomal	YBR041W (YPL147W and YKL188C) (YPL147W and YKL188C)	Fat1-p (Pxa1-p and Pxa2-p)
H2CIp GLXtp FA80tp FA80tp FA260tp FA260tp FA181COAabcp FA181COAabcp FA161tp FA161COAabcp FA160tOAabcp FA160tOAabcp FA160tOAabcp FA160tOAabcp FA141tp FA141COAabcp FA141tp FA141COAabcp FA140tp FA140COAabcp	Homocysteine peroxisomal transport via proton symport water transport by diffusion, peroxisomal glyoxylate transport, peroxisomal fatty acid peroxisomal ransport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acid peroxisomal transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system fatty acyl-CoA transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system fatty acid peroxisomal transport via ABC system	mal-L[x] + oaa[c] <==> mal-L[c] + oaa[x] h[c] + hcys-L[c] <==> h[x] + hcys-L[x] h2c[c] <==> h[x] + hcys-L[x] glx[c] <==> glx[x] octa[c] -> octa[x] hexc[c] -> hexc[x] ttc[c] -> hcx[x] atp[x] + h2c[x] + ocdycacoa[c]> adp[x] + h[x] + ocdycacoa[x] + pi[x] atp[x] + h2c[x] + odecoa[c]> adp[x] + h[x] + odecoa[x] + pi[x] atp[x] + h2c[x] + stcoa[c]> adp[x] + h[x] + pi[x] + stcoa[x] hcea[c]> hdcea[x] atp[x] + h2c[x] + hdcoa[c]> adp[x] + h[x] + pi[x] + stcoa[x] hcea[c]> hdcea[x] atp[x] + h2c[x] + hdcoa[c]> adp[x] + h[x] + pi[x] + pi[x] atp[x] + h2c[x] + pmtcoa[c]> adp[x] + h[x] + pi[x] + pmtcoa[x] ttdcea[c]> ttdcea[x] atp[x] + h2c[x] + tdecoa[c]> adp[x] + h[x] + pi[x] + tdecoa[x] ttdcea[c]> ttdcea[x] atp[x] + h2c[x] + tdecoa[c]> adp[x] + h[x] + pi[x] + tdecoa[x] ttdcea[c]> ttdcea[x] atp[x] + h2c[x] + tdcoa[c]> adp[x] + h[x] + pi[x] + tdecoa[x] ttdcea[c]> ttdcea[x]	Transport, Peroxisomal	YBR041W (YPL147W and YKL188C)	Fat1-p (Pxa1-p and Pxa2-p)
H2Otp GLXtp FA80tp FA80tp FA260tp FA240tp FA181COAabcp FA180COAabcp FA180COAabcp FA161tD FA161COAabcp FA161tOAabcp FA161COAabcp FA160COAabcp FA160COAabcp FA141tp FA141COAabcp FA141tp	Homocysteine peroxisomal transport via proton symport water transport by diffusion, peroxisomal glyoxylate transport, peroxisomal fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acid peroxisomal transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system fatty acyl-CoA transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system fatty acid peroxisomal system fatty acid peroxisomal system fatty acid pe	mal-L[x] + oaa[c] <==> mal-L[c] + oaa[x] h[c] + hcys-L[c] <==> h[x] + hcys-L[x] h2c[c] <==> h[x] + hcys-L[x] glx[c] <==> glx[x] octa[c] -> octa[x] hexc[c]> hcxc[x] tttc[c]> ttc[x] atp[x] + h2o[x] + ocdycacoa[c]> adp[x] + h[x] + ocdycacoa[x] + pi[x] atp[x] + h2o[x] + odecoa[c]> adp[x] + h[x] + odecoa[x] + pi[x] atp[x] + h2o[x] + stcoa[c]> adp[x] + h[x] + pi[x] + stcoa[x] hdcea[c]> hdcea[x] atp[x] + h2o[x] + hdcoa[c]> adp[x] + h[x] + hdcoa[x] + pi[x] atp[x] + h2o[x] + hdcoa[c]> adp[x] + h[x] + pi[x] + stcoa[x] hdcea[c]> hdcea[x] atp[x] + h2o[x] + pmtcoa[c]> adp[x] + h[x] + pi[x] + pmtcoa[x] ttdcea[c]> ttdcea[x] atp[x] + h2o[x] + tdecoa[c]> adp[x] + h[x] + pi[x] + tdecoa[x] ttdcea[c]> ttdcea[x]	Transport, Peroxisomal	YBR041W (YPL147W and YKL188C) (YPL147W and YKL188C)	Fat1-p (Pxa1-p and Pxa2-p)
H2CIp GLXtp FA80tp FA80tp FA260tp FA260tp FA181COAabcp FA181COAabcp FA161tp FA161COAabcp FA160tOAabcp FA160tOAabcp FA160tOAabcp FA160tOAabcp FA141tp FA141COAabcp FA141tp FA141COAabcp FA140tp FA140COAabcp	Homocysteine peroxisomal transport via proton symport water transport by diffusion, peroxisomal glyoxylate transport, peroxisomal fatty acid peroxisomal ransport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acid peroxisomal transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system fatty acyl-CoA transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system fatty acid peroxisomal transport via ABC system	mal-L[x] + oaa[c] <==> mal-L[c] + oaa[x] h[c] + hcys-L[c] <==> h[x] + hcys-L[x] h2c[c] <==> h[x] + hcys-L[x] glx[c] <==> glx[x] octa[c] -> octa[x] hexc[c] -> hexc[x] ttc[c] -> hcx[x] atp[x] + h2c[x] + ocdycacoa[c]> adp[x] + h[x] + ocdycacoa[x] + pi[x] atp[x] + h2c[x] + odecoa[c]> adp[x] + h[x] + odecoa[x] + pi[x] atp[x] + h2c[x] + stcoa[c]> adp[x] + h[x] + pi[x] + stcoa[x] hcea[c]> hdcea[x] atp[x] + h2c[x] + hdcoa[c]> adp[x] + h[x] + pi[x] + stcoa[x] hcea[c]> hdcea[x] atp[x] + h2c[x] + hdcoa[c]> adp[x] + h[x] + pi[x] + pi[x] atp[x] + h2c[x] + pmtcoa[c]> adp[x] + h[x] + pi[x] + pmtcoa[x] ttdcea[c]> ttdcea[x] atp[x] + h2c[x] + tdecoa[c]> adp[x] + h[x] + pi[x] + tdecoa[x] ttdcea[c]> ttdcea[x] atp[x] + h2c[x] + tdecoa[c]> adp[x] + h[x] + pi[x] + tdecoa[x] ttdcea[c]> ttdcea[x] atp[x] + h2c[x] + tdcoa[c]> adp[x] + h[x] + pi[x] + tdecoa[x] ttdcea[c]> ttdcea[x]	Transport, Peroxisomal	YBR041W (YPL147W and YKL188C) (YPL147W and YKL188C)	Fat1-p (Pxa1-p and Pxa2-p)
H2CIp GLXtp FA80tp FA80tp FA260tp FA260tp FA260tp FA181COAabcp FA181COAabcp FA181COAabcp FA161tp FA161COAabcp FA160tp FA160COAabcp FA160tp FA160COAabcp FA140tp FA141COAabcp FA140tp FA141COAabcp FA140tp FA140COAabcp FA1420tp	Homocysteine peroxisomal transport via proton symport water transport by diffusion, peroxisomal glyoxylate transport, peroxisomal fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acid peroxisomal transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system fatty acyl-CoA transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system fatty acid peroxisomal system fatty acid peroxisomal via ABC system f	mal-L[x] + oaa[c] <==> mal-L[c] + oaa[x] h[c] + hcys-L[c] <==> h[x] + hcys-L[x] h[c] + hcys-L[c] <==> h[x] + hcys-L[x] h[c] = x > h2o[x] g[x] <==> g[x]x octa[c] -> octa[x] hexc[c] -> hexc[x] tt[c] -> tt[x] atp[x] + h2o[x] + ocdycacoa[c]> adp[x] + h[x] + ocdycacoa[x] + pi[x] atp[x] + h2o[x] + odecoa[c]> adp[x] + h[x] + odecoa[x] + pi[x] atp[x] + h2o[x] + stcoa[c]> adp[x] + h[x] + pi[x] + stcoa[x] hdcea[c]> hdcea[x] atp[x] + h2o[x] + hdcoa[c]> adp[x] + h[x] + pi[x] + stcoa[x] hdcea[c]> hdcea[x] atp[x] + h2o[x] + hdcoa[c]> adp[x] + h[x] + pi[x] + pmtcoa[x] ttdcea[c]> hdcea[x] atp[x] + h2o[x] + pmtcoa[c]> adp[x] + h[x] + pi[x] + pmtcoa[x] ttdcea[c]> ttdcea[x] atp[x] + h2o[x] + tdccoa[c]> adp[x] + h[x] + pi[x] + tdccoa[x] ttdcea[c]> ttdcea[x] atp[x] + h2o[x] + tdccoa[c]> adp[x] + h[x] + pi[x] + tdccoa[x] ddca[c]> ddca[x] ddca[c]> ddca[x] ddca[c]> ddca[x]	Transport, Peroxisomal	YBR041W (YPL147W and YKL188C) (YPL147W and YKL188C)	Fat1-p (Pxa1-p and Pxa2-p)
H2OIp GLXtp FA80tp FA80tp FA260tp FA260tp FA181COAabcp FA181COAabcp FA161tp FA161COAabcp FA160tOAabcp FA160tOAabcp FA160tOAabcp FA160tOAabcp FA140tD FA141COAabcp FA141tp FA141COAabcp FA140tp FA140toAabcp FA140tp FA140to	Homocysteine peroxisomal transport via proton symport water transport by diffusion, peroxisomal glyoxylate transport, peroxisomal fatty acid peroxisomal ransport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acid peroxisomal transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system fatty acyl-CoA transport via ABC system fatty acyl-CoA transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system fatty acid peroxisomal system fatty acid peroxisomal system fatty acid peroxisomal system fatty acid peroxisomal system fatty acid per	mal-L[x] + oaa[c] <==> mal-L[c] + oaa[x] h[c] + hcys-L[c] <==> h[x] + hcys-L[x] h[c] + hcys-L[c] <==> h[x] + hcys-L[x] h[c] = x > h2o[x] g[x] <==> g[x]x octa[c] -> octa[x] hexc[c] -> hexc[x] tt[c] -> tt[x] atp[x] + h2o[x] + ocdycacoa[c]> adp[x] + h[x] + ocdycacoa[x] + pi[x] atp[x] + h2o[x] + odecoa[c]> adp[x] + h[x] + odecoa[x] + pi[x] atp[x] + h2o[x] + stcoa[c]> adp[x] + h[x] + pi[x] + stcoa[x] hdcea[c]> hdcea[x] atp[x] + h2o[x] + hdcoa[c]> adp[x] + h[x] + pi[x] + stcoa[x] hdcea[c]> hdcea[x] atp[x] + h2o[x] + hdcoa[c]> adp[x] + h[x] + pi[x] + pmtcoa[x] ttdcea[c]> hdcea[x] atp[x] + h2o[x] + pmtcoa[c]> adp[x] + h[x] + pi[x] + pmtcoa[x] ttdcea[c]> ttdcea[x] atp[x] + h2o[x] + tdccoa[c]> adp[x] + h[x] + pi[x] + tdccoa[x] ttdcea[c]> ttdcea[x] atp[x] + h2o[x] + tdccoa[c]> adp[x] + h[x] + pi[x] + tdccoa[x] ddca[c]> ddca[x] ddca[c]> ddca[x] ddca[c]> ddca[x]	Transport, Peroxisomal	YBR041W (YPL147W and YKL188C) (YPL147W and YKL188C)	Fat1-p (Pxa1-p and Pxa2-p)
H2CIp GLXtp FA80tp FA80tp FA260tp FA240tp FA182COAabcp FA181COAabcp FA180COAabcp FA161tD FA161COAabcp FA160tp FA160COAabcp FA140tp FA141COAabcp FA140tp FA140COAabcp FA120tp FA120tp FA120tp FA120tp FA120tp	Homocysteine peroxisomal transport via proton symport water transport by diffusion, peroxisomal glyoxylate transport, peroxisomal fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acid peroxisomal transport fatty acid peroxisomal transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system fatty acyl-CoA transport via ABC system fatty acyl-CoA peroxisomal transport via ABC system fatty acid peroxisomal system fatty acid peroxisomal via ABC system f	mal-L[x] + oaa[c] <==> mal-L[c] + oaa[x] h[c] + hcys-L[c] <==> h[x] + hcys-L[x] h[c] <==> y[x]x g[x] <==> g[x]x octa[x] hexc[c] -> hexc[x] ttc[c] -> hcx[x] atp[x] + h2o[x] + ocdycacoa[c] -> adp[x] + h[x] + ocdycacoa[x] + pi[x] atp[x] + h2o[x] + odecoa[c]> adp[x] + h[x] + odecoa[x] + pi[x] atp[x] + h2o[x] + stcoa[c]> adp[x] + h[x] + pi[x] + stcoa[x] hdcea[c]> hdcea[x] atp[x] + h2o[x] + hdcoa[c]> adp[x] + h[x] + pi[x] + stcoa[x] hdcea[c]> hdcea[x] atp[x] + h2o[x] + hdcoa[c]> adp[x] + h[x] + pi[x] + pi[x] ttdcea[c]> hdca[x] atp[x] + h2o[x] + pmtcoa[c]> adp[x] + h[x] + pi[x] + pmtcoa[x] ttdcea[c]> ttdcea[x] atp[x] + h2o[x] + tdecoa[c]> adp[x] + h[x] + pi[x] + tdecoa[x] ttdcea[c]> ttdcea[x] atp[x] + h2o[x] + tdecoa[c]> adp[x] + h[x] + pi[x] + tdecoa[x] ttdcea[c]> ttdcea[x] atp[x] + h2o[x] + tdcoa[c]> adp[x] + h[x] + pi[x] + tdcoa[x] ddca[c]> ddca[x]	Transport, Peroxisomal	YBR041W (YPL147W and YKL188C) (YPL147W and YKL188C)	Fat1-p (Pxa1-p and Pxa2-p)

CRNCARtp	parmiting apotulografting corrier paravisamal	ocrafyl + crafel - > corafel + crafyl	1	Transport Borovisamal		
	carnitine-acetylcarnitine carrier, peroxisomal	acrn[x] + crn[c]> acrn[c] + crn[x]		Transport, Peroxisomal		
CO2tp	CO2 peroxisomal transport	co2[c] <==> co2[x]		Transport, Peroxisomal		
CITtop	citrate/isocitrate antiport into peroxisome	cit[c] + icit[x] <==> cit[x] + icit[c]		Transport, Peroxisomal		
CITtap	citrate/malate antiport into peroxisome	cit[x] + mal-L[c] <==> cit[c] + mal-L[x]		Transport, Peroxisomal	YPR128C	Anti n
ATPtp-H	ADP/ATP transporter, peroxisomal	adp[x] + atp[c] + h[x]> adp[c] + atp[x] + h[c]		Transport, Peroxisomal	YPR128C	Ant1-p
ATP2tp_H ASPGLUtp	AMP/ATP transporter, peroxisomal	amp[x] + atp[c] + h[x]> amp[c] + atp[x] + h[c]		Transport, Peroxisomal	TFK126C	Ant1-p
ACtp	aspartate-glutamate peroxisomal shuttle acetate transport, peroxisomal	asp-L[c] + glu-L[x] <==> asp-L[x] + glu-L[c] ac[c] <==> ac[x]		Transport, Peroxisomal Transport, Peroxisomal		
ACRNtp						1
4H2OGLTtp	acetylcarnitine transport out of peroxisome 4. bydroxy, 2. oxoglutarate peroxisomal transport via diffusion	acrn[x]> acrn[c] 4b2odHcl <> 4b2odHvl		Transport, Peroxisomal		1
34HPPt2p	4-hydroxy-2-oxoglutarate peroxisomal transport via diffusion 3.44 bydroxy-phenyl pyruyate peroxisomal transport via proton symport	4h2oglt[c] <==> 4h2oglt[x] 34hpp[c] + h[c] <==> 34hpp[x] + h[x]		Transport, Peroxisomal Transport, Peroxisomal		1
TREt2v	3-(4-hydroxyphenyl)pyruvate peroxisomal transport via proton symport	34hpp[c] + h[c] <==> 34hpp[x] + h[x]				-
PStv_SC	trehalose vacuolar transport via proton symport phosphatidylserine vacuolar transport, yeast-specific	h[c] + tre[c] <==> h[v] + tre[v] ps_SC[c] <==> ps_SC[v]		Transport, Vacuolar		1
Plt2v	phosphate vacuolar transport, yeast-specific phosphate vacuolar transport via proton symport	h[c] + pi[c] <==> h[v] + pi[v]		Transport, Vacuolar Transport, Vacuolar		
PEtv_SC	phosphatidylethanolamine vacuolar transport, yeast-specific	pe_SC[c] <==> pe_SC[v]		Transport, Vacuolar		1
H2Otv	H2O transport, vacuolar	h2o[c] <==> h2o[v]		Transport, Vacuolar		1
GLCtv	glucose transport, vacuolar	glc-D[c] <==> glc-D[v]		Transport, Vacuolar		+
CO2tv	CO2 vacuolar transport	co2[c] <==> co2[v]		Transport, Vacuolar		+
COZIV	COZ Vacadiai italisport	302[0] 1 002[v]		Tyrosine, Tryptophan, and		1
TYRTRSm	tyrosyl-tRNA synthetase, mitochondrial	[m] : atp + trnatyr + tyr-L> amp + ppi + tyrtma	EC-6.1.1.1	Phenylalanine Metabolism	YPL097W	Msy1-m
TYRTRS	tyrosyl-tRNA synthetase	[c] : atp + trnatyr + tyr-L> amp + ppi + tyrtrna	EC-6.1.1.1	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YGR185C	Tys1
TYRTAp	tyrosine transaminase, peroxisomal	[x] : akg + tyr-L <==> 34hpp + glu-L	EC-2.6.1.5	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YLR027C	Aat2-p
				Tyrosine, Tryptophan, and		
TYRTAm	tyrosine transaminase, mitochondrial	[m] : akg + tyr-L <==> 34hpp + glu-L	EC-2.6.1.5	Phenylalanine Metabolism Tyrosine, Tryptophan, and	YKL106W	Aat1-m (Aro8) or (
TYRTAi	tyrosine transaminase, irreversible	[c] : 34hpp + glu-L> akg + tyr-L	EC-2.6.1.5	Phenylalanine Metabolism	(YGL202W or YHR137W)	
TYRTA	tyrosine transaminase	[c] : akg + tyr-L <==> 34hpp + glu-L	EC-2.6.1.5	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YLR027C	Aat2
TRPTRSm	Tryptophanyl-tRNA synthetase, mitochondrial	[m] : atp + trnatrp + trp-L> amp + ppi + trptrna	EC-6.1.1.2	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YDR268W	Msw1-m
				Tyrosine, Tryptophan, and		
TRPTRS	Tryptophanyl-tRNA synthetase	[c] : atp + trnatrp + trp-L> amp + ppi + trptrna	EC-6.1.1.2	Phenylalanine Metabolism Tyrosine, Tryptophan, and	YOL097C	Wrs1
TRPS1	tryptophan synthase (indoleglycerol phosphate)	[c] : 3ig3p + ser-L> g3p + h2o + trp-L	EC-4.2.1.20 EC-	Phenylalanine Metabolism Tyrosine, Tryptophan, and	YGL026C	Trp5
TRPO2	L-Tryptophan:oxygen 2,3-oxidoreductase (decyclizing)	[c] : o2 + trp-L> Lfmkynr		Phenylalanine Metabolism	YJR078W	Bna2
SPMDAT1	Spermidine acetyltransferase	[c] : accoa + spmd> N1aspmd + coa + h	EC-2.3.1.57	Tyrosine, Tryptophan, and Phenylalanine Metabolism		
SHKK	shikimate kinase	[c] : atp + skm> adp + h + skm5p	EC-2.7.1.71	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YDR127W	Aro1
SHK3D		[c] : 3dhsk + h + nadph> nadp + skm		Tyrosine, Tryptophan, and Phenylalanine Metabolism	YDR127W	Aro1
	shikimate dehydrogenase	[6] . билок (п. пация -> паци (окт		Tyrosine, Tryptophan, and		
PSCVTi	3-phosphoshikimate 1-carboxyvinyltransferase, irreversible	[c] : pep + skm5p> 3psme + pi	EC-2.5.1.19	Phenylalanine Metabolism Tyrosine, Tryptophan, and	YDR127W	Aro1
PRAII	phosphoribosylanthranilate isomerase (irreversible)	[c] : pran> 2cpr5p	EC-5.3.1.24	Phenylalanine Metabolism Tyrosine, Tryptophan, and	YDR007W	Trp1
PPNDH	prephenate dehydratase	[c] : h + pphn> co2 + h2o + phpyr	EC-4.2.1.51	Phenylalanine Metabolism	YNL316C	Pha2
PPND2	prephenate dehydrogenase (NADP)	[c] : nadp + pphn> 34hpp + co2 + nadph	EC-1.3.1.13	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YBR166C	Tyr1
PPND	prephenate dehydrogenase	[c] : nad + pphn> 34hpp + co2 + nadh	EC-1.3.1.12	Tyrosine, Tryptophan, and Phenylalanine Metabolism		
POLYAO2	poylamine oxidase	[c] : N1sprm + h2o + o2> N1aspmd + aproa + h2o2		Tyrosine, Tryptophan, and Phenylalanine Metabolism		
				Tyrosine, Tryptophan, and		
POLYAO	polyamine oxidase	[c] : N1aspmd + h2o + o2> aproa + aprut + h2o2		Phenylalanine Metabolism Tyrosine, Tryptophan, and		
PHETRSm	phenylalanyl-tRNA synthetase, mitochondrial	[m] : atp + phe-L + trnaphe> amp + phetrna + ppi	EC-6.1.1.20	Phenylalanine Metabolism Tyrosine, Tryptophan, and	YPR047W	Msf1-m
PHETRS	Phenylalanyl-tRNA synthetase	[c] : atp + phe-L + trnaphe> amp + phetrna + ppi	EC-6.1.1.20	Phenylalanine Metabolism	(YFL022C and YLR060W)	Frs
PHETA1	phenylalanine transaminase	[c] : akg + phe-L <==> glu-L + phpyr	EC-2.6.1.58	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YHR137W	Aro9
PCLAD	picolinic acid decarboxylase	[c] : cmusa + h> am6sa + co2	EC-4.1.1.45	Tyrosine, Tryptophan, and Phenylalanine Metabolism		
MACACI	maleylacetoacetate isomerase	[c] : 4mlacac> 4fumacac		Tyrosine, Tryptophan, and Phenylalanine Metabolism		
			EC-	Tyrosine, Tryptophan, and Phenylalanine Metabolism	VDI 000M	Pag4
	kynurenine 3-monooxygenase	[c] : Lkynr + h + nadph + o2> h2o + hLkynr + nadp		Tyrosine, Tryptophan, and	YBL098W	Bna4
	kynureninase	[c] : Lkynr + h2o> ala-L + anth + h	EC-3.7.1.3	Phenylalanine Metabolism Tyrosine, Tryptophan, and	YLR231C	Bna5
INDPYRD	Indole-3-pyruvate carboxylase	[c]: h + indpyr <==> co2 + id3acald	EC-4.1.1.74	Phenylalanine Metabolism Tyrosine, Tryptophan, and	YDR380W	Aro10
IGPS	indole-3-glycerol-phosphate synthase	[c] : 2cpr5p + h> 3ig3p + co2 + h2o	EC-4.1.1.48	Phenylalanine Metabolism	YKL211C	Trp3
HKYNH	3-Hydroxy-L-kynurenine hydrolase	[c] : h2o + hLkynr> 3hanthrn + ala-L		Tyrosine, Tryptophan, and Phenylalanine Metabolism	YLR231C	Bna5
HGNTOR	Homogentisate:oxygen 1,2-oxidoreductase (decyclizing)	[c] : hgentis + o2> 4mlacac + h	EC- 1.13.11.5	Tyrosine, Tryptophan, and Phenylalanine Metabolism		
				Tyrosine, Tryptophan, and Phenylalanine Metabolism		
FUIVIAC	fumarylacetoacetase	[c] : 4fumacac + h2o> acac + fum + h	EC-3.7.1.2	rnenyiaianine метаронsm		

FKYNH	N-Formyl-L-kynurenine amidohydrolase	[c] : Lfmkynr + h2o> Lkynr + for + h	EC-3.5.1.9	Tyrosine, Tryptophan, and Phenylalanine Metabolism		
DIAT	diamine transaminase	[c] : accoa + sprm> N1sprm + coa + h	EC-2.6.1.29	Tyrosine, Tryptophan, and Phenylalanine Metabolism		
DHQTi	3-dehydroquinate dehydratase, irreversible	[c] : 3dhq> 3dhsk + h2o	EC-4.2.1.10	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YDR127W	Aro1
DHQS	3-dehydroquinate synthase	[c] : 2dda7p> 3dhq + pi		Tyrosine, Tryptophan, and Phenylalanine Metabolism	YDR127W	Aro1
DDPAm	2-deoxy-D-arabino-heptulosonate 7-phosphate synthetase, mitochondrial	[m] : e4p + h2o + pep> 2dda7p + pi	FC-4 1 2 15	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YDR035W	Aro3-m
				Tyrosine, Tryptophan, and		(Aro4) or (
DDPA	3-deoxy-D-arabino-heptulosonate 7-phosphate synthetase	[c]: e4p + h2o + pep> 2dda7p + pi		Phenylalanine Metabolism Tyrosine, Tryptophan, and	(YBR249C or YDR035W)	
CHORS	chorismate synthase	[c] : 3psme> chor + pi		Phenylalanine Metabolism Tyrosine, Tryptophan, and	YGL148W	Aro2
CHORM	chorismate mutase	[c] : chor> pphn	EC-5.4.99.5	Phenylalanine Metabolism Tyrosine, Tryptophan, and	YPR060C	Aro7
САТр	catalase A, peroxisomal	[x] : (2) h2o2> (2) h2o + o2	EC-1.11.1.6	Phenylalanine Metabolism Tyrosine, Tryptophan, and	YDR256C	Cta1-p
CAT	catalase	[c] : (2) h2o2> (2) h2o + o2	EC-1.11.1.6	Phenylalanine Metabolism Tyrosine, Tryptophan, and	YGR088W	Ctt1
ANPRT	anthranilate phosphoribosyltransferase	[c] : anth + prpp> ppi + pran	EC-2.4.2.18	Phenylalanine Metabolism	YDR354W	Trp4
AMID3	amidase	[c] : h2o + iad> ind3ac + nh4	EC-3.5.1.4	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YDR242W	Amd2
AMID2	amidase	[c]: h2o + pad> nh4 + pac	EC-3.5.1.4	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YDR242W	Amd2
AM6SAD	aminomuconate-semialdehyde dehydrogenase	[c]: am6sa + h2o + nad> amuco + (2) h + nadh	EC-1.2.1.32	Tyrosine, Tryptophan, and Phenylalanine Metabolism		
ALDD2ym	aldehyde dehydrogenase (acetylaldehyde, NADP), mitochondrial	[m] : acald + h2o + nadp> ac + (2) h + nadph		Tyrosine, Tryptophan, and Phenylalanine Metabolism	YOR374W	Ald4-m
ALDD2y	aldehyde dehydrogenase (acetaldehyde, NADP)	[c]: acald + h2o + nadp> ac + (2) h + nadph		Tyrosine, Tryptophan, and Phenylalanine Metabolism	YPL061W	Ald6
				Tyrosine, Tryptophan, and		
ALDD2xm	aldehyde dehydrogenase (acetylaldehyde, NAD), mitochondrial	[m]: acald + h2o + nad> ac + (2) h + nadh	EC-1.2.1.3	Phenylalanine Metabolism Tyrosine, Tryptophan, and	YOR374W	Ald4-m (Ald4-m) or (
ALDD20ym	aldehyde dehydrogenase (indole-3-acetaldehyde, NADP), mitochondrial	[m]: h2o + id3acald + nadp> (2) h + ind3ac + nadph		Phenylalanine Metabolism Tyrosine, Tryptophan, and	(YOR374W or YER073W)	Ald5-m)
ALDD20y	aldehyde dehydrogenase (indole-3-acetaldehyde, NADP)	[c]: h2o + id3acald + nadp> (2) h + ind3ac + nadph		Phenylalanine Metabolism Tyrosine, Tryptophan, and	YPL061W	Ald6
ALDD20xm	aldehyde dehydrogenase (indole-3-acetaldehyde, NAD), mitochondrial	[m]: h2o + id3acald + nad> (2) h + ind3ac + nadh		Phenylalanine Metabolism Tyrosine, Tryptophan, and	YOR374W	Ald4-m (Ald2) or (
ALDD19x	aldehyde dehydrogenase (phenylacetaldehyde, NAD)	[c]: h2o + nad + pacald> (2) h + nadh + pac	EC-1.2.1.39	Phenylalanine Metabolism	(YMR170C or YMR169C)	Ald3)
3HAO	3-hydroxyanthranilate 3,4-dioxygenase	[c] : 3hanthm + o2> cmusa + h	EC- 1.13.11.6	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YJR025C	Bna1
34HPPOR	4-Hydroxyphenylpyruvate:oxygen oxidoreductase	[c] : 34hpp + o2> co2 + hgentis	EC- 1.13.11.27	Tyrosine, Tryptophan, and Phenylalanine Metabolism		
VALTRSm	valyl-tRNA synthetase, mitochondrial	[m] : atp + trnaval + val-L> amp + ppi + valtrna	EC-6.1.1.9	Valine, leucine, and isoleucine metabolism	YGR094W	Vas1-m
VALTRS	Valyl-tRNA synthetase	[c] : atp + trnaval + val-L> amp + ppi + valtrna	EC-6.1.1.9	Valine, leucine, and isoleucine metabolism	YGR094W	Vas1
VALTA	valine transaminase	[c] : akg + val-L <==> 3mob + glu-L	FC-2.6.1.42	Valine, leucine, and isoleucine metabolism	YJR148W	Bat2
OMCDCm	2-oxo-4-methyl-3-carboxypentanoate decarboxylation, mitochondrial	[m] : 3c4mop + h> 4mop + co2		Valine, leucine, and isoleucine metabolism	YHR208W	Bat1-m
				Valine, leucine, and isoleucine		
OMCDC	2-Oxo-4-methyl-3-carboxypentanoate decarboxylation	[c] : 3c4mop + h> 4mop + co2		Metabolism Valine, leucine, and isoleucine	YJR148W	Bat2
LEUTRSm	leucyl-tRNA synthetase, mitochondrial	[m] : atp + leu-L + trnaleu> amp + leutrna + ppi	EC-6.1.1.4	metabolism Valine, leucine, and isoleucine	YLR382C	Nam2-m
LEUTRS	Leucyl-tRNA synthetase	[c] : atp + leu-L + trnaleu> amp + leutrna + ppi	EC-6.1.1.4	metabolism Valine, leucine, and isoleucine	YPL160W	Cdc60
LEUTAm	leucine transaminase, mitochondrial	[m]: akg + leu-L <==> 4mop + glu-L	EC-2.6.1.6	metabolism Valine, leucine, and isoleucine	YHR208W	Bat1-m
LEUTA	leucine transaminase	[c] : akg + leu-L <==> 4mop + glu-L	EC-2.6.1.6	metabolism Valine, leucine, and isoleucine	YJR148W	Bat2
KARA2im	ketol-acid reductoisomerase (2-Aceto-2-hydroxybutanoate), mitochondrial	[m] : 2ahbut + h + nadph> 23dhmp + nadp	EC-1.1.1.86	metabolism	YLR355C	IIv5-m
KARA1im	acetohydroxy acid isomeroreductase, mitochondrial	[m] : alac-S + h + nadph> 23dhmb + nadp	EC-1.1.1.86	Valine, leucine, and isoleucine metabolism	YLR355C	llv5-m
IPPSm	2-isopropylmalate synthase, mitochondrial	[m]: 3mob + accoa + h2o> 3c3hmp + coa + h	EC-4.1.3.12	Valine, leucine, and isoleucine metabolism	YNL104C	Leu4-m
IPPS	2-isopropylmalate synthase	[c]: 3mob + accoa + h2o> 3c3hmp + coa + h	EC-4.1.3.12	Valine, leucine, and isoleucine metabolism	(YNL104C or YOR108W)	(Leu4) or (Leu5)
IPPMIb	2-isopropylmalate hydratase	[c]: 2ippm + h2o <==> 3c3hmp	EC-4.2.1.33	Valine, leucine, and isoleucine metabolism	YGL009C	Leu1
IPPMIa	3-isopropylmalate dehydratase	[c] : 3c2hmp <==> 2ippm + h2o		Valine, leucine, and isoleucine metabolism	YGL009C	Leu1
				Valine, leucine, and isoleucine		
IPMD	3-isopropylmalate dehydrogenase	[c] : 3c2hmp + nad> 3c4mop + h + nadh		metabolism Valine, leucine, and isoleucine	YCL018W	Leu2
ILETRSm	isoleucyl-tRNA synthetase, mitochondrial	[m] : atp + ile-L + trnaile> amp + iletrna + ppi	EC-6.1.1.5	metabolism Valine, leucine, and isoleucine	YPL040C	Ism1-m
ILETRS	Isoleucyl-tRNA synthetase	[c] : atp + ile-L + tmaile> amp + iletrna + ppi	EC-6.1.1.5	metabolism	YBL076C	lls1

				Valine, leucine, and isoleucine		
ILETAm	isoleucine transaminase, mitochondrial	[m] : akg + ile-L <==> 3mop + glu-L	EC-2.6.1.42	metabolism	YHR208W	Bat1-m
				Valine, leucine, and isoleucine		
ILETA	isoleucine transaminase	[c] : akg + ile-L <==> 3mop + glu-L	EC-2.6.1.42	metabolism	YJR148W	Bat2
				Valine, leucine, and isoleucine		
DHAD2m	dihydroxy-acid dehydratase (2,3-dihydroxy-3-methylpentanoate), mitochondrial	[m] : 23dhmp> 3mop + h2o		metabolism	YJR016C	Ilv3-m
				Valine, leucine, and isoleucine		
DHAD1m	dihydroxy-acid dehydratase (2,3-dihydroxy-3-methylbutanoate), mitochondrial	[m] : 23dhmb> 3mob + h2o	EC-4.2.1.9	metabolism	YJR016C	Ilv3-m
				Valine, leucine, and isoleucine	(YCL009C and YMR108W	
ACLSm	acetolactate synthase, mitochondrial	[m] : h + (2) pyr> alac-S + co2	EC-4.1.3.18	metabolism)	IIv26-m
				Valine, leucine, and isoleucine	(YCL009C and YMR108W	
ACHBSm	2-aceto-2-hydroxybutanoate synthase, mitochondrial	[m] : 2obut + h + pyr> 2ahbut + co2	EC-4.1.3.18	metabolism)	IIv26-m
XYLTD_D	xylitol dehydrogenase (D-xyulose-forming)	[c] : nad + xylt> h + nadh + xylu-D	EC-1.1.1.9	Xylose Metabolism	YLR070C	Xyl2
XYLR	xylose reductase	[c] : h + nadph + xyl-D> nadp + xylt		Xylose Metabolism	YHR104W	Gre3
XYLK	xylulokinase	[c] : atp + xylu-D> adp + h + xu5p-D	EC-2.7.1.17	Xylose Metabolism	YGR194C	Xks1

BIOMASS REACTION
(1.1348) 138Dg(n+ (0.4588) ala-L+ (0.046) amp + (0.1607) arg-L+ (0.1017) asn-L+ (0.2975) asp-L+ (59.276) atp + (0.0447) cmp + (0.0066) cys-L+ (0.0036) damp + (0.0024) dcmp + (0.0024) dcmp + (0.0036) dtmp + (0.0007) ergst + (0.1054) gin-L+ (0.2904) gly + (0.5185) glycogen + (0.046) gmp + (59.276) h2o + (0.0663) his-L+ (0.1927) ila-L+ (0.2962) hys-L+ (0.8079) mannan + (0.0507) met-L+ (0.00006) pa_SC + (0.00006) pa_SC + (0.000045) pe_SC + (0.1339) phe-L+ (0.1647) pro-L+ (0.000017) ps_SC + (0.000053) ptd1ino_SC + (0.1854) ser-L+ (0.02) so4 + (0.1914) thr-L+ (0.0024) trp-L+ (0.00066) triglyc_SC + (0.0284) trp-L+ (0.0205) yrr-L+ (0.0599) ump + (0.2646) val-L+ (0.0015) zymst -> (59.276) adap + (59.

ABBREVIATION	METABOLITE NAME	COMPARTMENT	FORMULA	CHARGE
10fthf	10-Formyltetrahydrofolate	cytosol	C20H22N7O7	-1
10fthf	10-Formyltetrahydrofolate	mitochondrion	C20H22N7O7	-1
* 12dgr_SC	1,2-Diacylglycerol, yeast-specific	cytosol	C3540H6644O500	0
13BDglcn	1,3-beta-D-Glucan	cytosol	C6H10O5	0
13BDglcn	1,3-beta-D-Glucan	extracellular	C6H10O5	0
13dampp	1,3-Diaminopropane	cytosol	C3H12N2	
13dpg	3-Phospho-D-glyceroyl phosphate	cytosol	C3H4O10P2	2 -4
14glun	(1,4-alpha-D-Glucosyl)n	cytosol	C6H12O6	0
1Dgali	1-alpha-D-Galactosyl-myo-inositol	cytosol	C12H22O11	0
* 1ag3p_SC	1-Acyl-sn-glycerol 3-phosphate	cytosol	C1920H3622O700P100	-200
* 1agly3p_SC	1-Acyl-glycerone 3-phosphate, yeast-specific	cytosol	C1920H3422O700P100	-200
1p3h5c	L-1-Pyrroline-3-hydroxy-5-carboxylate	cytosol	C5H6NO3	-1
1p3h5c	L-1-Pyrroline-3-hydroxy-5-carboxylate	mitochondrion	C5H6NO3	-1
1pyr5c	1-Pyrroline-5-carboxylate	cytosol	C5H6NO2	-1
1pyr5c	1-Pyrroline-5-carboxylate	mitochondrion	C5H6NO2	-1
23dhmb	(R)-2,3-Dihydroxy-3-methylbutanoate	mitochondrion	C5H9O4	-1
				-1 -1
23dhmp	(R)-2,3-Dihydroxy-3-methylpentanoate	mitochondrion	C6H11O4	
23dpg	3-Phospho-D-glycerol phosphate	cytosol	C3H3O10P2	-5
0.5	(S)-2-[5-Amino-1-(5-phospho-D-ribosyl)imidazole-4-		040145140405	_
25aics	carboxamido]succinate	cytosol	C13H15N4O12P	-4
	2,5-Diamino-6-hydroxy-4-(5'-phosphoribosylamino)-			
25dhpp	pyrimidine	cytosol	C9H14N5O8P	-2 -1
2ahbut	(S)-2-Aceto-2-hydroxybutanoate	mitochondrion	C6H9O4	-1
	2-Amino-4-hydroxy-6-hydroxymethyl-7,8-			
2ahhmd	dihydropteridine diphosphate	mitochondrion	C7H8N5O8P2	-3
	2-Amino-4-hydroxy-6-hydroxymethyl-7,8-			
2ahhmp	dihydropteridine	mitochondrion	C7H9N5O2	0
·	1-(2-Carboxyphenylamino)-1-deoxy-D-ribulose 5-			
2cpr5p	phosphate	cytosol	C12H13NO9P	-3
	2-Dehydro-3-deoxy-D-arabino-heptonate 7-	ĺ		
2dda7p	phosphate	cytosol	C7H10O10P	-3
	2-Dehydro-3-deoxy-D-arabino-heptonate 7-	5,000.		
2dda7p	phosphate	mitochondrion	C7H10O10P	-3
2dhp	2-Dehydropantoate	cytosol	C6H9O4	-3 -1
2dhp	2-Dehydropantoate	mitochondrion	C6H9O4	-1
2dr1p	2-Decrydioparticate 2-Decrydioparticate 2-Decrydioparticate	cytosol	C5H9O7P	-1
2dr5p	2-Deoxy-D-ribose 1-phosphate	cytosol	C5H9O7P	-2 -2 0
2hhxdal	2-Hydroxy-hexadecanal		C16H32O2	-2
		cytosol		-2
2ippm	2-Isopropylmaleate	cytosol	C7H8O4	-2
0	2-Methyl-4-amino-5-hydroxymethylpyrimidine		001101120700	,
2mahmp	diphosphate	cytosol	C6H8N3O7P2	-3
2mcit	2-Methylcitrate	cytosol	C7H7O7	-3 -3 -1
2mcit	2-Methylcitrate	mitochondrion	C7H7O7	-3
2obut	2-Oxobutanoate	cytosol	C4H5O3	-1
2obut	2-Oxobutanoate	mitochondrion	C4H5O3	-1
2ohph_5	2-Octaprenyl-6-hydroxyphenol (5 repeating units)	cytosol	C36H54O2	0
2ohph_5	2-Octaprenyl-6-hydroxyphenol (5 repeating units)	nucleus	C36H54O2	0
	2-Octaprenyl-6-methoxy-1,4-benzoquinol (5			
2ombzl_5	repeating units)	mitochondrion	C37H56O3	0
	2-Octaprenyl-3-methyl-5-hydroxy-6-methoxy-1,4-			
2omhmbl_5	benzoquinol (5 repeating units)	mitochondrion	C38H58O4	0
	2-Octaprenyl3-methyl-6-methoxy-1,4-benzoquinol (5			
2ommbl_5	repeating units)	mitochondrion	C38H58O3	0
	i op oag ao)			
2omph_5	2-Octaprenyl-6-methoxyphenol (5 repeating units)	cytosol	C37H56O2	0
20111011_0	2 Octopicity o methoxyphonol (o repeating time)	oy to do!	001110002	
2omph_5	2-Octaprenyl-6-methoxyphenol (5 repeating units)	mitochondrion	C37H56O2	0
2011pH_3	2-Octaprenty-o-methoxyphenor (3 repeating units)	mitochondrion	037113002	U
	1	nucleus	C27H56O2	_
Jomph 5	2 Octobronul 6 methovamber of /F reposting and the		C37H56O2	0
2omph_5	2-Octaprenyl-6-methoxyphenol (5 repeating units)		00011540	
2oph_5	2-Octaprenylphenol (5 repeating units)	cytosol	C36H54O	0
2oph_5 2oxoadp	2-Octaprenylphenol (5 repeating units) 2-Oxoadipate	cytosol cytosol	C6H6O5	
2oph_5 2oxoadp 2oxoadp	2-Octaprenylphenol (5 repeating units) 2-Oxoadipate 2-Oxoadipate	cytosol cytosol mitochondrion	C6H6O5 C6H6O5	
2oph_5 2oxoadp 2oxoadp 2pg	2-Octaprenylphenol (5 repeating units) 2-Oxoadipate 2-Oxoadipate D-Glycerate 2-phosphate	cytosol cytosol mitochondrion cytosol	C6H6O5 C6H6O5 C3H4O7P	
2oph_5 2oxoadp 2oxoadp 2pg 34hpp	2-Octaprenylphenol (5 repeating units) 2-Oxoadipate 2-Oxoadipate D-Glycerate 2-phosphate 3-(4-Hydroxyphenyl)pyruvate	cytosol cytosol mitochondrion cytosol cytosol	C6H6O5 C6H6O5 C3H4O7P C9H7O4	
2oph_5 2oxoadp 2oxoadp 2pg 34hpp 34hpp	2-Octaprenylphenol (5 repeating units) 2-Oxoadipate 2-Oxoadipate D-Glycerate 2-phosphate 3-(4-Hydroxyphenyl)pyruvate 3-(4-Hydroxyphenyl)pyruvate	cytosol cytosol mitochondrion cytosol	C6H6O5 C6H6O5 C3H4O7P C9H7O4 C9H7O4	-2 -2 -3 -1 -1
2oph_5 2oxoadp 2oxoadp 2pg 34hpp	2-Octaprenylphenol (5 repeating units) 2-Oxoadipate 2-Oxoadipate D-Glycerate 2-phosphate 3-(4-Hydroxyphenyl)pyruvate	cytosol cytosol mitochondrion cytosol cytosol	C6H6O5 C6H6O5 C3H4O7P C9H7O4	

35cdamp	3',5'-Cyclic dAMP	cytosol	C10H11N5O5P	-1
35cgmp	3',5'-Cyclic GMP	cytosol	C10H11N5O7P	-1
35cimp	3',5'-Cyclic IMP	cytosol	C10H10N4O7P	-1
3c2hmp	3-Carboxy-2-hydroxy-4-methylpentanoate	cytosol	C7H10O5	-2
3c3hmp	3-Carboxy-3-hydroxy-4-methylpentanoate	cytosol	C7H10O5	-2
3c3hmp	3-Carboxy-3-hydroxy-4-methylpentanoate	mitochondrion	C7H10O5	-2
3c4mop	3-Carboxy-4-methyl-2-oxopentanoate	cytosol	C7H8O5	-2 -2 -2 -2 -2 -1
3c4mop	3-Carboxy-4-methyl-2-oxopentanoate	mitochondrion	C7H8O5	-2
3dhq	3-Dehydroquinate	cytosol	C7H9O6	-1
3dhsk	3-Dehydroshikimate	cytosol	C7H7O5	-1
3dsphgn	3-Dehydrosphinganine	cytosol	C18H38NO2	1
3hacoa	(S)-3-Hydroxyacyl-CoA	peroxisome	C24H35N7O18P3RS	-4
3hanthrn	3-Hydroxyanthranilate	cytosol	C7H7NO3	O
3hdcoa	(S)-3-Hydroxydecanoyl-CoA	peroxisome	C31H50N7O18P3S	-4
3hddcoa	(S)-3-Hydroxydodecanoyl-CoA	peroxisome	C33H54N7O18P3S	-4
3hhdcoa	(S)-3-Hydroxyhexadecanoyl-CoA	peroxisome	C37H62N7O18P3S	-4 -4
3hodcoa	(S)-3-Hydroxyoctadecanoyl-CoA	peroxisome	C39H66N7O18P3S	-4
3htdcoa	(S)-3-Hydroxytetradecanoyl-CoA	peroxisome	C35H58N7O18P3S	-4
3hxccoa	(S)-3-Hydroxyhexacosyl-CoA	peroxisome	C47H82N7O18P3S	-4
3ig3p	C'-(3-Indolyl)-glycerol 3-phosphate	cytosol	C11H12NO6P	-2
3mob	3-Methyl-2-oxobutanoate	cytosol	C5H7O3	-4 -2 -1
3mob	3-Methyl-2-oxobutanoate	mitochondrion	C5H7O3	-1
3mop	(S)-3-Methyl-2-oxopentanoate	cytosol	C6H9O3	-1
3mop	(S)-3-Methyl-2-oxopentanoate	mitochondrion	C6H9O3	-1
3oacoa	3-Oxoacyl-CoA	peroxisome	C24H33N7O18P3RS	-4
3odcoa	3-Oxodecanoyl-CoA	peroxisome	C31H48N7O18P3S	-4
3oddcoa	3-Oxododecanoyl-CoA	peroxisome	C33H52N7O18P3S	-4
3ohdcoa	3-Oxohexadecanoyl-CoA	peroxisome	C37H60N7O18P3S	-4 -4
3ohodcoa	3-Oxooctadecanoyl-CoA	peroxisome	C39H64N7O18P3S	-4
3ohxccoa	3-Oxohexacosyl-CoA	peroxisome	C47H80N7O18P3S	-4
00.111.0000	o onemonaccoji con	po. 0000		
3ophb_5	3-Octaprenyl-4-hydroxybenzoate (5 repeating units)	cytosol	C37H53O3	-1
		-,		
3ophb_5	3-Octaprenyl-4-hydroxybenzoate (5 repeating units)	mitochondrion	C37H53O3	-1
3otdcoa	3-Oxotetradecanoyl-CoA	peroxisome	C35H56N7O18P3S	
3pg	3-Phospho-D-glycerate	cytosol	C3H4O7P	-3
3php	3-Phosphohydroxypyruvate	cytosol	C3H2O7P	-3
3psme	5-O-(1-Carboxyvinyl)-3-phosphoshikimate	cytosol	C10H9O10P	-4 -3 -3 -4
44mctr	4,4-dimethylcholesta-8,14,24-trienol	cytosol	C29H46O	O
44mzym	4,4-dimethylzymosterol	cytosol	C29H48O	C
4aabutn	4-Acetamidobutanoate	cytosol	C6H10NO3	-1
4abut	4-Aminobutanoate	cytosol	C4H9NO2	O
4abut	4-Aminobutanoate	extracellular	C4H9NO2	0
4abut	4-Aminobutanoate	mitochondrion	C4H9NO2	O
4abutn	4-Aminobutanal	cytosol	C4H10NO	1
4abutn	4-Aminobutanal	mitochondrion	C4H10NO	1
4abz	4-Aminobenzoate	cytosol	C7H6NO2	-1
4abz	4-Aminobenzoate	mitochondrion	C7H6NO2	-1
4adcho	4-amino-4-deoxychorismate	cytosol	C10H10NO5	-1
4ahmmp	4-Amino-5-hydroxymethyl-2-methylpyrimidine	cytosol	C6H9N3O	C
4ampm	4-Amino-2-methyl-5-phosphomethylpyrimidine	cytosol	C6H8N3O4P	
4fumacac	4-Fumarylacetoacetate	cytosol	C8H6O6	-2 -2 1
4gudbd	4-Guanidinobutanamide	cytosol	C5H13N4O	1
4gudbutn	4-Guanidinobutanoate	cytosol	C5H11N3O2	0
4h2oglt	4-Hydroxy-2-oxoglutarate	cytosol	C5H4O6	
4h2ogit 4h2ogit	4-Hydroxy-2-oxoglutarate	mitochondrion	C5H4O6	-2 -2 -2 -1
4h2oglt	4-Hydroxy-2-oxoglutarate	peroxisome	C5H4O6	-2
4hbz	4-Hydroxybenzoate	cytosol	C7H5O3	1
4hbz	4-Hydroxybenzoate	mitochondrion	C7H5O3	-1
4hglusa	L-4-Hydroxyglutamate semialdehyde	mitochondrion	C5H9NO4	-1
4hpro-LT	trans-4-Hydroxy-L-proline	cytosol	C5H9NO3	0
4hpro-LT	trans-4-Hydroxy-L-proline	mitochondrion	C5H9NO3	0
4hthr	4-Hydroxy-L-threonine	cytosol	C4H9NO4	0
4mhetz	4-Methyl-5-(2-hydroxyethyl)-thiazole	cytosol	C6H9NOS	0
4mlacac	4-Maleylacetoacetate	cytosol	C8H6O6	
4macac 4mop	4-Mateylacetoacetate 4-Methyl-2-oxopentanoate	cytosol	C6H9O3	-2 -1
1 11100	14-ivietriyi-2-uxuperitariuale	CytOSOI	COURCO	I - I
	4 Methyl 2 evenenteneste	mitochondrian	CEHOO3	4
4mop 4mpetz	4-Methyl-2-oxopentanoate 4-Methyl-5-(2-phosphoethyl)-thiazole	mitochondrion cytosol	C6H9O3 C6H8NO4PS	-1 -2

4mzym	4-methylzymosterol	cytosol	C28H46O	1 0
4mzym_int1	4-Methylzymosterol intermediate 1	cytosol	C29H46O3	
4mzym_int2	4-Methylzymosterol intermediate 2	cytosol	C28H44O	Č
4pasp	4-Phospho-L-aspartate	cytosol	C4H6NO7P	
4ppan	D-4'-Phosphopantothenate	cytosol	C9H15NO8P	-2 -3 -3
4ppcys	N-((R)-4-Phosphopantothenoyl)-L-cysteine	cytosol	C12H20N2O9PS	3
4r5au	4-(1-D-Ribitylamino)-5-aminouracil	cytosol	C9H16N4O6	Č
Hodu	5-amino-1-(5-phospho-D-ribosyl)imidazole-4-	Cytosoi	03111014400	
5aizc	carboxylate	cytosol	C9H11N3O9P	-3
5aop	5-Amino-4-oxopentanoate	cytosol	C5H9NO3	C
5aop 5aop	5-Amino-4-oxopentanoate	extracellular	C5H9NO3	C
5aop 5aop	5-Amino-4-oxopentanoate	mitochondrion	C5H9NO3	C
5aprbu	5-Amino-4-oxoperitarioate 5-Amino-6-(5'-phosphoribitylamino)uracil	cytosol	C9H15N4O9P	
5apru	5-Amino-6-(5'-phosphoribosylamino)uracil	cytosol	C9H13N4O9P	-2 -2 -4
5dpmev	(R)-5-Diphosphomevalonate	cytosol	C6H10O10P2	-2
5fthf	5-Formyltetrahydrofolate	cytosol	C20H21N7O7	
5fthf	5-Formyltetrahydrofolate	mitochondrion	C20H21N7O7	-2 -2 -2
5mta	5-Methylthioadenosine	cytosol	C11H15N5O3S	-2
5mthf	5-Methyltetrahydrofolate	cytosol	C20H24N7O6	-1
5mthf		mitochondrion	C20H24N7O6	-1
	5-Methyltetrahydrofolate		C6H10O7P	-1
5pmev	(R)-5-Phosphomevalonate	cytosol	C12H22O11	-3 C
6dg	D-Gal-alpha-1->6D-Glucose 6-Phospho-D-gluconate	cytosol		-3
6pgc		cytosol	C6H10O10P	-3
6pgl	6-phospho-D-glucono-1,5-lactone	cytosol	C6H9O9P	-2
6pgl	6-phospho-D-glucono-1,5-lactone	endoplasmic reticulum	C6H9O9P	-2 -2 0
8aonn	8-Amino-7-oxononanoate	cytosol	C9H17NO3	
8aonn	8-Amino-7-oxononanoate	extracellular	C9H17NO3	C
ACP	acyl carrier protein	cytosol	C11H21N2O7PRS	-1
ACP	acyl carrier protein	mitochondrion	C11H21N2O7PRS	-1
Dara14lac	D-Arabinono-1,4-lactone	cytosol	C5H8O5	C
L2aadp	L-2-Aminoadipate	cytosol	C6H10NO4	-1
L2aadp6sa	L-2-Aminoadipate 6-semialdehyde	cytosol	C6H11NO3	C
Lfmkynr	L-Formylkynurenine	cytosol	C11H12N2O4	C
Lkynr	L-Kynurenine	cytosol	C10H12N2O3	C
N1aspmd	N1-Acetylspermidine	cytosol	C9H23N3O	2
N1sprm	N1-Acetylspermine	cytosol	C12H31N4O	3
NPmehis	N(pai)-Methyl-L-histidine	cytosol	C7H11N3O2	С
Sfglutth	S-Formylglutathione	cytosol	C11H16N3O7S	-1
Ssq23epx	(S)-Squalene-2,3-epoxide	cytosol	C30H50O	С
Ssq23epx	(S)-Squalene-2,3-epoxide	endoplasmic reticulum	C30H50O	С
aacoa	Acetoacetyl-CoA	cytosol	C25H36N7O18P3S	-4
aacoa	Acetoacetyl-CoA	mitochondrion	C25H36N7O18P3S	-4
abt	L-Arabinitol	cytosol	C5H12O5	C
abt	L-Arabinitol	extracellular	C5H12O5	C
ac	Acetate	cytosol	C2H3O2	-1
ac	Acetate	extracellular	C2H3O2	-1
ac	Acetate	mitochondrion	C2H3O2	-1
ac	Acetate	peroxisome	C2H3O2	-1
acACP	Acetyl-ACP	cytosol	C13H23N2O8PRS	-1
acACP	Acetyl-ACP	mitochondrion	C13H23N2O8PRS	-1
acac	Acetoacetate	cytosol	C4H5O3	-1
acald	Acetaldehyde	cytosol	C2H4O	C
acald	Acetaldehyde	extracellular	C2H4O	C
acald	Acetaldehyde	mitochondrion	C2H4O	C
accoa	Acetyl-CoA	cytosol	C23H34N7O17P3S	-4
accoa	Acetyl-CoA	mitochondrion	C23H34N7O17P3S	-4
accoa	Acetyl-CoA	nucleus	C23H34N7O17P3S	-4
accoa	Acetyl-CoA	peroxisome	C23H34N7O17P3S	-4
acg5p	N-Acetyl-L-glutamyl 5-phosphate	mitochondrion	C7H9NO8P	-4 -3 -1
acg5sa	N-Acetyl-L-glutamate 5-semialdehyde	mitochondrion	C7H10NO4	-1
acgam1p	N-Acetyl-D-glucosamine 1-phosphate	cytosol	C8H14NO9P	-2
acgam6p	N-Acetyl-D-glucosamine 6-phosphate	cytosol	C8H14NO9P	-2 -2 -2 0
acglu	N-Acetyl-L-glutamate	mitochondrion	C7H9NO5	-2
achms	O-Acetyl-L-homoserine	cytosol	C6H11NO4	7
acoa	Acyl-CoA	peroxisome	C22H31N7O17P3RS	-4
acorn	N2-Acetyl-L-ornithine	mitochondrion	C7H14N2O3	C
acrn	O-Acetylcarnitine	cytosol	C9H17NO4	C
		-		C
acrn	O-Acetylcarnitine	mitochondrion	C9H17NO4	1

acrn	O-Acetylcarnitine	peroxisome	C9H17NO4	0
acser	O-Acetyl-L-serine	cytosol	C5H9NO4	0
acybut	gamma-Amino-gamma-cyanobutanoate	cytosol	C5H8N2O2	0
ade	Adenine	cytosol	C5H5N5	0
ade	Adenine	extracellular	C5H5N5	0
ade	Adenine	mitochondrion	C5H5N5	0
adn	Adenosine	cytosol	C10H13N5O4	0
adn	Adenosine	extracellular	C10H13N5O4	0
adn	Adenosine	mitochondrion	C10H13N5O4	0
adp	ADP	cvtosol	C10H12N5O10P2	
adp	ADP	Golgi apparatus	C10H12N5O10P2	-3
adp	ADP	mitochondrion	C10H12N5O10P2	-3
adp	ADP	nucleus	C10H12N5O10P2	-3
adp	ADP	vacuole	C10H12N5O10P2	-3 -3 -3 -3 -3 -3 -2 -2
adp	ADP	peroxisome	C10H12N5O10P2	-3
adprib	ADPribose	cytosol	C15H21N5O14P2	-0
<u> </u>	ADPribose	mitochondrion	C15H21N5O14P2	-2
adprib				-2
ahcys	S-Adenosyl-L-homocysteine	cytosol mitochondrion	C14H20N6O5S	0
ahcys	S-Adenosyl-L-homocysteine		C14H20N6O5S	
ahcys	S-Adenosyl-L-homocysteine	nucleus	C14H20N6O5S	0
a b dt	2-Amino-4-hydroxy-6-(erythro-1,2,3-	auta a a l	COLI42NEC42D2	_
ahdt	trihydroxypropyl)dihydropteridine triphosphate	cytosol	C9H13N5O13P3	-3
	5-Amino-1-(5-Phospho-D-ribosyl)imidazole-4-			=
aicar	carboxamide	cytosol	C9H13N4O8P	-2
air	5-amino-1-(5-phospho-D-ribosyl)imidazole	cytosol	C8H12N3O7P	-2 -2 -2 -2 -2 -2 -2
akg	2-Oxoglutarate	cytosol	C5H4O5	-2
akg	2-Oxoglutarate	extracellular	C5H4O5	-2
akg	2-Oxoglutarate	mitochondrion	C5H4O5	-2
akg	2-Oxoglutarate	nucleus	C5H4O5	-2
akg	2-Oxoglutarate	peroxisome	C5H4O5	-2
ala-B	beta-Alanine	cytosol	C3H7NO2	
ala-L	L-Alanine	cytosol	C3H7NO2	0
ala-L	L-Alanine	extracellular	C3H7NO2	0
ala-L	L-Alanine	mitochondrion	C3H7NO2	0
alac-S	(S)-2-Acetolactate	mitochondrion	C5H7O4	-1
alatrna	L-Alanyl-tRNA(Ala)	cytosol	C3H6NOR	1
allphn	Allophanate	cytosol	C2H3N2O3	-1
alltn	Allantoin	cytosol	C4H6N4O3	0
alltn	Allantoin	extracellular	C4H6N4O3	0
alltt	Allantoate	cytosol	C4H7N4O4	-1
alltt	Allantoate	extracellular	C4H7N4O4	-1
alpam	S-aminomethyldihydrolipoamide	mitochondrion	C9H21N2OS2	1
alpro	S-Aminomethyldihydrolipoylprotein	mitochondrion	CH6NS2X	1
am6sa	2-Aminomuconate 6-semialdehyde	cytosol	C6H7NO3	0
amet	S-Adenosyl-L-methionine	cytosol	C15H23N6O5S	1
amet	S-Adenosyl-L-methionine	extracellular	C15H23N6O5S	
amet	S-Adenosyl-L-methionine	mitochondrion	C15H23N6O5S	
amet	S-Adenosyl-L-methionine	nucleus	C15H23N6O5S	1
ametam	S-Adenosylmethioninamine	cytosol	C14H24N6O3S	2
amob	S-Adenosyl-4-methylthio-2-oxobutanoate	cytosol	C15H19N5O6S	0
	AMP	cytosol	C10H12N5O7P	
amp	AMP	mitochondrion	C10H12N5O7P	-2 -2
amp				-2
amp	AMP	peroxisome	C10H12N5O7P	-2 -1
amuco	2-Aminomuconate	cytosol	C6H6NO4	
anth	Anthranilate	cytosol	C7H6NO2	-1
ap4a	P1,P4-Bis(5'-adenosyl) tetraphosphate	cytosol	C20H24N10O19P4	-4
ap4g	P1-(5'-adenosyl),P4-(5'-guanosyl) tetraphosphate	cytosol	C20H24N10O20P4	-4
арер	Nalpha-Acetylpeptide	cytosol	C6H7N2O4R2	-1
aproa	3-Aminopropanal	cytosol	C3H8NO	1
aprop	alpha-Aminopropiononitrile	cytosol	C3H7N2	1
aprut	N-Acetylputrescine	cytosol	C6H15N2O	1
aps	Adenosine 5'-phosphosulfate	cytosol	C10H12N5O10PS	-2
arab-D	D-Arabinose	cytosol	C5H10O5	C
arab-D	D-Arabinose	extracellular	C5H10O5	0
				C
arab-L	L-Arabinose	cytosol	C5H10O5	
arab-L arab-L	L-Arabinose L-Arabinose	cytosol extracellular	C5H10O5 C5H10O5	0
		- ·		

arg-L	L-Arginine	mitochondrion	C6H15N4O2	1
argsuc	N(omega)-(L-Arginino)succinate	cytosol	C10H17N4O6	1
argtrna	L-Arginyl-tRNA(Arg)	cytosol	C6H14N4OR	2
argtrna	L-Arginyl-trivi(Arg)	mitochondrion	C6H14N4OR	2
asn-L	L-Asparagine	cytosol	C4H8N2O3	0
asn-L	L-Asparagine	extracellular	C4H8N2O3	0
asn-L	L-Asparagine	mitochondrion	C4H8N2O3	0
asntrna	L-Asparaginyl-tRNA(Asn)	cytosol	C4H7N2O2R	1
asntrna	L-Asparaginyl-tRNA(Asn)	mitochondrion	C4H7N2O2R	1
asp-L	L-Aspartate	cytosol	C4H6NO4	-1
asp-L	L-Aspartate	extracellular	C4H6NO4	-1
asp-L	L-Aspartate	mitochondrion	C4H6NO4	-1
asp-L	L-Aspartate	nucleus	C4H6NO4	-1
asp-L	L-Aspartate	peroxisome	C4H6NO4	-1
aspsa	L-Aspartate 4-semialdehyde	cytosol	C4H7NO3	0
asptrna	L-Aspartyl-tRNA(Asp)	cytosol	C4H5NO3R	0
asptrna	L-Aspartyl-tRNA(Asp)	mitochondrion	C4H5NO3R	0
atp	ATP	cytosol	C10H12N5O13P3	-4
atp	ATP	Golgi apparatus	C10H12N5O13P3	-4
atp	ATP	mitochondrion	C10H12N5O13P3	-4
atp	ATP	nucleus	C10H12N5O13P3	-4
atp	ATP	vacuole	C10H12N5O13P3	-4
atp	ATP	peroxisome	C10H12N5O13P3	-4
b124tc	But-1-ene-1,2,4-tricarboxylate	mitochondrion	C7H5O6	-3
btn	Biotin	cytosol	C10H15N2O3S	-1
btn	Biotin	extracellular	C10H15N2O3S	-1
camp	cAMP	cytosol	C10H11N5O6P	-1
caphis	2-(3-Carboxy-3-aminopropyl)-L-histidine	cytosol	C10H16N4O4	0
cbasp	N-Carbamoyl-L-aspartate	cytosol	C5H6N2O5	
cbasp	N-Carbamoyl-L-aspartate	nucleus	C5H6N2O5	-2
cbasp	Carbamoyl phosphate	cytosol	CH2NO5P	-2 -2 -2 -2
cbp	Carbamoyl phosphate	nucleus	CH2NO5P CH2NO5P	-2
cdp	CDP		C9H12N3O11P2	-3
cdp	CDP	cytosol nucleus	C9H12N3O11P2	-3 -3
cdpchol	CDPcholine		C14H25N4O11P2	-3 -1
capchol	CDPcholine	cytosol		-1
* adadaa CC	CDDdiagodahyaaral yaaat anasifia	outocol.	C4440H7744N300O1500 P200	200
* cdpdag_SC	CDPdiacylglycerol, yeast-specific	cytosol		-200
* adadaa CC	CDDdiagodahyaaral yaaat anasifia	mitochondrion	C4440H7744N300O1500 P200	200
* cdpdag_SC	CDPdiacylglycerol, yeast-specific CDPethanolamine		C11H19N4O11P2	-200
cdpea		cytosol		-1
cer1_24	Ceramide-1 (Sphinganine:n-C24:0)	cytosol	C42H85NO3	0
cer1_26	Ceramide-1 (Sphinganine:n-C26:0)	cytosol	C44H89NO3	0
cer2'_24	Ceramide-2' (Sphinganine:n-C24:0OH)	cytosol	C42H85NO4	0
cer2'_26	Ceramide-2' (Sphinganine:n-C26:0OH)	cytosol	C44H89NO4	0
cer2_24	Ceramide-2 (Phytosphingosine:n-C24:0)	cytosol	C42H85NO4	0
cer2_26	Ceramide-2 (Phytosphingosine:n-C26:0)	cytosol	C44H89NO4	0
cer3_24	Ceramide-3 (Phytosphingosine:n-C24:0OH)	cytosol	C42H85NO5	0
cer3_26	t caramada 2 (Dhartasahingasinan COC.OOLI)	Lovitocol	C44H89NO5	0
cgly	Ceramide-3 (Phytosphingosine:n-C26:0OH)	cytosol		
	Cys-Gly	cytosol	C5H10N2O3S	0
ch4s	Cys-Gly Methanethiol	cytosol cytosol	C5H10N2O3S CH4S	0
ch4s chitin	Cys-Gly Methanethiol Chitin	cytosol cytosol	C5H10N2O3S CH4S C8H13NO5	0 0 0
ch4s chitin chitos	Cys-Gly Methanethiol Chitin Chitosan	cytosol cytosol cytosol	C5H10N2O3S CH4S C8H13NO5 C6H11NO4	0
ch4s chitin chitos chol	Cys-Gly Methanethiol Chitin Chitosan Choline	cytosol cytosol cytosol cytosol	C5H10N2O3S CH4S C8H13NO5 C6H11NO4 C5H14NO	0 0 0
ch4s chitin chitos chol	Cys-Gly Methanethiol Chitin Chitosan Choline Choline	cytosol cytosol cytosol cytosol cytosol extracellular	C5H10N2O3S CH4S C8H13NO5 C6H11NO4 C5H14NO C5H14NO	0 0 0 0 1 1
ch4s chitin chitos chol	Cys-Gly Methanethiol Chitin Chitosan Choline Choline Choline Choline	cytosol cytosol cytosol cytosol cytosol extracellular cytosol	C5H10N2O3S CH4S C8H13NO5 C6H11NO4 C5H14NO C5H14NO C5H13NO4P	0 0 0 0 1 1 -1
ch4s chitin chitos chol	Cys-Gly Methanethiol Chitin Chitosan Choline Choline Choline Choline phosphate Chorismate	cytosol cytosol cytosol cytosol cytosol extracellular cytosol cytosol	C5H10N2O3S CH4S C8H13NO5 C6H11NO4 C5H14NO C5H14NO C5H13NO4P C10H8O6	0 0 0 1 1 -1 -2
ch4s chitin chitos chol chol cholp chor cit	Cys-Gly Methanethiol Chitin Chitosan Choline Choline Choline Chorismate Citrate	cytosol cytosol cytosol cytosol cytosol extracellular cytosol cytosol cytosol	C5H10N2O3S CH4S C8H13NO5 C6H11NO4 C5H14NO C5H14NO C5H13NO4P C10H8O6 C6H5O7	0 0 0 1 1 -1 -2 -3
ch4s chitin chitos chol chol cholp chor cit	Cys-Gly Methanethiol Chitin Chitosan Choline Choline Choline Chorismate Citrate Citrate	cytosol cytosol cytosol cytosol extracellular cytosol cytosol extracellular	C5H10N2O3S CH4S C8H13NO5 C6H11NO4 C5H14NO C5H14NO C5H13NO4P C10H8O6 C6H5O7	0 0 0 1 1 -1 -2 -3 -3
ch4s chitin chitos chol chol cholp chor cit cit	Cys-Gly Methanethiol Chitin Chitosan Choline Choline Choline Chorismate Citrate Citrate Citrate Citrate	cytosol cytosol cytosol cytosol cytosol extracellular cytosol cytosol cytosol	C5H10N2O3S CH4S C8H13NO5 C6H11NO4 C5H14NO C5H14NO C5H13NO4P C10H8O6 C6H5O7 C6H5O7	0 0 0 1 1 -1 -2 -3 -3
ch4s chitin chitos chol chol cholp chor cit cit cit	Cys-Gly Methanethiol Chitin Chitosan Choline Choline Choline Choline phosphate Chorismate Citrate Citrate Citrate Citrate Citrate Citrate	cytosol cytosol cytosol cytosol extracellular cytosol cytosol extracellular	C5H10N2O3S CH4S C8H13NO5 C6H11NO4 C5H14NO C5H14NO C5H13NO4P C10H8O6 C6H5O7 C6H5O7	0 0 0 1 1 -1 -2 -3 -3 -3 -3
ch4s chitin chitos chol chol cholp chor cit cit	Cys-Gly Methanethiol Chitin Chitosan Choline Choline Choline Chorismate Citrate Citrate Citrate Citrate	cytosol cytosol cytosol cytosol extracellular cytosol cytosol extracellular cytosol cytosol cytosol extracellular	C5H10N2O3S CH4S C8H13NO5 C6H11NO4 C5H14NO C5H14NO C5H13NO4P C10H8O6 C6H5O7 C6H5O7	0 0 0 1 1 -1 -2 -3 -3
ch4s chitin chitos chol chol cholp chor cit cit cit	Cys-Gly Methanethiol Chitin Chitosan Choline Choline Choline Choline phosphate Chorismate Citrate Citrate Citrate Citrate Citrate Citrate	cytosol cytosol cytosol cytosol cytosol extracellular cytosol cytosol cytosol cytosol extracellular mitochondrion peroxisome	C5H10N2O3S CH4S C8H13NO5 C6H11NO4 C5H14NO C5H14NO C5H13NO4P C10H8O6 C6H5O7 C6H5O7	0 0 0 1 1 -1 -2 -3 -3 -3
ch4s chitin chitos chol chol cholp chor cit cit cit cit citr-L	Cys-Gly Methanethiol Chitin Chitosan Choline Choline Choline Chorismate Citrate Citrate Citrate Citrate Citrate Citrate Citrate Citrate Citrate L-Citrulline	cytosol cytosol cytosol cytosol cytosol extracellular cytosol cytosol cytosol cytosol extracellular mitochondrion peroxisome cytosol	C5H10N2O3S CH4S C8H13NO5 C6H11NO4 C5H14NO C5H14NO C5H13NO4P C10H8O6 C6H5O7 C6H5O7 C6H5O7 C6H5O7 C6H5O7	0 0 0 1 1 1 -1 -2 -3 -3 -3 -3 0
ch4s chitin chitos chol chol cholp chor cit cit cit cit citr-L * clpn_SC	Cys-Gly Methanethiol Chitin Chitosan Choline Choline Choline Choline phosphate Chorismate Citrate Citrate Citrate Citrate Citrate Citrate Citrate Citrate Citrate Country Country Cardiolipin, yeast-specific	cytosol cytosol cytosol cytosol cytosol extracellular cytosol cytosol cytosol extracellular mitochondrion peroxisome cytosol mitochondrion	C5H10N2O3S CH4S C8H13NO5 C6H11NO4 C5H14NO C5H14NO C5H14NO C5H13NO4P C10H8O6 C6H5O7 C6H5O7 C6H5O7 C6H5O7 C6H5O7 C6H13N3O3 C7380H13688O1700P200	0 0 0 1 1 1 -1 -2 -3 -3 -3 -3 0
ch4s chitin chitos chol chol chor cit cit cit cit citr-L * clpn_SC cmaphis	Cys-Gly Methanethiol Chitin Chitosan Choline Choline Choline Choline phosphate Chorismate Citrate Citrate Citrate Citrate Citrate Citrate Citrate Citrate C	cytosol cytosol cytosol cytosol cytosol extracellular cytosol cytosol cytosol extracellular mitochondrion peroxisome cytosol mitochondrion	C5H10N2O3S CH4S C8H13NO5 C6H11NO4 C5H14NO C5H14NO C5H14NO C5H13NO4P C10H8O6 C6H5O7 C6H5O7 C6H5O7 C6H5O7 C6H13N3O3 C7380H13688O1700P200 C11H18N4O4	0 0 0 1 1 1 -1 -2 -3 -3 -3 -3 0

co2	CO2	cytosol	CO2	0
co2	CO2	extracellular	CO2	0
co2	CO2	Golgi apparatus	CO2	0
co2	CO2	mitochondrion	CO2	0
co2	CO2	nucleus	CO2	0
co2	CO2	vacuole	CO2	0
			CO2	0
co2	CO2	peroxisome		
coa	Coenzyme A	cytosol	C21H32N7O16P3S	-4
coa	Coenzyme A	mitochondrion	C21H32N7O16P3S	-4
coa	Coenzyme A	nucleus	C21H32N7O16P3S	-4
coa	Coenzyme A	peroxisome	C21H32N7O16P3S	-4
cpppg3	Coproporphyrinogen III	cytosol	C36H40N4O8	-4
crn	L-Carnitine	cytosol	C7H15NO3	0
crn	L-Carnitine	extracellular	C7H15NO3	0
crn	L-Carnitine	mitochondrion	C7H15NO3	0
crn	L-Carnitine	peroxisome	C7H15NO3	0
csn	Cytosine	cytosol	C4H5N3O	0
csn	Cytosine	extracellular	C4H5N3O	0
ctp	CTP	cytosol	C9H12N3O14P3	-4
ctp	CTP	mitochondrion	C9H12N3O14P3	-4
cys-L	L-Cysteine	cytosol	C3H7NO2S	0
cys-L	L-Cysteine	extracellular	C3H7NO2S	0
cyst-L	L-Cystathionine	cytosol	C7H14N2O4S	0
cyst-L	L-Cystathionine	peroxisome	C7H14N2O4S	0
cystrna	L-Cysteinyl-tRNA(Cys)	cytosol	C3H6NOSR	1
cytd	Cytidine	cytosol	C9H13N3O5	0
cytd	Cytidine	extracellular	C9H13N3O5	0
dad-2	Deoxyadenosine	cytosol	C10H13N5O3	0
dad-2	Deoxyadenosine	extracellular	C10H13N5O3	0
dadp	dADP	cytosol	C10H12N5O9P2	-3
dadp	dADP	nucleus	C10H12N5O9F2	-3
* dagpy_SC	diacylglycerol pyrophosphate, yeast-specific		C3540H6544O1100P200	-300
	dAMP	cytosol	C10H12N5O6P	
damp		cytosol		-2 1
dann	7,8-Diaminononanoate	cytosol	C9H21N2O2	
dann	7,8-Diaminononanoate	extracellular	C9H21N2O2	1
datp	dATP	cytosol	C10H12N5O12P3	-4
db4p	3,4-dihydroxy-2-butanone 4-phosphate	cytosol	C4H7O6P	-2
dc2coa	trans-Dec-2-enoyl-CoA	peroxisome	C31H48N7O17P3S	-4
dca	Decanoate (n-C10:0)	cytosol	C10H19O2	-1
dca dca	Decanoate (n-C10:0)	peroxisome	C10H19O2	-1
dca dca dcaACP	Decanoate (n-C10:0) Decanoyl-ACP (n-C10:0ACP)	peroxisome mitochondrion	C10H19O2 C21H39N2O8PRS	-1 -1
dca dca dcaACP dcacoa	Decanoate (n-C10:0) Decanoyl-ACP (n-C10:0ACP) Decanoyl-CoA (n-C10:0CoA)	peroxisome mitochondrion cytosol	C10H19O2 C21H39N2O8PRS C31H50N7O17P3S	-1 -1 -4
dca dca dcaACP dcacoa dcacoa	Decanoate (n-C10:0) Decanoyl-ACP (n-C10:0ACP) Decanoyl-CoA (n-C10:0CoA) Decanoyl-CoA (n-C10:0CoA)	peroxisome mitochondrion cytosol peroxisome	C10H19O2 C21H39N2O8PRS C31H50N7O17P3S C31H50N7O17P3S	-1 -1 -4 -4
dca dca dcaACP dcacoa dcacoa dcamp	Decanoate (n-C10:0) Decanoyl-ACP (n-C10:0ACP) Decanoyl-CoA (n-C10:0CoA) Decanoyl-CoA (n-C10:0CoA) N6-(1,2-Dicarboxyethyl)-AMP	peroxisome mitochondrion cytosol peroxisome cytosol	C10H19O2 C21H39N2O8PRS C31H50N7O17P3S C31H50N7O17P3S C14H14N5O11P	-1 -1 -4 -4
dca dca dcaACP dcacoa dcacoa dcamp dcdp	Decanoate (n-C10:0) Decanoyl-ACP (n-C10:0ACP) Decanoyl-CoA (n-C10:0CoA) Decanoyl-CoA (n-C10:0CoA) N6-(1,2-Dicarboxyethyl)-AMP dCDP	peroxisome mitochondrion cytosol peroxisome cytosol cytosol	C10H19O2 C21H39N2O8PRS C31H50N7O17P3S C31H50N7O17P3S C14H14N5O11P C9H12N3O10P2	-1 -1 -4 -4 -4 -3
dca dca dcaACP dcacoa dcacoa dcacoa dcamp dcdp dcdp	Decanoate (n-C10:0) Decanoyl-ACP (n-C10:0ACP) Decanoyl-CoA (n-C10:0CoA) Decanoyl-CoA (n-C10:0CoA) N6-(1,2-Dicarboxyethyl)-AMP dCDP dCDP	peroxisome mitochondrion cytosol peroxisome cytosol	C10H19O2 C21H39N2O8PRS C31H50N7O17P3S C31H50N7O17P3S C14H14N5O11P	-1 -1 -4 -4 -4 -3
dca dca dcaACP dcacoa dcacoa dcacoa dcamp dcdp dcdp dcmp	Decanoate (n-C10:0) Decanoyl-ACP (n-C10:0ACP) Decanoyl-CoA (n-C10:0CoA) Decanoyl-CoA (n-C10:0CoA) N6-(1,2-Dicarboxyethyl)-AMP dCDP dCDP dCMP	peroxisome mitochondrion cytosol peroxisome cytosol cytosol nucleus cytosol	C10H19O2 C21H39N2O8PRS C31H50N7O17P3S C31H50N7O17P3S C14H14N5O11P C9H12N3O10P2 C9H12N3O10P2 C9H12N3O7P	-1 -1 -4 -4 -4 -3
dca dca dcaACP dcacoa dcacoa dcacoa dcamp dcdp dcdp dcmp dctp	Decanoate (n-C10:0) Decanoyl-ACP (n-C10:0ACP) Decanoyl-CoA (n-C10:0CoA) Decanoyl-CoA (n-C10:0CoA) N6-(1,2-Dicarboxyethyl)-AMP dCDP dCDP dCMP dCTP	peroxisome mitochondrion cytosol peroxisome cytosol cytosol nucleus cytosol cytosol	C10H19O2 C21H39N2O8PRS C31H50N7O17P3S C31H50N7O17P3S C14H14N5O11P C9H12N3O10P2 C9H12N3O10P2 C9H12N3O7P C9H12N3O13P3	-1 -1 -4 -4 -4 -3 -3 -2 -4
dca dca dcaACP dcacoa dcacoa dcacoa dcamp dcdp dcdp dcmp	Decanoate (n-C10:0) Decanoyl-ACP (n-C10:0ACP) Decanoyl-CoA (n-C10:0CoA) Decanoyl-CoA (n-C10:0CoA) N6-(1,2-Dicarboxyethyl)-AMP dCDP dCDP dCMP	peroxisome mitochondrion cytosol peroxisome cytosol cytosol nucleus cytosol	C10H19O2 C21H39N2O8PRS C31H50N7O17P3S C31H50N7O17P3S C14H14N5O11P C9H12N3O10P2 C9H12N3O10P2 C9H12N3O7P	-1 -1 -4 -4 -4 -3 -3 -2 -4
dca dca dcaACP dcacoa dcacoa dcacoa dcamp dcdp dcdp dcmp dctp	Decanoate (n-C10:0) Decanoyl-ACP (n-C10:0ACP) Decanoyl-CoA (n-C10:0CoA) Decanoyl-CoA (n-C10:0CoA) N6-(1,2-Dicarboxyethyl)-AMP dCDP dCDP dCMP dCTP	peroxisome mitochondrion cytosol peroxisome cytosol cytosol nucleus cytosol cytosol	C10H19O2 C21H39N2O8PRS C31H50N7O17P3S C31H50N7O17P3S C14H14N5O11P C9H12N3O10P2 C9H12N3O10P2 C9H12N3O7P C9H12N3O13P3	-1 -1 -4 -4 -4 -3 -3 -2 -4 0
dca dca dcaACP dcacoa dcacoa dcacoa dcamp dcdp dcdp dcmp dctp dcyt	Decanoate (n-C10:0) Decanoyl-ACP (n-C10:0ACP) Decanoyl-CoA (n-C10:0CoA) Decanoyl-CoA (n-C10:0CoA) N6-(1,2-Dicarboxyethyl)-AMP dCDP dCDP dCMP dCTP Deoxycytidine	peroxisome mitochondrion cytosol peroxisome cytosol cytosol nucleus cytosol cytosol cytosol cytosol cytosol	C10H19O2 C21H39N2O8PRS C31H50N7O17P3S C31H50N7O17P3S C14H14N5O11P C9H12N3O10P2 C9H12N3O10P2 C9H12N3O7P C9H12N3O13P3 C9H13N3O4	-1 -1 -4 -4 -4 -3 -3 -2 -4
dca dca dcaACP dcacoa dcacoa dcamp dcdp dcdp dcmp dctp dcyt	Decanoate (n-C10:0) Decanoyl-ACP (n-C10:0ACP) Decanoyl-CoA (n-C10:0CoA) Decanoyl-CoA (n-C10:0CoA) N6-(1,2-Dicarboxyethyl)-AMP dCDP dCDP dCMP dCTP Deoxycytidine Deoxycytidine	peroxisome mitochondrion cytosol peroxisome cytosol cytosol nucleus cytosol cytosol cytosol cytosol cytosol extracellular	C10H19O2 C21H39N2O8PRS C31H50N7O17P3S C31H50N7O17P3S C14H14N5O11P C9H12N3O10P2 C9H12N3O10P2 C9H12N3O7P C9H12N3O13P3 C9H13N3O4 C9H13N3O4	-1 -1 -4 -4 -4 -3 -3 -2 -4 0
dca dca dcaACP dcacoa dcacoa dcamp dcdp dcdp dcmp dctp dcyt dcyt dd2coa	Decanoate (n-C10:0) Decanoyl-ACP (n-C10:0ACP) Decanoyl-CoA (n-C10:0CoA) Decanoyl-CoA (n-C10:0CoA) N6-(1,2-Dicarboxyethyl)-AMP dCDP dCDP dCMP dCTP Deoxycytidine Deoxycytidine trans-Dodec-2-enoyl-CoA	peroxisome mitochondrion cytosol peroxisome cytosol cytosol nucleus cytosol cytosol cytosol cytosol cytosol cytosol cytosol extracellular peroxisome	C10H19O2 C21H39N2O8PRS C31H50N7O17P3S C31H50N7O17P3S C14H14N5O11P C9H12N3O10P2 C9H12N3O10P2 C9H12N3O7P C9H12N3O13P3 C9H13N3O4 C9H13N3O4 C33H52N7O17P3S	-1 -1 -4 -4 -4 -3 -3 -2 -4 0 0
dca dca dcaACP dcacoa dcacoa dcamp dcdp dcdp dcmp dctp dcyt dcyt dd2coa ddca	Decanoate (n-C10:0) Decanoyl-ACP (n-C10:0ACP) Decanoyl-CoA (n-C10:0CoA) Decanoyl-CoA (n-C10:0CoA) N6-(1,2-Dicarboxyethyl)-AMP dCDP dCDP dCMP dCTP Deoxycytidine Deoxycytidine trans-Dodec-2-enoyl-CoA Dodecanoate (n-C12:0) Dodecanoate (n-C12:0)	peroxisome mitochondrion cytosol peroxisome cytosol cytosol nucleus cytosol cytosol cytosol cytosol cytosol cytosol cytosol extracellular peroxisome cytosol peroxisome	C10H19O2 C21H39N2O8PRS C31H50N7O17P3S C31H50N7O17P3S C14H14N5O11P C9H12N3O10P2 C9H12N3O10P2 C9H12N3O7P C9H12N3O13P3 C9H13N3O4 C9H13N3O4 C33H52N7O17P3S C12H23O2	-1 -1 -4 -4 -3 -3 -2 -4 0 0
dca dca dcaACP dcacoa dcacoa dcamp dcdp dcdp dctp dctp dcyt dd2coa ddca ddca	Decanoate (n-C10:0) Decanoyl-ACP (n-C10:0ACP) Decanoyl-CoA (n-C10:0CoA) Decanoyl-CoA (n-C10:0CoA) N6-(1,2-Dicarboxyethyl)-AMP dCDP dCDP dCMP dCTP Deoxycytidine Deoxycytidine trans-Dodec-2-enoyl-CoA Dodecanoate (n-C12:0) Dodecanoyl-ACP (n-C12:0ACP)	peroxisome mitochondrion cytosol peroxisome cytosol cytosol nucleus cytosol cytosol cytosol cytosol cytosol cytosol cytosol cytosol extracellular peroxisome cytosol	C10H19O2 C21H39N2O8PRS C31H50N7O17P3S C31H50N7O17P3S C31H50N7O17P3S C14H14N5O11P C9H12N3O10P2 C9H12N3O10P2 C9H12N3O7P C9H12N3O13P3 C9H13N3O4 C9H13N3O4 C33H52N7O17P3S C12H23O2 C12H23O2 C23H43N2O8PRS	-1 -1 -4 -4 -3 -3 -2 -4 0 0 -4 -1
dca dca dcaACP dcacoa dcacoa dcamp dcdp dcdp dcmp dctp dcyt dcyt dd2coa ddca ddca ddcaACP	Decanoate (n-C10:0) Decanoyl-ACP (n-C10:0ACP) Decanoyl-CoA (n-C10:0CoA) Decanoyl-CoA (n-C10:0CoA) N6-(1,2-Dicarboxyethyl)-AMP dCDP dCDP dCMP dCTP Deoxycytidine Deoxycytidine trans-Dodec-2-enoyl-CoA Dodecanoate (n-C12:0) Dodecanoyl-ACP (n-C12:0ACP) Dodecanoyl-ACP (n-C12:0ACP)	peroxisome mitochondrion cytosol peroxisome cytosol cytosol nucleus cytosol cytosol cytosol cytosol cytosol extracellular peroxisome cytosol peroxisome cytosol mitochondrion	C10H19O2 C21H39N2O8PRS C31H50N7O17P3S C31H50N7O17P3S C14H14N5O11P C9H12N3O10P2 C9H12N3O10P2 C9H12N3O7P C9H12N3O13P3 C9H13N3O4 C9H13N3O4 C33H52N7O17P3S C12H23O2 C12H23O2 C23H43N2O8PRS C23H43N2O8PRS	-1 -4 -4 -4 -3 -3 -2 -4 0 0 -4 -1 -1
dca dca dcaACP dcacoa dcacoa dcamp dcdp dcdp dctp dctp dcyt dd2coa ddca ddcaACP ddcaACP ddcaACP ddcacoa	Decanoate (n-C10:0) Decanoyl-ACP (n-C10:0ACP) Decanoyl-CoA (n-C10:0CoA) Decanoyl-CoA (n-C10:0CoA) N6-(1,2-Dicarboxyethyl)-AMP dCDP dCDP dCMP dCTP Deoxycytidine Deoxycytidine trans-Dodec-2-enoyl-CoA Dodecanoate (n-C12:0) Dodecanoyl-ACP (n-C12:0ACP) Dodecanoyl-CoA (n-C12:0CoA)	peroxisome mitochondrion cytosol peroxisome cytosol cytosol nucleus cytosol cytosol cytosol cytosol extracellular peroxisome cytosol peroxisome cytosol mitochondrion cytosol	C10H19O2 C21H39N2O8PRS C31H50N7O17P3S C31H50N7O17P3S C31H50N7O17P3S C14H14N5O11P C9H12N3O10P2 C9H12N3O10P2 C9H12N3O7P C9H12N3O13P3 C9H13N3O4 C9H13N3O4 C33H52N7O17P3S C12H23O2 C12H23O2 C23H43N2O8PRS C23H43N2O8PRS C33H54N7O17P3S	-1 -4 -4 -4 -3 -3 -2 -4 0 0 -4 -1 -1 -1
dca dca dcaACP dcacoa dcacoa dcamp dcdp dcdp dcmp dctp dcyt dcyt dd2coa ddcaACP ddcaACP ddcaACP ddcacoa ddcacoa	Decanoate (n-C10:0) Decanoyl-ACP (n-C10:0ACP) Decanoyl-CoA (n-C10:0CoA) Decanoyl-CoA (n-C10:0CoA) N6-(1,2-Dicarboxyethyl)-AMP dCDP dCDP dCMP dCTP Deoxycytidine Deoxycytidine trans-Dodec-2-enoyl-CoA Dodecanoate (n-C12:0) Dodecanoyl-ACP (n-C12:0ACP) Dodecanoyl-CoA (n-C12:0CoA) Dodecanoyl-CoA (n-C12:0CoA) Dodecanoyl-CoA (n-C12:0CoA)	peroxisome mitochondrion cytosol peroxisome cytosol cytosol nucleus cytosol cytosol cytosol cytosol extracellular peroxisome cytosol peroxisome cytosol peroxisome cytosol peroxisome cytosol mitochondrion cytosol peroxisome	C10H19O2 C21H39N2O8PRS C31H50N7O17P3S C31H50N7O17P3S C31H50N7O17P3S C14H14N5O11P C9H12N3O10P2 C9H12N3O7P C9H12N3O7P C9H12N3O13P3 C9H13N3O4 C9H13N3O4 C33H52N7O17P3S C12H23O2 C12H23O2 C23H43N2O8PRS C23H43N2O8PRS C33H54N7O17P3S C33H54N7O17P3S	-1 -4 -4 -4 -3 -3 -2 -4 0 0 -4 -1 -1 -1 -1 -4
dca dca dcaACP dcacoa dcacoa dcamp dcdp dcdp dctp dctp dcyt dd2coa ddca ddcaACP ddcaACP ddcaACP ddcacoa ddcacoa ddcacoa ddcacoa	Decanoate (n-C10:0) Decanoyl-ACP (n-C10:0ACP) Decanoyl-CoA (n-C10:0CoA) Decanoyl-CoA (n-C10:0CoA) N6-(1,2-Dicarboxyethyl)-AMP dCDP dCDP dCMP dCTP Deoxycytidine Deoxycytidine trans-Dodec-2-enoyl-CoA Dodecanoate (n-C12:0) Dodecanoyl-ACP (n-C12:0ACP) Dodecanoyl-ACP (n-C12:0CoA) Dodecanoyl-CoA (n-C12:0CoA) Dodecanoyl-CoA (n-C12:0CoA) dGDP	peroxisome mitochondrion cytosol peroxisome cytosol cytosol nucleus cytosol cytosol cytosol extracellular peroxisome cytosol peroxisome cytosol peroxisome cytosol peroxisome cytosol mitochondrion cytosol peroxisome cytosol	C10H19O2 C21H39N2O8PRS C31H50N7O17P3S C31H50N7O17P3S C31H50N7O17P3S C14H14N5O11P C9H12N3O10P2 C9H12N3O7P C9H12N3O7P C9H12N3O7P C9H13N3O4 C9H13N3O4 C33H52N7O17P3S C12H23O2 C12H23O2 C23H43N2O8PRS C33H54N7O17P3S C33H54N7O17P3S C33H54N7O17P3S C10H12N5O10P2	-1 -4 -4 -4 -3 -3 -2 -4 0 0 -4 -1 -1 -1 -1 -4
dca dca dcaACP dcacoa dcacoa dcamp dcdp dcdp dctp dctp dcyt dd2coa ddca ddcaACP ddcaACP ddcaACP ddcacoa ddcacoa ddcacoa ddcacoa ddca	Decanoate (n-C10:0) Decanoyl-ACP (n-C10:0ACP) Decanoyl-CoA (n-C10:0CoA) Decanoyl-CoA (n-C10:0CoA) N6-(1,2-Dicarboxyethyl)-AMP dCDP dCDP dCMP dCTP Deoxycytidine Deoxycytidine trans-Dodec-2-enoyl-CoA Dodecanoate (n-C12:0) Dodecanoyl-ACP (n-C12:0ACP) Dodecanoyl-ACP (n-C12:0CoA) Dodecanoyl-CoA (n-C12:0CoA) Dodecanoyl-CoA (n-C12:0CoA) dGDP dGDP	peroxisome mitochondrion cytosol peroxisome cytosol cytosol nucleus cytosol cytosol cytosol cytosol extracellular peroxisome cytosol peroxisome cytosol peroxisome cytosol mitochondrion cytosol peroxisome cytosol peroxisome	C10H19O2 C21H39N2O8PRS C31H50N7O17P3S C31H50N7O17P3S C31H50N7O17P3S C14H14N5O11P C9H12N3O10P2 C9H12N3O7P C9H12N3O7P C9H12N3O13P3 C9H13N3O4 C9H13N3O4 C33H52N7O17P3S C12H23O2 C12H23O2 C23H43N2O8PRS C23H43N2O8PRS C33H54N7O17P3S C33H54N7O17P3S C10H12N5O10P2 C10H12N5O10P2	-1 -4 -4 -4 -3 -3 -2 -4 0 0 -4 -1 -1 -1 -1 -4
dca dca dcaACP dcacoa dcacoa dcamp dcdp dcdp dctp dctp dcyt dd2coa ddcaACP ddcaACP ddcaACP ddcacoa ddcacoa ddcacoa ddcaroa ddcaroa ddcaroa ddcaroa ddcaroa dgdp dgdp dgmp	Decanoate (n-C10:0) Decanoyl-ACP (n-C10:0ACP) Decanoyl-CoA (n-C10:0CoA) Decanoyl-CoA (n-C10:0CoA) N6-(1,2-Dicarboxyethyl)-AMP dCDP dCDP dCMP dCTP Deoxycytidine Deoxycytidine trans-Dodec-2-enoyl-CoA Dodecanoate (n-C12:0) Dodecanoyl-ACP (n-C12:0ACP) Dodecanoyl-ACP (n-C12:0CoA) Dodecanoyl-CoA (n-C12:0CoA) Dodecanoyl-CoA (n-C12:0CoA) Dodecanoyl-CoA (n-C12:0CoA) dGDP dGMP	peroxisome mitochondrion cytosol peroxisome cytosol cytosol nucleus cytosol cytosol cytosol cytosol extracellular peroxisome cytosol peroxisome cytosol peroxisome cytosol mitochondrion cytosol peroxisome cytosol peroxisome cytosol peroxisome cytosol peroxisome cytosol cytosol peroxisome cytosol	C10H19O2 C21H39N2O8PRS C31H50N7O17P3S C31H50N7O17P3S C31H50N7O17P3S C14H14N5O11P C9H12N3O10P2 C9H12N3O7P C9H12N3O7P C9H12N3O13P3 C9H13N3O4 C9H13N3O4 C33H52N7O17P3S C12H23O2 C12H23O2 C23H43N2O8PRS C23H43N2O8PRS C33H54N7O17P3S C33H54N7O17P3S C10H12N5O10P2 C10H12N5O10P2 C10H12N5O7P	-1 -4 -4 -4 -3 -3 -2 -4 0 0 -4 -1 -1 -1 -1 -4
dca dca dcaACP dcacoa dcacoa dcamp dcdp dcdp dctp dctp dcyt dd2coa ddcaACP ddcaACP ddcaACP ddcacoa ddcacoa ddcacoa ddcacoa ddcacoa ddcacoa ddcacoa dgdp dgdp dgmp dgsn	Decanoate (n-C10:0) Decanoyl-ACP (n-C10:0ACP) Decanoyl-CoA (n-C10:0CoA) Decanoyl-CoA (n-C10:0CoA) N6-(1,2-Dicarboxyethyl)-AMP dCDP dCDP dCMP dCTP Deoxycytidine Deoxycytidine trans-Dodec-2-enoyl-CoA Dodecanoate (n-C12:0) Dodecanoyl-ACP (n-C12:0ACP) Dodecanoyl-ACP (n-C12:0CoA) Dodecanoyl-CoA (n-C12:0CoA)	peroxisome mitochondrion cytosol peroxisome cytosol cytosol nucleus cytosol cytosol cytosol cytosol extracellular peroxisome cytosol peroxisome cytosol peroxisome cytosol mitochondrion cytosol peroxisome cytosol peroxisome cytosol cytosol cytosol cytosol cytosol cytosol cytosol cytosol	C10H19O2 C21H39N2O8PRS C31H50N7O17P3S C31H50N7O17P3S C31H50N7O17P3S C14H14N5O11P C9H12N3O10P2 C9H12N3O7P C9H12N3O7P C9H12N3O13P3 C9H13N3O4 C9H13N3O4 C33H52N7O17P3S C12H23O2 C12H23O2 C12H23O2 C23H43N2O8PRS C23H43N2O8PRS C33H54N7O17P3S C33H54N7O17P3S C10H12N5O10P2 C10H12N5O10P2 C10H12N5O7P C10H13N5O4	-1 -4 -4 -4 -3 -3 -2 -4 0 0 -4 -1 -1 -1 -1 -4 -4 -3 -3 -3 -2 0
dca dca dcaACP dcacoa dcacoa dcamp dcdp dcdp dctp dctp dcyt dd2coa ddcaACP ddcaACP ddcaACP ddcacoa ddcacoa ddcacoa ddcacoa ddcacoa ddcacoa dgdp dgdp dgmp dgsn dgsn	Decanoate (n-C10:0) Decanoyl-ACP (n-C10:0ACP) Decanoyl-CoA (n-C10:0CoA) Decanoyl-CoA (n-C10:0CoA) N6-(1,2-Dicarboxyethyl)-AMP dCDP dCDP dCMP dCTP Deoxycytidine Deoxycytidine trans-Dodec-2-enoyl-CoA Dodecanoate (n-C12:0) Dodecanoyl-ACP (n-C12:0ACP) Dodecanoyl-ACP (n-C12:0CoA) Dodecanoyl-CoA (n-C12:0CoA)	peroxisome mitochondrion cytosol peroxisome cytosol cytosol nucleus cytosol cytosol cytosol extracellular peroxisome cytosol peroxisome cytosol peroxisome cytosol mitochondrion cytosol peroxisome cytosol cytosol cytosol extracellular	C10H19O2 C21H39N2O8PRS C31H50N7O17P3S C31H50N7O17P3S C31H50N7O17P3S C14H14N5O11P C9H12N3O10P2 C9H12N3O7P C9H12N3O7P C9H12N3O13P3 C9H13N3O4 C9H13N3O4 C33H52N7O17P3S C12H23O2 C12H23O2 C12H23O2 C23H43N2O8PRS C23H43N2O8PRS C33H54N7O17P3S C33H54N7O17P3S C10H12N5O10P2 C10H12N5O10P2 C10H12N5O7P C10H13N5O4 C10H13N5O4	-1 -4 -4 -4 -3 -3 -2 -4 0 0 -4 -1 -1 -1 -1 -4 -4 -3 -3 -3 -3 -3 -0 -0 -0 -0 -0 -0 -0 -0 -0 -0 -0 -0 -0
dca dca dcaACP dcacoa dcacoa dcamp dcdp dcdp dctp dctp dcyt ddyt ddcaACP ddcaACP ddcaACP ddcaCoa	Decanoate (n-C10:0) Decanoyl-ACP (n-C10:0ACP) Decanoyl-CoA (n-C10:0CoA) Decanoyl-CoA (n-C10:0CoA) N6-(1,2-Dicarboxyethyl)-AMP dCDP dCDP dCMP dCMP Deoxycytidine Deoxycytidine Deoxycytidine trans-Dodec-2-enoyl-CoA Dodecanoate (n-C12:0) Dodecanoyl-ACP (n-C12:0ACP) Dodecanoyl-ACP (n-C12:0ACP) Dodecanoyl-CoA (n-C12:0CoA)	peroxisome mitochondrion cytosol peroxisome cytosol cytosol nucleus cytosol cytosol cytosol extracellular peroxisome cytosol peroxisome cytosol peroxisome cytosol mitochondrion cytosol peroxisome cytosol peroxisome cytosol cytosol peroxisome cytosol peroxisome cytosol cytosol nucleus cytosol extracellular	C10H19O2 C21H39N2O8PRS C31H50N7O17P3S C31H50N7O17P3S C31H50N7O17P3S C14H14N5O11P C9H12N3O10P2 C9H12N3O7P C9H12N3O7P C9H12N3O13P3 C9H13N3O4 C9H13N3O4 C33H52N7O17P3S C12H23O2 C12H23O2 C12H23O2 C23H43N2O8PRS C23H43N2O8PRS C33H54N7O17P3S C33H54N7O17P3S C10H12N5O10P2 C10H12N5O10P2 C10H12N5O7P C10H13N5O4 C10H13N5O4 C10H13N5O4 C10H12N5O13P3	-1 -4 -4 -4 -3 -3 -2 -4 0 0 -4 -1 -1 -1 -1 -4 -4 -3 -3 -3 -2 0 0 0 -4 -4 -4 -4 -4 -6 -7 -7 -7 -7 -7 -7 -7 -7 -7 -7 -7 -7 -7
dca dca dcaACP dcacoa dcacoa dcamp dcdp dcdp dctp dctp dcyt dd2coa ddcaACP ddcaACP ddcaACP ddcacoa	Decanoate (n-C10:0) Decanoyl-ACP (n-C10:0ACP) Decanoyl-CoA (n-C10:0CoA) Decanoyl-CoA (n-C10:0CoA) N6-(1,2-Dicarboxyethyl)-AMP dCDP dCDP dCMP dCTP Deoxycytidine Deoxycytidine trans-Dodec-2-enoyl-CoA Dodecanoate (n-C12:0) Dodecanoyl-ACP (n-C12:0ACP) Dodecanoyl-ACP (n-C12:0ACP) Dodecanoyl-CoA (n-C12:0CoA)	peroxisome mitochondrion cytosol peroxisome cytosol cytosol nucleus cytosol cytosol cytosol extracellular peroxisome cytosol peroxisome cytosol peroxisome cytosol mitochondrion cytosol peroxisome cytosol peroxisome cytosol cytosol peroxisome cytosol	C10H19O2 C21H39N2O8PRS C31H50N7O17P3S C31H50N7O17P3S C31H50N7O17P3S C14H14N5O11P C9H12N3O10P2 C9H12N3O7P C9H12N3O7P C9H12N3O13P3 C9H13N3O4 C9H13N3O4 C33H52N7O17P3S C12H23O2 C12H23O2 C12H23O2 C23H43N2O8PRS C23H43N2O8PRS C33H54N7O17P3S C33H54N7O17P3S C10H12N5O10P2 C10H12N5O10P2 C10H12N5O7P C10H13N5O4 C10H13N5O4 C10H13N5O4 C10H12N5O13P3 C3H6O3	-1 -1 -4 -4 -4 -3 -3 -2 -4 0 0 0 -4 -1 -1 -1 -1 -4 -4 -3 -3 -2 0 0 0 0 0
dca dca dcaACP dcacoa dcacoa dcamp dcdp dcdp dctp dctp dcyt dd2coa ddcaACP ddcaACP ddcaACP ddcacoa	Decanoate (n-C10:0) Decanoyl-ACP (n-C10:0ACP) Decanoyl-CoA (n-C10:0CoA) Decanoyl-CoA (n-C10:0CoA) N6-(1,2-Dicarboxyethyl)-AMP dCDP dCDP dCMP dCTP Deoxycytidine Deoxycytidine trans-Dodec-2-enoyl-CoA Dodecanoate (n-C12:0) Dodecanoyl-ACP (n-C12:0ACP) Dodecanoyl-ACP (n-C12:0ACP) Dodecanoyl-CoA (n-C12:0CoA) Dodecanoyl-CoA (n-C12:0CoA)	peroxisome mitochondrion cytosol peroxisome cytosol cytosol nucleus cytosol cytosol cytosol extracellular peroxisome cytosol peroxisome cytosol peroxisome cytosol mitochondrion cytosol peroxisome cytosol peroxisome cytosol cytosol peroxisome cytosol	C10H19O2 C21H39N2O8PRS C31H50N7O17P3S C31H50N7O17P3S C31H50N7O17P3S C14H14N5O11P C9H12N3O10P2 C9H12N3O7P C9H12N3O13P3 C9H13N3O4 C9H13N3O4 C9H13N3O4 C33H52N7O17P3S C12H23O2 C12H23O2 C23H43N2O8PRS C23H43N2O8PRS C33H54N7O17P3S C33H54N7O17P3S C10H12N5O10P2 C10H12N5O10P2 C10H12N5O7P C10H13N5O4 C10H13N5O4 C10H13N5O4 C10H12N5O13P3 C3H6O3 C3H6O3 C3H5O6P	-1 -1 -4 -4 -4 -3 -3 -2 -4 0 0 0 -4 -1 -1 -1 -1 -4 -4 -3 -3 -2 0 0 0 0 0
dca dca dcaACP dcacoa dcacoa dcamp dcdp dcdp dctp dctp dcyt dd2coa ddcaACP ddcaACP ddcaACP ddcacoa ddagp dgp dgsn dgsn dgtp dha dhap	Decanoate (n-C10:0) Decanoyl-ACP (n-C10:0ACP) Decanoyl-CoA (n-C10:0CoA) Decanoyl-CoA (n-C10:0CoA) N6-(1,2-Dicarboxyethyl)-AMP dCDP dCDP dCMP dCTP Deoxycytidine Deoxycytidine trans-Dodec-2-enoyl-CoA Dodecanoate (n-C12:0) Dodecanoyl-ACP (n-C12:0ACP) Dodecanoyl-ACP (n-C12:0ACP) Dodecanoyl-CoA (n-C12:0CoA)	peroxisome mitochondrion cytosol peroxisome cytosol cytosol nucleus cytosol cytosol extracellular peroxisome cytosol peroxisome cytosol peroxisome cytosol peroxisome cytosol mitochondrion cytosol peroxisome cytosol peroxisome cytosol mitochondrion	C10H19O2 C21H39N2O8PRS C31H50N7O17P3S C31H50N7O17P3S C31H50N7O17P3S C14H14N5O11P C9H12N3O10P2 C9H12N3O7P C9H12N3O7P C9H12N3O13P3 C9H13N3O4 C9H13N3O4 C33H52N7O17P3S C12H23O2 C12H23O2 C23H43N2O8PRS C23H43N2O8PRS C33H54N7O17P3S C33H54N7O17P3S C10H12N5O10P2 C10H12N5O10P2 C10H12N5O7P C10H13N5O4 C10H13N5O4 C10H13N5O4 C10H12N5O13P3 C3H6O3 C3H5O6P C3H5O6P	-1 -1 -4 -4 -4 -3 -3 -2 -4 0 0 0 -4 -1 -1 -1 -1 -4 -4 -3 -3 -2 0 0 0 0 0
dca dca dcaACP dcacoa dcacoa dcamp dcdp dcdp dctp dctp dcyt dd2coa ddcaACP ddcaACP ddcaACP ddcacoa ddcay dcgp dcyt ddcay dcay ddca	Decanoate (n-C10:0) Decanoyl-ACP (n-C10:0ACP) Decanoyl-CoA (n-C10:0CoA) Decanoyl-CoA (n-C10:0CoA) N6-(1,2-Dicarboxyethyl)-AMP dCDP dCDP dCMP dCTP Deoxycytidine Deoxycytidine trans-Dodec-2-enoyl-CoA Dodecanoate (n-C12:0) Dodecanoyl-ACP (n-C12:0ACP) Dodecanoyl-ACP (n-C12:0ACP) Dodecanoyl-CoA (n-C12:0CoA) Dodecanoyl-CoA (n-C12:0CoA)	peroxisome mitochondrion cytosol peroxisome cytosol cytosol nucleus cytosol cytosol cytosol extracellular peroxisome cytosol peroxisome cytosol peroxisome cytosol mitochondrion cytosol peroxisome cytosol peroxisome cytosol cytosol peroxisome cytosol	C10H19O2 C21H39N2O8PRS C31H50N7O17P3S C31H50N7O17P3S C31H50N7O17P3S C14H14N5O11P C9H12N3O10P2 C9H12N3O7P C9H12N3O13P3 C9H13N3O4 C9H13N3O4 C9H13N3O4 C33H52N7O17P3S C12H23O2 C12H23O2 C23H43N2O8PRS C23H43N2O8PRS C33H54N7O17P3S C33H54N7O17P3S C10H12N5O10P2 C10H12N5O10P2 C10H12N5O7P C10H13N5O4 C10H13N5O4 C10H13N5O4 C10H12N5O13P3 C3H6O3 C3H6O3 C3H5O6P	-1 -4 -4 -4 -3 -3 -2 -4 0 0 -4 -1 -1 -1 -1 -4 -4 -3 -3 -3 -2 0 0 0 -4 -4 -4 -4 -4 -6 -7 -7 -7 -7 -7 -7 -7 -7 -7 -7 -7 -7 -7

dhlam	Dihydrolipoamide	mitochondrion	C8H17NOS2	0
dhlpro	Dihydrolipolprotein	mitochondrion	H2S2X	0
	2-Amino-4-hydroxy-6-(D-erythro-1,2,3-			
dhnpt	trihydroxypropyl)-7,8-dihydropteridine	cytosol	C9H14N5O4	1
	2-Amino-4-hydroxy-6-(D-erythro-1,2,3-			
dhnpt	trihydroxypropyl)-7,8-dihydropteridine	mitochondrion	C9H14N5O4	1
dhor-S	(S)-Dihydroorotate	cytosol	C5H5N2O4	-1
dhor-S	(S)-Dihydroorotate	nucleus	C5H5N2O4	-1
dhpmp	Dihydroneopterin monophosphate	cytosol	C9H13N5O7P	-1
dhpt	Dihydropteroate	cytosol	C14H13N6O3	-1
dhpt	Dihydropteroate	mitochondrion	C14H13N6O3	-1
din	Deoxyinosine	cytosol	C10H12N4O4	0
din	Deoxyinosine	extracellular	C10H12N4O4	0
dmlz	6,7-Dimethyl-8-(1-D-ribityl)lumazine	cytosol	C13H18N4O6	0
dmpp	Dimethylallyl diphosphate	cytosol	C5H9O7P2	-3
dnad	Deamino-NAD+	cytosol	C21H24N6O15P2	-3 -2 -2 0
dnad	Deamino-NAD+	mitochondrion	C21H24N6O15P2	-2
dolichol	Dolichol	cytosol	C15H28O	0
dolmanp	Dolichyl phosphate D-mannose	endoplasmic reticulum	C21H38O9P	-1
dolp	Dolichol phosphate	cytosol	C15H27O4P	-2
dolp	Dolichol phosphate	endoplasmic reticulum	C15H27O4P	-2
dpcoa	Dephospho-CoA	cytosol	C21H33N7O13P2S	-2 -2 -2 -2 0
dpcoa	Dephospho-CoA	mitochondrion	C21H33N7O13P2S	-2
drib	Deoxyribose	cytosol	C5H10O4	
dtbt	Dethiobiotin	cytosol	C10H17N2O3	-1
dtdp	dTDP	cytosol	C10H13N2O11P2	-3 -2 -4
dtmp	dTMP	cytosol	C10H13N2O8P	-2
dttp	dTTP	cytosol	C10H13N2O14P3	
dttp	dTTP	extracellular	C10H13N2O14P3	-4 -3 -3 -2 -2 0
dudp	dUDP	cytosol	C9H11N2O11P2	-3
dudp	dUDP	nucleus	C9H11N2O11P2	-3
dump	dUMP	cytosol	C9H11N2O8P	-2
dump	dUMP	nucleus	C9H11N2O8P	-2
duri	Deoxyuridine	cytosol	C9H12N2O5	
duri	Deoxyuridine	extracellular	C9H12N2O5	0
dutp	dUTP	cytosol	C9H11N2O14P3	-4
e4hglu	L-erythro-4-Hydroxyglutamate	cytosol	C5H8NO5	-1
e4hglu	L-erythro-4-Hydroxyglutamate	mitochondrion	C5H8NO5	-1
e4hglu	L-erythro-4-Hydroxyglutamate	peroxisome	C5H8NO5	-1
e4p	D-Erythrose 4-phosphate	cytosol	C4H7O7P	-2 -2 -2
e4p	D-Erythrose 4-phosphate	mitochondrion	C4H7O7P	-2
eig3p		ICVICEOL	IC GUONION GD	
epist	D-erythro-1-(Imidazol-4-yl)glycerol 3-phosphate	cytosol	C6H9N2O6P	
·	episterol	cytosol	C28H46O	0
epm	episterol Epimelibiose	cytosol cytosol	C28H46O C12H22O11	0
epm ergst	episterol Epimelibiose Ergosterol	cytosol cytosol	C28H46O C12H22O11 C28H44O	0
epm ergst ergst	episterol Epimelibiose Ergosterol Ergosterol	cytosol cytosol cytosol extracellular	C28H46O C12H22O11 C28H44O C28H44O	0 0 0
epm ergst ergst ergst	episterol Epimelibiose Ergosterol Ergosterol Ergosterol	cytosol cytosol cytosol extracellular endoplasmic reticulum	C28H46O C12H22O11 C28H44O C28H44O C28H44O	0 0 0 0
epm ergst ergst ergst ergst ergtetrol	episterol Epimelibiose Ergosterol Ergosterol Ergosterol Ergosterol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol	cytosol cytosol cytosol extracellular endoplasmic reticulum cytosol	C28H46O C12H22O11 C28H44O C28H44O C28H44O C28H44O	0 0 0 0 0
epm ergst ergst ergst ergterol ergtetrol	episterol Epimelibiose Ergosterol Ergosterol Ergosterol Ergosterol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol	cytosol cytosol cytosol extracellular endoplasmic reticulum cytosol endoplasmic reticulum	C28H46O C12H22O11 C28H44O C28H44O C28H44O C28H44O C28H42O C28H42O	0 0 0 0 0 0
epm ergst ergst ergst ergtetrol ergtetrol ergtrol	episterol Epimelibiose Ergosterol Ergosterol Ergosterol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol ergosta-5,7,24(28)-trienol	cytosol cytosol cytosol extracellular endoplasmic reticulum cytosol endoplasmic reticulum cytosol	C28H46O C12H22O11 C28H44O C28H44O C28H44O C28H42O C28H42O C28H42O C28H44O	0 0 0 0 0 0 0
epm ergst ergst ergst ergtetrol ergtetrol ergtrol etha	episterol Epimelibiose Ergosterol Ergosterol Ergostarol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol ergosta-5,7,24(28)-trienol Ethanolamine	cytosol cytosol cytosol extracellular endoplasmic reticulum cytosol endoplasmic reticulum cytosol cytosol	C28H46O C12H22O11 C28H44O C28H44O C28H44O C28H42O C28H42O C28H42O C28H44O C2H8NO	0 0 0 0 0 0 0 0 0
epm ergst ergst ergst ergtetrol ergtetrol ergtrol etha ethamp	episterol Epimelibiose Ergosterol Ergosterol Ergostarol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol ergosta-5,7,24(28)-trienol Ethanolamine Ethanolamine phosphate	cytosol cytosol cytosol extracellular endoplasmic reticulum cytosol endoplasmic reticulum cytosol cytosol cytosol	C28H46O C12H22O11 C28H44O C28H44O C28H44O C28H42O C28H42O C28H44O C28H44O C2H8NO C2H7NO4P	0 0 0 0 0 0 0 0 0 0
epm ergst ergst ergst ergtetrol ergtetrol ergtrol etha ethamp etoh	episterol Epimelibiose Ergosterol Ergosterol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol ergosta-5,7,24(28)-trienol Ethanolamine Ethanolamine phosphate Ethanol	cytosol cytosol cytosol extracellular endoplasmic reticulum cytosol endoplasmic reticulum cytosol cytosol cytosol cytosol cytosol	C28H46O C12H22O11 C28H44O C28H44O C28H44O C28H42O C28H42O C28H44O C2H8NO C2H7NO4P C2H6O	0 0 0 0 0 0 0 0 0 0 1 1 -1
epm ergst ergst ergst ergtetrol ergtetrol ergtrol etha ethamp etoh etoh	episterol Epimelibiose Ergosterol Ergosterol Ergosterol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol ergosta-5,7,24(28)-trienol Ethanolamine Ethanolamine phosphate Ethanol Ethanol	cytosol cytosol cytosol extracellular endoplasmic reticulum cytosol endoplasmic reticulum cytosol cytosol cytosol cytosol cytosol extracellular	C28H46O C12H22O11 C28H44O C28H44O C28H44O C28H42O C28H42O C28H44O C2H8NO C2H7NO4P C2H6O	0 0 0 0 0 0 0 0 0 0 1 1 -1
epm ergst ergst ergst ergtetrol ergtetrol ergtrol etha ethamp etoh etoh	episterol Epimelibiose Ergosterol Ergosterol Ergosterol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol ergosta-5,7,24(28)-tetraen-3beta-ol ergosta-5,7,24(28)-trienol Ethanolamine Ethanolamine phosphate Ethanol Ethanol	cytosol cytosol cytosol extracellular endoplasmic reticulum cytosol endoplasmic reticulum cytosol cytosol cytosol cytosol extracellular mitochondrion	C28H46O C12H22O11 C28H44O C28H44O C28H44O C28H42O C28H42O C28H44O C2H8NO C2H7NO4P C2H6O C2H6O	0 0 0 0 0 0 0 0 0 0 1 1 -1
epm ergst ergst ergst ergst ergtetrol ergtetrol ergtrol etha ethamp etoh etoh etoh	episterol Epimelibiose Ergosterol Ergosterol Ergosterol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol ergosta-5,7,24,(28)-tetraen-3beta-ol ergosta-5,7,24(28)-trienol Ethanolamine Ethanolamine phosphate Ethanol Ethanol Ethanol D-Fructose 1-phosphate	cytosol cytosol cytosol extracellular endoplasmic reticulum cytosol endoplasmic reticulum cytosol cytosol cytosol cytosol extracellular mitochondrion cytosol	C28H46O C12H22O11 C28H44O C28H44O C28H44O C28H42O C28H42O C28H44O C2H8NO C2H7NO4P C2H6O C2H6O C2H6O C2H6O C6H11O9P	0 0 0 0 0 0 0 0 0 1 1 -1 0 0 0
epm ergst ergst ergst ergst ergtetrol ergtetrol ergtrol etha ethamp etoh etoh f1p f26bp	episterol Epimelibiose Ergosterol Ergosterol Ergosterol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol ergosta-5,7,24(28)-trienol Ethanolamine Ethanolamine phosphate Ethanol Ethanol Ethanol D-Fructose 1-phosphate D-Fructose 2,6-bisphosphate	cytosol cytosol cytosol extracellular endoplasmic reticulum cytosol endoplasmic reticulum cytosol cytosol cytosol cytosol extracellular mitochondrion cytosol cytosol	C28H46O C12H22O11 C28H44O C28H44O C28H44O C28H42O C28H42O C28H42O C2H8NO C2H7NO4P C2H6O C2H6O C2H6O C2H6O C6H11O9P C6H10O12P2	0 0 0 0 0 0 0 0 0 1 1 -1 0 0 0 0
epm ergst ergst ergst ergst ergtetrol ergtetrol ergtrol etha ethamp etoh etoh f1p f26bp f6p	episterol Epimelibiose Ergosterol Ergosterol Ergosterol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol ergosta-5,7,24(28)-trienol Ethanolamine Ethanolamine phosphate Ethanol Ethanol Ethanol D-Fructose 1-phosphate D-Fructose 6-phosphate	cytosol cytosol cytosol extracellular endoplasmic reticulum cytosol endoplasmic reticulum cytosol cytosol cytosol cytosol extracellular mitochondrion cytosol cytosol cytosol	C28H46O C12H22O11 C28H44O C28H44O C28H44O C28H42O C28H42O C28H42O C28H44O C2H8NO C2H7NO4P C2H6O C2H6O C2H6O C2H6O C6H11O9P C6H10O12P2 C6H11O9P	0 0 0 0 0 0 0 0 0 1 1 -1 0 0 0 0
epm ergst ergst ergst ergst ergtetrol ergtetrol ergtrol etha ethamp etoh etoh f1p f26bp f6p f6p-B	episterol Epimelibiose Ergosterol Ergosterol Ergosterol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol ergosta-5,7,24(28)-trienol Ethanolamine Ethanolamine phosphate Ethanol Ethanol Ethanol D-Fructose 1-phosphate D-Fructose 6-phosphate beta-D-Fructose 6-phosphate	cytosol cytosol cytosol extracellular endoplasmic reticulum cytosol endoplasmic reticulum cytosol cytosol cytosol cytosol extracellular mitochondrion cytosol cytosol cytosol cytosol	C28H46O C12H22O11 C28H44O C28H44O C28H44O C28H42O C28H42O C28H42O C2H8NO C2H7NO4P C2H6O C2H6O C2H6O C6H11O9P C6H11O9P C6H11O9P C6H11O9P	0 0 0 0 0 0 0 0 0 1 1 -1 0 0 0 0
epm ergst ergst ergst ergst ergtetrol ergtetrol ergtrol etha ethamp etoh etoh f1p f26bp f6p f6p-B fad	episterol Epimelibiose Ergosterol Ergosterol Ergosterol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol ergosta-5,7,24(28)-trienol Ethanolamine Ethanolamine Ethanol Ethanol Ethanol Ethanol D-Fructose 1-phosphate D-Fructose 6-phosphate beta-D-Fructose 6-phosphate FAD	cytosol cytosol cytosol extracellular endoplasmic reticulum cytosol endoplasmic reticulum cytosol cytosol cytosol cytosol extracellular mitochondrion cytosol cytosol cytosol cytosol cytosol cytosol	C28H46O C12H22O11 C28H44O C28H44O C28H44O C28H42O C28H42O C28H42O C2H8NO C2H7NO4P C2H6O C2H6O C2H6O C6H11O9P C6H11O9P C6H11O9P C6H11O9P C6H11O9P C6H11O9P C27H31N9O15P2	0 0 0 0 0 0 0 0 0 1 1 -1 0 0 0 0
epm ergst ergst ergst ergst ergterol ergtetrol ergtrol etha ethamp etoh etoh f1p f26bp f6p f6p-B fad fad	episterol Epimelibiose Ergosterol Ergosterol Ergosterol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol ergosta-5,7,24(28)-trienol Ethanolamine Ethanolamine phosphate Ethanol Ethanol Ethanol D-Fructose 1-phosphate D-Fructose 6-phosphate beta-D-Fructose 6-phosphate FAD FAD	cytosol cytosol cytosol extracellular endoplasmic reticulum cytosol endoplasmic reticulum cytosol cytosol cytosol cytosol extracellular mitochondrion cytosol cytosol cytosol cytosol cytosol cytosol cytosol cytosol cytosol	C28H46O C12H22O11 C28H44O C28H44O C28H44O C28H42O C28H42O C28H42O C28H44O C2H8NO C2H7NO4P C2H6O C2H6O C2H6O C6H11O9P C6H11O9P C6H11O9P C6H11O9P C6H11O9P C27H31N9O15P2 C27H31N9O15P2	0 0 0 0 0 0 0 0 0 1 1 -1 0 0 0 0
epm ergst ergst ergst ergst ergst ergtetrol ergtetrol ergtrol etha ethamp etoh etoh f1p f26bp f6p f6p-B fad fad fadh2	episterol Epimelibiose Ergosterol Ergosterol Ergosterol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol ergosta-5,7,24(28)-trienol Ethanolamine Ethanolamine Ethanolamine phosphate Ethanol Ethanol D-Fructose 1-phosphate D-Fructose 2,6-bisphosphate D-Fructose 6-phosphate beta-D-Fructose 6-phosphate FAD FAD FAD	cytosol cytosol cytosol extracellular endoplasmic reticulum cytosol endoplasmic reticulum cytosol cytosol cytosol cytosol extracellular mitochondrion cytosol mitochondrion mitochondrion	C28H46O C12H22O11 C28H44O C28H44O C28H44O C28H42O C28H42O C28H42O C28H44O C2H8NO C2H7NO4P C2H6O C2H6O C2H6O C6H11O9P C6H11O9P C6H11O9P C6H11O9P C7H31N9O15P2 C27H31N9O15P2 C27H33N9O15P2	0 0 0 0 0 0 0 0 0 1 1 -1 0 0 0 0
epm ergst ergst ergst ergst ergst ergtetrol ergtetrol ergtrol etha ethamp etoh etoh f1p f26bp f6p f6p-B fad fad fadh2 fald	episterol Epimelibiose Ergosterol Ergosterol Ergosterol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol ergosta-5,7,24(28)-trienol Ethanolamine Ethanolamine Ethanol Ethanol Ethanol D-Fructose 1-phosphate D-Fructose 2,6-bisphosphate D-Fructose 6-phosphate beta-D-Fructose 6-phosphate FAD FAD FAD FAD FAD FAD FOrmaldehyde	cytosol cytosol cytosol extracellular endoplasmic reticulum cytosol endoplasmic reticulum cytosol cytosol cytosol cytosol extracellular mitochondrion cytosol	C28H46O C12H22O11 C28H44O C28H44O C28H44O C28H42O C28H42O C28H42O C28H44O C2H8NO C2H7NO4P C2H6O C2H6O C2H6O C6H1109P C6H1109P C6H1109P C6H1109P C27H31N9O15P2 C27H33N9O15P2 CC7H33N9O15P2 CH2O	0 0 0 0 0 0 0 0 0 1 1 -1 0 0 0 0 0 0 0 0
epm ergst ergst ergst ergst ergst ergterol ergtetrol ergtrol etha ethamp etoh etoh f1p f26bp f6p f6p-B fad fad fadh2 fald fdp	episterol Epimelibiose Ergosterol Ergosterol Ergosterol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol ergosta-5,7,24(28)-trienol Ethanolamine Ethanolamine Ethanol Ethanol Ethanol D-Fructose 1-phosphate D-Fructose 2,6-bisphosphate D-Fructose 6-phosphate beta-D-Fructose 6-phosphate FAD FAD FAD FAD FAD FADH2 Formaldehyde D-Fructose 1,6-bisphosphate	cytosol cytosol cytosol extracellular endoplasmic reticulum cytosol endoplasmic reticulum cytosol cytosol cytosol cytosol extracellular mitochondrion cytosol	C28H46O C12H22O11 C28H44O C28H44O C28H44O C28H42O C28H42O C28H42O C28H44O C2H8NO C2H7NO4P C2H6O C2H6O C2H6O C6H11O9P C6H11O9P C6H11O9P C6H11O9P C27H31N9O15P2 C27H31N9O15P2 C27H33N9O15P2 CH2O C6H10O12P2	0 0 0 0 0 0 0 0 0 0 1 1 -1 0 0 0 0 0 0 0
epm ergst ergst ergst ergst ergst ergterol ergterol ergtrol etha ethamp etoh etoh f1p f26bp f6p f6p-B fad fad fadh2 fald fdp fe2	episterol Epimelibiose Ergosterol Ergosterol Ergosterol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol ergosta-5,7,24(28)-trienol Ethanolamine Ethanolamine Ethanolamine phosphate Ethanol Ethanol Ethanol D-Fructose 1-phosphate D-Fructose 2,6-bisphosphate D-Fructose 6-phosphate beta-D-Fructose 6-phosphate FAD FAD FAD FAD FAD FADH2 Formaldehyde D-Fructose 1,6-bisphosphate Fe2+	cytosol cytosol cytosol extracellular endoplasmic reticulum cytosol endoplasmic reticulum cytosol cytosol cytosol cytosol extracellular mitochondrion cytosol mitochondrion mitochondrion cytosol cytosol cytosol mitochondrion	C28H46O C12H22O11 C28H44O C28H44O C28H44O C28H42O C28H42O C28H42O C28H44O C2H8NO C2H7NO4P C2H6O C2H6O C2H6O C6H11O9P C6H11O9P C6H11O9P C6H11O9P C27H31N9O15P2 C27H31N9O15P2 C27H33N9O15P2 C27H33N9O15P2 CH2O C6H10O12P2 Fe	0 0 0 0 0 0 0 0 0 0 1 1 -1 0 0 0 0 0 0 0
epm ergst ergst ergst ergst ergst ergterol ergtetrol ergterol etha ethamp etoh etoh f1p f26bp f6p f6p-B fad fad fadh2 fald fdp fe2 fecost	episterol Epimelibiose Ergosterol Ergosterol Ergosterol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol ergosta-5,7,24(28)-trienol Ethanolamine Ethanolamine phosphate Ethanol Ethanol Ethanol D-Fructose 1-phosphate D-Fructose 2,6-bisphosphate D-Fructose 6-phosphate beta-D-Fructose 6-phosphate FAD	cytosol cytosol cytosol extracellular endoplasmic reticulum cytosol endoplasmic reticulum cytosol cytosol cytosol cytosol extracellular mitochondrion cytosol mitochondrion mitochondrion cytosol cytosol cytosol cytosol cytosol	C28H46O C12H22O11 C28H44O C28H44O C28H44O C28H42O C28H42O C28H42O C28H44O C2H8NO C2H7NO4P C2H6O C2H6O C2H6O C6H11O9P C6H11O9P C6H11O9P C7H31N9O15P2 C27H31N9O15P2 C27H33N9O15P2 CH2O C6H10O12P2 Fe C28H46O	00 00 00 00 00 00 00 11 1 00 00 00 2 4 4 2 2 2 2 2 2 2
epm ergst ergst ergst ergst ergst ergterol ergtetrol ergtrol etha ethamp etoh etoh f1p f26bp f6p f6p-B fad fad fadh2 fald fdp fe2	episterol Epimelibiose Ergosterol Ergosterol Ergosterol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol Ergosta-5,7,22,24,(28)-tetraen-3beta-ol ergosta-5,7,24(28)-trienol Ethanolamine Ethanolamine Ethanolamine phosphate Ethanol Ethanol Ethanol D-Fructose 1-phosphate D-Fructose 2,6-bisphosphate D-Fructose 6-phosphate beta-D-Fructose 6-phosphate FAD FAD FAD FAD FAD FADH2 Formaldehyde D-Fructose 1,6-bisphosphate Fe2+	cytosol cytosol cytosol extracellular endoplasmic reticulum cytosol endoplasmic reticulum cytosol cytosol cytosol cytosol extracellular mitochondrion cytosol mitochondrion mitochondrion cytosol cytosol cytosol mitochondrion	C28H46O C12H22O11 C28H44O C28H44O C28H44O C28H42O C28H42O C28H42O C28H44O C2H8NO C2H7NO4P C2H6O C2H6O C2H6O C6H11O9P C6H11O9P C6H11O9P C6H11O9P C27H31N9O15P2 C27H31N9O15P2 C27H33N9O15P2 C27H33N9O15P2 CH2O C6H10O12P2 Fe	0 0 0 0 0 0 0 0 0 0 1 1 -1 0 0 0 0 0 0 0

fmettrna	N-Formylmethionyl-tRNA	mitochondrion	C6H9NO2SR	(
fmn	FMN	cytosol	C17H19N4O9P	-2
fmn	FMN	extracellular	C17H19N4O9P	-2
fmn	FMN	mitochondrion	C17H19N4O9P	-2
focytc	Ferrocytochrome c	mitochondrion	C42H53FeN8O6S2	
for	Formate	cytosol	CH1O2	-1
for	Formate	extracellular	CH1O2	-1
for	Formate	mitochondrion	CH1O2	-1
	2-(Formamido)-N1-(5-phospho-D-			
fpram	ribosyl)acetamidine	cytosol	C8H15N3O8P	_*
	5-Formamido-1-(5-phospho-D-ribosyl)imidazole-4-			
fprica	carboxamide	cytosol	C10H13N4O9P	-2
frdp	Farnesyl diphosphate	cytosol	C15H25O7P2	-(
fru	D-Fructose	cytosol	C6H12O6	(
fru	D-Fructose	extracellular	C6H12O6	(
fum	Fumarate	cytosol	C4H2O4	-2
fum	Fumarate	extracellular	C4H2O4	
fum	Fumarate	mitochondrion	C4H2O4	-2 -2 -2
g1p	D-Glucose 1-phosphate	cytosol	C6H11O9P	-/
g3p	Glyceraldehyde 3-phosphate	cytosol	C3H5O6P	
g5p g6p	D-Glucose 6-phosphate	cytosol	C6H11O9P	
g6p	D-Glucose 6-phosphate	endoplasmic reticulum	C6H11O9P	-2 -2
g6p-B	beta-D-glucose 6-phosphate	cytosol	C6H11O9P	-2
	D-Galactose	cytosol	C6H12O6	-2
gal				
gal	D-Galactose	extracellular	C6H12O6	(
gal1p	alpha-D-Galactose 1-phosphate	cytosol	C6H11O9P	-2
gam1p	D-Glucosamine 1-phosphate	cytosol	C6H13NO8P	′
gam6p	D-Glucosamine 6-phosphate	cytosol	C6H13NO8P	-1
gam6p	D-Glucosamine 6-phosphate	extracellular	C6H13NO8P	-1
gar	N1-(5-Phospho-D-ribosyl)glycinamide	cytosol	C7H14N2O8P	-1
gcald	Glycolaldehyde	cytosol	C2H4O2	(
gcald	Glycolaldehyde	extracellular	C2H4O2	(
gcald	Glycolaldehyde	mitochondrion	C2H4O2	(
gdp	GDP	cytosol	C10H12N5O11P2	-(
gdp	GDP	Golgi apparatus	C10H12N5O11P2	-(
gdp	GDP	mitochondrion	C10H12N5O11P2	-(
gdp	GDP	nucleus	C10H12N5O11P2	-(
gdpmann	GDP-D-mannose	cytosol	C16H23N5O16P2	-2
gdpmann	GDP-D-mannose	Golgi apparatus	C16H23N5O16P2	-2
ggl	Galactosylglycerol	cytosol	C9H18O8	(
glc-D	D-Glucose	cytosol	C6H12O6	(
glc-D	D-Glucose	extracellular	C6H12O6	
glc-D	D-Glucose	vacuole	C6H12O6	(
gln-L	L-Glutamine	cytosol	C5H10N2O3	(
gln-L	L-Glutamine	extracellular	C5H10N2O3	
				(
gln-L	L-Glutamine	nucleus	C5H10N2O3	(
glntrna	L-Glutaminyl-tRNA(Gln)	cytosol	C5H9N2O2R	
glp	Glycylpeptide	cytosol	C4H7N2O3R	(
glu-L	L-Glutamate	cytosol	C5H8NO4	
glu-L	L-Glutamate	extracellular	C5H8NO4	-1
glu-L	L-Glutamate	mitochondrion	C5H8NO4	
glu-L	L-Glutamate	nucleus	C5H8NO4	-1
glu-L	L-Glutamate	peroxisome	C5H8NO4	_^
glu5p	L-Glutamate 5-phosphate	cytosol	C5H8NO7P	-2
glu5sa	L-Glutamate 5-semialdehyde	cytosol	C5H9NO3	(
glu5sa	L-Glutamate 5-semialdehyde	mitochondrion	C5H9NO3	(
gluala	5-L-Glutamyl-L-alanine	cytosol	C8H13N2O5	^
glucys	gamma-L-Glutamyl-L-cysteine	cytosol	C8H13N2O5S	
glutrna	L-Glutamyl-tRNA(Glu)	cytosol	C5H7NO3R	(
glutrna	L-Glutamyl-tRNA(Glu)	mitochondrion	C5H7NO3R	
glx	Glyoxylate	cytosol	C2H1O3	
glx	Glyoxylate	peroxisome	C2H1O3	
				- (
gly	Glycine	cytosol	C2H5NO2	
gly	Glycine	extracellular	C2H5NO2	(
gly	Glycine	mitochondrion	C2H5NO2	(
glyald	D-Glyceraldehyde	cytosol	C3H6O3	(
glyc	Glycerol	cytosol	C3H8O3	(
glyc	Glycerol	extracellular	C3H8O3	(

glyc3p	Glycerol 3-phosphate	cytosol	C3H7O6P	-2
glyc3p	Glycerol 3-phosphate	mitochondrion	C3H7O6P	-2 -2 0
glycogen	glycogen	cytosol	C6H10O5	0
glytrna	Glycyl-tRNA(Gly)	cytosol	C2H4NOR	1
gmp	GMP	cytosol	C10H12N5O8P	
gmp	GMP	Golgi apparatus	C10H12N5O8P	-2 -2 -4
gp4g	P1,P4-Bis(5'-guanosyl) tetraphosphate	cytosol	C20H24N10O21P4	-4
grdp	Geranyl diphosphate	cytosol	C10H17O7P2	-3
gsn	Guanosine	cytosol	C10H13N5O5	0
gsn	Guanosine	extracellular	C10H13N5O5	0
gsn	Guanosine	mitochondrion	C10H13N5O5	0
gthox	Oxidized glutathione	cytosol	C20H30N6O12S2	-2
gthox	Oxidized glutathione	extracellular	C20H30N6O12S2	-2
gthrd	Reduced glutathione	cytosol	C10H16N3O6S	-2 -1
gthrd	Reduced glutathione	mitochondrion	C10H16N3O6S	-1
gtp	GTP	cytosol	C10H12N5O14P3	-4
gtp	GTP	mitochondrion	C10H12N5O14P3	-4
gua	Guanine	cytosol	C5H5N5O	0
gua	Guanine	extracellular	C5H5N5O	0
	Guanine	mitochondrion	C5H5N5O	0
gua h	H+	cytosol	Н	1
h	H+	extracellular	H	1
	H+		Н	1
h h	H+	Golgi apparatus mitochondrion	Н	1
h	H+	nucleus	Н	1
h	H+	endoplasmic reticulum	Н	1
h	H+	vacuole	Н	1
h	H+	peroxisome	Н	1
h2o	H2O	cytosol	H2O	0
h2o	H2O	extracellular	H2O	0
h2o	H2O	Golgi apparatus	H2O	0
h2o	H2O	mitochondrion	H2O	0
h2o	H2O	nucleus	H2O	0
h2o	H2O	endoplasmic reticulum	H2O	0
h2o	H2O	vacuole	H2O	0
h2o	H2O	peroxisome	H2O	0
h2o2	Hydrogen peroxide	cytosol	H2O2	0
h2o2	Hydrogen peroxide	peroxisome	H2O2	0
h2s	Hydrogen sulfide	cytosol	H2S	0
		cytocol	C10H12N2O4	
hLkynr	3-Hydroxy-L-kynurenine	cytosol		0
hcit	2-Hydroxybutane-1,2,4-tricarboxylate	mitochondrion	C7H7O7	-3
	2-Hydroxybutane-1,2,4-tricarboxylate 2-Hydroxybutane-1,2,4-tricarboxylate	mitochondrion nucleus		
hcit hcit hco3	2-Hydroxybutane-1,2,4-tricarboxylate 2-Hydroxybutane-1,2,4-tricarboxylate Bicarbonate	mitochondrion nucleus cytosol	C7H7O7 C7H7O7 CHO3	-3 -3 -1
hcit hcit hco3 hco3	2-Hydroxybutane-1,2,4-tricarboxylate 2-Hydroxybutane-1,2,4-tricarboxylate Bicarbonate Bicarbonate	mitochondrion nucleus cytosol mitochondrion	C7H7O7 C7H7O7 CHO3 CHO3	-3 -3 -1 -1
hcit hcit hco3 hco3	2-Hydroxybutane-1,2,4-tricarboxylate 2-Hydroxybutane-1,2,4-tricarboxylate Bicarbonate Bicarbonate Bicarbonate	mitochondrion nucleus cytosol mitochondrion nucleus	C7H7O7 C7H7O7 CHO3 CHO3 CHO3	-3 -3 -1 -1 -1
hcit hcit hco3 hco3 hco3 hco3	2-Hydroxybutane-1,2,4-tricarboxylate 2-Hydroxybutane-1,2,4-tricarboxylate Bicarbonate Bicarbonate Bicarbonate L-Homocysteine	mitochondrion nucleus cytosol mitochondrion nucleus cytosol	C7H7O7 C7H7O7 CHO3 CHO3 CHO3 CHO3 C4H9NO2S	-3 -3 -1 -1 -1 0
hcit hcit hco3 hco3 hco3 hco3 hcys-L hcys-L	2-Hydroxybutane-1,2,4-tricarboxylate 2-Hydroxybutane-1,2,4-tricarboxylate Bicarbonate Bicarbonate Bicarbonate L-Homocysteine L-Homocysteine	mitochondrion nucleus cytosol mitochondrion nucleus cytosol peroxisome	C7H7O7 C7H7O7 CHO3 CHO3 CHO3 CHO3 C4H9NO2S C4H9NO2S	-3 -3 -1 -1 -1 0 0
hcit hcit hco3 hco3 hco3 hco3 hcys-L hcys-L hdca	2-Hydroxybutane-1,2,4-tricarboxylate 2-Hydroxybutane-1,2,4-tricarboxylate Bicarbonate Bicarbonate Bicarbonate L-Homocysteine L-Homocysteine Hexadecanoate (n-C16:0)	mitochondrion nucleus cytosol mitochondrion nucleus cytosol peroxisome cytosol	C7H7O7 C7H7O7 CHO3 CHO3 CHO3 CHO3 C4H9NO2S C4H9NO2S C16H31O2	-3 -3 -1 -1 -1 0 0
hcit hcit hco3 hco3 hco3 hcys-L hcys-L hdca hdca	2-Hydroxybutane-1,2,4-tricarboxylate 2-Hydroxybutane-1,2,4-tricarboxylate Bicarbonate Bicarbonate Bicarbonate L-Homocysteine L-Homocysteine Hexadecanoate (n-C16:0) Hexadecanoate (n-C16:0)	mitochondrion nucleus cytosol mitochondrion nucleus cytosol peroxisome cytosol extracellular	C7H7O7 C7H7O7 CHO3 CHO3 CHO3 C4H9NO2S C4H9NO2S C16H31O2 C16H31O2	-3 -3 -1 -1 -1 0 0 -1 -1
hcit hcit hco3 hco3 hco3 hcys-L hcys-L hdca hdca	2-Hydroxybutane-1,2,4-tricarboxylate 2-Hydroxybutane-1,2,4-tricarboxylate Bicarbonate Bicarbonate Bicarbonate L-Homocysteine L-Homocysteine Hexadecanoate (n-C16:0) Hexadecanoate (n-C16:0)	mitochondrion nucleus cytosol mitochondrion nucleus cytosol peroxisome cytosol extracellular peroxisome	C7H7O7 C7H7O7 CHO3 CHO3 CHO3 C4H9NO2S C4H9NO2S C16H31O2 C16H31O2	-3 -3 -1 -1 -1 0 0 -1 -1 -1
hcit hcit hco3 hco3 hco3 hcys-L hcys-L hdca hdca	2-Hydroxybutane-1,2,4-tricarboxylate 2-Hydroxybutane-1,2,4-tricarboxylate Bicarbonate Bicarbonate Bicarbonate L-Homocysteine L-Homocysteine Hexadecanoate (n-C16:0) Hexadecanoate (n-C16:0) hexadecanoate (n-C16:1)	mitochondrion nucleus cytosol mitochondrion nucleus cytosol peroxisome cytosol extracellular	C7H7O7 C7H7O7 CHO3 CHO3 CHO3 C4H9NO2S C4H9NO2S C16H31O2 C16H31O2 C16H31O2 C16H31O2	-3 -3 -1 -1 -1 0 0 -1 -1 -1
hcit hcit hco3 hco3 hco3 hcys-L hcys-L hdca hdca	2-Hydroxybutane-1,2,4-tricarboxylate 2-Hydroxybutane-1,2,4-tricarboxylate Bicarbonate Bicarbonate Bicarbonate L-Homocysteine L-Homocysteine Hexadecanoate (n-C16:0) Hexadecanoate (n-C16:0) hexadecanoate (n-C16:1) hexadecenoate (n-C16:1)	mitochondrion nucleus cytosol mitochondrion nucleus cytosol peroxisome cytosol extracellular peroxisome	C7H7O7 C7H7O7 CHO3 CHO3 CHO3 C4H9NO2S C4H9NO2S C16H31O2 C16H31O2	-3 -3 -1 -1 -1 0 0 -1 -1 -1 -1
hcit hcit hco3 hco3 hco3 hcys-L hcys-L hdca hdca hdca	2-Hydroxybutane-1,2,4-tricarboxylate 2-Hydroxybutane-1,2,4-tricarboxylate Bicarbonate Bicarbonate Bicarbonate L-Homocysteine L-Homocysteine Hexadecanoate (n-C16:0) Hexadecanoate (n-C16:0) hexadecanoate (n-C16:1) hexadecenoate (n-C16:1)	mitochondrion nucleus cytosol mitochondrion nucleus cytosol peroxisome cytosol extracellular peroxisome cytosol	C7H7O7 C7H7O7 CHO3 CHO3 CHO3 C4H9NO2S C4H9NO2S C16H31O2 C16H31O2 C16H31O2 C16H29O2 C16H29O2	-3 -3 -1 -1 -1 0 0 -1 -1 -1 -1 -1
hcit hcit hco3 hco3 hco3 hcys-L hcys-L hdca hdca hdca hdca hdcea	2-Hydroxybutane-1,2,4-tricarboxylate 2-Hydroxybutane-1,2,4-tricarboxylate Bicarbonate Bicarbonate Bicarbonate L-Homocysteine L-Homocysteine Hexadecanoate (n-C16:0) Hexadecanoate (n-C16:0) hexadecanoate (n-C16:1) hexadecenoate (n-C16:1)	mitochondrion nucleus cytosol mitochondrion nucleus cytosol peroxisome cytosol extracellular peroxisome cytosol extracellular	C7H7O7 C7H7O7 CHO3 CHO3 CHO3 C4H9NO2S C4H9NO2S C16H31O2 C16H31O2 C16H31O2 C16H29O2 C16H29O2	-3 -3 -1 -1 -1 0 0 -1 -1 -1 -1 -1
hcit hcit hco3 hco3 hco3 hcys-L hcys-L hdca hdca hdca hdca hdcea hdcea	2-Hydroxybutane-1,2,4-tricarboxylate 2-Hydroxybutane-1,2,4-tricarboxylate Bicarbonate Bicarbonate Bicarbonate L-Homocysteine L-Homocysteine Hexadecanoate (n-C16:0) Hexadecanoate (n-C16:0) hexadecanoate (n-C16:1) hexadecenoate (n-C16:1)	mitochondrion nucleus cytosol mitochondrion nucleus cytosol peroxisome cytosol extracellular peroxisome cytosol extracellular peroxisome cytosol extracellular	C7H7O7 C7H7O7 CHO3 CHO3 CHO3 C4H9NO2S C4H9NO2S C16H31O2 C16H31O2 C16H31O2 C16H29O2 C16H29O2	-3 -3 -1 -1 -1 0 0 0 -1 -1 -1 -1 -1 -1 -4
hcit hcit hco3 hco3 hco3 hcys-L hcys-L hdca hdca hdca hdcea hdcea hdcea hdcoa	2-Hydroxybutane-1,2,4-tricarboxylate 2-Hydroxybutane-1,2,4-tricarboxylate Bicarbonate Bicarbonate Bicarbonate L-Homocysteine L-Homocysteine Hexadecanoate (n-C16:0) Hexadecanoate (n-C16:0) hexadecanoate (n-C16:1) hexadecenoate (n-C16:1) hexadecenoate (n-C16:1)	mitochondrion nucleus cytosol mitochondrion nucleus cytosol peroxisome cytosol extracellular peroxisome cytosol extracellular peroxisome cytosol extracellular peroxisome cytosol	C7H7O7 C7H7O7 CHO3 CHO3 CHO3 CHO3 C4H9NO2S C4H9NO2S C16H31O2 C16H31O2 C16H31O2 C16H29O2 C16H29O2 C16H29O2 C37H60N7O17P3S	-3 -3 -1 -1 -1 -0 0 0 -1 -1 -1 -1 -1 -1 -4 -4
hcit hcit hco3 hco3 hco3 hcys-L hcys-L hdca hdca hdca hdcea hdcea hdcea hdcoa hdcoa	2-Hydroxybutane-1,2,4-tricarboxylate 2-Hydroxybutane-1,2,4-tricarboxylate Bicarbonate Bicarbonate Bicarbonate L-Homocysteine L-Homocysteine Hexadecanoate (n-C16:0) Hexadecanoate (n-C16:0) hexadecanoate (n-C16:1) hexadecenoate (n-C16:1) hexadecenoate (n-C16:1) hexadecenoate (n-C16:1) Hexadecenoate (n-C16:1)	mitochondrion nucleus cytosol mitochondrion nucleus cytosol peroxisome cytosol extracellular peroxisome cytosol extracellular peroxisome cytosol extracellular peroxisome cytosol extracellular peroxisome cytosol peroxisome	C7H7O7 C7H7O7 CHO3 CHO3 CHO3 CHO3 C4H9NO2S C4H9NO2S C16H31O2 C16H31O2 C16H31O2 C16H29O2 C16H29O2 C16H29O2 C37H60N7O17P3S C37H60N7O17P3S	-3 -3 -3 -1 -1 -1 -0 0 0 -1 -1 -1 -1 -1 -1 -4 -4 -4
hcit hcit hco3 hco3 hco3 hcys-L hcys-L hdca hdca hdca hdcea hdcea hdcea hdcoa hdcoa hddcoa	2-Hydroxybutane-1,2,4-tricarboxylate 2-Hydroxybutane-1,2,4-tricarboxylate Bicarbonate Bicarbonate Bicarbonate L-Homocysteine L-Homocysteine Hexadecanoate (n-C16:0) Hexadecanoate (n-C16:0) Hexadecanoate (n-C16:1) hexadecenoate (n-C16:1) hexadecenoate (n-C16:1) hexadecenoate (n-C16:1) Hexadecenoate (n-C16:1) Hexadecenoyl-CoA (n-C16:1CoA) Hexadecenoyl-CoA (n-C16:1CoA)	mitochondrion nucleus cytosol mitochondrion nucleus cytosol peroxisome cytosol extracellular peroxisome cytosol extracellular peroxisome cytosol extracellular peroxisome cytosol extracellular peroxisome cytosol peroxisome	C7H7O7 C7H7O7 CHO3 CHO3 CHO3 CHO3 C4H9NO2S C4H9NO2S C16H31O2 C16H31O2 C16H31O2 C16H29O2 C16H29O2 C16H29O2 C37H60N7O17P3S C37H60N7O17P3S	-3 -3 -3 -1 -1 -1 -0 0 0 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1
hcit hcit hco3 hco3 hco3 hcys-L hcys-L hdca hdca hdca hdcea hdcea hdcea hdcoa hdcoa hdcoa hdcoa hdd2coa hdeACP	2-Hydroxybutane-1,2,4-tricarboxylate 2-Hydroxybutane-1,2,4-tricarboxylate Bicarbonate Bicarbonate Bicarbonate L-Homocysteine L-Homocysteine Hexadecanoate (n-C16:0) Hexadecanoate (n-C16:0) Hexadecanoate (n-C16:1) hexadecenoate (n-C16:1) hexadecenoate (n-C16:1) hexadecenoate (n-C16:1) Hexadecenoate (n-C16:1) Hexadecenoate (n-C16:1) Hexadecenoyl-CoA (n-C16:1CoA) Hexadecenoyl-CoA (n-C16:1CoA) Hexadecenoyl-CoA (n-C16:1CoA)	mitochondrion nucleus cytosol mitochondrion nucleus cytosol peroxisome cytosol extracellular peroxisome cytosol extracellular peroxisome cytosol extracellular peroxisome cytosol extracellular peroxisome cytosol peroxisome cytosol	C7H7O7 C7H7O7 CHO3 CHO3 CHO3 CHO3 C4H9NO2S C4H9NO2S C16H31O2 C16H31O2 C16H31O2 C16H29O2 C16H29O2 C16H29O2 C37H60N7O17P3S C37H60N7O17P3S C27H49N2O8PRS	-3 -3 -3 -1 -1 -1 -0 0 0 -1 -1 -1 -1 -1 -1 -4 -4 -4
hcit hcit hco3 hco3 hco3 hcys-L hcys-L hdca hdca hdca hdcea hdcea hdcea hdcoa hdcACP	2-Hydroxybutane-1,2,4-tricarboxylate 2-Hydroxybutane-1,2,4-tricarboxylate Bicarbonate Bicarbonate Bicarbonate L-Homocysteine L-Homocysteine Hexadecanoate (n-C16:0) Hexadecanoate (n-C16:0) Hexadecanoate (n-C16:1) hexadecenoate (n-C16:1) hexadecenoate (n-C16:1) hexadecenoate (n-C16:1) Hexadecenoate (n-C16:1) Hexadecenoyl-CoA (n-C16:1CoA) Hexadecenoyl-CoA (n-C16:1CoA) Hexadecenoyl-CoA (n-C16:1CoA) Hexadecenoyl-ACP (n-C16:1ACP)	mitochondrion nucleus cytosol mitochondrion nucleus cytosol peroxisome cytosol extracellular peroxisome cytosol extracellular peroxisome cytosol extracellular peroxisome cytosol extracellular peroxisome cytosol peroxisome cytosol peroxisome cytosol mitochondrion	C7H7O7 C7H7O7 CHO3 CHO3 CHO3 CHO3 C4H9NO2S C4H9NO2S C16H31O2 C16H31O2 C16H31O2 C16H29O2 C16H29O2 C16H29O2 C37H60N7O17P3S C37H60N7O17P3S C27H49N2O8PRS C27H49N2O8PRS	-3 -3 -3 -1 -1 -1 -0 0 0 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1
hcit hcit hco3 hco3 hco3 hco3 hcys-L hcys-L hdca hdca hdca hdca hdcea hdcea hdcea hdcoa hdcoa hdcoa hdcoa hdcoa hdcoa hdcACP hdeACP hexc	2-Hydroxybutane-1,2,4-tricarboxylate 2-Hydroxybutane-1,2,4-tricarboxylate Bicarbonate Bicarbonate Bicarbonate L-Homocysteine L-Homocysteine Hexadecanoate (n-C16:0) Hexadecanoate (n-C16:0) Hexadecanoate (n-C16:1) hexadecanoate (n-C16:1) hexadecenoate (n-C16:1) hexadecenoate (n-C16:1) Hexadecenoate (n-C16:1) Hexadecenoyl-CoA (n-C16:1CoA) Hexadecenoyl-CoA (n-C16:1CoA) Hexadecenoyl-CoA (n-C16:1ACP) Hexadecenoyl-ACP (n-C16:1ACP) hexadecenoyl-ACP (n-C16:1ACP) hexacosanoate (n-C26:0)	mitochondrion nucleus cytosol mitochondrion nucleus cytosol peroxisome cytosol extracellular peroxisome cytosol extracellular peroxisome cytosol extracellular peroxisome cytosol peroxisome cytosol peroxisome cytosol peroxisome cytosol peroxisome cytosol peroxisome cytosol	C7H7O7 C7H7O7 CHO3 CHO3 CHO3 CHO3 C4H9NO2S C4H9NO2S C16H31O2 C16H31O2 C16H31O2 C16H29O2 C16H29O2 C16H29O2 C37H60N7O17P3S C37H60N7O17P3S C37H60N7O17P3S C27H49N2O8PRS C27H49N2O8PRS C26H51O2	-3 -3 -3 -1 -1 -1 -1 -0 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1
hcit hcit hcit hco3 hco3 hco3 hco3 hcys-L hdca hdca hdca hdcea hdcea hdcea hdcoa hdcoa hdcoa hdcoa hdcACP hdeACP hexc hexc hexccoa	2-Hydroxybutane-1,2,4-tricarboxylate 2-Hydroxybutane-1,2,4-tricarboxylate Bicarbonate Bicarbonate Bicarbonate L-Homocysteine L-Homocysteine Hexadecanoate (n-C16:0) Hexadecanoate (n-C16:0) Hexadecanoate (n-C16:1) hexadecanoate (n-C16:1) hexadecenoate (n-C16:1) hexadecenoate (n-C16:1) Hexadecenoate (n-C16:1) Hexadecenoate (n-C16:1) Hexadecenopl-CoA (n-C16:1CoA) Hexadecenoyl-CoA (n-C16:1CoA) Hexadecenoyl-CoA (n-C16:1ACP) Hexadecenoyl-ACP (n-C16:1ACP) Hexadecenoyl-ACP (n-C16:1ACP) hexacosanoate (n-C26:0) Hexacosanoate (n-C26:0)	mitochondrion nucleus cytosol mitochondrion nucleus cytosol peroxisome cytosol extracellular peroxisome cytosol extracellular peroxisome cytosol extracellular peroxisome cytosol peroxisome cytosol peroxisome cytosol peroxisome cytosol peroxisome cytosol mitochondrion cytosol peroxisome cytosol	C7H7O7 C7H7O7 CHO3 CHO3 CHO3 CHO3 C4H9NO2S C4H9NO2S C16H31O2 C16H31O2 C16H31O2 C16H29O2 C16H29O2 C16H29O2 C37H60N7O17P3S C37H60N7O17P3S C37H60N7O17P3S C27H49N2O8PRS C27H49N2O8PRS C26H51O2 C26H51O2 C26H51O2 C47H82N7O17P3S	-3 -3 -3 -1 -1 -1 -1 -0 -1 -1 -1 -1 -4 -4 -4 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1
hcit hcit hcit hco3 hco3 hco3 hco3 hcys-L hdca hdca hdca hdcea hdcea hdcea hdcoa hdcoa hdcoa hdcoa hdcACP hdeACP hexc hexc hexc hexccoa	2-Hydroxybutane-1,2,4-tricarboxylate 2-Hydroxybutane-1,2,4-tricarboxylate Bicarbonate Bicarbonate Bicarbonate L-Homocysteine L-Homocysteine Hexadecanoate (n-C16:0) Hexadecanoate (n-C16:0) Hexadecanoate (n-C16:1) hexadecenoate (n-C16:1) hexadecenoate (n-C16:1) Hexadecenoate (n-C16:1) Hexadecenoate (n-C16:1) Hexadecenoate (n-C16:1) Hexadecenopl-CoA (n-C16:1CoA) Hexadecenoyl-CoA (n-C16:1CoA) Hexadecenoyl-CoA (n-C16:1ACP) Hexadecenoyl-ACP (n-C16:1ACP) Hexadecenoyl-ACP (n-C16:1ACP) Hexadecenoyl-ACP (n-C16:0) Hexacosanoate (n-C26:0) Hexacosanoyl-CoA (n-C26:0CoA) Hexacosanoyl-CoA (n-C26:0CoA)	mitochondrion nucleus cytosol mitochondrion nucleus cytosol peroxisome cytosol extracellular peroxisome cytosol extracellular peroxisome cytosol extracellular peroxisome cytosol peroxisome cytosol peroxisome cytosol peroxisome cytosol mitochondrion cytosol peroxisome cytosol peroxisome cytosol peroxisome	C7H7O7 C7H7O7 CHO3 CHO3 CHO3 CHO3 C4H9NO2S C4H9NO2S C16H31O2 C16H31O2 C16H31O2 C16H29O2 C16H29O2 C16H29O2 C37H60N7O17P3S C37H60N7O17P3S C37H60N7O17P3S C27H49N2O8PRS C27H49N2O8PRS C26H51O2 C26H51O2 C47H82N7O17P3S C47H82N7O17P3S	-3 -3 -3 -1 -1 -1 -1 -0 -1 -1 -1 -1 -4 -4 -4 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1
hcit hcit hcit hco3 hco3 hco3 hco3 hcys-L hdca hdca hdca hdcea hdcea hdcea hdcoa hdcoa hdcoa hdcACP hdeACP hexc hexc hexccoa hgentis	2-Hydroxybutane-1,2,4-tricarboxylate 2-Hydroxybutane-1,2,4-tricarboxylate Bicarbonate Bicarbonate Bicarbonate L-Homocysteine L-Homocysteine Hexadecanoate (n-C16:0) Hexadecanoate (n-C16:0) Hexadecanoate (n-C16:1) hexadecenoate (n-C16:1) hexadecenoate (n-C16:1) Hexadecenoate (n-C16:1) Hexadecenoate (n-C16:1) Hexadecenoate (n-C16:1) Hexadecenopl-CoA (n-C16:1CoA) Hexadecenoyl-CoA (n-C16:1CoA) Hexadecenoyl-CoA (n-C16:1ACP) Hexadecenoyl-ACP (n-C16:1ACP) Hexadecenoyl-ACP (n-C16:1ACP) Hexadecenoyl-ACP (n-C16:0) Hexacosanoate (n-C26:0) Hexacosanoyl-CoA (n-C26:0CoA) Hexacosanoyl-CoA (n-C26:0CoA) Hexacosanoyl-CoA (n-C26:0CoA)	mitochondrion nucleus cytosol mitochondrion nucleus cytosol peroxisome cytosol extracellular peroxisome cytosol extracellular peroxisome cytosol extracellular peroxisome cytosol peroxisome cytosol peroxisome cytosol peroxisome cytosol mitochondrion cytosol peroxisome cytosol peroxisome cytosol peroxisome cytosol	C7H7O7 C7H7O7 CHO3 CHO3 CHO3 CHO3 C4H9NO2S C4H9NO2S C16H31O2 C16H31O2 C16H31O2 C16H29O2 C16H29O2 C16H29O2 C37H60N7O17P3S C37H60N7O17P3S C37H60N7O17P3S C27H49N2O8PRS C27H49N2O8PRS C27H49N2O8PRS C26H51O2 C26H51O2 C47H82N7O17P3S C47H82N7O17P3S C47H82N7O17P3S	-3 -3 -3 -1 -1 -1 -0 0 0 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1
hcit hcit hco3 hco3 hco3 hco3 hcys-L hcys-L hdca hdca hdca hdcea hdcea hdcea hdcoa hdcoa hdcoa hdcACP hdeACP hexc hexc hexccoa hgentis hicit	2-Hydroxybutane-1,2,4-tricarboxylate 2-Hydroxybutane-1,2,4-tricarboxylate Bicarbonate Bicarbonate Bicarbonate L-Homocysteine L-Homocysteine Hexadecanoate (n-C16:0) Hexadecanoate (n-C16:0) Hexadecanoate (n-C16:1) hexadecenoate (n-C16:1) hexadecenoate (n-C16:1) Hexadecenoate (n-C16:1) Hexadecenoate (n-C16:1) Hexadecenoate (n-C16:1) Hexadecenopl-CoA (n-C16:1CoA) Hexadecenoyl-CoA (n-C16:1CoA) Hexadecenoyl-CoA (n-C16:1ACP) Hexadecenoyl-ACP (n-C16:1ACP) Hexadecenoyl-ACP (n-C16:1ACP) Hexadecenoyl-ACP (n-C16:0CoA) Hexacosanoate (n-C26:0) Hexacosanoyl-CoA (n-C26:0CoA) Hexacosanoyl-CoA (n-C26:0CoA) Homogentisate Homoisocitrate	mitochondrion nucleus cytosol mitochondrion nucleus cytosol peroxisome cytosol extracellular peroxisome cytosol extracellular peroxisome cytosol extracellular peroxisome cytosol peroxisome cytosol peroxisome cytosol peroxisome cytosol mitochondrion cytosol peroxisome cytosol mitochondrion cytosol peroxisome cytosol peroxisome cytosol	C7H7O7 C7H7O7 CHO3 CHO3 CHO3 CHO3 CHO9 C4H9NO2S C4H9NO2S C16H31O2 C16H31O2 C16H31O2 C16H29O2 C16H29O2 C16H29O2 C37H60N7O17P3S C37H60N7O17P3S C37H60N7O17P3S C27H49N2O8PRS C27H49N2O8PRS C26H51O2 C26H51O2 C47H82N7O17P3S C47H82N7O17P3S C8H7O4 C7H7O7	-3 -3 -3 -1 -1 -1 -1 -0 0 0 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1
hcit hcit hco3 hco3 hco3 hco3 hcys-L hcys-L hdca hdca hdca hdcea hdcea hdcea hdcoa hdcoa hdcoa hdcACP hdeACP hexc hexc hexccoa hgentis hicit his-L	2-Hydroxybutane-1,2,4-tricarboxylate 2-Hydroxybutane-1,2,4-tricarboxylate Bicarbonate Bicarbonate Bicarbonate L-Homocysteine L-Homocysteine Hexadecanoate (n-C16:0) Hexadecanoate (n-C16:0) Hexadecanoate (n-C16:1) hexadecenoate (n-C16:1) hexadecenoate (n-C16:1) Hexadecenoate (n-C16:1) Hexadecenoate (n-C16:1) Hexadecenoate (n-C16:1) Hexadecenoyl-CoA (n-C16:1CoA) Hexadecenoyl-CoA (n-C16:1CoA) Hexadecenoyl-CoA (n-C16:1ACP) Hexadecenoyl-ACP (n-C16:1ACP) Hexadecenoyl-ACP (n-C16:1ACP) Hexadecenoyl-ACP (n-C16:0) Hexacosanoate (n-C26:0) Hexacosanoate (n-C26:0CoA) Hexacosanoyl-CoA (n-C26:0CoA) Homogentisate Homoisocitrate L-Histidine	mitochondrion nucleus cytosol mitochondrion nucleus cytosol peroxisome cytosol extracellular peroxisome cytosol extracellular peroxisome cytosol extracellular peroxisome cytosol peroxisome cytosol peroxisome cytosol peroxisome cytosol mitochondrion cytosol peroxisome cytosol peroxisome cytosol mitochondrion cytosol peroxisome cytosol peroxisome cytosol	C7H7O7 C7H7O7 CHO3 CHO3 CHO3 CHO3 C4H9NO2S C4H9NO2S C16H31O2 C16H31O2 C16H31O2 C16H29O2 C16H29O2 C16H29O2 C37H60N7O17P3S C37H60N7O17P3S C37H60N7O17P3S C27H49N2O8PRS C27H49N2O8PRS C26H51O2 C26H51O2 C47H82N7O17P3S C47H82N7O17P3S C47H82N7O17P3S C8H7O4 C7H7O7 C6H9N3O2	-3 -3 -3 -3 -1 -1 -1 -1 -0 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1
hcit hcit hco3 hco3 hco3 hco3 hcys-L hcys-L hdca hdca hdca hdcea hdcea hdcea hdcoa hdcoa hdcoa hdcACP hdeACP hexc hexc hexccoa hgentis hicit	2-Hydroxybutane-1,2,4-tricarboxylate 2-Hydroxybutane-1,2,4-tricarboxylate Bicarbonate Bicarbonate Bicarbonate L-Homocysteine L-Homocysteine Hexadecanoate (n-C16:0) Hexadecanoate (n-C16:0) Hexadecanoate (n-C16:1) hexadecenoate (n-C16:1) hexadecenoate (n-C16:1) Hexadecenoate (n-C16:1) Hexadecenoate (n-C16:1) Hexadecenoate (n-C16:1) Hexadecenopl-CoA (n-C16:1CoA) Hexadecenoyl-CoA (n-C16:1CoA) Hexadecenoyl-CoA (n-C16:1ACP) Hexadecenoyl-ACP (n-C16:1ACP) Hexadecenoyl-ACP (n-C16:1ACP) Hexadecenoyl-ACP (n-C16:0CoA) Hexacosanoate (n-C26:0) Hexacosanoyl-CoA (n-C26:0CoA) Hexacosanoyl-CoA (n-C26:0CoA) Homogentisate Homoisocitrate	mitochondrion nucleus cytosol mitochondrion nucleus cytosol peroxisome cytosol extracellular peroxisome cytosol extracellular peroxisome cytosol extracellular peroxisome cytosol peroxisome cytosol peroxisome cytosol peroxisome cytosol mitochondrion cytosol peroxisome cytosol mitochondrion cytosol peroxisome cytosol peroxisome cytosol	C7H7O7 C7H7O7 CHO3 CHO3 CHO3 CHO3 CHO9 C4H9NO2S C4H9NO2S C16H31O2 C16H31O2 C16H31O2 C16H29O2 C16H29O2 C16H29O2 C37H60N7O17P3S C37H60N7O17P3S C37H60N7O17P3S C27H49N2O8PRS C27H49N2O8PRS C26H51O2 C26H51O2 C47H82N7O17P3S C47H82N7O17P3S C8H7O4 C7H7O7	-3 -3 -3 -1 -1 -1 -0 0 0 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1

histd	L-Histidinol	cytosol	C6H12N3O	1
histrna	L-Histidyl-tRNA(His)	cytosol	C6H8N3OR	1
histrna	L-Histidyl-tRNA(His)	mitochondrion	C6H8N3OR	1
hmbil	Hydroxymethylbilane	cytosol	C40H38N4O17	-8
hmgcoa	Hydroxymethylglutaryl-CoA	cytosol	C27H39N7O20P3S	-5
hmgcoa	Hydroxymethylglutaryl-CoA	mitochondrion	C27H39N7O20P3S	-5
hom-L	L-Homoserine	cytosol	C4H9NO3	-5 0
hpglu	Tetrahydropteroyltri-L-glutamate	cytosol	C24H34N8O12	0
hxan	Hypoxanthine	cytosol	C5H4N4O	0
hxan	Hypoxanthine	extracellular	C5H4N4O	0
hxc2coa	trans-Hexacos-2-enoyl-CoA	peroxisome	C47H80N7O17P3S	-4
hxdcal	Hexadecanal	cytosol	C16H32O	0
iad	Indole-3-acetamide	cytosol	C10H10N2O	0
iasp	Iminoaspartate	cytosol	C4H4NO4	-1
icit	Isocitrate	cytosol	C6H5O7	
icit	Isocitrate	mitochondrion	C6H5O7	-3 -3 -3
icit	Isocitrate	peroxisome	C6H5O7	-3 -3
id3acald	Indole-3-acetaldehyde	cytosol	C10H9NO	0
id3acald	Indole-3-acetaldehyde	mitochondrion	C10H9NO	0
idp	IDP	cytosol	C10H9NO C10H11N4O11P2	0
	IDP			-3 -3
idp		mitochondrion	C10H11N4O11P2	-3
ile-L	L-Isoleucine	cytosol	C6H13NO2	0
ile-L	L-Isoleucine	extracellular	C6H13NO2	0
ile-L	L-Isoleucine	mitochondrion	C6H13NO2	0
iletrna	L-IsoleucyI-tRNA(IIe)	cytosol	C6H12NOR	1
iletrna	L-Isoleucyl-tRNA(IIe)	mitochondrion	C6H12NOR	1
imacp	3-(Imidazol-4-yl)-2-oxopropyl phosphate	cytosol	C6H7N2O5P	-2 -2
imp	IMP	cytosol	C10H11N4O8P	-2
ind3ac	Indole-3-acetate	cytosol	C10H8NO2	-1
ind3ac	Indole-3-acetate	mitochondrion	C10H8NO2	-1
ind3acnl	Indole-3-acetonitrile	cytosol	C10H8N2	0
indpyr	Indolepyruvate	cytosol	C11H8NO3	-1
inost	myo-Inositol	cytosol	C6H12O6	0
inost	myo-Inositol	extracellular	C6H12O6	0
	,			
ins	Inosine	cytosol	C10H12N4O5	0
ins ins	Inosine Inosine		C10H12N4O5	
ins	Inosine Inosine Inositol phosphorylceramide, ceramide-1 (24C),	cytosol		0
	Inosine Inosine Inositol phosphorylceramide, ceramide-1 (24C), yeast-specific	cytosol	C10H12N4O5 C4800H9500N100O1100 P100	0
ins	Inosine Inosine Inositol phosphorylceramide, ceramide-1 (24C), yeast-specific Inositol phosphorylceramide, ceramide-1 (26C),	cytosol extracellular	C10H12N4O5 C4800H9500N100O1100 P100 C5000H9900N100O1100	0
ins	Inosine Inosine Inositol phosphorylceramide, ceramide-1 (24C), yeast-specific Inositol phosphorylceramide, ceramide-1 (26C), yeast-specific	cytosol extracellular	C10H12N4O5 C4800H9500N100O1100 P100	0
ins * ipc124_SC	Inosine Inosine Inositol phosphorylceramide, ceramide-1 (24C), yeast-specific Inositol phosphorylceramide, ceramide-1 (26C), yeast-specific Inositol phosphorylceramide, ceramide-2 (24C),	cytosol extracellular cytosol	C10H12N4O5 C4800H9500N100O1100 P100 C5000H9900N100O1100	-100
ins * ipc124_SC	Inosine Inosine Inositol phosphorylceramide, ceramide-1 (24C), yeast-specific Inositol phosphorylceramide, ceramide-1 (26C), yeast-specific	cytosol extracellular cytosol	C10H12N4O5 C4800H9500N100O1100 P100 C5000H9900N100O1100 P100	-100
ins * ipc124_SC * ipc126_SC	Inosine Inosine Inositol phosphorylceramide, ceramide-1 (24C), yeast-specific Inositol phosphorylceramide, ceramide-1 (26C), yeast-specific Inositol phosphorylceramide, ceramide-2 (24C),	cytosol extracellular cytosol cytosol	C10H12N4O5 C4800H9500N100O1100 P100 C5000H9900N100O1100 P100 C4800H9500N100O1200	-100
ins * ipc124_SC * ipc126_SC	Inosine Inosine Inositol phosphorylceramide, ceramide-1 (24C), yeast-specific Inositol phosphorylceramide, ceramide-1 (26C), yeast-specific Inositol phosphorylceramide, ceramide-2 (24C), yeast-specific	cytosol extracellular cytosol cytosol	C10H12N4O5 C4800H9500N100O1100 P100 C5000H9900N100O1100 P100 C4800H9500N100O1200 P100	-100 -100 -100
ins * ipc124_SC * ipc126_SC * ipc224_SC	Inosine Inosine Inositol phosphorylceramide, ceramide-1 (24C), yeast-specific Inositol phosphorylceramide, ceramide-1 (26C), yeast-specific Inositol phosphorylceramide, ceramide-2 (24C), yeast-specific Inositol phosphorylceramide, ceramide-2 (26C),	cytosol extracellular cytosol cytosol	C10H12N4O5 C4800H9500N100O1100 P100 C5000H9900N100O1100 P100 C4800H9500N100O1200 P100 C5000H9900N100O1200	-100 -100 -100
ins * ipc124_SC * ipc126_SC * ipc224_SC	Inosine Inosine Inositol phosphorylceramide, ceramide-1 (24C), yeast-specific Inositol phosphorylceramide, ceramide-1 (26C), yeast-specific Inositol phosphorylceramide, ceramide-2 (24C), yeast-specific Inositol phosphorylceramide, ceramide-2 (26C), yeast-specific	cytosol extracellular cytosol cytosol	C10H12N4O5 C4800H9500N100O1100 P100 C5000H9900N100O1100 P100 C4800H9500N100O1200 P100 C5000H9900N100O1200 P100	-100 -100 -100 -100
ins * ipc124_SC * ipc126_SC * ipc224_SC * ipc226_SC	Inosine Inosine Inositol phosphorylceramide, ceramide-1 (24C), yeast-specific Inositol phosphorylceramide, ceramide-1 (26C), yeast-specific Inositol phosphorylceramide, ceramide-2 (24C), yeast-specific Inositol phosphorylceramide, ceramide-2 (26C), yeast-specific Inositol phosphorylceramide, ceramide-3 (24C),	cytosol extracellular cytosol cytosol cytosol	C10H12N4O5 C4800H9500N100O1100 P100 C5000H9900N100O1100 P100 C4800H9500N100O1200 P100 C5000H9900N100O1200 P100 C4800H9500N100O1300	-100 -100 -100 -100
ins * ipc124_SC * ipc126_SC * ipc224_SC * ipc226_SC	Inosine Inosine Inositol phosphorylceramide, ceramide-1 (24C), yeast-specific Inositol phosphorylceramide, ceramide-1 (26C), yeast-specific Inositol phosphorylceramide, ceramide-2 (24C), yeast-specific Inositol phosphorylceramide, ceramide-2 (26C), yeast-specific Inositol phosphorylceramide, ceramide-2 (26C), yeast-specific Inositol phosphorylceramide, ceramide-3 (24C), yeast-specific	cytosol extracellular cytosol cytosol cytosol	C10H12N4O5 C4800H9500N100O1100 P100 C5000H9900N100O1100 P100 C4800H9500N100O1200 P100 C5000H9900N100O1200 P100 C4800H9500N100O1300 P100 C4800H9500N100O1300 P100	-100 -100 -100 -100 -100
ins * ipc124_SC * ipc126_SC * ipc224_SC * ipc226_SC * ipc324_SC	Inosine Inosine Inositol phosphorylceramide, ceramide-1 (24C), yeast-specific Inositol phosphorylceramide, ceramide-1 (26C), yeast-specific Inositol phosphorylceramide, ceramide-2 (24C), yeast-specific Inositol phosphorylceramide, ceramide-2 (26C), yeast-specific Inositol phosphorylceramide, ceramide-3 (24C), yeast-specific Inositol phosphorylceramide, ceramide-3 (24C), yeast-specific Inositol phosphorylceramide, ceramide-3 (26C),	cytosol extracellular cytosol cytosol cytosol cytosol cytosol	C10H12N4O5 C4800H9500N100O1100 P100 C5000H9900N100O1100 P100 C4800H9500N100O1200 P100 C5000H9900N100O1200 P100 C4800H9500N100O1300 P100 C4800H9500N100O1300 P100 C5000H9900N100O1300	-100 -100 -100 -100 -100 -100 -100 -3
ins * ipc124_SC * ipc126_SC * ipc224_SC * ipc226_SC * ipc324_SC * ipc326_SC	Inosine Inosine Inositol phosphorylceramide, ceramide-1 (24C), yeast-specific Inositol phosphorylceramide, ceramide-1 (26C), yeast-specific Inositol phosphorylceramide, ceramide-2 (24C), yeast-specific Inositol phosphorylceramide, ceramide-2 (26C), yeast-specific Inositol phosphorylceramide, ceramide-3 (24C), yeast-specific Inositol phosphorylceramide, ceramide-3 (24C), yeast-specific Inositol phosphorylceramide, ceramide-3 (26C), yeast-specific Isopentenyl diphosphate	cytosol extracellular cytosol cytosol cytosol cytosol cytosol	C10H12N4O5 C4800H9500N100O1100 P100 C5000H9900N100O1100 P100 C4800H9500N100O1200 P100 C5000H9900N100O1200 P100 C4800H9500N100O1300 P100 C5000H9900N100O1300 P100 C5000H9900N100O1300 P100	-100 -100 -100 -100 -100 -100 -100 -3
ins * ipc124_SC * ipc126_SC * ipc224_SC * ipc226_SC * ipc324_SC * ipc326_SC ipdp	Inosine Inosine Inositol phosphorylceramide, ceramide-1 (24C), yeast-specific Inositol phosphorylceramide, ceramide-1 (26C), yeast-specific Inositol phosphorylceramide, ceramide-2 (24C), yeast-specific Inositol phosphorylceramide, ceramide-2 (26C), yeast-specific Inositol phosphorylceramide, ceramide-3 (24C), yeast-specific Inositol phosphorylceramide, ceramide-3 (24C), yeast-specific Inositol phosphorylceramide, ceramide-3 (26C), yeast-specific	cytosol extracellular cytosol cytosol cytosol cytosol cytosol cytosol cytosol	C10H12N4O5 C4800H9500N100O1100 P100 C5000H9900N100O1100 P100 C4800H9500N100O1200 P100 C5000H9900N100O1200 P100 C4800H9500N100O1300 P100 C5000H9900N100O1300 P100 C5000H9900N100O1300 P100 C5H9O7P2	-100 -100 -100 -100 -100 -100 -100 -3
ins * ipc124_SC * ipc126_SC * ipc224_SC * ipc226_SC * ipc324_SC * ipc326_SC ipdp itaccoa itacon	Inosine Inosine Inositol phosphorylceramide, ceramide-1 (24C), yeast-specific Inositol phosphorylceramide, ceramide-1 (26C), yeast-specific Inositol phosphorylceramide, ceramide-2 (24C), yeast-specific Inositol phosphorylceramide, ceramide-2 (26C), yeast-specific Inositol phosphorylceramide, ceramide-2 (26C), yeast-specific Inositol phosphorylceramide, ceramide-3 (24C), yeast-specific Inositol phosphorylceramide, ceramide-3 (26C), yeast-specific Isopentenyl diphosphate Itaconyl-CoA	cytosol extracellular cytosol cytosol cytosol cytosol cytosol cytosol cytosol cytosol mitochondrion mitochondrion	C10H12N4O5 C4800H9500N100O1100 P100 C5000H9900N100O1100 P100 C4800H9500N100O1200 P100 C5000H9900N100O1200 P100 C4800H9500N100O1300 P100 C5000H9900N100O1300 P100 C5000H9900N100O1300 P100 C5H9O7P2 C26H35N7O19P3S	-100 -100 -100 -100 -100 -100 -100 -3
ins * ipc124_SC * ipc126_SC * ipc224_SC * ipc226_SC * ipc324_SC * ipc326_SC ipdp itaccoa itacon itp	Inosine Inosine Inositol phosphorylceramide, ceramide-1 (24C), yeast-specific Inositol phosphorylceramide, ceramide-1 (26C), yeast-specific Inositol phosphorylceramide, ceramide-2 (24C), yeast-specific Inositol phosphorylceramide, ceramide-2 (26C), yeast-specific Inositol phosphorylceramide, ceramide-2 (26C), yeast-specific Inositol phosphorylceramide, ceramide-3 (24C), yeast-specific Inositol phosphorylceramide, ceramide-3 (26C), yeast-specific Isopentenyl diphosphate Itaconyl-CoA Itaconate	cytosol extracellular cytosol cytosol cytosol cytosol cytosol cytosol cytosol mitochondrion mitochondrion cytosol	C10H12N4O5 C4800H9500N100O1100 P100 C5000H9900N100O1100 P100 C4800H9500N100O1200 P100 C5000H9900N100O1200 P100 C4800H9500N100O1300 P100 C5000H9900N100O1300 P100 C5H9O7P2 C26H35N7O19P3S C5H4O4 C10H11N4O14P3	-100 -100 -100 -100 -100 -100 -3 -5 -2 -4
ins * ipc124_SC * ipc126_SC * ipc224_SC * ipc226_SC * ipc324_SC * ipc326_SC ipdp itaccoa itacon	Inosine Inosine Inositol phosphorylceramide, ceramide-1 (24C), yeast-specific Inositol phosphorylceramide, ceramide-1 (26C), yeast-specific Inositol phosphorylceramide, ceramide-2 (24C), yeast-specific Inositol phosphorylceramide, ceramide-2 (26C), yeast-specific Inositol phosphorylceramide, ceramide-3 (24C), yeast-specific Inositol phosphorylceramide, ceramide-3 (24C), yeast-specific Inositol phosphorylceramide, ceramide-3 (26C), yeast-specific Isopentenyl diphosphate Itaconyl-CoA Itaconate ITP ITP	cytosol extracellular cytosol cytosol cytosol cytosol cytosol cytosol cytosol mitochondrion mitochondrion cytosol mitochondrion	C10H12N4O5 C4800H9500N100O1100 P100 C5000H9900N100O1100 P100 C4800H9500N100O1200 P100 C5000H9900N100O1200 P100 C4800H9500N100O1300 P100 C5000H9900N100O1300 P100 C5000H9900N100O1300 P100 C5H9O7P2 C26H35N7O19P3S C5H4O4	-100 -100 -100 -100 -100 -100 -100 -3 -5 -2 -4 -4
ins * ipc124_SC * ipc126_SC * ipc224_SC * ipc226_SC * ipc324_SC * ipc326_SC ipdp itaccoa itacon itp itp	Inosine Inosine Inositol phosphorylceramide, ceramide-1 (24C), yeast-specific Inositol phosphorylceramide, ceramide-1 (26C), yeast-specific Inositol phosphorylceramide, ceramide-2 (24C), yeast-specific Inositol phosphorylceramide, ceramide-2 (26C), yeast-specific Inositol phosphorylceramide, ceramide-3 (24C), yeast-specific Inositol phosphorylceramide, ceramide-3 (24C), yeast-specific Inositol phosphorylceramide, ceramide-3 (26C), yeast-specific Isopentenyl diphosphate Itaconyl-CoA Itaconate ITP ITP K+	cytosol extracellular cytosol cytosol cytosol cytosol cytosol cytosol cytosol mitochondrion mitochondrion cytosol mitochondrion cytosol mitochondrion cytosol	C10H12N4O5 C4800H9500N100O1100 P100 C5000H9900N100O1100 P100 C4800H9500N100O1200 P100 C5000H9900N100O1200 P100 C4800H9500N100O1300 P100 C5000H9900N100O1300 P100 C5000H9900N100O1300 P100 C5H9O7P2 C26H35N7O19P3S C5H4O4 C10H11N4O14P3 K	-100
ins * ipc124_SC * ipc126_SC * ipc224_SC * ipc226_SC * ipc324_SC * ipc326_SC ipdp itaccoa itacon itp itp k k	Inosine Inosine Inositol phosphorylceramide, ceramide-1 (24C), yeast-specific Inositol phosphorylceramide, ceramide-1 (26C), yeast-specific Inositol phosphorylceramide, ceramide-2 (24C), yeast-specific Inositol phosphorylceramide, ceramide-2 (26C), yeast-specific Inositol phosphorylceramide, ceramide-3 (24C), yeast-specific Inositol phosphorylceramide, ceramide-3 (24C), yeast-specific Inositol phosphorylceramide, ceramide-3 (26C), yeast-specific Isopentenyl diphosphate Itaconyl-CoA Itaconate ITP ITP K+ K+	cytosol extracellular cytosol cytosol cytosol cytosol cytosol cytosol cytosol mitochondrion mitochondrion cytosol mitochondrion cytosol extracellular	C10H12N4O5 C4800H9500N100O1100 P100 C5000H9900N100O1100 P100 C4800H9500N100O1200 P100 C5000H9900N100O1200 P100 C4800H9500N100O1300 P100 C5000H9900N100O1300 P100 C5H9O7P2 C26H35N7O19P3S C5H4O4 C10H11N4O14P3 K	-100 -100 -100 -100 -100 -100 -100 -100
ins * ipc124_SC * ipc126_SC * ipc224_SC * ipc226_SC * ipc324_SC * ipc326_SC ipdp itaccoa itacon itp itp k k lac-D	Inosine Inosine Inositol phosphorylceramide, ceramide-1 (24C), yeast-specific Inositol phosphorylceramide, ceramide-1 (26C), yeast-specific Inositol phosphorylceramide, ceramide-2 (24C), yeast-specific Inositol phosphorylceramide, ceramide-2 (26C), yeast-specific Inositol phosphorylceramide, ceramide-3 (24C), yeast-specific Inositol phosphorylceramide, ceramide-3 (26C), yeast-specific Inositol phosphorylceramide, ceramide-3 (26C), yeast-specific Isopentenyl diphosphate Itaconyl-CoA Itaconate ITP ITP K+ K+ C+ D-Lactate	cytosol extracellular cytosol cytosol cytosol cytosol cytosol cytosol cytosol mitochondrion mitochondrion cytosol mitochondrion cytosol extracellular cytosol	C10H12N4O5 C4800H9500N100O1100 P100 C5000H9900N100O1100 P100 C4800H9500N100O1200 P100 C5000H9900N100O1200 P100 C4800H9500N100O1300 P100 C5000H9900N100O1300 P100 C5H9O7P2 C26H35N7O19P3S C5H4O4 C10H11N4O14P3 K K C3H5O3	-100 -100 -100 -100 -100 -100 -100 -101 -
ins * ipc124_SC * ipc126_SC * ipc224_SC * ipc226_SC * ipc324_SC * ipc326_SC ipdp itaccoa itacon itp itp k k lac-D lac-D	Inosine Inosine Inositol phosphorylceramide, ceramide-1 (24C), yeast-specific Inositol phosphorylceramide, ceramide-1 (26C), yeast-specific Inositol phosphorylceramide, ceramide-2 (24C), yeast-specific Inositol phosphorylceramide, ceramide-2 (26C), yeast-specific Inositol phosphorylceramide, ceramide-3 (24C), yeast-specific Inositol phosphorylceramide, ceramide-3 (26C), yeast-specific Inositol phosphorylceramide, ceramide-3 (26C), yeast-specific Isopentenyl diphosphate Itaconyl-CoA Itaconate ITP ITP K+ K+ D-Lactate D-Lactate D-Lactate	cytosol extracellular cytosol cytosol cytosol cytosol cytosol cytosol cytosol cytosol mitochondrion mitochondrion cytosol mitochondrion cytosol extracellular cytosol mitochondrion	C10H12N4O5 C4800H9500N100O1100 P100 C5000H9900N100O1100 P100 C4800H9500N100O1200 P100 C5000H9900N100O1200 P100 C4800H9500N100O1300 P100 C5000H9900N100O1300 P100 C5H9O7P2 C26H35N7O19P3S C5H4O4 C10H11N4O14P3 K K C3H5O3 C3H5O3	-100 -100 -100 -100 -100 -100 -100 -101 -
ins * ipc124_SC * ipc126_SC * ipc224_SC * ipc226_SC * ipc324_SC * ipc326_SC ipdp itaccoa itacon itp itp k k lac-D lac-D lac-L	Inosine Inosine Inositol phosphorylceramide, ceramide-1 (24C), yeast-specific Inositol phosphorylceramide, ceramide-1 (26C), yeast-specific Inositol phosphorylceramide, ceramide-2 (24C), yeast-specific Inositol phosphorylceramide, ceramide-2 (26C), yeast-specific Inositol phosphorylceramide, ceramide-3 (24C), yeast-specific Inositol phosphorylceramide, ceramide-3 (26C), yeast-specific Inositol phosphorylceramide, ceramide-3 (26C), yeast-specific Isopentenyl diphosphate Itaconyl-CoA Itaconate ITP ITP K+ K+ D-Lactate D-Lactate L-Lactate	cytosol extracellular cytosol cytosol cytosol cytosol cytosol cytosol cytosol cytosol mitochondrion mitochondrion cytosol mitochondrion cytosol extracellular cytosol mitochondrion cytosol extracellular cytosol mitochondrion cytosol	C10H12N4O5 C4800H9500N100O1100 P100 C5000H9900N100O1100 P100 C4800H9500N100O1200 P100 C5000H9900N100O1200 P100 C4800H9500N100O1300 P100 C5000H9900N100O1300 P100 C5H9O7P2 C26H35N7O19P3S C5H4O4 C10H11N4O14P3 K K C3H5O3 C3H5O3 C3H5O3	-100 -100 -100 -100 -100 -100 -100 -101 -
ins * ipc124_SC * ipc126_SC * ipc224_SC * ipc226_SC * ipc324_SC * ipc326_SC ipdp itaccoa itacon itp itp k k lac-D lac-D lac-L lac-L	Inosine Inosine Inositol phosphorylceramide, ceramide-1 (24C), yeast-specific Inositol phosphorylceramide, ceramide-1 (26C), yeast-specific Inositol phosphorylceramide, ceramide-2 (24C), yeast-specific Inositol phosphorylceramide, ceramide-2 (26C), yeast-specific Inositol phosphorylceramide, ceramide-3 (24C), yeast-specific Inositol phosphorylceramide, ceramide-3 (26C), yeast-specific Inositol phosphorylceramide, ceramide-3 (26C), yeast-specific Isopentenyl diphosphate Itaconyl-CoA Itaconate ITP ITP K+ K+ C-Lactate D-Lactate L-Lactate L-Lactate	cytosol extracellular cytosol cytosol cytosol cytosol cytosol cytosol cytosol cytosol mitochondrion mitochondrion cytosol mitochondrion cytosol extracellular cytosol mitochondrion cytosol extracellular cytosol extracellular	C10H12N4O5 C4800H9500N100O1100 P100 C5000H9900N100O1100 P100 C4800H9500N100O1200 P100 C5000H9900N100O1200 P100 C4800H9500N100O1300 P100 C5000H9900N100O1300 P100 C5H9O7P2 C26H35N7O19P3S C5H4O4 C10H11N4O14P3 K K C3H5O3 C3H5O3 C3H5O3 C3H5O3	-100 -100 -100 -100 -100 -100 -100 -101
ins * ipc124_SC * ipc126_SC * ipc224_SC * ipc226_SC * ipc324_SC * ipc326_SC ipdp itaccoa itacon itp itp k k lac-D lac-D lac-L lac-L lac-L	Inosine Inosine Inositol phosphorylceramide, ceramide-1 (24C), yeast-specific Inositol phosphorylceramide, ceramide-1 (26C), yeast-specific Inositol phosphorylceramide, ceramide-2 (24C), yeast-specific Inositol phosphorylceramide, ceramide-2 (26C), yeast-specific Inositol phosphorylceramide, ceramide-3 (24C), yeast-specific Inositol phosphorylceramide, ceramide-3 (26C), yeast-specific Inositol phosphorylceramide, ceramide-3 (26C), yeast-specific Isopentenyl diphosphate Itaconyl-CoA Itaconate ITP ITP K+ K+ D-Lactate D-Lactate L-Lactate L-Lactate L-Lactate L-Lactate L-Lactate	cytosol extracellular cytosol cytosol cytosol cytosol cytosol cytosol cytosol cytosol mitochondrion mitochondrion cytosol extracellular cytosol mitochondrion cytosol extracellular cytosol extracellular mitochondrion	C10H12N4O5 C4800H9500N100O1100 P100 C5000H9900N100O1100 P100 C4800H9500N100O1200 P100 C5000H9900N100O1200 P100 C4800H9500N100O1300 P100 C5000H9900N100O1300 P100 C5H9O7P2 C26H35N7O19P3S C5H4O4 C10H11N4O14P3 K K C3H5O3 C3H5O3 C3H5O3 C3H5O3 C3H5O3	-100 -100 -100 -100 -100 -100 -100 -100
ins * ipc124_SC * ipc126_SC * ipc224_SC * ipc226_SC * ipc324_SC * ipc326_SC ipdp itaccoa itacon itp itp k k lac-D lac-D lac-L lac-L lac-L lald-L	Inosine Inosine Inositol phosphorylceramide, ceramide-1 (24C), yeast-specific Inositol phosphorylceramide, ceramide-1 (26C), yeast-specific Inositol phosphorylceramide, ceramide-2 (24C), yeast-specific Inositol phosphorylceramide, ceramide-2 (26C), yeast-specific Inositol phosphorylceramide, ceramide-3 (24C), yeast-specific Inositol phosphorylceramide, ceramide-3 (26C), yeast-specific Inositol phosphorylceramide, ceramide-3 (26C), yeast-specific Isopentenyl diphosphate Itaconyl-CoA Itaconate ITP ITP K+ K+ C-Lactate L-Lactate	cytosol extracellular cytosol cytosol cytosol cytosol cytosol cytosol cytosol cytosol mitochondrion mitochondrion cytosol extracellular cytosol mitochondrion cytosol extracellular cytosol extracellular mitochondrion mitochondrion cytosol mitochondrion cytosol mitochondrion cytosol mitochondrion	C10H12N4O5 C4800H9500N100O1100 P100 C5000H9900N100O1100 P100 C4800H9500N100O1200 P100 C5000H9900N100O1200 P100 C4800H9500N100O1300 P100 C5000H9900N100O1300 P100 C5H9O7P2 C26H35N7O19P3S C5H4O4 C10H11N4O14P3 K K C3H5O3 C3H5O3 C3H5O3 C3H5O3 C3H5O3 C3H5O3 C3H5O3 C3H6O2	-100 -100 -100 -100 -100 -100 -100 -100
ins * ipc124_SC * ipc126_SC * ipc224_SC * ipc226_SC * ipc324_SC * ipc326_SC ipdp itaccoa itacon itp itp k k lac-D lac-D lac-L lac-L lald-L lanost	Inosine Inosine Inositol phosphorylceramide, ceramide-1 (24C), yeast-specific Inositol phosphorylceramide, ceramide-1 (26C), yeast-specific Inositol phosphorylceramide, ceramide-2 (24C), yeast-specific Inositol phosphorylceramide, ceramide-2 (26C), yeast-specific Inositol phosphorylceramide, ceramide-3 (24C), yeast-specific Inositol phosphorylceramide, ceramide-3 (26C), yeast-specific Inositol phosphorylceramide, ceramide-3 (26C), yeast-specific Isopentenyl diphosphate Itaconyl-CoA Itaconate ITP ITP K+ K+ C-Lactate L-Lactate	cytosol extracellular cytosol cytosol cytosol cytosol cytosol cytosol cytosol cytosol mitochondrion mitochondrion cytosol extracellular cytosol mitochondrion cytosol extracellular cytosol extracellular mitochondrion cytosol extracellular cytosol extracellular cytosol extracellular mitochondrion cytosol extracellular mitochondrion cytosol	C10H12N4O5 C4800H9500N100O1100 P100 C5000H9900N100O1100 P100 C4800H9500N100O1200 P100 C5000H9900N100O1200 P100 C4800H9500N100O1300 P100 C5000H9900N100O1300 P100 C5H9O7P2 C26H35N7O19P3S C5H4O4 C10H11N4O14P3 K K C3H5O3 C3H5OO	-100 -100 -100 -100 -100 -100 -100 -100
ins * ipc124_SC * ipc126_SC * ipc224_SC * ipc226_SC * ipc324_SC * ipc326_SC ipdp itaccoa itacon itp itp k k lac-D lac-D lac-L lac-L lac-L lanost leu-L	Inosine Inositol phosphorylceramide, ceramide-1 (24C), yeast-specific Inositol phosphorylceramide, ceramide-1 (26C), yeast-specific Inositol phosphorylceramide, ceramide-2 (24C), yeast-specific Inositol phosphorylceramide, ceramide-2 (26C), yeast-specific Inositol phosphorylceramide, ceramide-3 (24C), yeast-specific Inositol phosphorylceramide, ceramide-3 (26C), yeast-specific Inositol phosphorylceramide, ceramide-3 (26C), yeast-specific Isopentenyl diphosphate Itaconyl-CoA Itaconate ITP ITP K+ K+ D-Lactate L-Lactate	cytosol extracellular cytosol cytosol cytosol cytosol cytosol cytosol cytosol cytosol mitochondrion mitochondrion cytosol extracellular cytosol mitochondrion cytosol extracellular cytosol extracellular cytosol extracellular mitochondrion cytosol extracellular cytosol extracellular mitochondrion cytosol extracellular mitochondrion cytosol cytosol cytosol	C10H12N4O5 C4800H9500N100O1100 P100 C5000H9900N100O1100 P100 C4800H9500N100O1200 P100 C5000H9900N100O1200 P100 C4800H9500N100O1300 P100 C5000H9900N100O1300 P100 C5900H9900N100O1300 P100 C5H9O7P2 C26H35N7O19P3S C5H4O4 C10H11N4O14P3 K K C3H5O3 C3H5O3 C3H5O3 C3H5O3 C3H5O3 C3H5O3 C3H5O3 C3H5O3 C3H5O3 C3H5OO C6H13NO2	-100 -100 -100 -100 -100 -100 -100 -100
ins * ipc124_SC * ipc126_SC * ipc224_SC * ipc226_SC * ipc324_SC * ipc326_SC ipdp itaccoa itacon itp itp k k lac-D lac-D lac-L lac-L lac-L lanost leu-L leu-L	Inosine Inosine Inositol phosphorylceramide, ceramide-1 (24C), yeast-specific Inositol phosphorylceramide, ceramide-1 (26C), yeast-specific Inositol phosphorylceramide, ceramide-2 (24C), yeast-specific Inositol phosphorylceramide, ceramide-2 (26C), yeast-specific Inositol phosphorylceramide, ceramide-3 (24C), yeast-specific Inositol phosphorylceramide, ceramide-3 (26C), yeast-specific Inositol phosphorylceramide, ceramide-3 (26C), yeast-specific Isopentenyl diphosphate Itaconyl-CoA Itaconate ITP ITP K+ K+ C-Lactate L-Lactate	cytosol extracellular cytosol cytosol cytosol cytosol cytosol cytosol cytosol cytosol mitochondrion mitochondrion cytosol extracellular cytosol mitochondrion cytosol extracellular cytosol extracellular mitochondrion cytosol cytosol extracellular	C10H12N4O5 C4800H9500N100O1100 P100 C5000H9900N100O1100 P100 C4800H9500N100O1200 P100 C5000H9900N100O1200 P100 C4800H9500N100O1300 P100 C5000H9900N100O1300 P100 C5H9O7P2 C26H35N7O19P3S C5H4O4 C10H11N4O14P3 K K C3H5O3	-100 -100 -100 -100 -100 -100 -100 -100
ins * ipc124_SC * ipc126_SC * ipc224_SC * ipc226_SC * ipc324_SC * ipc326_SC ipdp itaccoa itacon itp itp k k lac-D lac-D lac-L lac-L lac-L lanost leu-L leu-L	Inosine Inosine Inositol phosphorylceramide, ceramide-1 (24C), yeast-specific Inositol phosphorylceramide, ceramide-1 (26C), yeast-specific Inositol phosphorylceramide, ceramide-2 (24C), yeast-specific Inositol phosphorylceramide, ceramide-2 (26C), yeast-specific Inositol phosphorylceramide, ceramide-3 (24C), yeast-specific Inositol phosphorylceramide, ceramide-3 (26C), yeast-specific Inositol phosphorylceramide, ceramide-3 (26C), yeast-specific Isopentenyl diphosphate Itaconyl-CoA Itaconate ITP ITP K+ K+ C-Lactate L-Lactate	cytosol extracellular cytosol cytosol cytosol cytosol cytosol cytosol cytosol cytosol mitochondrion mitochondrion cytosol extracellular cytosol mitochondrion cytosol extracellular cytosol extracellular mitochondrion	C10H12N4O5 C4800H9500N100O1100 P100 C5000H9900N100O1100 P100 C4800H9500N100O1200 P100 C5000H9900N100O1200 P100 C4800H9500N100O1300 P100 C5000H9900N100O1300 P100 C5900H9900N100O1300 P100 C5H9O7P2 C26H35N7O19P3S C5H4O4 C10H11N4O14P3 K K C3H5O3	-100 -100 -100 -100 -100 -100 -100 -100
ins * ipc124_SC * ipc126_SC * ipc224_SC * ipc226_SC * ipc324_SC * ipc326_SC ipdp itaccoa itacon itp itp k k lac-D lac-D lac-L lac-L lac-L lanost leu-L leu-	Inosine Inosine Inositol phosphorylceramide, ceramide-1 (24C), yeast-specific Inositol phosphorylceramide, ceramide-1 (26C), yeast-specific Inositol phosphorylceramide, ceramide-2 (24C), yeast-specific Inositol phosphorylceramide, ceramide-2 (26C), yeast-specific Inositol phosphorylceramide, ceramide-3 (24C), yeast-specific Inositol phosphorylceramide, ceramide-3 (26C), yeast-specific Inositol phosphorylceramide, ceramide-3 (26C), yeast-specific Isopentenyl diphosphate Itaconyl-CoA Itaconate ITP ITP K+ K+ C-Lactate L-Lactate L-Leucine L-Leucine L-Leucine L-Leucine L-Leucine L-Leucyl-tRNA(Leu)	cytosol extracellular cytosol cytosol cytosol cytosol cytosol cytosol cytosol cytosol mitochondrion mitochondrion cytosol extracellular cytosol mitochondrion cytosol extracellular cytosol extracellular mitochondrion	C10H12N4O5 C4800H9500N100O1100 P100 C5000H9900N100O1100 P100 C4800H9500N100O1200 P100 C5000H9900N100O1200 P100 C4800H9500N100O1300 P100 C5000H9900N100O1300 P100 C5000H9900N100O1300 P100 C5H9O7P2 C26H35N7O19P3S C5H4O4 C10H11N4O14P3 K K C3H5O3	-100 -100 -100 -100 -100 -100 -100 -100
ins * ipc124_SC * ipc126_SC * ipc224_SC * ipc226_SC * ipc326_SC ipdp itaccoa itacon itp itp k k lac-D lac-D lac-L lac-L lad-L lanost leu-L leu-L leu-L	Inosine Inosine Inositol phosphorylceramide, ceramide-1 (24C), yeast-specific Inositol phosphorylceramide, ceramide-1 (26C), yeast-specific Inositol phosphorylceramide, ceramide-2 (24C), yeast-specific Inositol phosphorylceramide, ceramide-2 (26C), yeast-specific Inositol phosphorylceramide, ceramide-3 (24C), yeast-specific Inositol phosphorylceramide, ceramide-3 (26C), yeast-specific Inositol phosphorylceramide, ceramide-3 (26C), yeast-specific Isopentenyl diphosphate Itaconyl-CoA Itaconate ITP ITP K+ K+ C-Lactate L-Lactate	cytosol extracellular cytosol cytosol cytosol cytosol cytosol cytosol cytosol cytosol mitochondrion mitochondrion cytosol extracellular cytosol mitochondrion cytosol extracellular cytosol extracellular mitochondrion	C10H12N4O5 C4800H9500N100O1100 P100 C5000H9900N100O1100 P100 C4800H9500N100O1200 P100 C5000H9900N100O1200 P100 C4800H9500N100O1300 P100 C5000H9900N100O1300 P100 C5900H9900N100O1300 P100 C5H9O7P2 C26H35N7O19P3S C5H4O4 C10H11N4O14P3 K K C3H5O3	-100 -100 -100 -100 -100 -100 -100 -100

lgt-S	(R)-S-Lactoylglutathione	mitochondrion	C13H20N3O8S	-1
lpam	Lipoamide	mitochondrion	C8H15NOS2	0
Ipro	Lipoylprotein	mitochondrion	S2X	0
lys-L	L-Lysine	cytosol	C6H15N2O2	1
		extracellular	C6H15N2O2	1
lys-L	L-Lysine	mitochondrion		1
lys-L	L-Lysine		C6H15N2O2	1
lystrna	L-Lysine-tRNA (Lys)	cytosol	C6H14N2OR	2
lystrna	L-Lysine-tRNA (Lys)	mitochondrion	C6H14N2OR	2
	alpha-D-mannosyl-beta-D-mannosyl-			
m1macchitppdol	diacylchitobiosyldiphosphodolichol	Golgi apparatus	C43H74N2O27P2	-2
	(alpha-D-mannosyl)2-beta-D-mannosyl-			
m2macchitppdol	diacetylchitobiosyldiphosphodolichol	Golgi apparatus	C49H84N2O32P2	-2
	(alpha-D-mannosyl)3-beta-D-mannosyl-			
m3macchitppdol	diacetylchitodiphosphodolichol	Golgi apparatus	C55H94N2O37P2	-2
	(alpha-D-Mannosyl)4-beta-D-mannosyl-			
m4macchitppdol	diacetylchitobiosyldiphosphodolichol	Golgi apparatus	C61H104N2O42P2	-2
	beta-D-	osigi apparatus	001111011120121	
macchitppdol	Mannosyldiacetylchitobiosyldiphosphodolichol	Golgi apparatus	C37H64N2O22P2	_2
mal-L	L-Malate	cytosol	C4H4O5	-2
				-2 -2 -2
mal-L	L-Malate	extracellular	C4H4O5	-2
mal-L	L-Malate	mitochondrion	C4H4O5	-2
mal-L	L-Malate	peroxisome	C4H4O5	-2
malACP	Malonyl-[acyl-carrier protein]	cytosol	C14H22N2O10PRS	-2 -2 -2 -2
malACP	Malonyl-[acyl-carrier protein]	mitochondrion	C14H22N2O10PRS	-2
malcoa	Malonyl-CoA	cytosol	C24H33N7O19P3S	-5
malcoa	Malonyl-CoA	mitochondrion	C24H33N7O19P3S	-5
malt	Maltose	cytosol	C12H22O11	0
malt	Maltose	extracellular	C12H22O11	0
	D-Mannose	cytosol	C6H12O6	0
man				-
man	D-Mannose	extracellular	C6H12O6	0
man1p	D-Mannose 1-phosphate	cytosol	C6H11O9P	-2
man6p	D-Mannose 6-phosphate	cytosol	C6H11O9P	-2
mannan	Mannan	cytosol	C6H10O5	0
mannan	Mannan	endoplasmic reticulum	C6H10O5	0
melib	Melibiose	cytosol	C12H22O11	0
melib	Melibiose	extracellular	C12H22O11	0
melt	melibiitol	cytosol	C12H24O11	0
met-L	L-Methionine	cytosol	C5H11NO2S	0
met-L	L-Methionine	extracellular	C5H11NO2S	0
met-L	L-Methionine	mitochondrion	C5H11NO2S	0
			C20H20N7O6	
methf	5,10-Methenyltetrahydrofolate	cytosol		-1
methf	5,10-Methenyltetrahydrofolate	mitochondrion	C20H20N7O6	-1
mettrna	L-Methionyl-tRNA (Met)	cytosol	C5H10NOSR	1
mettrna	L-Methionyl-tRNA (Met)	mitochondrion	C5H10NOSR	1
mev-R	(R)-Mevalonate	cytosol	C6H11O4	-1
mhpglu	5-Methyltetrahydropteroyltri-L-glutamate	cytosol	C25H36N8O12	0
mi145tp-D	1D-myo-Inositol 1,4,5-trisphosphate	cytosol	C6H9O15P3	-6
mi1p-D	1D-myo-Inositol 1-phosphate	cytosol	C6H11O9P	-2
	mannose-(inositol-P)2-ceramide, ceramide-1 (24C),	5,000	C6000H11500N100O240	_
* mip2c124_SC	yeast-specific	cytosol	0P200	-200
1111p2C124_0C	mannose-(inositol-P)2-ceramide, ceramide-1 (26C),	Cytosoi	C6200H11900N100O240	-200
*	, , , , , , , , , , , , , , , , , , , ,			200
* mip2c126_SC	yeast-specific	cytosol	0P200	-200
	mannose-(inositol-P)2-ceramide, ceramide-2 (24C),		C6000H11500N100O250	
* mip2c224_SC	yeast-specific	cytosol	0P200	-200
	mannose-(inositol-P)2-ceramide, ceramide-2 (26C),		C6200H11900N100O250	
* mip2c226_SC	yeast-specific	cytosol	0P200	-200
	mannose-(inositol-P)2-ceramide, ceramide-3 (24C),		C6000H11500N100O260	
* mip2c324_SC	yeast-specific	cytosol	0P200	-200
p200200	mannose-(inositol-P)2-ceramide, ceramide-3 (26C),	Syless.	C6200H11900N100O260	
* mip2c326_SC	yeast-specific	cytosol	0P200	-200
1111p20320_30		Cylusui		-200
*i404 00	mannose-inositol phosphorylceramide, ceramide-1		C5400H10500N100O160	400
* mipc124_SC	(24C), yeast-specific	cytosol	0P100	-100
	mannose-inositol phosphorylceramide, ceramide-1		C5600H10900N100O160	
* mipc126_SC	(26C), yeast-specific	cytosol	0P100	-100
	mannose-inositol phosphorylceramide, ceramide-2		C5400H10500N100O170	
* mipc224_SC	(24C), yeast-specific	cytosol	0P100	-100
	mannose-inositol phosphorylceramide, ceramide-2	<u> </u>	C5600H10900N100O170	
* mipc226_SC	(26C), yeast-specific	cytosol	0P100	-100
pu 00	(-00), Jouet openio	5,1000.	0. 100	- 100

* mino224 SC	mannose-inositol phosphorylceramide, ceramide-3	outocol	C5400H10500N100O180 0P100	100
* mipc324_SC	(24C), yeast-specific mannose-inositol phosphorylceramide, ceramide-3	cytosol	C5600H10900N100O180	-100
* mipc326_SC	(26C)	cytosol	0P100	-100
mlthf	5,10-Methylenetetrahydrofolate	cytosol	C20H22N7O6	
mlthf	5,10-Methylenetetrahydrofolate	mitochondrion	C20H22N7O6	
mmet	S-Methyl-L-methionine	cytosol	C6H14NO2S	
mmet	S-Methyl-L-methionine	extracellular	C6H14NO2S	
mnl1p	D-Mannitol 1-phosphate	cytosol	C6H13O9P	-2
mthgxl	Methylglyoxal	cytosol	C3H4O2	
myrsACP	Myristoyl-ACP (n-C14:0ACP)	cytosol	C25H47N2O8PRS	
myrsACP	Myristoyl-ACP (n-C14:0ACP)	mitochondrion	C25H47N2O8PRS	-
n4abutn	N4-Acetylaminobutanal	cytosol	C6H11NO2	
na1	Sodium	cytosol	Na	
na1	Sodium	extracellular	Na	
nac	Nicotinate	cytosol	C6H4NO2	-
nac	Nicotinate	mitochondrion	C6H4NO2	-
nad	Nicotinamide adenine dinucleotide	cytosol	C21H26N7O14P2	-
nad	Nicotinamide adenine dinucleotide	mitochondrion	C21H26N7O14P2	-
nad	Nicotinamide adenine dinucleotide	peroxisome	C21H26N7O14P2	-
nadh	Nicotinamide adenine dinucleotide - reduced	cytosol	C21H27N7O14P2	
nadh	Nicotinamide adenine dinucleotide - reduced	mitochondrion	C21H27N7O14P2	-2
nadh	Nicotinamide adenine dinucleotide - reduced	peroxisome	C21H27N7O14P2	-2
nadp	Nicotinamide adenine dinucleotide phosphate	cytosol	C21H25N7O17P3	-:
nadp	Nicotinamide adenine dinucleotide phosphate	mitochondrion	C21H25N7O17P3	-1 -1 -1 -1 -1
nadp	Nicotinamide adenine dinucleotide phosphate	endoplasmic reticulum	C21H25N7O17P3	-:
nadp	Nicotinamide adenine dinucleotide phosphate	peroxisome	C21H25N7O17P3	-;
	Nicotinamide adenine dinucleotide phosphate -			
nadph	reduced	cytosol	C21H26N7O17P3	-4
Паарп	Nicotinamide adenine dinucleotide phosphate -	eyicco.	5211125111 5 111 5	
nadph	reduced	mitochondrion	C21H26N7O17P3	-4
паарп	Nicotinamide adenine dinucleotide phosphate -	mitoenerianen	0211120147 0 171 0	
nadph	reduced	endoplasmic reticulum	C21H26N7O17P3	-4
Паарп	Nicotinamide adenine dinucleotide phosphate -	chaopiasinie reticularii	0211120147 0 171 0	
nadph	reduced	peroxisome	C21H26N7O17P3	-4
ncam	Nicotinamide	cytosol	C6H6N2O	
ncam	Nicotinamide	mitochondrion	C6H6N2O	(
nh4	Ammonium	cytosol	H4N	
nh4	Ammonium	extracellular	H4N	
nh4		mitochondrion	H4N	
nh4	Ammonium Ammonium		H4N	
	Nicotinate D-ribonucleotide	peroxisome	C11H12NO9P	-2
nicrnt		cytosol		
nicrnt	Nicotinate D-ribonucleotide	mitochondrion	C11H12NO9P	- <u>-</u>
nmn	NMN	cytosol	C11H14N2O8P	
nmn	NMN	extracellular	C11H14N2O8P	
nmn	NMN	mitochondrion	C11H14N2O8P	
nmn	NMN	peroxisome	C11H14N2O8P	
02	02	cytosol	02	(
02	02	extracellular	02	(
02	02	mitochondrion	02	(
02	02	endoplasmic reticulum	02	(
o2	02	peroxisome	02	(
oaa	Oxaloacetate	cytosol	C4H2O5	-1 -1 -1
oaa	Oxaloacetate	mitochondrion	C4H2O5	-2
oaa	Oxaloacetate	peroxisome	C4H2O5	-2
ocACP	Octanoyl-ACP (n-C8:0ACP)	mitochondrion	C19H35N2O8PRS	
occoa	Octanoyl-CoA (n-C8:0CoA)	cytosol	C29H46N7O17P3S	-4
occoa	Octanoyl-CoA (n-C8:0CoA)	peroxisome	C29H46N7O17P3S	-4
ocdca	octadecanoate (n-C18:0)	cytosol	C18H35O2	-
ocdca	octadecanoate (n-C18:0)	extracellular	C18H35O2	
ocdcaACP	Octadecanoyl-ACP (n-C18:0ACP)	cytosol	C29H55N2O8PRS	-
ocdcaACP	Octadecanoyl-ACP (n-C18:0ACP)	mitochondrion	C29H55N2O8PRS	-
ocdcea	octadecenoate (n-C18:1)	cytosol	C18H33O2	-
ocdcea	octadecenoate (n-C18:1)	extracellular	C18H33O2	-
ocdcya	octadecynoate (n-C18:2)	cytosol	C18H31O2	
ocdcya	octadecynoate (n-C18:2)	extracellular	C18H31O2	-
ocdcyaACP	Octadecynoyl-ACP (n-C18:2ACP)	cytosol	C29H51N2O8PRS	-· -·

ocdycacoa	Octadecynoyl-CoA (n-C18:2CoA)	cytosol	C39H62N7O17P3S	-4
ocdycacoa	Octadecynoyl-CoA (n-C18:2CoA)	peroxisome	C39H62N7O17P3S	
octa	octanoate (n-C8:0)	cytosol	C8H15O2	-4 -1
octa	octanoate (n-C8:0)	peroxisome	C8H15O2	-1
	,			
octdp_5	all-trans-Octaprenyl diphosphate (5 repeating units)	cytosol	C30H49O7P2	-3
· -				
octdp_5	all-trans-Octaprenyl diphosphate (5 repeating units)	mitochondrion	C30H49O7P2	-3
octeACP	Octadecenoyl-ACP (n-C18:1ACP)	cytosol	C29H53N2O8PRS	-1
octeACP	Octadecenoyl-ACP (n-C18:1ACP)	mitochondrion	C29H53N2O8PRS	-1
od2coa	trans-Octadec-2-enoyl-CoA	peroxisome	C39H64N7O17P3S	-4
odecoa	Octadecenoyl-CoA (n-C18:1CoA)	cytosol	C39H64N7O17P3S	-4
odecoa	Octadecenoyl-CoA (n-C18:1CoA)	peroxisome	C39H64N7O17P3S	-4
oh1	hydroxide ion	cytosol	НО	-1
oh1	hydroxide ion	mitochondrion	НО	-1
ohpb	2-Oxo-3-hydroxy-4-phosphobutanoate	cytosol	C4H4O8P	-3
orn	Ornithine	cytosol	C5H13N2O2	1
orn	Ornithine	extracellular	C5H13N2O2	1
orn	Ornithine	mitochondrion	C5H13N2O2	1
orot	Orotate	cytosol	C5H3N2O4	-1
orot5p	Orotidine 5'-phosphate	cytosol	C10H10N2O11P	-3
oxag	Oxaloglutarate	cytosol	C7H5O7	-3 -3
oxag	Oxaloglutarate	mitochondrion	C7H5O7	
* pa_SC	Phosphatidate, yeast-specific	cytosol	C3540H6544O800P100	-200
* pa_SC	Phosphatidate, yeast-specific	mitochondrion	C3540H6544O800P100	-200
pac	Phenylacetic acid	cytosol	C8H7O2	-1
pacald	Phenylacetaldehyde	cytosol	C8H8O	0
pad	2-Phenylacetamide	cytosol	C8H9NO	0
palmACP	Palmitoyl-ACP (n-C16:0ACP)	cytosol	C27H51N2O8PRS	-1
palmACP	Palmitoyl-ACP (n-C16:0ACP)	mitochondrion	C27H51N2O8PRS	-1
pan4p	Pantetheine 4'-phosphate	cytosol	C11H21N2O7PS	-2
pan4p	Pantetheine 4'-phosphate	mitochondrion	C11H21N2O7PS	-2 -2 -1
pant-R	(R)-Pantoate	cytosol	C6H11O4	<u>-</u> -1
pant-R	(R)-Pantoate	mitochondrion	C6H11O4	-1
pap	Adenosine 3',5'-bisphosphate	cytosol	C10H11N5O10P2	-4
pap pap	Adenosine 3',5'-bisphosphate	extracellular	C10H11N5O10P2	-4
	Adenosine 3',5'-bisphosphate	mitochondrion	C10H11N5O10P2	-4
pap paps	3'-Phosphoadenylyl sulfate	cytosol	C10H11N5O13P2S	-
paps	3-Filospiloaderiyiyi sullate	Cytosoi	C4040H7844N100O800P	-4
* pc_SC	Phosphatidylcholine, yeast-specific	cytosol	100	0
pdx5p	Pyridoxine 5'-phosphate	cytosol	C8H10NO6P	-2
ράλορ	r yriddxirie 3 -priospriate	Cytosoi	C3740H7244N100O800P	-2
* no SC	nhoenhatidylethanolamine, yeast specific	cytocol	100	0
* pe_SC	phosphatidylethanolamine, yeast-specific	cytosol	C3740H7244N100O800P	0
* no CC	nhoonhatidulathanalamina, vaaat anaaifia	Colai apparatus		0
* pe_SC	phosphatidylethanolamine, yeast-specific	Golgi apparatus	100	0
* 00	de contra Calaba (contra de contra d		C3740H7244N100O800P	_
* pe_SC	phosphatidylethanolamine, yeast-specific	mitochondrion	100	0
			C3740H7244N100O800P	
* pe_SC	phosphatidylethanolamine, yeast-specific	vacuole	100	0
рер	Phosphoenolpyruvate	cytosol	C3H2O6P	-3 -3
рер	Phosphoenolpyruvate	mitochondrion	C3H2O6P	-3
pepd	peptide	cytosol	C2H4NO2RC2H2NOR	0
pepd	peptide	extracellular	C2H4NO2RC2H2NOR	0
* pg_SC	Phosphatidylglycerol, yeast-specific	mitochondrion	C3840H7244O1000P100	-100
* pgp_SC	Phosphatidylglycerophosphate, yeast-specific	mitochondrion	C3840H7144O1300P200	-300
phe-L	L-Phenylalanine	cytosol	C9H11NO2	0
phe-L	L-Phenylalanine	extracellular	C9H11NO2	0
phe-L	L-Phenylalanine	mitochondrion	C9H11NO2	0
	Protoheme	mitochondrion	C34H30FeN4O4	-2 1
pheme	Totolicine		I COLLIANI CON	
pheme phetrna	L-Phenylalanyl-tRNA(Phe)	cytosol	C9H10NOR	1
	L-Phenylalanyl-tRNA(Phe)	cytosol mitochondrion	C9H10NOR C9H10NOR	1 1
phetrna phetrna	L-Phenylalanyl-tRNA(Phe) L-Phenylalanyl-tRNA(Phe)	mitochondrion		1
phetrna phetrna phom	L-Phenylalanyl-tRNA(Phe) L-Phenylalanyl-tRNA(Phe) O-Phospho-L-homoserine	mitochondrion cytosol	C9H10NOR	1
phetrna phetrna phom phpyr	L-Phenylalanyl-tRNA(Phe) L-Phenylalanyl-tRNA(Phe) O-Phospho-L-homoserine Phenylpyruvate	mitochondrion cytosol cytosol	C9H10NOR C4H8NO6P C9H7O3	1 -2 -1
phetrna phetrna phom phpyr phthr	L-Phenylalanyl-tRNA(Phe) L-Phenylalanyl-tRNA(Phe) O-Phospho-L-homoserine Phenylpyruvate O-Phospho-4-hydroxy-L-threonine	mitochondrion cytosol cytosol cytosol	C9H10NOR C4H8NO6P C9H7O3 C4H8NO7P	1 -2 -1
phetrna phetrna phom phpyr phthr pi	L-Phenylalanyl-tRNA(Phe) L-Phenylalanyl-tRNA(Phe) O-Phospho-L-homoserine Phenylpyruvate O-Phospho-4-hydroxy-L-threonine Phosphate	mitochondrion cytosol cytosol cytosol cytosol	C9H10NOR C4H8NO6P C9H7O3 C4H8NO7P HO4P	1 -2 -1
phetrna phetrna phom phpyr phthr	L-Phenylalanyl-tRNA(Phe) L-Phenylalanyl-tRNA(Phe) O-Phospho-L-homoserine Phenylpyruvate O-Phospho-4-hydroxy-L-threonine	mitochondrion cytosol cytosol cytosol	C9H10NOR C4H8NO6P C9H7O3 C4H8NO7P	1

pi	Phosphate	nucleus	HO4P	_2
pi	Phosphate	vacuole	HO4P	-2
pi	Phosphate	peroxisome	HO4P	-2 -2 -2 -4 -4 -1
pmtcoa	Palmitoyl-CoA (n-C16:0CoA)	cytosol	C37H62N7O17P3S	-4
pmtcoa	Palmitoyl-CoA (n-C16:0CoA)	peroxisome	C37H62N7O17P3S	-4
pnto-R	(R)-Pantothenate	cytosol	C9H16NO5	-4
	(R)-Pantothenate	extracellular	C9H16NO5	-1
pnto-R				-1 -1
ppbng	Porphobilinogen	cytosol	C10H13N2O4	
ppcoa	Propanoyl-CoA	cytosol	C24H36N7O17P3S	-4 -2 -3 -3 -3 -2 -2 -2 -2
pphn	Prephenate	cytosol	C10H8O6	-2
ppi	Diphosphate	cytosol	HO7P2	-3
ppi	Diphosphate	mitochondrion	HO7P2	-3
ppi	Diphosphate	peroxisome	HO7P2	-3
ppp9	Protoporphyrin	mitochondrion	C34H32N4O4	-2
pppg9	Protoporphyrinogen IX	cytosol	C34H38N4O4	-2
pppg9	Protoporphyrinogen IX	mitochondrion	C34H38N4O4	-2
pram	5-Phospho-beta-D-ribosylamine	cytosol	C5H11NO7P	-1
pran	N-(5-Phospho-D-ribosyl)anthranilate	cytosol	C12H13NO9P	-3 -4
prbamp	1-(5-Phosphoribosyl)-AMP	cytosol	C15H19N5O14P2	-4
prbatp	1-(5-Phosphoribosyl)-ATP	cytosol	C15H19N5O20P4	-6
T T T T T T T T T T	1-(5-Phosphoribosyl)-5-[(5-	.,		
	phosphoribosylamino)methylideneamino]imidazole-4			
prfp	carboxamide	cytosol	C15H21N5O15P2	-4
рпр	5-[(5-phospho-1-deoxyribulos-1-	eytoeei	0.10112111001012	
	ylamino)methylideneamino]-1-(5-			
prlp	phosphoribosyl)imidazole-4-carboxamide	cytosol	C15H21N5O15P2	1
_ ' '	L-Proline	,		
pro-L		cytosol	C5H9NO2	
pro-L	L-Proline	extracellular	C5H9NO2	0
pro-L	L-Proline	mitochondrion	C5H9NO2	0
protrna	L-Prolyl-tRNA(Pro)	cytosol	C5H8NOR	1
prpp	5-Phospho-alpha-D-ribose 1-diphosphate	cytosol	C5H8O14P3	-5 -5
prpp	5-Phospho-alpha-D-ribose 1-diphosphate	mitochondrion	C5H8O14P3	-5
			C3840H7144N100O1000	
* ps_SC	phosphatidylserine, yeast-specific	cytosol	P100	-100
			C3840H7144N100O1000	
* ps_SC	phosphatidylserine, yeast-specific	Golgi apparatus	P100	-100
			C3840H7144N100O1000	
* ps_SC	phosphatidylserine, yeast-specific	mitochondrion	P100	-100
	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		C3840H7144N100O1000	
* ps_SC	phosphatidylserine, yeast-specific	vacuole	P100	-100
psd5p	Pseudouridine 5'-phosphate	cytosol	C9H11N2O9P	
pser-L	O-Phospho-L-serine	cytosol	C3H6NO6P	-2 -2
	·			
psph1p	Phytosphingosine 1-phosphate	cytosol	C18H39NO6P	-1 1
psphings	Phytosphingosine	cytosol	C18H40NO3	ı
*	phosphatidyl-1D-myo-inositol 3,4-bisphosphate,	l	044401174440400000000	=00
* ptd134bp_SC	yeast-specific	cytosol	C4140H7444O1900P300	-500
	1-Phosphatidyl-D-myo-inositol 4,5-bisphosphate,			
* ptd145bp_SC	yeast-specific	cytosol	C4140H7444O1900P300	-500
* ptd1ino_SC	phosphatidyl-1D-myo-inositol, yeast-specific	cytosol	C4140H7644O1300P100	-100
* ptd1ino_SC	phosphatidyl-1D-myo-inositol, yeast-specific	nucleus	C4140H7644O1300P100	-100
			C3940H7644N100O800P	
* ptd2meeta_SC	Phosphatidyl-N-dimethylethanolamine	cytosol	100	0
* ptd3ino_SC	phosphatidyl-1D-myo-3-inositol, yeast-specific	cytosol	C4140H7544O1600P200	-300
* ptd4ino SC	phosphatidyl-1D-myo-4-inositol, yeast specific	cytosol	C4140H7544O1600P200	-300
* ptd4ino_SC	phosphatidyl-1D-myo-4-inositol, yeast specific	nucleus	C4140H7544O1600P200	-300
F120_00	programme in the state of the s		C3840H7444N100O800P	
* ptdmeeta_SC	Phosphatidyl-N-methylethanolamine, yeast-specific	cytosol	100	0
ptrc ptumeeta_3C	Putrescine	cytosol	C4H14N2	
	Putrescine	extracellular		2 2 -1
ptrc			C4H14N2	
pyam5p	Pyridoxamine 5'-phosphate	cytosol	C8H12N2O5P	
pydam	Pyridoxamine	cytosol	C8H13N2O2	1
pydx	Pyridoxal	cytosol	C8H9NO3	0
pydx5p	Pyridoxal 5'-phosphate	cytosol	C8H8NO6P	-2 0
pydxn	Pyridoxine	cytosol	C8H11NO3	0
pyr	Pyruvate	cytosol	C3H3O3	-1
pyr	Pyruvate	extracellular	C3H3O3	-1
pyr	Pyruvate	mitochondrion	C3H3O3	-1
pyr	Pyruvate	peroxisome	C3H3O3	<u> </u>
	i yiavato	POLOVISOLIIC	0011000	- 1

q6	Ubiquinone-6	mitochondrion	C39H58O4
q6h2	Ubiquinol-6	mitochondrion	C39H60O4
quin	Quinolinate	cytosol	
quin	Quinolinate	mitochondrion	C7H3NO4
r1p	alpha-D-Ribose 1-phosphate	cytosol	C7H3NO4 C7H3NO4 C5H9O8P C5H9O8P C5H9O8P C18H32O16
r1p	alpha-D-Ribose 1-phosphate	mitochondrion	C5H9O8P
r5p	alpha-D-Ribose 5-phosphate	cytosol	C5H9O8P
raffin	Raffinose	cytosol	C18H32O16
rib-D	D-Ribose	cytosol	C5H10O5
rib-D	D-Ribose	extracellular	C5H10O5
ribfly	Riboflavin		C17H20N4O6
ribfly	Riboflavin	cytosol extracellular	C17H20N4O6
ribfly	Riboflavin	mitochondrion	C17H20N4O6
-			
ru5p-D	D-Ribulose 5-phosphate Sulfur	cytosol	
S		cytosol	
s17bp	Sedoheptulose 1,7-bisphosphate	cytosol	C7H12O13P2
s7p	Sedoheptulose 7-phosphate	cytosol	C7H13O10P C11H19N2O6
saccrp-L	L-Saccharopine	cytosol	
sbt-D	D-Sorbitol	cytosol	C6H14O6
sbt-D	D-Sorbitol	extracellular	C6H14O6
sbt-L	L-Sorbitol	cytosol	C6H14O6
sbt-L	L-Sorbitol	extracellular	C6H14O6
sdhlam	S-Succinyldihydrolipoamide	mitochondrion	C12H20NO4S2
ser-L	L-Serine	cytosol	C3H7NO3
ser-L	L-Serine	extracellular	C3H7NO3
ser-L	L-Serine	mitochondrion	C3H7NO3
sertrna	L-Seryl-tRNA(Ser)	cytosol	C3H6NO2R
shcl	Sirohydrochlorin	cytosol	C42H41N4O16
skm	Shikimate	cytosol	C7H9O5
skm5p	Shikimate 5-phosphate	cytosol	C7H8O8P O3S O4S O4S C18H39NO5P
so3	Sulfite	cytosol	O3S
so4	Sulfate	cytosol	O4S
so4	Sulfate	extracellular	O4S
sph1p	Sphinganine 1-phosphate	cytosol	C18H39NO5P
sphgn	Sphinganine	cytosol	C18H40NO2
spmd	Spermidine	cytosol	C7H22N3
spmd	Spermidine	extracellular	C7H22N3
sprm	Spermine	cytosol	C10H30N4
sprm	Spermine	extracellular	C10H30N4
sql	Squalene	cytosol	C30H50
sql	Squalene	endoplasmic reticulum	C30H50
srb-L	L-Sorbose	cytosol	C6H12O6
srb-L	L-Sorbose	extracellular	C6H12O6
stcoa	Stearoyl-CoA (n-C18:0CoA)	cytosol	C39H66N7O17P3S
stcoa	Stearoyl-CoA (n-C18:0CoA)	peroxisome	C39H66N7O17P3S
succ	Succinate	cytosol	
succ	Succinate	extracellular	C4H4O4 C4H4O4 C4H4O4 C25H35N7O19P3S
succ	Succinate	mitochondrion	C4H4O4
succoa	Succinyl-CoA	mitochondrion	C25H35N7O19P3S
suchms	O-Succinyl-L-homoserine	cytosol	C8H12NO6
sucr	Sucrose	cytosol	C12H22O11
sucr	Sucrose	extracellular	C12H22O11
sucsal	Succinic semialdehyde	cytosol	C4H5O3
tag6p-D	D-Tagatose 6-phosphate	cytosol	
tagdp-D	D-Tagatose 0-priospriate D-Tagatose 1,6-biphosphate	cytosol	C6H11O9P C6H10O12P2
td2coa	trans-Tetradec-2-enoyl-CoA	peroxisome	C35H56N7O17P3S
tdcoa	Tetradecanoyl-CoA (n-C14:0CoA)	cytosol	C35H58N7O17P3S
tdcoa	Tetradecanoyl-CoA (n-C14:0CoA)	peroxisome	C35H58N7O17P3S
tdeACP	Tetradecanoyi-CoA (ii-C14:0C0A)	cytosol	C25H45N2O8PRS
tdeACP	Tetradecenoyl-ACP (n-C14:1ACP)	mitochondrion	C25H45N2O8PRS
tdecoa	Tetradecenoyl-CoA (n-C14:1ACP)	cytosol	C35H56N7O17P3S
tdecoa	Tetradecenoyl-CoA (n-C14:1CoA) Tetradecenoyl-CoA (n-C14:1CoA)	peroxisome	C35H56N7O17P3S
	* , , , ,	'	
tglp	N-Tetradecanoylglycylpeptide	cytosol	C18H32N2O4R
thf	5,6,7,8-Tetrahydrofolate	cytosol	C19H22N7O6
thf	5,6,7,8-Tetrahydrofolate	mitochondrion	C19H22N7O6
thfglu	Tetrahydrofolyl-[Glu](2)	cytosol	C24H28N8O9 C12H17N4OS
thm thm	Thiamin Thiamin	cytosol extracellular	C12H17N4OS C12H17N4OS

thmmp	Thiamin monophosphate	cytosol	C12H16N4O4PS	-1
thmmp	Thiamin monophosphate	extracellular	C12H16N4O4PS	-1
thmpp	Thiamine diphosphate	cytosol	C12H16N4O7P2S	
thmpp	Thiamine diphosphate	extracellular	C12H16N4O7P2S	-2 -2 -3
thmtp	Thiamin triphosphate	cytosol	C12H16N4O10P3S	-3
thr-L	L-Threonine	cytosol	C4H9NO3	0
thr-L	L-Threonine	extracellular	C4H9NO3	C
thr-L	L-Threonine	mitochondrion	C4H9NO3	C
thrtrna	L-Threonyl-tRNA(Thr)	cytosol	C4H8NO2R	1
thrtrna	L-Threonyl-tRNA(Thr)	mitochondrion	C4H8NO2R	1
thym	Thymine	cytosol	C5H6N2O2	C
thym	Thymine	extracellular	C5H6N2O2	C
thymd	Thymidine	cytosol	C10H14N2O5	C
thymd	Thymidine	extracellular	C10H14N2O5	C
trdox	Oxidized thioredoxin	cytosol	X	C
trdox	Oxidized thioredoxin	mitochondrion	X	C
trdox	Oxidized thioredoxin	nucleus	X	C
trdrd	Reduced thioredoxin	cytosol	XH2	C
trdrd	Reduced thioredoxin	mitochondrion	XH2	C
trdrd	Reduced thioredoxin	nucleus	XH2	C
tre	Trehalose	cytosol	C12H22O11	C
tre	Trehalose	extracellular	C12H22O11	C
tre	Trehalose	vacuole	C12H22O11	C
tre6p	alpha,alpha'-Trehalose 6-phosphate	cytosol	C12H21O14P	-2
* triglyc_SC	triglyceride, yeast-specific	cytosol	C5160H9566O600	C
trnaala	tRNA(Ala)	cytosol	R	C
trnaarg	tRNA(Arg)	cytosol	R	C
trnaarg	tRNA(Arg)	mitochondrion	R	C
trnaasn	tRNA(Asn)	cytosol	R	C
trnaasn	tRNA(Asn)	mitochondrion	R	C
trnaasp	tRNA(Asp)	cytosol	R	C
trnaasp	tRNA(Asp)	mitochondrion	R	C
trnacys	tRNA(Cys)	cytosol	R	C
trnagln	tRNA(GIn)	cytosol	R	C
trnaglu	tRNA (Glu)	cytosol	R	C
trnaglu	tRNA (Glu)	mitochondrion	R	C
trnagly	tRNA(Gly)	cytosol	R	C
trnahis	tRNA(His)	cytosol	R	C
trnahis	tRNA(His)	mitochondrion	R	C
trnaile	tRNA(IIe)	cytosol	R	C
trnaile	tRNA(IIe)	mitochondrion	R	C
trnaleu	tRNA(Leu)	cytosol	R	(
trnaleu	tRNA(Leu)	mitochondrion	R	
trnalys	tRNA(Lys)	cytosol	R	C
trnalys	tRNA(Lys)	mitochondrion	R	C
trnamet	tRNA(Met)	cytosol	R	C
trnamet	tRNA(Met)	mitochondrion	R	C
trnaphe	tRNA(Phe)	cytosol	R	(
trnaphe	tRNA(Phe)	mitochondrion	R	(
trnapro	tRNA(Pro)	cytosol	R	(
trnaser	tRNA(Ser)	cytosol	R	(
trnathr	tRNA(Thr)	cytosol	R	(
trnathr	tRNA(Thr)	mitochondrion	R	(
trnatrp	tRNA(Trp)	cytosol	R	(
trnatrp	tRNA(Trp)	mitochondrion	R	
trnatyr	tRNA(Tyr)	cytosol	R	(
trnatyr	tRNA(Tyr) tRNA(Val)	mitochondrion	R R	(
trnaval	` '	cytosol		(
trnaval	tRNA(Val)	mitochondrion	R	
trp-L	L-Tryptophan	cytosol	C11H12N2O2	(
trp-L	L-Tryptophan	extracellular	C11H12N2O2	
trp-L	L-Tryptophan	mitochondrion	C11H12N2O2	(
trptrna	L-Tryptophanyl-tRNA(Trp)	cytosol	C11H11N2OR	1
trptrna	L-Tryptophanyl-tRNA(Trp)	mitochondrion	C11H11N2OR	1
ttc	tetracosanoate (n-C24:0)	cytosol	C24H47O2	-1
ttc	tetracosanoate (n-C24:0)	peroxisome	C24H47O2	-1
ttccoa	tetracosanoyl-CoA (n-C24:0CoA)	cytosol	C45H78N7O17P3S	-4 -4
ttccoa	tetracosanoyl-CoA (n-C24:0CoA)	peroxisome	C45H78N7O17P3S	-4

ttdca	tetradecanoate (n-C14:0)	cytosol	C14H27O2	
ttdca	tetradecanoate (n-C14:0)	extracellular	C14H27O2	-1
ttdca	tetradecanoate (n-C14:0)	peroxisome	C14H27O2	-1
ttdcea	tetradecenoate (n-C14:1)	cytosol	C14H25O2	-1
ttdcea	tetradecenoate (n-C14:1)	peroxisome	C14H25O2	-1
tyr-L	L-Tyrosine	cytosol	C9H11NO3	(
tyr-L	L-Tyrosine	extracellular	C9H11NO3	(
tyr-L	L-Tyrosine	mitochondrion	C9H11NO3	(
tyr-L	L-Tyrosine	peroxisome	C9H11NO3	(
tyrtrna	L-Tyrosyl-tRNA(Tyr)	cytosol	C9H10NO2R	•
tyrtrna	L-Tyrosyl-tRNA(Tyr)	mitochondrion	C9H10NO2R	·
udp	UDP	cytosol	C9H11N2O12P2	-3
udp	UDP	nucleus	C9H11N2O12P2	-3
udpacgal	UDP-N-acetyl-D-galactosamine	cytosol	C17H25N3O17P2	-2
udpg	UDPglucose	cytosol	C15H22N2O17P2	-2 -2 -2 -3 -4 -3 -4
udpgal	UDPgalactose	cytosol	C15H22N2O17P2	-2
ump	UMP	cytosol	C9H11N2O9P	-2
ump	UMP	nucleus	C9H11N2O9P	-2
uppg3	Uroporphyrinogen III	cytosol	C40H36N4O16	-8
ura	Uracil	cytosol	C4H4N2O2	(
ura	Uracil	extracellular	C4H4N2O2	(
urdglyc	(-)-Ureidoglycolate	cytosol	C3H5N2O4	-1
urea	Urea	cytosol	CH4N2O	(
urea	Urea	extracellular	CH4N2O	(
uri	Uridine	cytosol	C9H12N2O6	(
uri	Uridine	extracellular	C9H12N2O6	(
utp	UTP	cytosol	C9H11N2O15P3	-4
val-L	L-Valine	cytosol	C5H11NO2	(
val-L	L-Valine	extracellular	C5H11NO2	(
val-L	L-Valine	mitochondrion	C5H11NO2	(
valtrna	L-Valyl-tRNA(Val)	cytosol	C5H10NOR	·
valtrna	L-Valyl-tRNA(Val)	mitochondrion	C5H10NOR	·
xan	Xanthine	cytosol	C5H4N4O2	(
xan	Xanthine	extracellular	C5H4N4O2	(
xmp	Xanthosine 5'-phosphate	cytosol	C10H11N4O9P	-2
xtsn	Xanthosine	cytosol	C10H12N4O6	(
xtsn	Xanthosine	extracellular	C10H12N4O6	(
xu5p-D	D-Xylulose 5-phosphate	cytosol	C5H9O8P	-2
xyl-D	D-Xylose	cytosol	C5H10O5	-2
xyl-D	D-Xylose	extracellular	C5H10O5	(
xylt	Xylitol	cytosol	C5H12O5	(
xylt	Xylitol	extracellular	C5H12O5	(
xylu-D	D-Xylulose	cytosol	C5H10O5	(
zym int1	zymosterol intermediate 1	cytosol	C28H44O3	
zym_int2	zymosterol intermediate 2	cytosol	C27H42O	
zymst	zymosterol	cytosol	C27H44O	
zymst	zymosterol	extracellular	C27H44O	

 $^{^*}$ Metabolite represents 100 copies of this compound. For reactions involving this metabolite, the stoichiometric coefficients have been appropriately scaled (e.g., 1/100 or 2/100).

Key to deletion results

ORF ORF name
Name Gene name

Annotation Gene annotation (from SGD)
Ess sim Essential (YPD) simulation
Ess call Essential call (FP/TN)
Slow sim Slow growth simulation

Slow exp Slow growth experimental [Giaever02]

Slow call Slow growth call (FP/TN)

MMD sim Glucose minimal media simulation

MMD experimental (1=normal growth, 0=retarded growth)

MMD average of experimental scores

MMD call (FP/FN/TP/TN)
YPGal sim YP galactose simulation

YPGal exp YPGal experimental (1=normal growth, 0=retarded growth)

YPGal average of experimental scores

YPGal call (FP/FN/TP/TN)

YPD sim YPD simulation
YPD exp YPD experimental
YPD call YPD call (FP/FN/TP/TN)
YPDGE sim YPDGE experimental
YPDGE call YPDGE call (FP/FN/TP/TN)

YPG sim YPG simulation
YPG exp YPG experimental
YPG call (FP/FN/TP/TN)

YPE sim YPE simulation
YPE exp YPE experimental
YPE call (FP/FN/TP/TN)

YPL sim YPL simulation
YPL exp YPL experimental
YPL call (FP/FN/TP/TN)

Class Primary source for false prediction(s)

Explanation Detailed explanation for false prediction(s)

Forster et al Result in Forster et al. study - only false predictions are listed

Abbreviations for sources for false predictions

Acc Accumulation of a toxic intermediate

Bio Problems with in silico biomass constitution

Den Dead end in the in silico model
Dis Discrepancy in experimental data

Iso Problems with in silico gene-protein-reaction associations

Med Problems with in silico media composition
Mod Problems with in silico model structure

Oth Involvement of the gene in non-metabolic processes

Reg Missing transcriptional regulation
Unk Unknown source for false prediction

					ے	۵	_	_	۵	ø	_	Ē	фx	ve	all				sim	dxe	call	_		_								e et
ORF	ame		ss sim	ss call	ow sim	ow exp	ow ca	MD sim	MD ex	AIMD ave	MD call	Gal sim	Gal exp	PGal ave	PGal cal	/PD sim	PD exp	PD call	PDGE sim	PDGE exp	PDGE	/PG sim	PG exp	G call	/PE sim	/PE exp	PE call	/PL sim	PL exp	L call	Class	Explanation Explanation
		Annotation ADP/ATP translocator	NA.	ES	NA	NA	Š	2	Ξ	_	Ē TP	<u>}</u>	_	.06	⋝	_	_	<u> </u>				_	.03	_	1.12	1.03	TP 1		⊭ 1.03	,	NA	
TWKUSOC	AACT	Adenine aminohydrolase (adenine	INA	INA	INA	INA	INA		<u> </u>	0.04	IF	-	1 -0	1.06	IF I	.06	1.02 1	P	1.1	1.02	IF I	.11	.03	IF.	1.12	1.03	IF	.11	1.03	IF	INA	INA INA
YNL141W	AAH1	deaminase)	NA	NA	NA	NA	NA	1	1 -	0.01	TP	1	1 -0	.07	TP 1	.08	1 T	ΓP 1			TP 1				1.12		TP 1		1		NA	NA NA
YKL106W	AAT1	Aspartate aminotransferase	NA	NA	NA	NA	NA	1	1 -	0.04	TP	1	1 -(.05	TP 1	.08	D.98 T	ΓP 1	1.1	0.97	ΓP 1	.09 0).87	TP 1	1.11	0.82	TP	1.1 (0.84	TP	NA	NA NA
YLR027C	AAT2	Aspartate aminotransferase	NA	NA	NA	NA	NA	1	1	0.96	TP	1	1	0 -	TP 1	.08 0	0.93 T	ГР 1	1.1	0.83	-P 1	.08 0	0.74	FP 1	1.11	0.65	FP	1.1	0.87	TP	Unk	The model correctly predicts that the effect of the deletion is larger on non-fermentable carbon sources, but the predicted change in growth rate is too small for the slow growth criterion. The model does not predict higher growth of lactate than on other non-fermentable carbon sources though.
		Aminodeoxychorismate synthase			NA					0.04										1.01												
YGR037C	ACB1	Acyl-CoA-binding protein (ACBP)/diazepam binding inhibitor (DBI)/endozepine (EP)			NA		NA	0	1 (0.23	FN	0	1 -(1.04 F	₹N	0 0	0.93 F	FN.	0	0.97 F	-N	0 0).94 [FN	0	0.95	FN	0 (0.94	FN	Unk	Product of ACB1 is part of FAS complex; involved in termination of fatty acid synthesis and transport of newly synthesized acyl-CoA esters from the fatty acid synthetase to acyl-CoA-consuming processes, may also transport mediumand long-chain acyl CoA esters [MIPS]; since enzymatic mechanism is unknown and transport function is not well defined, may want to remove from FAS complex.
YNR016C		Acetyl CoA carboxylase	0		NA	NA	NA	NA	NA	NA	NA	NA I						A N		NA I			NA I			NA		NA	NA	NA	NA	NA NA
YBL015W	ACH1	Acetyl CoA hydrolase	NA	NA	NA	NA	NA	1	1 -	0.01	TP (0.99	1 -0	.05	TP 1	.08 1	1.03 T	ΓP 1	1.1	1.05	TP 1	1.1 1	.04	TP (0.96	1.06	TP 1	.11	1.06	TP	NA	NA NA
YLR304C	ACO1	Aconitase	NA	NA	1	3.6	FP	1	1 .	0.02	TP	1	1 (TD 4	00 0	2 06 5	D 1		0.75 F	-D 4	11 0	. 50	ED 4	1 12	0.50	ED.	11	0.6	FP	Iso	YJL200C codes for an isozyme for Aco1p, but Aco1p is probably the major isoform. NA
TLK304C	ACOT	Aconitase	INA	INA		3.0	FF		- '	0.02	IF	-	1 -0	1.04	IF I	.06 (J.00 F	P	1.1	0.75	FI	.11 ().59	r P	1.12	0.52	FF	. 1 1	0.6	FF	150	Acp1p used in synthesis of fatty-acyl ACPs, which are not
YKL192C		Acyl carrier protein	1	FP	NA	NA	NA	NA	NA	NA	NA	NA I	NA I	A A	1 AV	NA I	NA N	A N	NA	NA I	1 A	NA I	NA I	NA	NA	NA	NA	NA	NA	NA	Bio	required in the model. NA
		Acetyl CoA synthetase	_	_	NA	NA	NA	1	_		TP	1		.03	_					1.02											NA	NA NA
YLR153C	ACS2	Acetyl CoA synthetase Phosphoribosyl amino	0	IN	NA	NA	NA	NA	NA	NA	NA	NA I	NA I	1 AV	1 AV	NA I	NA N	1 AI	VA	NA I	NA I	VA I	NA I	NA	NA	NA	NA	NA	NA	NA	NA	NA FP
		imidazolesuccinocarbozamide																														Should be an adenine auxotroph [SGD] - should not grow
YAR015W	ADE1	synthetase	NA	NA	NA	NA	NA	0	1 (0.02	FN	1	1	0	TP 1	.08	0.97 T	ΓP 1	1.1	0.93	TP 1	.11 0	0.99	TP 1	1.12	0.97	TP 1	.11	0.95	TP	Med	normally on minimal media. NA
YNL220W	ADE12	Adenylosuccinate synthetase	NA	NA	1	4.5	FP	0	1 -	0.01	TN	1	1	0 -	TP 1	NA I	NA N	1 AI	NA	NA I	1 AV	NA I	NA I	NA	NA	NA	NA	NA	NA	NA	Med	
VI DOEOW	ADE40	A depute que sin eta luca e	,		NIA	NIA	NIA	NIA		NI A		NIA .				NIA .				NIA N					NIA	NIA	NIA	NIA	NI A		Mad	Null mutant is an adenine auxotroph [MIPS]. The deletion is
		Adenylosuccinate lyase 5-aminoimidazole-4-carboxamide ribonucleotide (AICAR) transformylase/IMP cyclohydrolase	NA NA		NA NA	NA NA		NA 1		0.01		NA I		0.01						NA N						NA 1.05					Med NA	
		5-aminoimidazole-4-carboxamide ribonucleotide (AICAR)																														
YMR120C	ADE17	transformylase/IMP cyclohydrolase	NA	NA	NA	NA	NA	1	1 -	0.02	TP	1	1 -0	.02	TP 1	.08 1	1.01 T	rP 1	1.1	1.01	TP 1	.11 1	.01	TP 1	1.12	1.02	TP 1	.11	1.02	ТР	NA	NA NA
		C1-tetrahydrofolate synthase	NA	_	NA	NA		0		2.08										0.99							TP 1		1		NA	Weak false negative FN
VMDOOOO	ADE 4	Phosphoribosylpyrophosphate						_	_	4.0						00	, ,			4.04	-						TD				NIA	NA NA
YMR300C	ADE4	amidotransferase Aminoimidazole ribotide	NA	NA	NA	NA	NA	0	0	4.2	TN	1	1 -(0.06	IP 1	.08	1 1	IP 1	1.1	1.01	IP 1	.11 1	1.02	IP 1	1.12	1	TP 1	.11	1	IP	NA	
YGL234W	ADE5,	synthetase glycinamide ribotide synthetase 5'-phosphoribosylformyl	NA	NA	NA	NA	NA	0	1 (0.95	FN	1	1 -0	.03	TP 1	.08	D.99 T	гР 1	1.1	0.99	ГР 1	.11	1	TP 1	1.12	1	TP 1	.11 (0.99	TP	Med	Should be an adenine auxotroph [SGD] - should not grow normally on minimal media.
YGR061C	ADE6	glycinamidine synthetase	NA	NA	NA	NA	NA	0	0	5.08	TN	1	1 -0	.02	TP 1	.08 1	1.03 T	гР 1	1.1	1.03	ГР 1	.11 1	.03	TP 1	1.12	1.04	TP 1	.11	1.03	TP	NA	NA NA
YDR408C	ADE8	Glycinamide ribotide transformylase	NA	NA	NA	NA	NA	0	1	1.1	TN	1	1	0 -	TP 1	.08	1 T	ΓP 1	1.1	1.01	ΓP 1	.11 1	1.02	TP 1	1.12	1.02	TP 1	.11	1.02	TP	NA	
																																Most likely a regulatory effect as this may be the only isozyme (out of five) active under severely glucose repressed
		Alcohol dehydrogenase				10.1				0	TP	1	1	0	TP 1	.08	0.76 F	P 1	1.1	0.87	ΓP 1	.11 1	1.12	TP 1	1.12	1.09	TP 1	.11	1.15	TP	Reg	conditions. NA
YMR303C	ADH2	Alcohol dehydrogenase II Alcohol dehydrogenase isoenzyme	NA	NA	NA	NA	NA	1	1 (0.13	۱P	1	1 -(.04	IP 1	.08	1 1	1	1.1	1	1 1	.11 1	.01	12 1	1.12	0.98	17 1	.11 (J.99	11	NA	NA NA
YMR083W	ADH3	III	NA	NA	NA	NA	NA	1	1	1.2	TP	1	1 -0	.01	TP 1	.08	D.98 T	TP 1	1.1	0.97	TP 1	.11	0.97	TP 1	1.12	0.93	TP 1	.11	0.95	TP	NA	NA NA
YGL256W	ADH4		NA	NA	NA	NA	NA	1	1 -	0.03	TP	1	1 -0	0.07	TP 1	.08 1	1.02 T	ГР 1	1.1	1.02	ΓP 1	.11 1	1.01	TP 1	1.12	1.03	TP 1	1.11	1.02	TP	NA	NA NA
VDD4.45\41	4 D. 15	Alcohol dehydrogenase isoenzyme	l ,,.		ļ ,	,				0.00	[, [[4.00						4.60					NI A	NA
	ADH5 ADK1	Adenylate kinase	NA NA				NA TN	0	1 -	0.03		0		0.04						1.02 T												
		Adenylate kinase mitochondrial																														
YER170W	ADK2	GTP:AMP phosphotransferase	NA	NA	NA	NA	NA	1	1 (0.04	TP	1	1 0	.02	TP 1	.08 1	1.01 T	TP 1	1.1	1.02	TP 1	.11 1	.02	TP 1	1.12	1.03	TP 1	.11	1.02	TP	NA	NA NA

												_		0	_				Ε	9	=											etal
ų,	me		ssim	ss call	Slow sim	w exp	w call	MMD sim	MD exp	имр аve	IMD call	/PGal sim	PGal exp	'PGal ave	PGal call	'PD sim	/PD exp	PD call	PDGE sim	PDGE exp	PDGE cal	PG sim	PG exp	PG call	'PE sim	PE exp	PE call	PL sim	dxe 7	L call	Class	Explanation Explanation
O. P.	Na	Annotation	Es	Ess	Slo	Sio	Sio	Σ	2	Σ	Σ	Ă.	γÞ	Σ.	ΥP	ΥP	γP	ΥP	ΥP	ΥP	ΥP	Ϋ́	γP	ΥP	∠	ΥP	Υ	∠	YPL	YPL	ਠੱ	Explanation There is an alternative pathway involving Pnp1p that can
																																substitute for the function of this adenosine kinase. This
YJR105W	ΔDO1	Adenosine kinase	ΝΔ	ΝΔ	NA	NA	NΔ	. 1	1	0.73	TP	1	1	0	TD	1 08	0.70	FD	11	0.8	FD	1 11	0.04	тр	1 12	0.00) TE	1.11	١١٥٥	и тр	Unl	activity of Pnp1p does not seem to have been established conclusively in the literature.
YCL025C		Amino acid permease			NA					-0.04		1	1	0		1.08																NA NA NA
		The acronym may be misleading. AGP3 has not been shown to be a																														
		general amino acid permease with																														
YFL055W	AGP3	broad substrate specificity Cytoplasmic alanyl-tRNA	NA	NA	NA	NA	NA	1	1	0.12	TP	1	1	-0.02	TP	1.08	1.03	TP	1.1	1.03	TP	1.11	0.99	TP	1.12	1.03	3 TF	1.11	1.0	1 TP	NA	NA NA
YOR335C	ALA1	synthetase gene	1	FP	NA	NA	NA	NA	NA	NA		NA																NA		NA	Oth	Protein synthesis not required in the model. NA
YMR170C YMR169C		Aldeyhde dehydrogenase Aldehyde dehydrogenase	NA NA		NA NA		_	1	1	0.08	TP TP	1	1	-0.04 0	TP TP	1.08	_	TP										1.11				NA NA NA
		Aldehyde dehydrogenase			NA		_	1	1	0.02	TP	1	1	-0.08	TP	1.08	1.01	TP		1.02		1.11						1.11				NA NA
YER073W	ALD5	Aldehyde dehydrogenase	NA	NA	NA	NA	NA	1	1	0.02	TP	1	1	-0.03	TP	1.08	1.01	TP	1.1	1.03	TP	1.11	1.07	TP	1.12	1.07	7 TF	1.11	1.0	6 TP	NA	NA NA The model uses a mitochondrial acetaldehyde
																																dehydrogenase in the deletion strain. In vivo this activity
YPL061W		Aldehyde dehydrogenase Basic amino acid permease	NA NA	_	NA			1	1	0.1	TP	1		-0.04	TP TP					0.91								1.11				c cannot fully compensate for the cytoplasmic activity. NA NA NA
YNL270C YML035C		AMP deaminase			NA NA			1	1	-0.01 -0.01	TP TP	1	1	-0.07 -0.01	TP	1.08	1.02	TP TP		0.99								1.11			NA NA	NA NA
		Amidase (putative)			NA			1	1	-0.02	TP	1	1	0	TP	1.08		TP		1.01			1					1.11			NA	NA NA
YPR128C	ANTT	Adenine nucleotide transporter Diadenosine 5',5"'-P1,P4-	NA	NA	NA	NA	NA	1	1	0.02	TP	1	1	-0.04	TP	1.08	1.01	IP	1.1	0.99	IP	1.11	0.99	IP	1.12	1	111	1.11	1.0	1 11	INA	NA NA
YCL050C	APA1	tetraphosphate phosphorylase I	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.07	TP	1.08	1.01	TP	1.1	1.04	TP	1.11	1.06	TP	1.12	1.07	7 TF	1.11	1.0	6 TP	NA	NA NA
YDR530C	APA2	5',5"'-P-1,P-4-tetraphosphate phosphorylase II	NA	NA	NA	NA	NA	. 1	1	-0.04	TP	1	1	-0.06	TP	1.08	1.02	TP	1.1	1.04	TP	1.11	1.03	TP	1.12	1.06	S TF	1.11	1.0	4 TP	NA	NA NA
\/ \ 41, 000\\	4 DT4	A		İ			Ī																									
YML022W	AP11	Adenine phosphoribosyltransferase	NA	NA	NA	NA	NA	1	1	1.41	TP	1	1	0	TP	1.08	0.96	TP	1.1	0.95	TP	1.11	0.96	TP	1.12	0.96	S TF	1.11	0.9	6 TP	NA	NA NA
		Similar to adenine																														
YDR441C	APT2	phosphoribosyltransferase; appears to be a nonfunctional pseudogene	NA	NA	NA	NA	NA	. 1	1	0.11	TP	1	1	-0.02	TP	1.08	0.99	TP	1.1	1	TP	1.11	0.97	TP	1.12	1.01	I TF	1.11	1.0	1 TP	NA	NA NA
YBR149W	ARA1	D-arabinose dehydrogenase	NA	NA	NA	NA	NA		1	0.01	TP	1	1	-0.03	TP	1.08	0.99	TP	1.1		TP	1.11	1	TP	1.12	0.98	3 TF	1.11	0.9	8 TP	NA	NA NA
YOL058W YJL071W		Arginosuccinate synthetase Acetylglutamate synthase	_	NA NA	NA NA	_	-	0	_	5.51 3.27	TN TP	1	1	-0.07 -0.06	TP TP	1.08	1.01		1.1	_	_	1.11						1.11			NA NA	
YJL088W	ARG3	Ornithine carbamoyltransferase	NA	NA	NA	NA	NA		1	2.1	TN	1	1	-0.01	ΤP	1.08	1.02	TP	1.1	1.03	TP	1.11	1.05	TP	1.12	1.04	1 TF	1.1	1.0	4 TP	NA	Weak false negative NA
YHR018C	ARG4	Argininosuccinate lyase N-acetyl-gamma-glutamyl-	NA	NA	NA	NA	NA	0	1	6.58	TN	1	1	0	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.03	TP	1.12	1.04	1 TF	1.1	1.0	3 TP	NA	Weak false negative NA
		phosphate reductase and																														
YER069W	ARG5	acetylglutamate kinase 3-dehydroquinate dehydratase (3-	NA	NA	NA	NA	NA	. 0	1	2.36	TN	1	1	-0.06	TP	1.08	1	TP	1.1	1.02	TP	1.11	1.02	TP	1.12	1.01	I TF	1.11	1.0	1 TP	NA	Weak false negative NA
		dehydroquinase) 3-dehydroquinate																														
		synthase epsp synthase pentafunctional arom																														
		polypeptide shikimate 5-																														FP for rich media - TN for MMD. There appears to be an
	ARO1	dehydrogenase shikimate kinase		NΑ	1 NA	10.5 NA		0	1	-0.03 -0.05		1		-0.03 -0.02		1.08		TP				1.11						1.11				d extra component in the in silico rich medium. NA NA NA
YGL148W		Chorismate synthase			NA		_	0	1	5.13		1	_	-0.02	_			TP		1.03		1.11						1.11				
		DAHP synthase; a.k.a. phospho-2-dehydro-3-deoxyheptonate																														
		aldolase, phenylalanine-inhibited;																														
		phospho-2-keto-3-deoxyheptonate aldolase; 2-dehydro-3-																														
		deoxyphosphoheptonate aldolase; 3																														
VDB03EW	A D O 2	deoxy-D-arabine-heptulosonate-7-	NIA.		NIA	NIA		,		0.00	TD	,	4	0.05	TD	4.00	4 04	TD	4.4	4.00			4.00	TD	4 40	4.00	. _		1 4 0		NIA	NA NA
1 DK035W	ARU3	phosphate synthase 3-deoxy-D-arabino-heptulosonate 7-	NA	INA	NA	NA	INA	Т	1	-0.03	12			-0.05	1P	1.08	1.01	112	1.1	1.03	IP.	1.11	1.03	۱P	1.12	1.06) 16	1.11	1.0	o IP	NA	NA NA
VPP240C	ABO4	phosphate (DAHP) synthase	NI A	N/A	NI A	NIA.	NIA			0.04			1	0.04	TD	1.00	1.00	TD	1.4	1.00	TD	1 11	1.00	ТЪ	1 40	1.0	J.,	1 4 4	4.0	4 T.	NIA.	NA NA
YBR249C YPR060C		isoenzyme Chorismate mutase			NA NA			0		0.04 3.64		1		-0.02																		NA NA NA
VGI 202/M		Aromatic amino acid aminotransferase	NIA	NIA	NA	NIA	NIA	1		0.05		1		-0.01														1.11				
YGL202W	ANU8	aniinullansierase	NA	INA	NA	NA	NA		H	0.05	117		_	-0.01	112	1.08	1.01	117	1.1	1	IP.	1.11	0.99	117	1.12	1.02	11	1.11	1 1	IP	NA	ARO8 should be able to complement ARO9 deletion on
VUD40714	ABOC	Aromatic amino acid		N. A	N.O.		N. C	_		0.40				0.00		4.00			4.4	4.00	TO		4.00	_	4.40	4.0					,	minimal media, but the gpr association might be wrong
YHK13/W	AKU9	aminotransferase II	NΑ	NΑ	NA	NA	NA	0	1	0.18	FΝ	1	1	-0.02	IΡ	1.08	1	ΠP	1.1	1.02	IΡ	1.11	1.03	IΡ	1.12	1.0	I I F	1.11	1.0	ijΙΡ	ISO	[Urrestarazu98]. NA

																													<u> </u>
			ء	_	sim	dxə	=	sim	Ω×	e Ve	call	Sin I	dxa	a c	E	9		'PDGE sim	(PDGE exp	E E	: .	call	Ε	9	=	۽ ا ۽	. -		i e i
	ORF	ıme	s sim	s call	Slow si)w e	Slow C	MMD s	MMD exp	MMD ave	MMD c	YPGal sim	r r Gal exp		YPD sim	YPD exp	YPD call	DGE	PDGE exp	YPG sim	YPG exp	PG	YPE sim	YPE exp	'PE call	(PL sim	dyo I I		Explanation
	ō :	Annotation Provides low levels of resistance	e to	Es	š	Š	š	Ē	Ē	Ē	Ξ	<u>}</u>	5	5		Ϋ́	7	Υ.	7 5		: }	7	7	7	¥	<u>}</u>	: }	: 0	Explanation $\underline{\mathcal{C}}$
YDL100	ARR	R4 arsenicals	NA NA	N.A	NA NA	A NA	NA	1	1	0.4	TP	1	1 -0.	.01 T	P 1.08				0.96 T								92 T	P N	
YPR145		N1 Asparagine synthetase			N/			1	1	0.05	TP	1			P 1.08				1.02 T	_									A NA NA
YGR124	W ASN	N2 Asparagine synthetase	NA	N.F	NA NA	A NA	NA	1	1	0.07	TP	1	1 0.	03 T	P 1.08	1.01	TP	1.1	1 T	P 1.1	11 1	TP	1.12	0.99	TP 1	.11 0.	99 T	P N	A NA NA
YDR321		P1 Asparaginase I intracellular isoz		N/				1	1		TP	1			P 1.08				0.99 T										
YPR026		H1 Acid trehalase P1 F1F0-ATPase alpha subunit			NA 0.9		NA TN				TP (1			P 0.98				1.01 T							.11 1.			
YBL099\	VAIP	P1 F1F0-A1Fase alpha suburili	NA	N/	4 0.9	11 4	IN	0.91	1	0	IP	J.82	1 -0.	.03 1	0.98	0.91	IP	0.24	0.81 1	N 0.1	14 0.5	6 IN	0.16	0.49	IN	0.05 0.	04 11	N N	Mitochondrial maintenance not required in the model in
YLR2950	C ATP	P14 ATP synthase subunit h	NA	N/	0.9	1 4.7	TN	0.91	1	0	TP (0.82	1 -0.	.01 T	P 0.98	0.73	FP (0.24	0.59 T	N 0.1	14 0.5	6 TN	0.16	0.52	TN (0.05 0	5 TI	N Ot	h primarily fermentative conditions. NA
YPL271\	,	ATP synthase epsilon P15 subunit nuclear encoded	NA.	NIA.	0.9	1 9.5	TN	0.91	4	-0.03	TD.	200		.03 T	P 0.98	0.72	ED (0.24	0.69 T	N O		0 TNI	0.46	0.54	TNI (0.05	 T	N O1	Mitochondrial maintenance not required in the model in h primarily fermentative conditions.
YDL004		P16 ATP synthase delta subunit	0.9		NA NA			NA	NA		NA			IA N			NA			IA N			NA		NA			A N	
																													Mitochondrial maintenance not required in the model in
YDR377	W ATP	P17 ATP synthase subunit f	NA	N/	A 0.9	1 3.3	TN	0.91	1	-0.03	TP (0.82	1 -0.	.04 T	P 0.98	0.83	FP (0.24	0.78 T	N 0.1	14 0.6	6 TN	0.16	0.66	TN (0.05 0.	59 T	N Of	h primarily fermentative conditions. NA
																													This is probably due to excessive respiration under the
																													simulation conditions - glucose vs oxygen limitation, may
YML081	CA ATP	P18 ATP synthase associated protein F(1)F(0)-ATPase complex beta	n NA	N/	A NA	A NA	NA	0.91	1	-0.02	TP (0.82	1 0.	15 T	P 0.98	1.03	TP (0.24	0.96 F	N 0.1	14 0.6	5 TN	0.16	0.63	TN (0.05 0.	35 T	N Me	d consider increasing maximum glc uptake in YPDGE medium. NA This is close enough to count as a correct prediction. With
YJR121\		P2 subunit	NA	N.A	NA NA	A NA	NA	0.91	1	0	TP (0.82	1 -0.	.02 T	P 0.98	0.86	FP (0.24	0.82 T	N 0.1	14 0.5	1 TN	0.16	0.55	TN (0.05 0.	53 TI	N Me	ed small changes in uptake rates this would be true negative. NA
YPR020	W ATP	P20 ATP synthase subunit g homolo	g NA	N.A	N/	A NA	NA	1	1	-0.04	TP	1	1 -0.	.02 T	P 1.08	1	TP	1.1	0.98 T	P 1.1	11 0.9	4 TP	1.12	0.95	TP 1	.11 0.	94 T	P N	
YPL0780	ATP	P4 F(1)F(0)-ATPase complex subu	nit b NA	N/	A 0.9	1 4.1	TN	0.91	1	0.19	TP	0.82	1 0.	15 T	P 0.98	0.83	FP (0.24	0.77 T	N 0.1	14 0.5	2 TN	0.16	0.51	TN	0.05 0.	54 TI	N Ot	Mitochondrial maintenance not required in the model in h primarily fermentative conditions.
		() ()																											
VDDOOG	_ _	ATP synthase subunit 5 oligomy						0.04		0.00		2.00		00 -	D 0 00	0.75		0.04	0.00				0.40						Mitochondrial maintenance not required in the model in
YDR298	CAIP	P5 sensitivity-conferring protein	NA	N/	1 0.9	1 7.7	IIN	0.91	1	-0.03	IP	J.82	1 -0.	.02 1	0.98	0.75	FP	0.24	0.66 T	N U.	14 0.5	3 IIN	0.16	0.53	IIN	1.05 0.	0/ 11	N OI	h primarily fermentative conditions. NA Mitochondrial maintenance not required in the model in
YKL0160		P7 ATP synthase d subunit	N/	_		1 3.7			1	-0.03	_								0.64 T										h primarily fermentative conditions. NA
YKL004\	V AUR	R1 Involved in phospolipid metaboli	ism 1	FF	N/	A NA	NA	NA	NA	NA	NA	NA N	IA N	IA N	A NA	NA	NA	NA	NA N	IA N	A NA	NA.	NA	NA	NA	NA N	A N	A Bi	o Sphingolipid synthesis not required in the model FP
YOR011	w AUS	S1 ATP-binding cassette (ABC) fan	nily NA	N.A	A NA	A NA	NA	1	1	-0.03	TP	1	1 (о Т	P 1.08	1.02	TP	1.1	1.02 T	P 1.1	11 1.0	з ТР	1.12	1.02	TP 1	.11 1.	03 T	P N	A NA NA
		Amino acid permease for leucing	-																										
YBR068 YDR046		P2 valine, and isoleucine (putative) P3 Valine transporter			A NA				_	-0.05	TP	1			P 1.08				1.03 T										
101040	C DAI	Valine transporter	INA	1 11/	1 14/-	1 11/4	INA	<u>'</u>		-0.03	15	-	1 -0.	.04 1	1.00	1.02	IF	1.1	1.04 1	- 1.	11 1.0	4 11	1.12	1.00	IF	.11 1.	00 1	r IV	BAT2 single deletion should not be lethal as there is a
																													mitochondrial isozyme (BAT1) - double deletion should be
		Branched-chain amino acid																											lethal. Bat1p currently does not catalyze valine transamination so this functionality should probably be added
YJR148\	V BAT	T2 transaminase	NA	N/	NA NA	A NA	NA	0	1	-0.04	FN	1	1 -0.	.01 T	P 0.69	1.03	FN	1.1	1.04 T	P 1.1	11 1.0	4 TP	1.12	1.06	TP 1	.11 1.	05 T	P Is	
VDD476		Geranylgeranyltransferase type T2 beta subunit	II	-	, NA	, I NIA	NIA.	NIA.	NI A	NIA		NIA	1A N		A NIA	NIA	NI A	NIA	NIA N	IA N		. NIA	NIA	NIA.	NIA	NIA N	, ,,	, D:	Quinone biosynthesis is not required in the model.
YPR176	DEI	Geranylgeranyltransferase type	II I	FF	NA	A NA	NA	NA	NA	NA	INA	NA N	IA N	IA IN	A NA	INA	INA	INA	NA N	IA N	A INA	NA	INA	INA	INA	NA IN	A IN	А БІ	O Quinone biosynthesis is not required in the model. FP
		alpha subunit (PGGTase-II, alph																											
YJL0310 YGR282		T4 subunit) L2 Cell wall endo-beta-1,3-glucana	1 se NA		NA NA				NA 1		NA TP	NA N			A NA P 1.08	NA 1.03	NA	NA 1 1	NA N	A N	A N/	NA 2 TD	1.12	NA 1 02	NA TD 4	NA N	A N	A Bi	O Quinone biosynthesis is not required in the model. NA NA NA NA
YGR286				_	A NA	_		1	1		TP	1			P 1.08				0.99 T										
		7,8-diamino-pelargonic acid																											
YNR058	w BIO:	aminotransferase (DAPA) aminotransferase	NA	N/	A NA	A NA	NA	1	1	-0.03	ТР	1	1 -0	02 T	P 1 08	1 04	TP	11	1.04 T	P 1 1	11 1 0	2 TP	1 12	1 06	TP 4	11 1	14 T	P N	A NA NA
		Dethiobiotin synthetase		_	_	A NA	_		-		_	1			_	-	_		1.03 T		_			_	_		_		
VNDOCC	C BIC	Transmembrane regulator of	\ \[\							0.00			1 2	00	D 4.00	1 00			4.00				4.40	4.05		,,[,		D	A NA
YNR056	C BIO	D5 KAPA/DAPA transport 3-hydroxyanthranilic acid	NA	N.F	N/	A NA	INA	1	1	-0.02	112	1	1 0.	US T	1.08	1.03	12	1.1	1.03 T	1.1	1.0	∠ IP	1.12	1.05	IP 1	.11 1.	J4 [r N	A NA NA
YJR0250		A1 dioxygenase			NA NA					-0.06		1	1 -0	.01 T	P 1.08	1.01	TP	1.1	1.02 T	P 1.1	11 1.0	2 TP	1.12	1.02	TP 1	.11 1.)2 T	P N	A NA NA
YJR078\ YBL098\		A2 Tryptophan 2,3-dioxygenase A4 Kynurenine 3-mono oxygenase			A NA					-0.03 0.05									1.05 T										
YLR2310		A5 Kynureninase			A NA					0.05		1							1.01 T										
		Quinolinate phosphoribosyl																											
YFR0470		A6 transferase H1 Beige protein homologue 1			A NA	A NA				-0.03 -0.01		1							1 T										A NA NA NA NA
YEL0630		N1 Arginine permease			A NA		NA		-	0.1		1	1 -0.	.03 T	P 1.08	0.99	TP	1.1	1.01 T	P 1.1	11 1.0	1 TP	1.12	0.99	TP 1	.11	Т	P N	A NA NA
YPL111\		R1 Arginase				NA NA				0.03			1 -0.	.06 T	P 1.08	1.01	TP	1.1	1.02 T	P 0.9	99 1	TP	1.11	0.98	TP 1	.03 0.	97 T		A NA NA
YLR438\ YML042		R2 Ornithine aminotransferase T2 Carnitine O-acetyltransferase				A NA				-0.03	TP								1.03 T										
YLR307		A1 Chitin deacetylase		NA NA						-0.04		1																	A NA NA

	Φ.		sim	call	sim	dxe.	call	sim	MD exp	MMD ave	call	Galsim	r F Gal exp	r Gal ave	YPD sim	YPD exp	PD call	PDGE sim	/PDGE exp	PDGE call	YPG sim	d exb	PG call	YPEsim	/PE exp	PEcall	SIM	dxe	call	υ	Explanation Explanation
OR.	lam	Annotation	SS	SS (Nois	Nois	No lo	AIMD		₩	Q W	P. I	5 0	Ď	9	PD	PD	PD	PD	PD	PG	PG	PG	PE	PE	J E	2	ا ل	١	Class	Explanation
		Chitin deacetylase	NA	NA	NA	NA	NA	1		0.05	TP	1	1 0.	_	P 1.0	_	2 TP	1.1	1	TP	1.11	1	_	_	_	TP 1	.11				NA NA
YAL038W	CDC19	Pyruvate kinase	1	FP	NA	NA	NA	NA N	NA	NA I	NA I	NA N	IA N	A N	A NA	N.A	NA.	NA	NA	NA	NA	NA	NA	NA	NA	NA N	1 A	1 AV	NΑ	Reg	Model has Pyk2p as an isozyme. Pyk2p may only be expressed under conditions of very low glycolytic flux [MIPS] FP Essential for nuclear and mitochondrial biosynthesis, which
YOR074C	CDC2	Thymidylate synthase	1	FP	NA	NA	NA	NA N	NΑ	NA I	NA	NA N	IA N	A N	A NA	NA	NA NA	NA	NA	NA	NA	NA	NA	NA	NA	NA N	1 A	A N	NΑ	Oth	
		Protein geranylgeranyltransferase																													
		type 1 polypeptide subunit LeucinetRNA ligase			NA NA		NΑ	NA N					IA N		A NA				NA NA												Quinone biosynthesis is not required in the model. NA Protein synthesis not required in the model NA
11 210011	0000	Louding INTO III	<u> </u>	Ë	14/1	107	14/	14/	-				.,, .,	, ,	74 147	147	100	14/1	10/1		14/1	10/1	10/	14/	14/1					Our	Essential for DNA synthesis, which is not required in our
		Thymidylate kinase			NA		NA	NA N					IA N		A NA				NA									1 AV			
YBR029C	CDS1	Phosphatidate cytidylyltransferase	0	IN	NA	NA	NA	NA N	NA	NA I	VA	NA N	IA N	A N	A NA	N.P	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA 1	NA I	1 AV	NΑ	NA	NA
																															related to fatty acids, which is essential for mitochondrial
YER061C	CEM1	Beta-keto-acyl synthase homolog	NA	NA	NA	NA	NA	1	1 ().55	TP	1	1 0.	05 T	P 1.0	8 0.8	1 FP	1.1	0.77	FP	1.11	0.57	FP ′	1.12	0.54	FP 1	.11 0	.54 F	Р	Oth	function. NA
YCL064C	CHA1	Catabolic serine (threonine) dehydratase	NA	NA	NA	NA	NA	1	1 -	0.03	TP	1	1 -0.	05 T	P 1.0	8 1.0	2 TP	1.1	1.02	TP	1.11	1.04	TP	1.12	1.05	TP 1	.11 1	.04	ГР	NA	NA NA
		Phosphatidyl-ethanolamine N-methyltransferase			NA			0		0.03		0	1 -0.				1 FN									FN					Catalyzes 1st step in pathway from PE to PC. Opi3p can also catalyze this step, but it is very inefficient; mutant cells are viable and not auxotrophic for choline or other phospholipid intermediates; membranes of mutants contain 10% PC and 40-50% PE (WT is 40-45% PC and 15-20% PE); this deletion is lethal in silico since we require fixed amounts of these specific phospholipids in our biomass (in vivo there is flexibility as to which phospholipids are used).
		Chitin synthase 1			NA					0.02		1		03 T			NA					NA				NA N					NA NA
		Chitin synthase 2	1	FP	NA	NA	NA	1	1	0	ТР	1	1 -0.	03 T	P NA	N/A	NA NA	NA	NA	NA	NA	NA	NA	NA	NA	NA N	1 AL	1 AV	NA.	Dis	Gene is listed as essential, but there is data for MMD and YPGal. In any case chitin synthesis is not required in the
YBR023C	CHS3	Chitin synthase 3		NA	NA	NA	NA	1	1 -	0.03	TP	1		03 T	P 1.0	8 1.0	1 TP	1.1	1	TP	1.11	1.01	TP ′	1.12	0.99	TP 1	.11 1	.01	ГΡ	NA	NA NA
		Citrate synthase			NA		NA	1	_		TP	1	_	02 T	P 1.0		9 TP		_							TP 1		.81		NA	NA NA
	CIT2 CIT3	Citrate synthase Citrate synthase	NA NA	_	NA NA	NA NA	NΑ	1	_		TP TP	1		07 T	P 1.0		2 TP	1.1	1.03	_			TP '			TP 1		.03		NA	NA NA NA
		Choline kinase			NA		NA	1	_	_	TP	1	_		P 1.0		9 TP														NA NA
YBR003W	COQ1	Hexaprenyl pyrophosphate synthetase Para hydroxybenzoate: polyprenyl	NA	NA	NA	NA	NA	1	1 (0.04	ТР	1	1 0.	09 T	P 1.0	8 0.9	5 TP	1.1	0.83	FP	1.11	0.48	FP '	1.12	0.45	FP 1	.11 0	.58 F	ъ	Bio	Quinone biosynthesis is not required in the model. NA
YNR041C	COQ2	transferase	NA	NA	NA	NA	NA	1	1 (0.01	TP	1	1 0.	11 T	P 1.0	8 0.9	5 TP	1.1	0.91	TP	1.11	0.56	FP	1.12	0.54	FP 1	.11 0	.52 F	ъ	Bio	Quinone biosynthesis is not required in the model. NA
VOI 0000	0000	3,4-dihydroxy-5- hexaprenylbenzoate			1	4.0		4					4	00 T	D 4.0				0.70		4.44	0.54	ED.	1.10	0.40	FD 4	44 0		-	D:-	O disease bissenth sale is not seen in the seed of
		methyltransferase C-methyltransferase (putative)	NA NA		1	4.3		1		0.21	TP	1							0.78												Quinone biosynthesis is not required in the model. NA Quinone biosynthesis is not required in the model NA
		Monooxygenase	_	_	NA	_		1	_	_	TP	1	1 0.		P 1.0				0.8											Bio	
		Coenzyme QH2 cytochrome c reductase 44 kDa core protein subunit Farnesyl transferase (putative)			0.9	4 NA	TN	0.89		0.03		1.82			P 0.9				0.77												Mitochondrial maintenance not required in the model in primarily fermentative conditions. NA Quinone biosynthesis is not required in the model NA
YLR038C								0.89																							This is probably due to excessive respiration under the simulation conditions - glucose vs oxygen limitation, may consider increasing maximum glc uptake in YPDGE medium. NA
YNL052W	COYE	Cytochrome c oxidase chain Va	NIA	NIA	NIA	NA	NΙΛ	1	1	0.03	тр	1	1 0	17 7	D 10	8 1 0	2 TD	1.1	0.94	тр	1 11	0.65	ED.	1 12	0.61	ED 4	11 0	69 1	ь	leo	COX5A is the dominant isoform - COX5B cannot fully compensate [SGD].
		Cytochrome c oxidase chain Vb				NA		1		0.03		1			P 1.0				1.01												
																		0.5	0.7-			0.00			0.01		0.5				Higher oxygen uptake rate or lower glucose uptake rate will
		Cytochrome c oxidase subunit			NA			0.89																							Mitochondrial maintenance not required in the model in
		Cytochrome c oxidase subunit VII Cytochrome c oxidase chain VIII						0.89											0.74												Null mutant is viable, but should be deficient in cellular respiration and cytochrome C oxidase activity [SGD] so there should be a growth defect on non-fermentable carbon
		,																													Higher oxygen uptake rate or lower glucose uptake rate will
YDL067C	COX9	Cytochrome c oxidase subunit VIIa Arginine specific carbamoyl	NA	NA	NA	NA	NA	0.89	1 ().14	TP C	.82	1 0.	05 T	P 0.9	8.0	2 FP	0.24	0.75	TN	0.14	0.53	TN (80.0	0.5	TN 0	.05 0	.52	ΓN	Med	make this deleterious in the model. NA
YOR303W	CPA1	phosphate synthetase	NA	NA	NA	NA	NA	0	1 (5.82	TN	1	1 -0	.1 T	P 1.0	8 1.0	2 TP	1.1	0.98	TP	1.11	0.98	TP	1.12	0.98	TP 1	.1 0	.98	ГР	NA	Weak false negative NA

			_		Ε	٩	=	Ε	9	Ð	=	Ē	dx	Ne	=	اء	ا ۵	_ -	sim	PDGE exp	ا ا		l_	_		1_	_				eta
ш	me		sim	call	w sim	e e	w ca	D sim	MD exp	MMD ave	MD call	/PGal sin	Gale	Gal ave	PGal cal	(PD sim	PD exp	PD call	PDGE sin	PDGE exp	(P.G. sim	dxe	3 call	/PE sim	(PE exp	call	/PL sim	dxə -	- call	Class	Explanation
ORF	Naı	Annotation	Ess	Ess	Slo	Slo	Slo	DIMIN	Z	Σ	M	Ϋ́	γP(Ϋ́	YP(YPI	ΥPI	4 2	YPI	YPI	ΛÞ	YPG	YPG	YPI	YPI	YPE	YPI	IЫ	YPI		
YJR109C		Carbamyl phosphate synthetase	NA	NA	NA	NA	NA	0	1	8.21	TN	1	1	0.07	TP	1.08	1.02	ΓP 1	1.1	1.03 T	P 1.1	11 1.03	3 TP	1.12	2 1.04	1 TP	1.1	1.04	TP	NA	Weak false negative NA
YNL130C		Sn-1,2-diacylglycerol cholinephosphotransferase	NA	ΝΔ	NA	NA	NΔ	1	1	0.03	TP	1	1	-0.04	тр	1.08	1 7	ΓP 1	1.1	1 T	D 1 .	11 0.99	ТР	1 12) n q	I TP	1 11	n 99	ТР	NA	NA NA
		Carnitine transporter			NA		NA	1	1	-0.03	TP	1	1	-0.06				ΓP 1		1.02 T							1.11	1.01		NA	NA NA
YDL142C	CRD1	Cardiolipin synthase	NA	NA	NA	NA	NA	1	1	0.01	TP	1	1	-0.02	TP	1.08	0.98	ΓP 1	1.1	0.99 T	P 1.1	11 0.93	3 TP	1.12	0.85	TP	1.11	0.93	TP	NA	
YBR036C	CSG2	Required for mannosylation of inositolphosphorylceramide (IPC)	NΙΛ	NIA	NA	NA	NA	1	1	-0.02	TP	1	1	-0.05	тр	1 00	1 02 7	TD 1		1 01 T	D 1 .	11 0.98	ть	1 12	0 00		1 11	1 01	тр	NΙΛ	NA NA
		Catalase A			NA				1	0.28		1	1	0.05			1.02					11 0.99					1.11	1.01		NA	
																															Lower oxygen uptake rate would correct this false negative
		Citrate tranporter		_	NA		_		1	-0.05		1	1	0.21								11 0.96									
YGR088W	CITT	Catalase I	NA	NA	NA	NA	NA	1	1	-0.02	IP	1	1	-0.07	IP	1.08	1 7	1 1	1.1	1.01 1	P 1.	11 1.01	I IP	1.12	2 1.02	2 112	1.11	1.01	IP	INA	INA NA
		17 kDa VO sector subunit dicyclohexylcarbodiimide																													
		binding subunit proteolipid vacuolar ATP synthase proteolipid C vacuolar ATPase V0 domain																													The cup5 null mutant is viable but lacks vacuolar (H)- ATPase activity, and is defective in vacuolar acidification, vacuole biogenesis, vacuolar protein targeting, and
YEL027W		subunit c (dicyclohexylcarbodiimide binding subunit) (17 kDa)	NA	NA	1	17.9	FP	1	1	-0.01	TP	1	1	0	TP	1.08	0.72 F	P 1	1.1	0.62 F	P 1.1	11 0.53	3 FP	1.12	2 0.58	3 FP	1.11	0.58	FP	Oth	endocytosis [SGD]. The slow growth phenotype could be due to problems in pH balancing.
VMI 0540	CVB3	L-lactate cytochrome c	NIA	NIA.	NI A	NIA.	NI A	,		0.04	TD	,	1	0	TD	1.00	1 04 3	rp .		1 04 -		11 4 04		1.40	1 00	, , , ,	0.04	1.07	EVI	N/1~-	Lower oxygen uptake rate would correct this false negative prediction.
YML054C	CYBZ	oxidoreductase cytochrome b2	NA	NA	NA	NA	NA	1	1	0.01	IP	1	1	0	IP	1.08	1.01	PT	1.1	1.04 1	71.	11 1.06) IP	1.12	2 1.08	3 IP	0.64	1.07	FN	ivied	prediction. NA cAMP synthesis not required in model as its primarily used as
YJL005W	CYR1	Adenylate cyclase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA N	NA N	AV	NA N	A N.	A NA	NA	NA	NA	NA	NA	NA	NA	Oth	a signaling molecule. FP This reaction is not used in complete media, because
YAL012W	CYS3	Cystathionine gamma-lyase	NA	NA	NA	NA	NA	1	1	0.29	TP	1	1	0.63	тр	1 08	0 94 7	TP 1	1	0.9 T	P 1 ·	11 0 67	7 FP	1 12	0.77	7 FP	1 11	0.88	ТР	Med	cysteine is available. Should only be a cysteine auxotroph [SGD].
171201211	0100	System of miss gamma tydes	147.	14/	147.	10/1			Ė	0.20				0.00		1.00	0.04			0.0 1	Ë	11 0.07	Ť	1.12	0.77	Ë		0.00	Ħ	Wied	
																															CYS4 null mutant is deficient in vacuolar ATPase activity and vacuolar acidification [MIPS]. The false positives could be
YGR155W	CYS4	Cystathionine beta-synthase	NA	NA	1	3.7	FP	1	1	0.11	TP	1	1	0.17	TP	1.08	0.91	ΓP 1	1.1	0.9 T	P 1.1	11 0.71	1 FP	1.12	0.72	2 FP	1.11	0.83	TP	Oth	due to pH balancing, which is not accounted for in the model. NA
																															This is now below the second in the second s
																															This is probably due to excessive respiration under the simulation conditions - glucose vs oxygen limitation, may
YOR065W	CYT1	Cytochrome c1	NA	NA	NA	NA	NA	0.89	1	0.02	TP	0.82	1	0.23	TP	0.98	0.96	ΓP 0.	.24	0.92 F	N 0.	14 0.62	2 TN	0.08	0.57	7 TN	0.17	0.61	TN	Med	consider increasing maximum glc uptake in YPDGE medium. NA
		Dihydroxyacetone kinase (putative) Dihydroxyacetone kinase			NA NA		NA NA	1	1	0.03	TP	1	1	0 -0.06								11 1.02 11 1.01									
		Allantoinase		_	NA		_	1	1	0.05	TP	1	1	-0.06	_	_	1.02	_	_		_	11 0.98	_	_			1.11	1.02	TP	NA	INA INA
	DAL2	Allantoicase		_	NA		_	1	1	0	TP	1	1	-0.05	_	_		ΓP 1	_	1.04 T	_	_	_	_	2 1.07			1.05	TP	NA	NA NA
		Ureidoglycolate hydrolase		_	NA		_	1	1	0.02	TP	1	1	0	TP			_	_		_	11 0.98	_	_		_		0.99	TP	NA	
		Allantoin permease Allantoate permease			NA NA			1	1	0.03	TP	1	1	-0.01	TP		1.02 T		1.1		P 1.1			1.12		I TP		1	TP	NA NA	NA NA NA
		Malate synthase 2			NA		_	1	1	-0.02 0	TP	1	1	-0.01	_							11 1.0 ² 11 0.98									INA INA INA
		Asparaginyl-tRNA synthetase	1	_	NA		_	NA	NA	NA	-	NA	NA		_		NA N			NA N				NA			NA	NA	_	Oth	
		Similar to rRNA methyltransferase																													
		(Caenorhabditis elegans) and hypothetical 28K protein (alkaline																													
		endoglucanase gene 5' region)																													
YFL001W	DEG1	from Bacillus sp.	NA	NA	1	3.5	FP	1	1	-0.02	TP	1	1	-0.02	TP	1.08	0.86 F	P 1	1.1	0.79 F	P 1.1	11 0.8	TP	1.12	0.8	TP	1.11	0.81	TP	Oth	Pseudouridine biosynthesis not required in the model. NA
VOD000M	DED4	Dibdasfalata as divetas				1	l		l																1	l			ll		Folate biosynthesis is not required in rich media. Lethality
1 UR 236W	DFR1	Dihydrofolate reductase Protein similar to bacterial seryl-	1	FP	NA	NA	NΑ	NA	NA	NA	NΑ	NA	NΑ	NΑ	IVA	AVI	NA N	NA N	NΑ	NA N	A N.	A NA	NA	NA	NA	NA	NA	NA	NΑ	ACC	may be due to toxicity of DHP [Bayly02]. FP
YHR011W		tRNA synthases	NA			6.5			1	-0.04			1	0.19	TP	1.08	0.74 F	P 1	1.1	0.65 F	P 1.1	11 0.54	4 FP	1.12	0.44	FP	1.11	0.49	FP	Oth	Protein synthesis not included in the model. NA
		Dicarboxylate transport protein			NA		_			-0.02												11 1.03									NA NA
		Dimethyladenosine transferase			NA		_		_																						Quinone biosynthesis is not required in the model FP
YPL265W	DIP5	Dicarboxylic amino acid permease D-lactate ferricytochrome c	NA	NA	NA	NA	NA	1	1	0	TP	1	1	0.03	TP	1.08	0.99	ΓP 1	1.1	0.96 T	P 1.1	11 0.87	7 TP	1.12	0.81	I TP	1.11	0.88	TP	NA	NA NA
YDL174C	DLD1	oxidoreductase	NA	NA	NA	NA	NA	1	1	0.01	TP	1	1									11 1.02									
YLR172C	DPH5	Diphthamide biosynthesis	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1									11 1									
		Dihydrosphingosine phosphate lyase (also known as sphingosine																													
YDR294C	DPL1	phosphate lyase)	NA	NA	NA	NA	NA	1	1	0.06	TP	1	1	-0.03	TP	1.08	1.01	TP 1	1.1	1.02 T	P 1.1	11 1.02	2 TP	1.12	2 1.04	1 TP	1.11	1.03	TP	NA	NA NA
		Dolichol phosphate mannose																													
YPR183W	DPM1	synthase Diacylglycerol pyrophosphate	0	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA N	NA N	NΑ	NA N	A N.	A NA	NA	NA	NA	NA	NA	NA	NA	NA	NA NA
YDR284C	DPP1	phosphatase	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	-0.03	TP .	1.08	1.01	TP 1	1.1	0.99 T	P 1.1	11 0.98	з тр	1.12	0.98	ТР	1.11	0.99	TP	NA	NA FN
																							-								

			_		sim	dxə	=	sim	<u>.</u>	e :	call	۽ اڇ	ave	l =	u	Q.	_	'PDGE sim	PDGE exp	. E	ء ا :	. =	۽	۵	l_	_	۵	_		Explanation Explanation
щ.	me		s sim	s call	is vi	(e) %	W C	MMD si	M exp	MMD ave	MMD	rPGal sim	YP Gal ave	/PGal cal	YPD sim	ҮРD ехр	/PD call		PDGE exp	YPG sim	YPG exp	PG call	YPE sim	(PE exp	PE call	/PL sim	L exp	L call	Class	st
ORF	Z	Annotation	Es	Es	Slo	Slo	Slo	Σ :			_					•	_	_		- /	_	_	_	_	-	-		YPL		
YLL018C	DPS1	Aspartyl-tRNA synthetase Urea amidolyase (contains urea	1	FP	NA	NA	NA	NA N	1 AI	1 AV	1 A	N AI	A NA	NA	NA	NA	NA	NA	NA N	IA N.	A N	A NA	NA	. NA	NA	NA	NA	NA	Oth	Protein synthesis not required in the model NA
		carboxylase and allophanate																												
		hydrolase)			NA								0.02						0.98 T											
YHL016C	DUR3	Urea active transport protein	NA	NA	NA	NA	NA	1	1 0	.04	ГР	1 1	-0.0	TP	1.08	1.01	TP	1.1	1.02 T	P 1.0	07 1.0	3 TF	1.11	1 1.04	1 TP	1.07	1.02	TP	NA	
																														Converts dUTP to dUMP preventing uracil incorporation into DNA [MIPS]. Since we do not include DNA replication in our
YBR252W	DUT1	DUTP pyrophosphatase	1	FP	NA	NA	NA	NA N	I AI	A A	1 AI	N A	A NA	NA	NA	NA	NA	NA	NA N	IA N	A N	A NA	NA	. NA	NA	NA	NA	NA	Oth	model, this function is unnecessary.
.																														Dys1p catalyzes first two steps in hypusine biosynthesis.
		Deoxyhypusine synthase Sulfite reductase (putative)	1 NA		NA NA	NA NA		NA N		NA N .28		NA N	A NA		NA 1.08				NA N											Hypusine is required in our model. FP NA NA
		ExtraCellular Mutant			NA		_	1	_	_	ГР	1 1	0.00	TP					1.04 T											
		Gamma-glutamyltransferase																												
		homolog			NA NA			0			TP N	1 1							0.99 T											NA NA Weak false negative NA
		Acetylornithine acetyltransferase Ethanolamine kinase	NA		NA		_	1	_	_	ΓP	1 1	-0.0	TP	1.08	1.03				P 1.				2 0.98			1.01		NA	NA NA
YGR254W						NA		1			ГР	1 1		7 TP	1.08				1.02 T								1.02			
VHD123\\\/	EDT1	Sn-1,2-diacylglycerol ethanolamine- and cholinephosphotranferase	NIA	NIA	NΙΛ	NA	NΙΛ	1	, ,	.05	гр	1 1	0.0		1 00	1.01	тр	1 1	1.02 T	D 4 .	11 1 0	12 TE	1 11	1 03	ТБ	1 11	1.02	тр	NΙΛ	NA NA
		Squalene monooxygenase	0					NA N				IA N			NA				NA N			A NA					NA			
YPL028W		Acetoacetyl CoA thiolase	0	TN			_	NA N				N AI			NA	NA			NA N			A NA							NA	NA FP
\/\ \D0070	ED04	Cytochrome P450 lanosterol 14a-	_			l	l		. II.					l							.			l	l				.	NA NA
		demethylase Mevalonate kinase	0		NA NA		_	NA N				N AI	A NA A NA		NA NA				NA N			A NA		NA NA			NA NA			NA NA NA
TWITTEGOTT	LIKOTZ	3-hydroxy-3-methylglutaryl	Ů		1471	147		14/	<u>" </u>				1,00	1.47.	14/1	1471		1471	10/	14.	/\ \\\		147.	147	1471	14/1	14/1		14/1	Deletion of ERG13 is lethal [Daum98]. Discrepancy between
YML126C	ERG13	coenzyme A synthase	0	TN	NA	NA	NA	NA N	1 AI	1 A	1 AI	N A	A NA	NA	0	0.96	FN	0	0.91 F	N C	0.9	2 FN	0	0.9	FN	0	0.9	FN	Dis	the two experimental studies.
																														Ergosterol can be synthesized by the model from zymosterol, which bypasses the reaction catalyzed by the ERG2 gene
YMR202W	ERG2	C-8 sterol isomerase	NA	NA	1	3.2	FP	1	1 0	.54	гР	1 1	0.16	l _{TP}	1.08	0.92	TP	1.1	0.76 F	P 1.1	11 0.8	6 TF	1.12	0.75	5 FP	1.11	0.73	FP	Mod	product. This bypass is probably incorrect.
		Farnesyl diphosphate synthetase												T		0.02			-											
		(FPP synthetase)	0		NA		_					N AI		NA					NA N			_		. NA			NA			
		Sterol C-14 reductase C-4 sterol methyl oxidase	NA 0		0 NA		TΝ	0 NA N				0 1 NA N	0 A NA	TN NA		0.79 NA	NA		0.62 T	N C			0 NA		TN NA		0.68 NA			
		C-3 sterol dehydrogenase	0	_	NA		_	NA N		_		VA N					NA	_		A N	_	_	NA		NA				NA	NA NA
YLR100W	ERG27	3-keto sterol reductase	0	TN	NA	NA	NA	NA N	1 Al	A A	1 A	N AI	A NA	NA	NA	NA	NA	NA	NA N	IA N	A N	A NA	NA	. NA	NA	NA	NA	NA	NA	NA NA
																														Ergosterol can be synthesized by the model from zymosterol, which bypasses the reaction catalyzed by the ERG3 gene
YLR056W	ERG3	C-5 sterol desaturase	NA	NA	1	5.5	FP	1	1 0	.06	гР	1 1	-0.0	↓ ITP	1.08	0.92	ТР	1.1	0.9 T	P 1.	11 0.8	2 TF	1.12	0.84	1 TP	1.11	0.92	ТР	Mod	product. This bypass is probably incorrect.
																														Erg4p catalyzes the last step in the synthesis of ergosterol.
																														when it is deleted, the precursor accounts for 90% of the
																														cell's sterol composition, suggesting that Erg4p is the only enzyme that can catalyze this reaction; ergosterol is
																														completely replaced by its precursor in the plasma
																														membrane of erg4 mutants; the mutant is viable, but there
																														are distinct defects relating to drug sensitivity [Zweytick00]; thus, this FN is a result of our biomass function, which
YGL012W	ERG4	Sterol C-24 reductase	NA	NA	NA	NA	NA	0	1 0	.03 F	N	0 1	0	FN	0	0.96	FN	0	0.96 F	N C	0.9	3 FN	0	1.01	I FN	0	0.95	FN	Bio	requires ergosterol.
		Cytochrome P450 involved in C-22				1			Ť					Ť				_	-				Ť	1						
		denaturation of the ergosterol side-							. .																					L.
YMR015C	ERG5	cnain	NA	NA	NA	NA	NA	1	1 0	.14	P	1 1	-0.1	TP	1.08	1	TP	1.1	1.03 T	P 1.1	11 1.0	04 TF	1.12	2 1.03	3 TP	1.11	1.04	TP	NA	NA FN Ergosterol can be synthesized by the model from zymosterol,
																														which bypasses the reaction catalyzed by the ERG6 gene
YML008C	ERG6	Ergosterol synthesis	NA	NA	1	3.2	FP	1	1 0	.36	ГР	1 1	0.02	TP	1.08	0.84	FP	1.1	0.81 F	P 1.	11 0.8	2 TF	1.12	0.78	TP.	1.11	0.72	FP	Mod	
YHR072W	EDO-	2,3-oxidosqualene-lanosterol	_			N. A	N. A	NIA.							N/A	NI A	NIC	NIA	NIA .						N. A	NIA	NI A	NIC	NIA	NA NA
		48 kDa phosphomevalonate kinase	0		NA NA			NA N					A NA			NA NA	NA	NA NA	NA N	A N	A N	A NA	NA NA	NA NA	NA	NA NA	NA	NA	NA	NA NA NA
YHR190W		Squalene synthetase	0		NA			NA N											NA N											NA NA
		Exo-1,3-beta-glucanase			NA			1		.05		1 1	0						1.01 T											NA NA
YDR261C	EXG2	Exo-1,3-beta-glucanase Long chain fatty acyl:CoA	NA	NA	NA	NA	NA	1	1 0	.03	Р	1 1	-0.0	2 TP	1.08	1	TP	1.1	1 T	P 1.1	11 1	TP	1.12	2 1	TP	1.11	1	TP	NA	NA NA
YOR317W	FAA1	synthetase	NA	NA	NA	NA	NA	1	1 -0	.04	ГР	1 1	0	ТР	1.08	1.01	TP	1.1	1.01 T	P 1.1	11 1.0	1 TF	1.12	2 1.01	ТР	1.11	1.01	ТР	NA	NA NA
		Acyl-CoA synthase			NA			1		0.01		1 1	-0.0						1.01 T											
		Long chain fatty acyl:CoA																												
YMR246W	FAA4	synthetase long-chain fatty acid:CoA ligase	NA	NΑ	NΑ	NA	NΑ	1	1 0	.03	гР	1 1	-0.0	ТР	1.08	1.01	ТР	1.1	1.02 T	P 1	11 1 0)4 TF	1 13	2 1 03	ТР	1.11	1.02	ТР	NA	NA NA
1011				, \	, \		. 47 (. 50			0.0		00								2	7.02					, .	TVA

	0		sim	call	sim	dxə	call	sim	exp	лмD ave	call	PGal sim	l exp	l ave	PGal call	mis	dxe	all	PDGE sim	PDGE exp	PDGE call	sim	dxe	call	im	dx	all	m.	dxə	call		er et al
ORF	ame	Annotation	S SS	SS C	Slow sim	No	low	MMD sim	IMD exp	MD	IMD	PGa	PGal	PGal	PGa	'PD sim	PD exp	PD call	PDG	PDG	PDG	PG sim	PG exp	PG	'PE sim	PE exp	PE call	'PL sim	YPL e	YPLo	Class	Explanation
YFR019W	FAB1	1-phosphatidylinositol-3-phosphate 5-kinase FAD synthetase				8.3 NA		1	1 NA	0	TP	1 NA I	1 -	_		1.08	0.63	FP	1.1	0.73 NA		1.11	<u> </u>		1.12	0.5	FP	1.11	0.54	FP		Mutation causes pleiotropic effects on nuclear migration and orientation, and separation of mitotic chromosomes (forms aploid and binucleate cells).Mutant has defects in vacuolar function and morphology [SGD]. Riboflavin biosynthesis is not required in the model FP
TDE043C	IADI	I AD Synthetase	<u> </u>	1 -	INA	INA	INA	INA	INA	INA	INA	INA	N/A	INA	INA	INA	INA	INA	INA	INA	INA	INA	INA	INA	INA	INA	INA	INA	INA	INA	Otti	INDUIAVIT DIOSYTUTESIS IS TIOL TEQUITED IT THE THOUGH
YKL182W	FAS1	Acetyl transferase dehydratase enoyl reductase malonyl/palmityl transferase pentafunctional enzyme	0	TN	NA	NA	NA	NA	NA	NA	NA	NA I	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA NA
YPL231W	FAS2	Fatty acid synthase alpha subuni	0	TN	NA	NA	NA	NA	NA	NA	NA	NA I	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NΑ	NA	NA	NA	NA		NA	NA	NA NA
YBR041W	FAT1	Fatty acid transporter 5,10-methenyltetrahydrofolate	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1 -	0.01	TP	1.08	1.01	TP	1.1	1	TP	1.11	0.99	TP	1.12	0.99	TP	1.11	1	TP	NA	NA NA
YER183C	FAU1	synthetase	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1 -	0.02	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.02	TP	1.12	1.03	ТР	1.11	1.02	TP	NA	NA NA
YKL060C	FBA1	Aldolase	0.19	TN	NA	NA	NA	NA	NA	NA	NA	NA I	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	In silico slow growth.
YLR377C	FBP1	Fructose-1,6-bisphosphatase	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	0	TP	1.08	1	TP	1.1	1	TP	1.11	0.85	TP	0.41	0.84	FN	0.89	0.88	TP	Med	Lower oxygen uptake rate would correct this false negative prediction.
YJL155C	FBP26	Fructose-2,6-bisphosphatase	NA	NA	NA	NA	NA	1	1	0.01	TP	1		0.05	_	1.08	1.01	TP	1.1	1.03	TP	1.11	0.96	TP	1.12	0.91	TP	1.11		TP	NA	NA NA
		Cytosine deaminase Purine-cytosine permease	NA NA		NA NA	NA NA	NA	1	_	-0.03 -0.02	TP TP	1		0.07	_	1.08	1.02 0.97	_	1.1	1.02	_	1.11	1.02	_	1.12	1.04	_	1.11	1.03		NA NA	NA NA NA
		Purine-cytosine permease	_	_	NA	NA	_	1	_		TP	1	_	0.04	_	1.08	1.02			1.02						1.02			1.03	_		NA NA
YER060WA	FCY22	Purine-cytosine permease	NA	NA	NA	NA	NA	1	1	-0.04	TP	1	1 (0.01	TP	1.08	1.01	TP	1.1	1.03	TP	1.11	1.04	TP	1.12	1.04	TP	1.11	1.04	TP	NA	NA NA
YCR034W	EEN1	1,3-beta-glucan synthase subunit (putative) ELO1 homolog	NA	NIA	NIA	NA	NIA	•	1	0.26	ENI	0	1	0.05	ENI	0	0.03	EN	0	0.04	EN	0	0.02	EN	0	0.91	EN	0	0.04	EN	Pio	Involved in synthesis of 1,3-beta-glucan, probable beta-1,3-glucan synthase subunit - unknown whether it is a catalytic subunit or GTP-binding subunit. Membranes of mutant cells have 90% less beta-1,3-glucan synthase activity - could an alternate subunit exist? This is lethal in silico because beta-1,3-glucan is required in biomass.
1 CRU34VV	FENI	Plasma Membrane H+-	INA	INA	NA	NA	INA	0	1	0.36	FIN	0	1 -	0.05	FIN	0	0.93	FIN	U	0.94	FIN	U	0.92	FIN	U	0.81	FIN	U	0.94	FIN	DIO	Pantothenate is necessary for CoA biosynthesis, which is not
YCR028C	FEN2	Pantothenate Symporter	NA	NA	1	3.1	FP	1	1	0.11	TP	1	1	0	TP	1.08	0.8	FP	1.1	0.8	FP	1.11	0.83	TP	1.12	0.77	FP	1.11	0.72	FP	Oth	required by the model. NA
YLR342W	FKS1	1,3-beta-D-glucan synthase	NA	NA	1	4.5	FP	1	1	-0.01	TP	1	1	0	TP	1.08	0.62	FP	1.1	0.74	FP	1.11	0.84	TP	1.12	0.84	TP	1.11	0.87	TP	Iso	There are three alternate isozymes in the model, but FKS1 deletion experimentally disrupts the enzymatic function significantly.
YMR306W	FKS3	Protein with similarity to Gls1p and Gls2p (GB:Z49212)	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1 -	0.05	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.03	TP	1.12	1.01	TP	1.11	1.02	TP	NA	NA NA
YIL134W	FLX1	FAD carrier protein	NA	NA	1	3.4	FP	1	1	-0.02	TP	1		0.01						1.03											Dis	There is no evidence of significant deleterious phenotype. Experimentally flx1 strain has low FMN/FAD ratio [MIPS]. The two studies also show conflicting results. NA
		Riboflavin kinase	1		NA			NA	NA 1	NA		NA I				NA	NA			NA			NA			NA			NA	NA	Bio	Riboflavin biosynthesis is not required in the model FP NA NA
		Methionyl-tRNA transformylase Dihydro-6-hydroxymethylpterin pyrophosphokinase dihydroneopteri n aldolase dihydropteroate synthetase			NA NA	NA NA		NA		0.42 NA		NA I								1.04 NA												Folate biosynthesis is not required in rich media. Lethality may be due to toxicity of DHP [Bayly02].
VCD267C	FOL 2	CTD systemydrates I			NIA	NIA		NIA	NIA	NIA	NI A	NIA I		NIA	NIA	NIA	N. A.	NI A	NIA	NIA	NIA	N14	NIA	NI A		NIA	NI A	NIA.	NIA	NI A	٨٥٥	Folate biosynthesis is not required in rich media. Lethality
YGR267C	I-OLZ	GTP-cyclohydrolase I		FP	NA	NA	NA	NA	NA	NA	INA	INA	NA	NA	INA	INA	INA	INA	AVI	NA	INA	INA	IVA	INA	INA	NA	ΝA	INA	NA	INA	ACC	may be due to toxicity of DHP [Bayly02]. FP Folate biosynthesis is not required in rich media. Lethality
YMR113W	FOL3	Dihydrofolate synthetase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA I	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Acc	may be due to toxicity of DHP [Bayly02].
YKR009C	FOX2	Multifunctional beta-oxidation protein	NA	NA	NA	NA	NA	1	1	0	TP	1	1 -	0.07	ТР	1.08	1.03	TP	1.1	1.05	TP	1.11	1,04	TP	1,12	1.07	TP	1,11	1.06	ТР	NA	NA NA
YLL043W	FPS1	Glycerol channel proteir	NA	NA	NA	NA	NA	1	-	-0.02	TP	1	1 -	0.04	TP	1.08	0.99	TP	1.08	1.02	TP	0.9	1.05	TP	1.12	1.03	TP	1.11	1.03	TP	NA	NA NA
YLR060W YFL022C		Phenylalanine-tRNA ligase subuni Phenylalanine-tRNA ligase subuni	_	_	NA NA	_	_	NA NA	NA					NA NA						NA NA												Protein synthesis not required in the model NA Protein synthesis not required in the model NA
	FUI1	Uridine permease			NA		_	NA 1		0.03		1								0.89												
		Fumarase (fumarate hydralase) Glutamate decarboxylase	NΑ		NA NA		NΑ	1	1		TP TP	1	1 (0.96												The model predicts a reduced growth rate, but the drop is not that large. NA NA NA
		Galactokinase				NA		1		-0.01	TP			2.08	TN	1.08	0.99	TP	1.1	0.97	TP	1.11	0.99	TP	1.12	0.98	TP	1.11	0.99	TP	NA	NA NA
YBR019C	GAL10	UDP-glucose 4-epimerase	NA	NA	NA	NA	NA	1	1	-0.01	TP	0.18	0 ;	3.14	TN	1.08	1.01	TP	1.1	1.01	TP	1.11	1.01	TP	1.12	0.99	TP	1.11	0.99	TP	NA	
YLR081W	GAL2	Galactose permease	NA	NA	NA	NA	NA	1	1	-0.04	TP	1	0	1.52	FP	1.08	1.01	TP	1.1	1.03	TP	1.11	1.03	TP	1.12	1.05	TP	1.11	1.04	TP	Iso	Gal2p is the high-affinity galactose transporter, which is known to be a major player in gal transport. Deletion of GAL2 drastically reduces growth on galactose [Douglas64]. Model includes other isozymes (HXT genes) that are not nearly as efficient for gal transport so disabling their gal transport ability should result correct prediction.

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ORF	ame		Ess sim	es call	Slow sim	Slow exp	MMD sim	MMD exp	ММD аve	MMD cal	PGal sım	YP Gal ave	YPGal cal	YPD exp	/PD call	rPDGE sim	PDGE cal	YPG sim	YPG exp	YPE sim	YPEexp	(PE call	YPL sim	YPL exp	rPL call		Forster
ō	ž	Annotation	ű	Ш	S	<u> </u>	ñΞ	Σ	Σ	Σ	<u> </u>	¥	F F	<u> </u>	⊁ :	÷ 5	=	¥	× 5	= =	×	۲	⊁	₹	7 5	Explanation	Ĕ
YBR018C	GAL 7	Galactose-1-phosphate uridyl transferase	NA	NA	NA	NA N	IA 1	1	-0.02	TP 0	18 0	5 37	TN 1 (1.01	TP 1	1 1	01 TE	1 11	1 T	P 1.12	1 1 0	1 TP	1 11	1 01	re N	A NA	NA
YKR039W		General amino acid permease		NA	_				0.02					8 1.01												A NA	NA
		Glycine decarboxylase complex T																									
YDR019C	GCV1	subunit	NA	NA	NA	NA N	IA 1	1	-0.03	TP 0	.99 1	-0.03	TP 1.0	1.03	TP 1	.09 1.	05 TF	1.03	1.05 T	P 0.87	7 1.0	8 TP	1.04	1.06	TP N	A NA	NA
		Glycine cleavage system P subunit glycine decarboxylase																									
YMR189W		complex P subunit glycine synthase P subunit		NA	NA	NA N	IA 1	1	0.02	TP 0	.99 1	-0.04	TP 1.0	0.99	TP 1	.09 1.0	01 TF	1.03	1.03 T	P 0.87	7 1.0	2 TP	1.04	1.02	TP N	A NA	NA
																										Should not be deleterious except when glycine is the only	
VAL044C		Glycine cleavage system H-protein subunit	NIA.	NIA	NIA	NA N	1 1	1	0	TD	00 1	0.01	TD 4	7 0 76	ED 1	00 0	77 55	1.02	06 5	D 0 0	7 0 5	o ED	1.04	0.55	-D D	nitrogen source [Nagarajan97]. Could also be due to complicated gene-protein-reaction associations.	NA
YAL044C	GCV3	Guanosine diphosphatase of Golgi	NA	INA	NA	NA N	IA I	+	U	TP 0	.99 1	-0.01	IP I.	0.76	FP I	.09 0.	// FF	1.03	0.6 F	P 0.87	0.5	8 FP	1.04	0.55	-P D	is complicated gene-protein-reaction associations.	INA
YEL042W	GDA1	membrane	NA	NA	NA	NA N	IA 1	1	-0.01	TP	1 1	-0.06	TP 1.0	0.97	TP 1	.1 0.	97 TF	1.11	1.02 T	P 1.12	0.9	9 TP	1.11	0.98	TP N	A NA	NA
YOR375C	CDH1	NADP-specific glutamate dehydrogenase	NA	NA	NA	NA N	IA 1	1	0.39	тр	1 1	0.03	TP 1.0	10 1	TD 1	.1 1.	01 TE	1 11	1 T	P 1.12	2 1	TP	1 11	1 -	TP N	A NA	NA
101(3/30	GDITI	NAD-dependent glutamate	INA	INA	INA	IN/A IN	1	+	0.55	IF	<u> </u>	-0.02	11 1.0	70 1	IF I	.1 1.	01 11	1.11	<u> </u>	F 1.12		IF	1.11	-	I		INA
YDL215C	GDH2	dehydrogenase	NA	NA	NA	NA N	IA 1	1	-0.06	TP	1 1	-0.05	TP 1.0	1.01	TP 1	.1 1.0	02 TF	1.11	1.03 T	P 1.12	2 1.0	5 TP	1.11	1.04	TP N	A NA	NA
		NADP-linked glutamate																									
YAL062W	GDH3	dehydrogenase	NA	NA	NA	NA N	IA 1	1	-0.03	TP	1 1	-0.02	TP 1.0	1.01	TP 1	1.1	04 TF	1.11	1.05 T	P 1.12	2 1.0	6 TP	1.11	1.05	TP N	A INA	NA
		Glucoseamine-6-phosphate synthase glutamine_fructose-6-																								Essential for synthesis of cell wall precursors (leading to	
YKL104C		phosphate amidotransferase	1	FP	NA	NA N	IA NA	NA	NA	NA I	IA NA	NA NA	NA N	A NA	NA N	N AIN	IA NA	NA	NA N	IA NA	. NA	NA NA	NA	1 AN	IA B	io chitin biosynthesis), which are not required in the model.	FP
		Permease involved in the uptake of																									
YCR098C	GIT1	glycerophosphoinositol (GroPIns)	NA	NA	NA	NA N	IA 1	1	0.03	TP	1 1	-0.02	TP 1.0	0.97	TP 1	.1 0.	94 TF	1.11	0.97 T	P 1.12	2 0.9	4 TP	1.11	0.97	TP N	A NA	NA
YEL011W	GLC3	1,4-glucan-6-(1,4-glucano)- transferase	NA	NA	NA	NA N	IA 1	1	-0.02	TP	1 1	0	TP 1.0	08 1	TD 1	1 1	01 TE	1 11	1.03 T	D 1 11	1 0	2 TD	1 11	1 01	re N	A NA	NA
YCL040W		Glucokinase		NA					0.02			-0.03							1.03 T							A NA	NA
																										Null mutants are glutamine auxotrophs [MIPS]. The deletion	
		Glutamine synthetase	1				IA NA					NA.	NA N			N AI			NA N							ed is lethal if glutamine is removed from the media.	NA
YOR168W	GLN4	Glutamine-tRNA ligase	1	FP	NA	NA N	IA NA	NA	NA	NA I	IA NA	NA NA	NA 1.0	1.03	TP 1	.1 1.	04 TF	1.11	1.04 T	P 1.12	2 1.0	6 TP	1.11	1.03	TP O	th Protein synthesis not required in the model	NA
YML004C	GLO1	Lactoylglutathione lyase (glyoxalase	NA	NA	NA	NA N	IA 1	1	0.01	TP	1 1	0	TP 1.0	08 1 03	TP 1	1 1	06 TE	1 11	1.07 T	P 1 12	1 0	7 TP	1 11	1 07	re N	A NA	NA
YDR272W		Glyoxylase-II		NA				_	0.07		1 1	_	TP 1.0						1.01 T					1.03		A NA	NA
YOR040W	GLO4	Glyoxylase-II	NA	NA	NA	NA N	IA 1	1	-0.03	TP	1 1	-0.07	TP 1.0)8 1	TP 1	.1 1.	02 TF	1.11	1.02 T	P 1.12	2 1.0	1 TP	1.11	1.01	TP N	A NA	NA
VDI 00 4144	0.54	Glutathione oxidoreductase EC																									
YPL091W YDL171C		1.6.4.2 Glutamate synthase (NADH)	_	NA NA	_				-0.03 0.29				TP 1.0	08 1 08 1.02		.1 1.				P 1.12			1.11			A NA A NA	NA NA
IBLITIO	OLIT	Gidamate synthase (IVADIT)	IVA	INA	INA	IVA	1/1	+	0.23		' '	-0.07	11 1.0	1.02			01 11	1.11	<u> </u>	1 1.12	0.3	3 11	1.11	-		Should be a glycine auxotroph when grown on glucose so	IVA
																										that the deletion strain should grow normally in complex	
YEL046C	GLY1	Threonine aldolase	NA	NA	1	5.5 F	P 1	1	0.03	TP	1 1	0	TP 1.0	0.71	FP 1	.1 0	.7 FF	1.11	0.83 T	P 1.12	2 0.7	7 FP	1.11	0.85	TP D	is media [Monschau97].	NA
VEL0470	CNIA 1	Glucosamine-phosphate N-	١,	FP	NIA	NIA N	IA NIA	. NA	NIA	NIA .		NIA.	NIA NI	A NIA	NIA N			NIA	NIA NI		NI A	. INIA	NIA	NIA N	, D	is N. Acatulalusacamina synthesis is not required in the model	NA
YFL017C		acetyltransferase 6-phosphogluconate	1	FP	NA	NA N	IA NA	NA	NA	NA I	IA NA	NA NA	NA N	A NA	NA I	N AI	IA NA	NA	NA N	IA NA	. INA	NA	NA	NA I	NA B	io N-Acetylglucosamine synthesis is not required in the model.	INA
		dehydrogenase, decarboxylating;																									
		converts 6-phosphogluconate +																									
		NADP to ribulose-5-phosphate +																									
YHR183W		NADPH + CO2 6-phosphogluconate	NA	NA	. 1	5 F	P 1	1	-0.01	TP	1 1	-0.04	TP 1.0	0.65	FP 1	.1 0.	82 FF	1.11	0.83 T	P 1.12	2 0.9	9 TP	1.11	0.95	TP Is	This is the major isozyme (80% of activity) [MIPS].	NA
YGR256W		dehydrogenase	NA	NA	NA	NA N	JA 1	1	-0.03	TP	1 1	0.03	TP 1 (1.02	TP 1	1 .	1 TE	1 11	0 99 T	P 1 12	1	ТР	1 11	1 .	re N	A NA	NA
		High affinity glutamine permease				NA N			0					1.03													NA
		Glycerol-3-phosphate																									
YDL022W	GPD1	dehydrogenase	NA	NA	NA	NA N	IA 1	1	-0.04	TP	1 1	-0.05	TP 1.0	1.03	TP 1	.1 1.0	06 TF	1.11	1.05 T	P 1.12	2 1.0	8 TP	1.11	1.06	TP N	A NA	NA
YOL059W	CDD2	Glycerol-3-phosphate dehydrogenase (NAD+)	NIA	NA	NA	NA N	1 1	1	0.24	тр	, ,	0	TD 1	1.01	TD 1	1 1	02 TE	1 11	1 02 T	D 1 11	1 0	4 TD	1 11	1 01	ro N	A NA	NA
		Glycogen phosphorylase			NA		IA 1	1	-0.02		1 1		TP 1.0	8 1.03	TP 1	1.1	1 TF	1.11	1 T							A NA	NA
		, 0. 1		<u> </u>																							
				FP	NA	NA N	IA NA	NA	NA	NA I	IA NA	NA NA	NA N	A NA	NA N	N AI	IA NA	NA	NA N	IA NA	. NA	NA NA	NA	1 AN	NA O	th Essential for sporulation, which is not required in our model.	FP
YKL152C		Phosphoglycerate mutase	1	гг							_																
		Similar to GPM1 (phosphoglycerate	1	FF																							۱ ا
		Similar to GPM1 (phosphoglycerate mutase); converts 3-	1	FF																							
YKL152C		Similar to GPM1 (phosphoglycerate			NA.		IA 1	1	0.03	TP	1 1	-0.05	TP 1.0	08 1.02	TP 1	1.1 1.0	04 TF	1.11	1.06 T	P 1.12	2 1.0	7 TP	1.11	1.07	TP N	A NA	NA
YKL152C YDL021W YOL056W	GPM2 GPM3	Similar to GPM1 (phosphoglycerate mutase); converts 3- phosphoglycerate to 2- phosphoglycerate in glycolysis Phosphoglycerate mutase	NA NA	NA NA	NA NA	NA N	IA 1	1	-0.01	TP	1 1	-0.03	TP 1.0	08 1.02 08 1	TP 1	.1 1.	01 TF	1.11	1.02 T	P 1.12	2 1.0	2 TP	1.11	1.02	TP N	A NA	NA
YKL152C YDL021W YOL056W YKL026C	GPM2 GPM3 GPX1	Similar to GPM1 (phosphoglycerate mutase); converts 3- phosphoglycerate to 2- phosphoglycerate in glycolysis	NA NA NA	NA NA NA	NA NA	NA N	IA 1 IA 1	1	-0.01	TP TP	1 1 1 1	-0.03 -0.04	TP 1.0	08 1.02 08 1 08 1.01 08 0.98	TP 1	i.1 1.0	01 TF 02 TF	1.11	1.02 T 0.99 T	P 1.12	2 1.0 2 1.0	2 TP 1 TP	1.11 1.11	1.02	TP N	A NA	

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			sim	all	sim	dxe	call	sim	MD exp	ave	call	l sim	ave	call	Ë	dxe	i all	'PDGE sim	PDGE exp	Ë	dxə	call	Ë	dxe	call	exp	all	"	Explanation Explanation
ORF	Vam.	Annotation	s ss	ss c	Nols	Nols	Nols	MIMD	/IMD	ммр аve	MM M	/PGal sim	(PGal ave	/PGal cal	YPD sim	YPD exp	/PD call	PDG	(PDGE	/PG sim	PG	/PG	/PE sim	/PE exp	PE (PLe	P.	Class	Explanation
YHR104W		Aldose reductase			NA		_	1		0.05	TP	1 .	1 -0.0)1 TP	1.08	0.99	TP 1	1.1	1 TF	1.11		_	1.12	0.99	TP 1.	_		NA	NA NA
YBR121C	GRS1	Glycine-tRNA ligase 1,3-beta-D-glucan synthase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA N	A NA	A NA	NA	NA I	1 AV	NA	NA NA	NA.	NA	NA	NA	NA	NA N	A NA	NA	Oth	Protein synthesis not required in the model NA
YGR032W	GSC2	catalytic component	NA	NA	NA	NA	NA	1	1 -	0.02	TP	1 .	-0.0)5 TP	1.08	1.02	TP 1	1.1 1	1.03 TF	1.11	1.02	TP	1.12	1.05	TP 1.	11 1.0	4 TP	NA	NA NA
YJL101C	GSH1	Gamma-glutamylcysteine synthetase	NA	NA	NA	NA	NA	1	1 -	0.02	ТР	1 .	0.2	2 TP	1.08	0.99	TP 1	1.1	1 TE	1.11	0.93	TP	1.12	0.94	TP 1.	11 0.9	4 TP	NA	NA NA
YOL049W		Glutathione synthetase			NA		NA	1			TP	1 '			1.08				1.02 TF										
YFR015C	GSY1	Glycogen synthase (UDP-glucose- starch glucosyltransferase)	NA	NA	NA	NA	NA	1	1 -	0.05	TP	1	-0.0)2 TP	1.08	1.03	TP 1	1.1 1	1.04 TF	1.11	1.03	TP	1.12	1.07	TP 1.	11 1.0	4 TP	NA	NA NA
YLR258W	GSY2	Glycogen synthase (UDP-glucose- starch glucosyltransferase)	NΔ	NΔ	NA	NA	NΑ	1	1 -	0.04	TP	1 .	1 -0 ()7 TP	1.08	1.03	TP 1	1 1 1	1.03 TF	1 11	1 03	TP	1 12	1.05	TP 1	11 1 0	5 TP	NΑ	NA NA
YDR454C		Guanylate kinase			NA		NA	NA				NA N			NA				NA NA						NA N			NA	
YHL032C	GUT1	Converts glycerol to glycerol-3- phosphate glyerol kinase	NΔ	NΔ	NA	NA	NA	1	1 -	0.01	TP	1 .	1 -0 (18 TP	1.08	1	TP 1	08 1	1.02 TF	0.9	0.98	TP	1 12	1	TP 1	11 1 0	1 TP	NΑ	NA NA
		Glycerol-3-phosphate					IVA	_	H																				
YIL155C YDR232W		dehydrogenase 5-aminolevulinate synthase			NA NA		NA	1	1		TP	1 NA N			1.08 NA				0.99 TF NA NA						TP 1. NA N				NA NA Heme biosynthesis not required in the model FP
		Uroporphyrinogen decarboxylase			NA			NA				NA N			NA				NA NA						NA N			Bio	
YDR044W		Coproporphyrinogen III oxidase	1		NA		_	NA		NA		NA N					1 AV			NA	NA	NA			NA N			Bio	
YFR014W	HEM14	Protoporphyrinogen oxidase	NΔ	NΔ	NA	NA	NA	NA	NΑ	NA	NΑ	NA N	Δ ΝΑ	ΔNA	1.08	0.82	FP 1	1 1 ().84 FF	1 11	0.85	TP	1 12	0.68	FP 1	11 0 7	4 FP	Acc	Heme is not required in the model. May also result in heme precursor accumulation in vivo [SGD].
		The second secon			1.0.	10.				10.					1.00	0.02			,,,,,,,	ļ	0.00	1		0.00	<u> </u>		Ť	7100	Only deemed to be essential in one study [Giaever02]. The
\(OD470\\\		Ferrochelatase (protoheme																									. _	D: .	other study [Steinmetz02] shows normal growth on all
YOR176W	HEM1	Delta-aminolevulinate dehydratase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA N	A NA	A NA	1.08	1.04	IP 1	1.1 1	1.04 TF	1.11	1.04	IP	1.12	1.03	IP 1.	11 1.0	4 IP	DIS	substrates. FP
YGL040C	HEM2	(porphobilinogen synthase)	1	FP	NA	NA	NA	NA	NA	NA	NA	NA N	A NA	NA NA	NA	NA	NA N	NA	NA NA	NA.	NA	NA	NA	NA	NA N	A NA	NA	Bio	Heme biosynthesis not required in the model.
		Phorphobilinogen deaminase																											Only deemed to be essential in one study [Giaever02]. The other study [Steinmetz02] shows normal growth on all
YDL205C	НЕМ3	(uroporphyrinogen synthase)	1	FP	NA	NA	NA	NA	NA	NA	NA	NA N	A NA	NA NA	1.08				1.04 TF										substrates. FP
YOR278W	HEM4	Uroporphyrinogen III synthase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA N	A NA	A NA	NA	NA	1 AV	NA	NA NA	NA.	NA	NA	NA	NA	NA N	A NA	NA	Bio	
																													Used as a histidine transporter in our model, but there are isozymes for this function. Lethality may be due to the role of
YGR191W	HIP1	Histidine permease	1	FP	NA	NA	NA	NA	NA	NA	NA	NA N	A NA	NA NA	NA	NA	NA N	NA	NA NA	NA	NA	NA	NA	NA	NA N	A NA	NA	Oth	Hip1p in Mg2+ transport.
YER055C		ATP phosphoribosyltransferase			NA			1			TP	1 1	-0.0	_	1.08				1.01 TF									NA	
YFR025C	HIS2	Histidinolphosphatase Imidazoleglycerol-phosphate	NA	NA	NA	NA	NA	1	1 -	0.04	TP	1 1	0.0	2 TP	1.08	1	TP 1	1.1).99 TF	1.11	1	TP	1.12	1.01	TP 1.	1 1	TP	NA	NA NA
YOR202W	HIS3	dehydratase	NA	NA	NA	NA	NA	1	1 -	0.01	TP	1 -	-0.0)8 TP	1.08	1.01	TP 1	1.1 1	1.02 TF	1.11	1.03	TP	1.12	1.03	TP 1.	11 1.0	2 TP	NA	NA NA
YCL030C	HIS4	Histidinol dehydrogenase	NA	NA	NA	NA	NA	1	1	0	TP	1 1	0		1.08				1.02 TF										
YIL116W	HIS5	Histidinol-phosphate aminotransferase	NIA	NIA	NA	NA	NA	1	1 -	0.01	тр	1 .)6 TD	1.08	1 01	TD 1	1 1 1	1.02 TF	1 11	1.04	тр	1 12	1.02	TD 1	11 1 0	л Д ТБ	NΙΛ	NA NA
TILITOVV	ПІЗЗ	Phosphoribosyl-5-amino-1-	INA	INA	INA	INA	INA	_	H	0.01	IF	_	-0.0	JO 1F	1.06	1.01	IF I	1.1	1.02 16	1.11	1.04	IF	1.12	1.02	IF I.	11 1.0	4 11	INA	IVA IVA
		phosphoribosyl-4-																									_		l
YIL020C	HIS6	imidazolecarboxiamide isomerase Glutamine	NA	NA	NA	NA	NA	1	1	0.09	TP	1 '	1 -0.0)6 TP	1.08	1.01	TP 1	1.1 1	1.01 TF	1.11	1.03	TP	1.12	1.03	TP 1.	11 1.0	3 TP	NA	NA NA
		amidotransferase:cyclase imidazole																											
		glycerol phosphate synthase																											
YBR248C	HIS7	(synonym) 3-hydroxy-3-methylglutaryl-	NA	NA	NA	NA	NA	1	1 -	0.01	TP	1 1	0.1	3 TP	1.08	1	TP 1	1.1	1 TF	1.11	1.01	TP	1.12	0.98	TP 1.	11 0.9	9 TP	NA	NA NA
		coenzyme A (HMG-CoA) reductase																											
YML075C	HMG1	isozyme	NA	NA	NA	NA	NA	1	1	0.06	TP	1 1	-0.0)2 TP	1.08	1.01	TP 1	1.1 1	1.01 TF	1.11	0.99	TP	1.12	1.01	TP 1.	1 1.0	1 TP	NA	NA NA
		3-hydroxy-3-methylglutaryl- coenzyme A (HMG-CoA) reductase																											
YLR450W	HMG2	isozyme	NA	NA	NA	NA	NA	1	1	0.04	TP	1	0	TP	1.08	0.99	TP 1	1.1).99 TF	1.11	0.98	TP	1.12	0.98	TP 1.	1 0.9	в ТР	NA	NA NA
		Arginine methyltransferase mono-																											
YBR034C	HMT1	and asymmetrically dimethylating enzyme	NΙΔ	ΝΔ	NΔ	NA	ΝΔ	1	1	0.06	тр	1		и Тр	1.08	1	TD 1	1 1 1	1.01 TF	1 11	1 02	тр	1 12	1 04	TD 1	11 1 0	2 TD	ΝΔ	NA NA
1010040	. mvi i i	Transporter (permease) for choline	14/4	1474	14/4	INA	IVA			0.00			0.0	7 15	1.00				1.01 11	1.11	1.02		1.12	7.04	1.	1.0	J 11 ²	1474	IVA
VOI 0770	LININA	and nitrogen mustard; share	N. A		NIA.	NIA.	NI A	,	1	0.04	_{TC}				4.00	4.04	TD				0.00	т.	4.40	4.04	TD .			NIA.	NA NA
YGL077C	minivi1	homology with UGA4 Fhit homolog, member of the	NA	NA	NA	NA	NA	1	1	0.31	12	1 '	-0.0	io IP	1.08	1.01	12 1	1.1 1	1.01 TF	1.11	0.99	IP	1.12	1.01	IP 1.	1.0	I IP	IVA	NA NA
		histidine triad superfamily of																											
YDR305C	HNT2	nucleotide binding-proteins	NA	NA	NA	NA	NA	1	1	0.03	TP	1 '	-0.0)3 TP	1.08	1.01	TP 1	1.1).99 TF	1.11	0.98	TP	1.12	0.97	TP 1.	11 0.9	8 TP	NA	
																													Homocysteine can be produced in the model using CYSTL
																													(Cys1p) and AHCi (Sah1p) reactions in addition to this
\\\ 5		Aspartic beta semi-aldehyde dehydrogenase				NA	NA		0 1	10.74			0	TP	1.08				1.03 TF										pathway, but neither of these reactions can be removed from

												۔	a	е	_				Ē	dx	all											et al
ORF	ame		ss sim	ss call	Slow sim	ом ехр	ow call	MMD sim	имD ехр	MMD ave	MMD call	YPGal sim	Gal exp	rPGal ave	/PGal cal	YPD sim	YPD exp	rPD call	YPDGE sim	/PDGE exp	PDGE cal	YPG sim	YPG exp	PG call	YPE sim	YPE exp	'PE call	YPL sim		YPL call	Class	ster
0	Z	Annotation	ш	Ш	S	<u>w</u>	S	Σ	Σ	Σ	Σ	⋝	>	>	-	>	> 3	× -	⋝	>	X	-	>	⋝	>	¥	⋝	-	>	⋝	O	Explanation Homocysteine can be produced in the model using CYSTL (Cys1p) and AHCi (Sah1p) reactions in addition to this
YER052C	НОМЗ	Aspartate kinase (L-aspartate 4-P-transferase) (EC 2.7.2.4)	NA	NA	NA	NA	NA	1	0	4.46	FP	1	1 (0.04	TP 1	.08	1 1	ΓP 1	1.1	1.02	ΓP 1	.11	1.03	TP ·	1.12	1.02	TP 1	.11	.05	TP	Unk	pathway, but neither of these reactions can be removed from the model.
		L-homoserine:NADP																														Homocysteine can be produced in the model using CYSTL (Cys1p) and AHCi (Sah1p) reactions in addition to this
YJR139C	НОМ6	oxidoreductase homoserine dehydrogenase	NA	NA	NA	NA	NA	1	0	9.11	FP	1	1 -	0.03	TP 1	.08	0.98 7	ГР 1	1.1	0.98	ΓP 1	.11	0.96	TP ·	1.12	0.91	TP 1	.11	0.97	TP	Unk	pathway, but neither of these reactions can be removed from the model.
YER062C		DL-glycerol-3-phosphatase	NA				NA	1		0.02	TP	1					1.01 1								1.12							
YDR399W	HPT1	Hypoxanthine guanine phosphoribosyltransferase	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	0	TP 1	.08	0.99 1	ГР 1	1.1	0.99	TP 1	.11	1.01	TP ·	1.12	1.01	TP 1	.11	.01	TP	NA	NA NA
YPR033C		Histidine-tRNA ligase		_	NA		NA	NA	NA		_	NA I			_			_	_	NA I	_	_	_	_	_	_	_	_	_	_		Protein synthesis not required in the model FP
YFR053C	HXK1	Hexokinase I (PI) (also called hexokinase A)	NA	NA	NA	NA	NA	1	1	-0.04	TP	1	1 -	0.05	TP 1	1.08	1.03 1	ΓP 1	1.1	1.04	TP 1	.11	1.03	TP	1.12	1.05	TP 1	.11	.04	TP	NA	NA NA
YGL253W	HXK2	Hexokinase II (PII) (also called hexokinase B)	NA	NA	NA	NA	NA	1	1	0.05	TP	1	1	0	TP 1	.08 (0.95 1	ΓP 1	1.1	1.02	ΓP 1	.11	1.07	TP ·	1.12	1.07	TP 1	.11	.07	TP	NA	NA NA
		Hexose transporter		_	NA		NA	1	-	0.03	TP	1			_		1.01 1	_	_		ΓP 1	_	_	_	1.12	_	_	_	_	_		
		High affinity hexose transporter Hexose transporter	NA NA		NA NA		NΑ	1	1	-0.05 0.1	TP	1		0.03	TP 1	.08 1	1.02 1	TP 1	_	0.97 ⁻	ΓΡ 1 ΓΡ 1	_	_	_	_	0.97 1.01	TP 1	.11 (0.97	_	NA NA	NA NA NA
		Hexose transporter		_	NA		NA	1	1	0.08	TP	1		0.04	TP 1	.08 1	1.02 7	ΓP 1	_	1.02	_	_	_	_	_	_	TP 1	.11 ′	.01		NA	NA NA
		High affinity hexose transporter-2	NA	_	_		NA	1	1	-0.01	TP	1	_	0.05	TP 1			ГР 1	_	1.06	_	_	1.07	_	_	1.07	_	.11 1	.07	_	NA	NA NA
		Low affinity glucose transporter High affinity glucose transporter	NA NA	_	NA NA		NA	1	1	-0.06 -0.01	TP TP	1		0.03	TP 1		1.01 T	TP 1	1.1	1.02	_	_	1.04 1.06		1.12	_	TP 1	_	.06		NA NA	NA NA NA
		Hexose transporter			NA		NA	1	1	0.85	TP	1	_	0.03	TP 1		1.01 1		1.1	1.04	_	_			1.12				.03	_	NA	
YJL214W		Hexose permease		_	NA		NA	1	1	0	TP	1		0.03	_			ΓP 1	_			.11	_	_	1.12	_	TP 1	_	_	_	NA	NA NA
YIR037W	HYR1	Glutathione-peroxidase (putative)	NA	NA	NA	NA	NA	1	1	0.03	TP	1	1	0 .	TP 1	.08	1 1	ΓP 1	1.1	0.97	ΓP 1	.11 (0.98	TP ·	1.12	0.96	TP 1	.11 ().97	TP	NA	NA NA
YER065C	ICL1	Isocitrate lyase	NA	NA	NA	NA	NA	1	1	-0.02	TP	1		0.04			1 1	ΓP 1	1.1	1	ΓP 1	.11	1.02	TP (0.79	0.99	FN 1	.08	1	TP	Med	
YPR006C	ICL2	2-methylisocitrate lyase	NA	NA	NA	NA	NA	1	1	0.03	TP	1	1 -	0.02	TP 1	.08 1	1.02 1	ΓP 1	1.1	1.02	ΓP 1	.11	1.02	TP ·	1.12	1.03	TP 1	.11 ′	.03	TP	NA	NA NA
YNL037C	IDH1	Isocitrate dehydrogenase 1 alpha-4- beta-4 subunit	NA	NA	1	4.7	FP	1	1	-0.06	TP	1	1 (0.02	TP I	NA	NA N	1 AV	NA	NA I	1 AV	NA	NA	NA	NA	NA	NA I	NA	NA I	NA	Unk	The model does not utilize this part of the TCA cycle.
VOD400W	IDIIIO	NAD-dependent isocitrate									-															. =0						The model does not use the corresponding reaction when grown on glycerol or lactate. In vivo there is a NAD/NADH
YOR136W	IDH2	dehydrogenase Isopentenyl	NA	NA	NA	NA	NA	1	1	0.96	IP	1	1 ().17	IP 1	.08 ().99 1	IP 1	1.1	0.88	IP 1	.11 (0.68	FP '	1.12	0.78	IP 1	.11	0.6	FP	Unk	balancing issue. NA
		diphosphate:dimethylallyl																														
YPL117C	IDI1	diphosphate isomerase (IPP isomerase)	0	TN	NA	NA	NA	NA	NA	NA	NA	NA I	NΑ	1 AN	NA I	NA	NA N	1 AV	NA	NA I	1 AV	NA	NA	NA	NA	NA	NA I	NA	NA I	NA	NA	NA NA
YDL066W	IDP1	NADP-dependent isocitrate dehydrogenase	NA	NA	NA	NA	NA	1	1	0.12	TP	1	1 (0.03	TP 1	1.08	1.01 T	ΓP 1	1.1	1.02	ΓP 1	.11	1.07	TP ·	1.12	1.05	TP 1	.11	.09	TP	NA	NA NA
YLR174W	IDP2	NADP-dependent isocitrate dehydrogenase	NA	NA	NA	NA	NA	1	1	0.04	TP	1	1	0	TP 1	.08	1 1	ΓP 1	1.1	1.01	ΓP 1	.11 (0.99	TP ·	1.12	1	TP 1	.11 (0.98	TP	NA	NA NA
YNL009W	IDP3	NADP-dependent isocitrate dehydrogenase	NA	NA	NA	NA	NA	1	1	0.03	TP	1	1 -	0.02	TP 1	1.08 1	1.04 T	ГР 1	1 1	1 -	ΓP 1	11	1.01	TP ·	1.12						NA	NA NA
YBL076C	ILS1	Isoleucine-tRNA synthetase		_	NA		NA	NA	NA	NA		NA I						A A	NA	NA I			NA				NA I					Protein synthesis not required in the model NA
YER086W	ILV1	Threonine deaminase	NA	_	_		NA	0	0	10.66	TN	1			_			_	_	0.98	_	_	_	_	1.12	_	_	_	_	_	NA	NA NA
YJR016C	ILV3	Dihydroxyacid dehydratase Acetohydroxyacid	0.64	TN	NA	NA	NA	NA	NA	NA	NA	NA I	NA	1 AN	NA I	NA	NA N	1 AV	NA	NA I	1 A	NA	NA	NA	NA	NA	1 AN	NA	NA I	NA	NA	In silico slow growth.
YLR355C	ILV5	reductoisomerase	0.64	TN	NA	NA	NA	NA	NA	NA	NA	NA I	NA	NA I	NA I	NA	NA N	1 A	NA	NA I	1 A	NA	NA	NA	NA	NA	NA I	NA	NA I	NA	NA	In silico slow growth.
		Acetolactate synthase regulatory																														Ilv6p is the regulatory subunit of phenylalanine transaminase [SGD]. Null mutant has defective retroinhibition by valine [Cullin96], but apparently this subunit is otherwise non-
	ILV6	subunit				NA		0		-0.01		1				0.69	1.01 F	-N 1	1.1	1.02	ΓP 1	.11	1.01	TP	1.12	1	TP 1	.11				essential for the enzymatic function.
YLR432W YML056C	IMD3 IMD4	IMP dehydrogenase homolog IMP dehydrogenase homolog			NA NA			1		0.02		1			TP 1	.08 1	1.01 T	TP 1	1.1	1.04	TP 1	.11			1.12						NΑ	
	INM1	Inositol monophosphatase			NA NA		NA NA	0	1	-0.06 0	FN	0		0.07						1.04 1.04 F												VDR287W may code for an isozyme for Inm1p. May not be lethal if inositol is in media.
		L-myo-inositol-1-phosphate							İ																							Null mutant is viable, but an inositol auxotroph [SGD]. This is consistent with in silico results. Thus, experiments may have
	INO1	synthase				NA			1	0.11																						some inositol in media.
	IPP1 IPT1	Inorganic pyrophosphatase Inositolphosphotransferase 1			NA NA		-	NA 1	NA 1	NA -0.05		NA I		NA 1			NA N			NA N			NA n ga				NA I				NA NA	
	ISM1	Isoleucine-tRNA ligase	NA					1		-0.03		1	1 -	0.03	TP 1	.08).69 F	P 1	1.1	0.66 F	P 1	.11 (0.48	FP '	1.12	0.45	FP 1	.11 ().56	FP	Oth	Protein synthesis not required in the model NA
	ITR1	Myo-inositol transporter			NA			1		0.09		1								1.03												NA NA
YOL103W	ITR2	Myo-inositol transporter	NA	NA	NA	NA	NA	1	1	0.03	TP	1	1 -	0.05	TP 1	.08 1	1.03	TP 1	1.1	1.02	TP 1	.11	1.01	TP	1.12	1.03	TP 1	.11 ′	.01	TP	NA	NA NA

			E	_	im	exp	sim	dx	ıve	all	sim	Gal ave	100	<u> </u>	dx	all	E S I	Eexp	in call	dx	all I	E	e =	₹ E	9	=			er et al
ORF	lame	Annotation	Ess sim	ss call	Slow sim	Slow exp	MMD	иМD ехр	MMD ave	MMD	/PGal sim	YPGal ave	/PGal cal	YPD sim	YPD exp	/PD call	PDGE SIM	(PDGE exp	YPG sim	YPG exp	YPG call	YPE SIM	YPE exp	YPL sim	YPL exp	YPL call	Class	Explanation	Forster
YKL217W		Carboxylic acid transporter protein		NA	NA	0, 0,			-0.02							T				0.99								Lower oxygen uptake rate would correct this false negative prediction.	NA
TRLZITVV	JEINT	Homolog	INA	INA	INA	INA IN	A 1	<u> </u>	-0.02	IF	-	1 -0.0	05 1	1.00	1.03	IF I	.1 1.	.01 1	1.11	0.99	IF I.	.12	- '	0.04	1.01	FIN	ivieu	Should definitely have a growth defect on non-fermentable	
YIL125W	KGD1	Alpha-ketoglutarate dehydrogenase	NA	NA	NA	NA N	A 1	1	0.02	TP	1	1 0.0)3 T	P 1.08	0.96	TP 1	.1 0.	.92 T	P 1.09	0.6	FP 1.	.11 0).66 F	P 1.1	0.66	FP	Unk	carbon sources. The model just adjusts the flux distribution to utilize more amino acids and dumps acetate.	o NA
		Alpha-ketoglutarate dehydrogenase complex dihydrolipoyl	:																									Should definitely have a growth defect on non-fermentable carbon sources. The model just adjusts the flux distribution to	
YDR148C		transsuccinylase component	NA	NA	NA	NA N	A 1	1	0.01	TP	1	1 0.0)6 T	P 1.08	1	TP 1	.1 0	.95 T	P 1.09	0.64	FP 1.	.11 0).71 F	P 1.1	0.6	FP	Unk	1 .	NA
YDR483W		Alpha-1,2-mannosyltransferase	_	NA		NA N			-0.03			1 0		P 1.08						1.04									NA
		Lysine-tRNA ligase Type II transmembrane protein	1 NA	FP NA	NA NA	NA N	_	_	NA 0	NA TP		IA N		A NA					NA NA	NA 1 1.04	NA N			A NA				Protein synthesis not required in the model NA	FP NA
101(09944	KIKI	Type ii transmembrane protein	INA	INA	INA	INA IN		+-	- 0	IF	-+	1 -0.0	03 1	1.00	1.03	1 -	. 1	.05 1	1.11	1.04	IF I.	. 12 1	1.00 1	1.11	1.05	IF	INA	IVA	INA
YKR061W	KTR2	Mannosyltransferase (putative) type 2 membrane protein		NA	NA	NA N	A 1	1	0.05	ТР	1	1 -0.0	06 T	P 1.08	1.02	TP 1	.1 1.	.03 T	P 1.11	1.03	TP 1.	.12 1	1.05 T	P 1.11	1.04	TP	NA	NA	NA
YBR205W	KTR3	Alpha-1,2-mannosyltransferase (putative)	NΙΔ	NΔ	NA	NA N	Δ 1	1	0.13	тр	1	1 -0.0	мт	P 1.08	1.02	TD 1	1 1	01 T	D 1 11	1	TP 1.	12	1 T	P 1.11	1	тр	ΝΔ	NA	N/
		Alpha-1,2-mannosyltransferase																											
YBR199W	KTR4	(putative)	NA	NA	NA	NA N	A 1	1	-0.05	TP	1	1 0.0)6 T	1.08	1.01	IP 1	.1 1.	.02 T	P 1.11	1.02	TP 1.	.12 1	T 80.1	P 1.11	1.03	ſΡ	NA	NA Affects cell wall composition, but should not necessarily have	N/
YNL029C	KTR5	Mannosyltransferase (putative)	NA	NA	1	4.2 FI	P 1	1	-0.02	TP	1	1 0	, Іт	P NA	NA I	VA N	IA N	NA N	IA NA	NA	NA N	I AL	NA IN	IA NA	NA	NA	Oth	a slow growth phenotype [MIPS].	NA
YPL053C		Mannosylphosphate transferase			NA		A 1	1	0.02											1.02							NA		NA
		Pyruvate dehydrogenase complex dihydrolipoamide acetyltransferase																											
YNL071W	LAT1	component (E2)	NA	NA	NA	NA N	A 1	1	0.01	TP	1	1 -0.0	03 T	P 1.08	1.02	TP 1	.1 0.	.99 T	P 1.11	0.78	FP 1.	.12 0).89 T	P 1.11	0.89	TP	Unk	The model can bypass the PDH complex if necessary.	N/
YMR296C	LCB1	Serine palmitoyltransferase component	1	FP	NA	NA N	A NA	NA	NA	NA	NA N	IA N	A N	A NA	NA I	NA N	IA N	NA N	IA NA	NA	NA N	JA I	NA N	IA NA	NA	NA	Bio	Sphingolipid synthesis not required in the model.	FF
YDR062W	LCB2	Serine palmitoyltransferase	1	FP	NA	NA N	ΔΝΔ	NΔ	ΝΔ	NΔ	NA N	IA N	ΔΝ	A NA	ΝΔΙ	NA N	ΙΔ Ν	MA N	ΙΔ ΝΙΔ	NΔ	NA N	. ΔΙ	NIA N	ΙΔ ΝΙΔ	NΔ	NΔ	Rio	Sphingolipid synthesis not required in the model.	FF
		Dihydrosphingosine-1-phosphate		Ħ																									
YJL134W	LCB3	phophatase Sphingoid long chain base (LCB)	NA	NA	NA	NA N	A 1	1	-0.02	TP	1	1 0) T	P 1.08	1.01	TP 1	.1 1.	.05 T	P 1.11	1.06	TP 1.	.12 1	1.07 T	P 1.11	1.06	TP	NA	NA .	N/
YOR171C	LCB4	kinase Sphingoid long chain base (LCB)	NA	NA	NA	NA N	A 1	1	0.23	TP	1	1 -0.0	07 T	P 1.08	1.01	TP 1	.1 1.	.01 T	P 1.11	1.02	TP 1.	.12	1 T	P 1.11	1	TP	NA	NA	N.
YLR260W YGL009C		kinase	_	NA NA	1 NA	4.2 FI			-0.02 -0.01					P 1.08						0.55								Sphingolipid synthesis not required in the model. NA	N.
1 GL009C	LEUI	Isopropylmalate isomerase Alpha-isopropylmalate synthase (2-	INA	INA	INA	INA IN	A 1	-	-0.01	IF	_	1 -0.0	03 1	1.00	1.03	IF I	.1 1.	.04 1	F 1.11	1.04	IF I.	. 12 1	1.07	F 1.11	1.05	IF	INA	IVA	IN.
YNL104C	LEU4	isopropylmalate synthase) Alpha-isopropylmalate synthase (2-	NA	NA	NA	NA N	A 1	1	-0.01	TP	1	1 -0.0	03 T	P 1.08	1.01	TP 1	.1 1.	.03 T	P 1.11	1.03	TP 1.	.12 1	1.04 T	P 1.11	1.04	TP	NA	NA	N.
YOR108W	LEU9	isopropylmalate synthase)	NA	NA	NA	NA N	A 1	1	-0.02	TP	1	1 -0.0	03 T	P 1.08	1.02	TP 1	.1 1.	.02 T	P 1.11	1.03	TP 1.	.12 1	1.04 T	P 1.11	1.03	TP	NA	NA	N.
		Dihydrolipoamide dehydrogenase precursor (mature protein is the E3																										Should definitely have a growth defect on non-fermentable	
VEL 0400		component of alpha-ketoacid	l	l																			_					carbon sources. The model just adjusts the flux distribution to	
YFL018C YDR503C		dehydrogenase complexes) Lipid phosphate phosphatase		NA	NA	3.7 FI		_	-0.03											1.03									N.
TDN303C	LITI	Alpha subunit of succinyl-CoA	INA	INA	INA	IN/A IN		-	-0.03	15	-	1 0	<u>'</u>	1.00	1.02	1 - 1	. 1 1.	.04 1	1.11	1.03	IF I.	. 12 1	1.07	1.11	1.03	IF	INA	IVA	111/
		ligase (synthetase; ATP-forming), a																											
VOD4 40W		mitochondrial enzyme of the TCA	l	l		l l		١.										. _					. _				.	NA	1,,
YOR142W	LSC1	cycle Beta subunit of succinyl-CoA ligase	NA	NA	NA	NA N	A 1	1	0.08	TP	1	1 -0.0	02 T	P 1.08	1	TP 1	.1	1 T	P 1.09	0.96	TP 1.	.11	1 1	P 1.1	0.98	TP	NA	NA .	N.
		(synthetase; ATP-forming), a mitochondrial enzyme of the TCA																											
YGR244C	LSC2		NA	NA	NA	NA N	A 1	1	0.38	TP	1	1 0	, Т	P 1.08	1,02	TP 1	.1 1	.03 т	P 1.09	0.98	TP 1	11 1	I.05 T	P 11	1.01	TP	NA	NA	N
YNL268W		Lysine permease						_	-0.01					P 1.08						1.01								NA	N/
YIR034C	LYS1	Saccharopine dehydrogenase	_	NA				_	2.88	TN	1									0.98								NA	N/
YIL094C		Homo-isocitrate dehydrogenase YDL131W (LYS21)	NA	NA	NA	NA N	A 0	0	5.15		1									1.03								NA	N/
YDL182W	LYS20	homolog homocitrate synthase	NA	NA	NA	NA N	A 1	1	0.3	TP	1	1 -0.0	04 T	P 1.08	1	TP 1	.1 1.	.01 T	P 1.11	1 1	TP 1.	.12 0).99 T	P 1.11	0.99	TP	NA	NA	N/
YDL131W	LYS21	YDL182W (LYS20) homolog homocitrate synthase	NA	NA	NA	NA N	A 1	1	-0.03	TP	1	1 -0 (03 T	P 1.08	1.02	TP 1	.1 1	.02 Т	P 1.11	1.04	TP 1	12 1	1.05 T	P 1.11	1.04	TP	NA	NA	N/
		Homoaconitase			NA				1.55											1.02									N/
YGL154C	LYS5	Alpha aminoadipate reductase phosphopantetheinyl transferase	NA	NA	NA	NA N	A 0	0	8.33	TN	1	1 0.0)1 T	P 1.08	1.02	TP 1	.1 1	.03 T	P 1.11	1.03	TP 1.	.12 1	1.05 T	P 1.11	1.03	TP	NA	NA	N/
		Seventh step in lysine biosynthesis																											
		pathway Malic enzyme		NA NA	NA NA	NA N			1.27 -0.01			1 -0.0 1 0	02 T	P 1.08	1.01	TP 1	.1 0.	.97 T	P 1.11	0.97	TP 1.	.12 1 .12 1	1.03 T	P 1.11	1.03	TP		INA INA	NA NA

												_		ο .				2	9	÷ =													et al
L.	me		s sim	s call	w sim	w exp	w call	MMD sim	MMD exp	ммр аve	MMD call	/PGal sim	Gal exp	YPGal ave	YPGal call	ا د	YPD call	YPDGE sim	/PDGF exp	PDGE cal	YPG sim	YPG exp	PG call	YPE sim	YPEexp	PEcall	YPL sim	YPL exp	L call				Forster e
ORF	Z	Annotation	Es	Es	Slow	Slo	Slo	2	Σ	Σ	Σ	Ϋ́P	Ϋ́	Y Y	۲ م ۲	<u> </u>	} }	Ϋ́	<u>م</u> ۷	Ϋ́	ΥP	ΥP	ΥP	Ϋ́	ΥP	Α.	. Y	Ϋ́	YPL	ċ	Explanation	n	<u>د</u>
		Alpha-glucoside transporter hexose																															
		transporter maltose permease		NA			NA	1			TP	1		.03 1			.01 TF)2 TF					2 1.0						NA NA		N/
		Maltase		_	NA	_	NA	1			TP	1			TP 1.0		.03 TF														NA NA		N/
		Maltose permease Maltase	NA		NA NA		NΑ	1		0.14	TP	1	_	.16 7	_		.97 TF														A NA A NA		NA NA
		Malonyl-CoA:ACP transferase			NA			1			TP	1			ΓP 1.0		1.8 FF														Component of phopholipids does not according to the contract of the contract o	of the mitochondrial FAS that supplies s to the mitochondrial membrane. The moc count for the formation of the mitochondrial	lel
		Malate dehydrogenase			NA	NA	_	1		0.01	TP	1		.03 1	ΓP 1.0		.01 TF					1 0.8									NA NA		N/
		Malate dehydrogenase			NA	NA	NA	1	1 -	0.03	TP	1	1 -0	.07 1	TP 1.0	08 1	.04 TF	1.1	1.0)6 TF	1.1	1 1.0	3 TF	1.12	2 1.0	6 TI	P 1.1	1 1.0	6 TP	N			N/
		Malate dehydrogenase		_	NA	_	NA	1		0.01	TP	1	_	0 1	ΓP 1.0		.02 TF	_				1 1.0				_	_		3 TP	N			N/
		Ammonia permease			NA		NA	1	_	0.25	TP	1			_		.01 TF)1 TF				1.12			P 1.1		TP	_	NA NA		N/
		Ammonia transport protein NH4+ transporter	NA NA	_	NA NA	NA NA	NA	1		0.01	TP	1	_	.03 1	TP 1.0	_	.03 TF	_				1 1.0 1 0.9							2 TP	N			NA NA
		Methionine-tRNA ligase			NA		NA	NA			NA	I NA I			IA N	_		1.1 A NA		A NA					2 0.9 NA							thesis not required in the model	N/
		Methionine metabolism			NA		_			1.55		1	_		TP 1.0																NA NA		N/
		Assimilatory sulfite reductase subunit				NA		1		0.29		1																			A NA		N/
		Methylenetetrahydrofolate																															
YPL023C	MET12	reductase (mthfr) (putative)	NA	NA	NA	NA	NA	1	1	0.33	TP	1	1 -0	.05 1	TP 1.0	08 1	.01 TF	1.1	1.0)2 TF	1.1	1 1.0	3 TF	1.12	2 1.0	3 TI	P 1.1	1 1.0	3 TP	N			N/
YGL125W	MET13	Methylenetetrahydrofolate reductase (mthfr) (putative)	NA	NA	NA	NA	NA	1	0	3.97	FP	1	1 -0	.01 7	TP 1.0	08	1 TE	1.1	0.9	99 TF	1.1	1 1	TF	1.12	2 1.0	2 TI	P 1.1	1 1.0	2 TP	ls		ne dominant isozyme, but the model contain sozyme (Met12p).	ns an N <i>A</i>
																																grow as sulfate as only sulfur source [Thon	
V((() 0040		A London Marco Discour		l															۱.,		١											mal media in experimental study has some	
YKL001C	ME I 14	Adenylylsulfate kinase	NA	NA	NA	NA	NA	0	1	0.18	ͰN	1	1 -0	1 80.0	IP 1.0	08 1.	.03 11	J 1.1	1.0)2 11-	1.1	1 1.0	2 11	1.12	2 1.0	2 11	P 1.1	1 1.0	12 TP	, IVI	d sulfur source	es. grow as sulfate as only sulfur source [Thon	NA
																																mal media in experimental study has some	
YPR167C	MET16	3'phosphoadenylylsulfate reductase	NA	NA	NA	NA	NA	0	1	0.64	FN	1	1 -0	.04 7	TP 1.0	08 1	.03 TF	1.1	1 1.0)2 TF	1.1	1 1	TF	1.12	2 1.0	зТ	P 1.1	1 1.0	3 TP	M	d sulfur source		N/
																																ine can be produced in the model using CY	
																															(Cys1p) and	d AHCi (Sah1p) reactions in addition to this	
																																ut neither of these reactions can be remove	
YLR303W	MET17	O-acetylhomoserine (thiol)-lyase	NA	NA	NA	NA	NA	1	0	2.78	FP	1	1	0 1	TP 1.0	08 1	.01 TF	2 1.1	1.0)1 TF	1.1	1 0.9	9 TF	1.12	2 1.0	1 TI	P 1.1	1 1.0	1 TP) Ui	k the model.		N/
YOL064C	METO	3'(2')5'-bisphosphate nucleotidase	NA	NIA	NA	NA	NΙΛ	0.99	1	1.33	тр	1	1	0 1	TD 1 /	م ا م	.84 FF	1 1	ا ا) E	1 1	1 0 0	4 TC	1 11	0 0	, 1 TI	0 1 1	1 0 0	E TD	Λ,		pably accumulates phosphoadenylyl sulfate ich is toxic [Thomas90].	N/
		ATP sulfurylase				NA				0.96		1																			NA NA	ichis toxic [momasso].	N/
131(01000	WILTS	Vitamin B12-(cobalamin)- independent isozyme of methionine	INA	INA	IVA	INA	IVA		Ť	0.30	"		1 -0	1.00	1	00 1	.01 11		1.0	/	1.1	+	T"	1.12	0.3	3 11	T	1 0.3	70 11		100		14/
YER091C	MET6	synthase (also called N5- methyltetrahydrofolate homocysteine methyltransferase or 5-methyltetrahydropteroyl triglutamate homocysteine methyltransferase)	NA	NA	NA	NA	NA	0	0	3.2	TN	0	1	0 F	-N (0	1 FN	N 0	1	FN	1 0	1.0	1 FN	0	1	FI	N O	1	FN	I Ui	homocysteine biosynthesis. at least not in k off excess ho		o drain FN
																																ad end in the model, but it should be part o	
VOR241W	METZ	Folylpolyalutamata synthetase	NΛ	NA	1	7.1	ED	1	1	0.01	тр	1	1 (102 7	FD 1.	00 0	74 50	0 11		72 55	11	1.05	0 55	1 1 1	2 0 4	0 51	D 11	1 0 5	:1 ED	D D	present in bo causes a peti f-Met-tRNA (metabolic conversions. Also the gene product cytoplam and mitochondia and its deletetite phenotype as the production of mitoch (necessary for mitochondrial translation) is	tion ondrial
10K241W	IVIE I /	Folylpolyglutamate synthetase S-Methylmethionine Homocysteine	INA	IVA		7.1	FP	-	-	0.01	12	-	1 -0	.02 1	F 1.0	00 0	74 F	1.1	0.7	3 FF	1.1	1 0.5	o FF	1.12	2 0.4	o FI	1.1	1 0.5	I FP	D	n disrupted [De	coouzavoj.	N/
YLL062C	MHT1	methylTransferase	NA	NA	NA	NA	NA	1	1 -	0.02	TP	1	1 -0	.03 1	ΓP 1.0	08 1	.01 TF	1.1	1.0)2 TF	1.1	1 1.0	3 TF	1.12	2 1.0	2 TI	P 1.1	1 1.0	2 TP	N	NA NA	licated in blocking mitochondrial protein imp	N/
																																s mitochondrial function [MIPS]. Model has	
YJR077C	MIR1	Product of gene unknown	NA	NA	NA	NA	NA	0.96	1	0.24	TP	0.96	1 ().1	TP 1	05 0	.98 TF	0.9	1 0.9	2 TF	0.9	2 0.6	4 FF	0.94	1 0.6	1 F	0.9	3 0.6	6 FP	0		resport phosphate into mitochondria.	NA NA
		C1-tetrahydrofolate synthase			NA			1		0.02		1					.01 TF															, , , , , , , , , , , , , , , , , , , ,	N/
		Carbon-catabolite sensitive malate					NA	1		0.05		1					.01 TF														A NA		NA
		synthase High affinity S-methylmethionine			NA										ΓP 1.0																		
		permease			NA		NA	1		0.03		1					1 TF														NA Drotoin overth	thesis not required in the second	N/
		Aspartyl-tRNA synthetase Glutamine-tRNA ligase	NA NA		NA 1	NA 6.3	_	1		0.02		1																				thesis not required in the model thesis not required in the model	NA NA
1000000	WIGET	Phenylalanyl-tRNA synthetase	IVA	IVA	_	0.3		-	-	0.03	11	+	1 -0	.02 1	- 1.0	00 0	7 1 5		0.0	,, ,,	1.1	1 0.5	JFF	1.14	0.5	9 [7]	1.1	1 0.5	,5		i i rotolii syritii	noolo not required in the model	INF
YPR047W	MSF1	alpha subunit	NA	NA	1	3.7	FP	1	1	0.01	TP	1	1 -0	.01 7	TP 1.0	0 80	79 FF	1.1	0.6	69 FF	1.1	1 0.4	9 FF	1.12	0.4	5 FI	P 1.1	1 0.5	3 FP	0	h Protein synth	thesis not required in the model.	N/
YNL073W	MSK1	Lysine-tRNA ligase	NA	NA	1	4.9	FP	1	1	0	TP	1	1 -0	.01 1	TP 1.0	08 0	74 FF	1.1	0.	7 FF	1.1	1 0.5	1 FF	1.12	2 0.5	2 Fi	P 1.1	1 0.5	8 FP	0	h Protein synth	thesis not required in the model	N/

					u.	Ω.	_	E 9		=	Ë	dx	ıve	<u> </u>	۵		sim	exp	call	_	۵				_					et al
T.	ame		ss sim	ss call	ow sim	ow exp	ow call	MD sim	MMD ave	MD ca	PGal s	Gale	PGal a	PGal ca	/PD exp	PD call	PDGE sim	PDGE exp	PDGE	/PG sim	PG exp	/PG call	إ	PEexp	/PL sim	/PL exp	/PL call	Class		Forster
0		Annotation	ü	ш	S	S	S	ΣΣ		Σ	> 3		_	_		_	_	_	_		→ :	≻	_		- >	_	_		Explanation	<u>к</u>
		Methionine-tRNA ligase Arginyl-tRNA synthetase	NA NA		1 NA	5.9 F		1 1		TP	1			TP 1.0		FP FP		0.65			0.43 F				P 1.1				Protein synthesis not required in the model Protein synthesis not required in the model	NA NA
THRU91C	MSKI	Arginyi-trina synthetase	NA	NΑ	NA	NA I	VA	1 1	0	IP	1	1 -0	0.03	TP 1.0	8 0.71	FP	1.1	0.67	FP	1.11	0.53	-P 1.1	2 0.	.52 FI	P 1.1	1 0.5	4 FP	Oth	Protein synthesis not required in the moder	INA
YDR208W	MSS4		1	FP	NA	NA I			NA NA		NA N			NA NA				NA				NA NA			A NA			Oth	Phospholipid produced by this reaction leads to a dead end (1D-myo-Inositol 1,4,5-trisphosphate = IP3). This metabolite is used in other cellular processes such as signaling.	FP
		Tryptophan-tRNA ligase	NA		1	4.3 F		1 1	-0.02	_		1 0		TP 1.0															Protein synthesis not required in the model	NA
YPL097W		Tyrosine-tRNA ligase	NA	NA	NA	NA N	NA	1 1	-0.02	TP	1	1 -0	0.02	TP 1.0	8 0.74	FP	1.1	0.69	FP	1.11	0.55 F	P 1.1	2 0.	.48 FI	P 1.1	1 0.5	5 FP	Oth	Protein synthesis not required in the model	NA
		NAD-dependent 5,10-																												
VKDOSOW		methylenetetrahydrafolate	NIA.	NI A	NIA	NIA A			0.05	TD				TD 4 0		L TD	4.4	4 00	TD	4 4 4	4 00 3	FD 4.4		04		4 4 0		NIA	NA	NIA
YGR055W		dehydrogenase High affinity methionine permease	NA		NA NA	A AN		1 1 1 1	-0.05 0.29					TP 1.0															INA	NA NA
TGRUSSW	WUPT	Very low affinity methionine	NA	INA	NA	NA I	NA	1 1	0.29	IP	1	1 -0	0.05	TP 1.0	8 1.02	IP	1.1	1.01	IP	1.11	1.01	P 1.1	2 1.	.02 11	P 1.1	1 1.0	2 112	INA	INA	INA
VIII OSEWI	MUD	permease	NIA	NIA	NA	NA N	NIA.	1 1	0.05	тр	1	1 0	. 07	TP 1.0	0 1	TD	11	1 01	тр	1 11	1 02 7	TD 4.4	2 0	00 T	D 1 1	1 1	ТП	NA	NA	NA
YHL036W		Choline phosphate	NA	INA	IVA	INA I	NA.	1 1	-0.05	IF	-	1 -0	7.07	11.0	0 1	IF	1.1	1.01	IF	1.11	1.02	F 1.1	2 0.	.99 11	1.1	<u> </u>	IF	INA	IVA	INA
YGR007W	MUQ1	cytidylyltransferase (also called phosphoethanolamine cytidylyltransferase or phosphocholine cytidylyltransferase)	NA	NA	NA	NA N	NA_	1 1	0.3	TP	1	1 -0	0.03	TP 1.0	8 1.03	тР	1.1	1.01	TP	1.11	0.99	ΓP 1.1	2 1.	.02 TI	P 1.1	1 1	TP	NA	NA	NA
\/\ID0.40\\/		Mevalonate pyrophosphate				l.				l			l.		١			١ ا									l		NIA.	
		decarboxylase	0	TN	NA	NA N		NA NA						NA NA							NA N								NA	NA
		Leucine-tRNA ligase	NA	NA	1	11.2 F	_	1 1	-0.01	_	1			TP 1.0							0.51 F								Protein synthesis not required in the model	NA
YDL040C	NA I 1	N-terminal acetyltransferase	NA	NA	1	3.8 F	FP	1 1	-0.04	TP	1	1 -0	0.02	TP 1.0	8 0.89	TP	1.1	0.87	TP	1.11	0.88	P 1.1	2 0).8 T	P 1.1	1 0.8	9 TP	Oth	Protein N-terminal acetylation not required in the model	NA
YGR147C	NAT2	N alpha-acetyltransferase	1	FP	NA	NA N	NA N	NA NA	NA NA	NA	NA N	1 A	1 AV	NA 1.0	8 0.9	TP	1.1	0.89	TP	1.11	0.96	ГР 1.1	2 0.	.96 TI	P 1.1	1 0.9	6 TP	Dis	Only deemed to be essential in one study [Giaever02]. The other study [Steinmetz02] shows normal growth on all substrates.	FP
YMR145C	NDE1	Hypothetical ORF	NA	NA	NA	NA I	NΑ	1 1	-0.01	TP	1	1 -0	0.02	TP 1.0	8 1.02	TP	1.1	1.04	TP	1.11	1.05	TP 1.1	2 1.	.05 TI	P 1.1	1 1.0	5 TP	NA	NA	NA
YDL085W	NDE2	Hypothetical ORF	NA	NA	NA	NA N	NΑ	1 1	0.26	TP	1	1 -0	0.07	TP 1.0	8 1.02	TP	1.1	1.03	TP	1.11	1.03	ΓP 1.1	2 1.	.03 T	P 1.1	1 1.0	2 TP	NA	NA	NA
YML120C	NDI1	NADH dehydrogenase (ubiquinone)	NΔ	NΔ	NA	NA I	NΔ	1 1	-0.03	тр	1	1 -0	0.03	TP 1.0	8 0 08	тр	1 1	0.97	ТР	1 11	0.65	D 1 1	2 0	03 T	D 11	1 06	1 FD	Unk	The model will ferment glycerol or lactate in a ndi1 strain, bu the yields are much lower than the wild type strain yield.	t NA
		Putative Na+/H+ antiporter	NA	_	NA	NA N		1 1	-0.03		1	1 0	0.03	TP 1.0	0 1 01	TD	1.1	1.01	TD	1.11	1.02	F 1.1	2 0.	02 T	D 1.1	1 1 0.0	4 TD	NIA	MA	NA
TENTOVV	INDAT	Nit protein, nitrilase superfamily	INA	INA	IVA	INA I	NA	' '	-0.03	IF	-	1 -0	1.02	11.0	0 1.01	IF	1.1	1.01	IF	1.11	1.02	F 1.1	2 1.	.02 11	1.1	1 1.0	+ 115	INA	IVA	INA
YJL126W	NIT2	member	NIA	NΙΛ	NA	NA N	NIA.	1 1	0.72	тр	1	1 0	07	TP 1.0	0 1 01	тр	11	1 02	тр	1 11	1 02 7	TD 1 1	2 1	01 T	D 1 1	1 1 0	ть	NΙΛ	NΛ	NA
13L120VV	INITZ	Nit protein, nitrilase superfamily	INA	INA	INA	INA I	N/A	<u>' </u>	0.72	1.5	-	1 -0	7.07	1.0	0 1.01	IF	1.1	1.02	IF	1.11	1.03	F 1.1	2 1.	.01 11	1.1	1 1.0	2 11	INA	IVA	INA
YLR351C	NIT3	member	NA	NΙΛ	NA	NA N	NIA.	1 1	-0.03	тр	1	1 0	0.6	TP 1.0	0 1 02	ть	11	1 04	тр	1 11	1 04 7	TD 1 1	2 1	06 T	D 1 1	1 1 0	ть	NΙΛ	NΛ	NA
TENSSTO		Nicotinamide/nicotinic acid	INA	INA	INA	INA I	NA.		-0.03	115		1 -0	7.03	11.0	0 1.00) IF	1.1	1.04	IF	1.11	1.04	1.1	2 1.	.00 11	1.1	1 1.0	J 1F	INA	IVA	INA
YLR328W	NMA1	mononucleotide adenylyltransferase	NA	NA	NA	NA N	NΑ	1 1	-0.01	TP	1	1 -0	0.03	TP 1.0	8 1.05	TP	1.1	1.05	TP	1.11	1.04	TP 1.1	2 1.	.08 TI	P 1.1	1 1.0	6 TP	NA	NA	NA
YGR010W		Nicotinamide/nicotinic acid mononucleotide adenylyltransferase	NA	NA	NA	NA N	NA	1 1	0.38	TP	1	1 -0	0.03	TP 1.0	8 1.03	тР	1.1	1.01	TP	1.11	1.01	ГР 1.1	2 1.	.03 TI	P 1.1	1 1.0	2 TP	NA	NA	NA
																													Metabolite produced by this reaction is a dead-end (N-	
YLR195C	NMT1	N-myristoyl transferase	1	FP	NA	NA N	1 AV	NA NA	NA	NA	NA N	1 A	1 AV	NA NA	NA NA	NA	NA	NA	NA	NA	NA N	NA NA	A N	NA N	A NA	N/	NA	Den	Tetradecanoylglycylpeptide).	FP
V0D5		Nicotinate																											Also potentially involved in cromatin silencing through	
		phosphoribosyltransferase	NA	_	1	4.8 F	FP	1 1	0	TP	1			TP 1.0	_	TP		_	TP		0.97								adjusting the NAD/NADH balance.	NA
		NADH pyrophosphatase 1	NA	NA	NA	NA N	NA	1 1	0.04	TP	1			TP 1.0	_	_		1.02	_			TP 1.1			P 1.1		_		NA NA	NA
YDR001C		Neutral trehalase	NA	NA	NA		_	1 1	0.02	TP	1			TP 1.0					_				_		P 1.1				NA	NA
		Neutral trehalase	NA		NA	NA N		1 1						TP 1.0	_						1.01					_	_		NA	NA
YKL120W	OAC1	Oxaloacetate transport protein	NA	NA	NA	NA N	NA	1 1	-0.04	TP	1	1 -0	0.05	TP 1.0	8 1.02	TP	1.1	1.02	TP	1.11	1.01	TP 1.1	2 1.	.03 T	P 1.1	1 1.0	2 TP	NA		NA
YKL055C		3-oxoacyl-[acyl-carrier-protein] reductase	NA	NΔ	1	5.7 F	FP	1 1	0.09	TP	1	1 -0	0.02	TP 1.0	8 0 75	; FP	11	0.73	FP	1 11	0.47 F	TP 1 1	2 0	45 FI	P 1 1	1 0 5	S FP	Oth	It has been proposed that the role of the mitochondrial fatty acid synthase is to provide phospholipids for the mitochondrial inner membrane and that the disruption of genes in the FAS (including OAR1) would lead into inability properly synthesize the inner membrane [Schneider97].	c NA
2000		Mitochondrial 2-oxodicarboxylate	,	, .		<u> </u>		+	0.00			+		1.0	3.70			5.75		7	J/ I					. 0.0	+	5.11	, , , , , , , , , , , , , , , , , , , ,	
YPL134C		transport protein	NA	NA	NA	NA N	NA	1 1	-0.01	TP	1	1 -0	0.05	TP 1.0	8 1.01	TP	1.1	1.01	TP	1.11	1.01	TP 1.1	2	1 TI	P 1.1	1 1.0	1 TP	NA	NA	NA
		Mitochondrial 2-oxodicarboxylate																												
		transport protein	NA		NA	NA N			-0.02					TP 1.0																NA
YGL055W	OLE1	Delta-9-fatty acid desaturase	0	TN	NA	NA N	1 AV	NA NA	NA	NA	NA N	1 A	1 AV	NA NA	NA	NA	NA	NA	NA	NA	NA N	NA NA	A N	NA N	A NA	N/	NA	NA	NA	NA

Name Ess sim Row sim MMD call NPGal exp PPG a lex PPG a	YPL exp	TPL exp	Class	Explanation
	0 1.03	03 FN	Ti di m m al is m st	The activities catalyzed by this gene are totally lost when it is disrupted, but mutants are viable. The cells accumulate mmPE and membrane is devoid of PC [MIPS]. Surpsingly, mutant were not strict choline auxotrophs (choline req'd for an alternate route to produce PC). Reason why cells are viable is unknown; it has been speculated that a mutation in CHO2 may alter its substrate specificity (CHO2 catalyzes 1st of 3 steps in pathway from PE to PC, OPI3 primarily catalyzes and and 3rd steps, can also catalyze 1st step but is very nefficient).
Mitochondrial integral membrane YOR130C ORT1 protein, ornithine transporter NA NA NA NA NA O 1 4.31 TN 1 1 -0.04 TP 1.08 1.01 TP 1.1 1.03 TP 1.11 1.02 TP 1.12 1.02 TP 1.1	11 1.02	02 TP	NA W	Weak false negative NA
YJR051W OSM1 Osmotic growth protein NA NA NA NA NA NA 1 1 1 0.27 TP 1 1 1 -0.03 TP 1.08 1.02 TP 1.1 1.03 TP 1.11 1.03 TP 1.12 1.04 TP 1.	11 1.04	04 TP	NA N	NA NA
YDR538W PAD1 Phenylacrylic acid decarboxylase NA NA NA NA NA NA NA NA NA NA NA NA NA		03 TP		NA NA NA
Phosphoenolpyruvate				Lower oxygen uptake rate would correct this false negative
YKR097W PCK1 carboxylkinase	93 1.04	04 TP	Med p	orediction. NA
	IA NA	IA NA	Bio N	N-Acetylglucosamine synthesis is not required in the model. FP
Cholinephosphate cytidylyltransferase phosphorylcholi	11 0.99	99 TP		
Pyruvate dehydrogenase alpha YER178W PDA1 subunit (E1 alpha) NA NA NA NA NA NA 1 1 1 0.35 TP 1 1 1 0.28 TP 1.08 1 TP 1.1 0.96 TP 1.11 0.78 FP 1.12 0.79 TP 1.	11 0.9	9 TP		Pyruvate dehydrogenase (coded by PDA1 & PDB1) is not used by the model when grown on glycerol.
Pyruvate dehydrogenase beta YBR221C PDB1 subunit (E1 beta) NA NA NA NA NA NA 1 1 1 0.09 TP 1 1 0 TP 1.08 0.93 TP 1.1 0.91 TP 1.11 0.66 FP 1.12 0.71 FP 1.			Р	Pyruvate dehydrogenase (coded by PDA1 & PDB1) is not used by the model when grown on glycerol or ethanol.
15 15 15 15 15 15 15 15 15 15 15 15 15 1	11 0.0	.0 11	Т	There are three alternate isozymes in the model , but PDC1 deletion alone is sufficient to reduce PDC activity significantly
YLR044C PDC1 Pyruvate decarboxylase NA NA 1 3.8 FP 1 1 1 -0.03 TP 1 1 1 -0.03 TP 1.08 1 TP 1.1 1 TP 1.11 1 TP 1.12 0.97 TP 1.	11 0.99	99 TP		enough to result in a slow growth phenotype. NA
YLR134W PDC5 Pyruvate decarboxylase				NA NA
YGR087C PDC6 Pyruvate decarboxylase isozyme	11 1.02	02 TP	NA N	NA NA
YGL248W PDE1 phosphodiesterase, low affinity NA NA NA NA NA NA 1 1 1 2.85 TP 1 1 1 -0.03 TP 1.08 0.99 TP 1.1 0.99 TP 1.11 0.98 TP 1.12 0.97 TP 1.	11 0.98	98 TP	NA N	NA NA
YOR360C PDE2 phosphodiesterase	11 0.99	99 TP	NA N	NA NA
YBR035C PDX3 phosphate oxidase	11 0.61	61 FP		The whole pyridoxine metabolism is a dead end in the model. NA
YBL030C PET9 ADP/ATP translocator 1 FP NA NA NA NA NA NA NA NA NA NA NA NA NA	11 1.03	03 TP	of	Only deemed to be essential in one study [Giaever02]. The other study [Steinmetz02] shows normal growth on all substrates.
YGR240C PFK1 Phosphofructokinase alpha subunit NA NA 0.19 4.8 TN 0.18 1 -0.01 TN 0.19 1 0 TN 0.2 0.89 FN 1.06 0.95 TP 1.1 1.05 TP 1.12 1.08 TP 1.1	11 1.05	05 TP	Dis [S	Slow growth in [Giaever02], but apparently normal growth in Steinmetz02].
YMR205C PFK2 Phosphofructokinase beta subunit NA NA 0.19 16.7 TN 0.18 1 -0.01 TN 0.19 1 -0.03 TN 0.2 0.7 TN 1.06 0.76 FP 1.1 0.95 TP 1.12 1.01 TP 1.	11 0.97	97 TP		n YPDGE media the max glc uptake in the simulation is too ow to cause pfk2 to have a growth defect.
YIL107C PFK26 6-phosphofructose-2-kinase NA NA NA NA NA 1 1 1 0.02 TP 1 1 1 0.1 TP 1.08 1 TP 1.1 0.98 TP 1.11 0.99 TP 1.12 0.96 TP 1.				NA NA
YOL136C PFK276-phosphofructo-2-kinase				NA NA NA NA NA
YCR012W PGK1 3-phosphoglycerate kinase 0.1 TN NA NA NA NA NA NA NA NA NA NA NA NA NA		IA NA		n silico slow growth. NA NA
Phosphoglucomutase minor YKL127W PGM1 isoform NA NA NA NA NA NA NA NA 1 1 -0.05 TP 1 1 -0.04 TP 1.08 1.01 TP 1.1 1.04 TP 1.11 1.03 TP 1.12 1.05 TP 1.	11 1.04	04 TP	NA N	NA NA
			P th	Pgm2p is major isomform of phosphoglucomutase. Maybe he minor isoform (Pgm1p) can't fully compensate for loss of
YMR105C PGM2 Phosphoglucomutase	11 1	1 TP		
YCL004W PGS1 synthase 1 FP NA NA NA NA NA NA NA NA NA NA NA NA NA			Dis m	Should not be absolutely essential [SGD]. Disrupts nitochondrial function somewhat.
YNL316C PHA2 Prephenate dehydratase NA NA NA NA NA NA NA NA NA NA NA NA NA				
YDR481C PHO8 Repressible alkaline phosphatase NA NA NA NA NA NA NA NA NA NA NA NA NA				
YML123C PHO84 Inorganic phosphate transporter NA NA NA NA NA 1 1 1 -0.03 TP 1 1 1 -0.02 TP 1.08 0.96 TP 1.1 0.83 FP 1.11 0.85 TP 1.12 0.82 TP 1.			Ti tra	There are multiple alternative isozymes for the phosphate ransporters, but Pho84p may be the dominant one under some conditions.
YCR037C PHO87Phosphate permease NA NA NA NA NA NA 1 1 1 0.02 TP 1 1 1 0 TP 1.08 1 TP 1.1 1 TP 1.1 1.01 TP 1.12 1 TP 1.2	11 1.01	01 TP	NA N	NA NA
YBR296C PHO8 Na+/Pi symporter (putative) NA NA NA NA NA NA NA NA NA NA NA NA NA				
YJL198W PHO9(Low-affinity phosphate transporter NA NA NA NA NA NA NA NA NA NA NA NA NA				

																			-	۵ =											<u> </u>
			sim	=	sim	exp	call	Sign	dxə	ave	call	l sim	PGal exp	/PGal ave	8	<u>ڇ</u>	d z	DOCE eim		PDGE exp	E	d X	la:	<u>ء</u>	Q.	call	<u>.</u> <u>E</u>	dxe	call		ster et
ORF	lame	Annotation	SS S	ss call	Nol	NO!	No	MMD sim	IMD exp	имр аve	IMD call	PGal sim	PGa	PGa	PGa	'PD sim	PD exp		3		/PG sim	PG exp	PG call	/PE sim	/PE exp	PE	/PL sim	/PLe	/PL c	Class	Explanation Is
		Amotation	Ш	Ш	S	S	S	2	2		2	<u> </u>	_	> ;	_	>	> >	>		> >		· >		<u> </u>	<u> </u>		<u> </u>	>	>	0	Phospholipid produced by this reaction leads to a dead-end
VAIL OCTIVI	DIKA	Phosphatidulinasital 4 kinasa	١,		NIA.	l NIA	NIA.	NIA.	NI A	NIA	NI A	NIA I					NIA NI	A N		NIA NI	, ,		NI A	NIA	NIA	. INTA	NIA.	NIA.		Don	(1D-myo-Inositol 1,4,5-trisphosphate). Also Stt4p is an
	PIK1 PIS1	Phosphatidylinositol 4-kinase Phosphatidylinositol synthase	0	TN	NA NA			NA NA	NA	NA NA		NA I			1 Al			A N		NA N		A NA		NA NA			NA			NA	isozyme. FP
		Phosphoinositide-specific																													
YPL268W	PLC1	phospholipase C	NA	NA	1	14.8	3 FP	1	1	-0.02	TP	1	1 -(0.01 7	TP 1	.08 0).72 F	P 1.	.1 (0.7 FI	1.1	11 0.88	B TP	1.12	2 0.8	1 TP	1.11	0.89	TP	Oth	Also involved in kinetochore function. NA This is the major isoform of the cytosolic ATPase, but in the
																															model a minor isoform can compensate for the function.
		Diameter ATD																													Deletion of the minor isoform (which contains Pma2p instead
		Plasma membrane H+-ATPase Plasma membrane ATPase	NA		NA NA			NA 1		-0.04		NA I	NA	NA N 0.01 T	NA N	.08 1	NA N	A N	A N	.03 TI	1.1	A NA	NA 3 TP	1.12	NA 2 1.0	NA 3 TP	1.11	1.03	TP	ISO NA	of Pma1p) is not lethal experimentally. FP NA NA
		Mannose-6-phosphate isomerase	0		NA		NA		NA	NA		NA I		NA N			NA N			NA N				NA			NA			NA	NA NA
VCD024CA	DMD4	Proteolipid associated with plasma	NIA.	NI A	NIA	NIA.		0.05	_	0.04	TD	0.00	4	04	NI O				00 4	00 T	1.0	7 4 0	_ TD	4.00		4	4.04		1	Mad	If oxygen uptake rate on YPGal is increased the pmp1 growth rate increases to that of the wild type. NA
YCR024CA	PIVIPT	membrane H(+)-ATPase (Pma1p) Proteolipid associated with plasma	NA	NA	NA	. NA	INA	0.85	1	0.04	IP	0.23	1 (1.01 F	N U	1.99	1.03 1	P 1.	03 1	.03 11	1.0	1.02	2 112	1.03	3 1	IP	1.04	1	IP	Med	rate increases to that of the wild type. NA If oxygen uptake rate on YPGal is increased the pmp2 growth
YEL017CA	PMP2	membrane H(+)-ATPase (Pma1p)	NA	NA	NA	. NA	NA	0.85	1	0.33	TP	0.23	1	0 F	N 0	.99 1	1.02 T	P 1.	03 1	.03 TI	1.0	7 1.0	з ТР	1.03	3 1.0	4 TP	1.04	1.03	TP	Med	
		Dolichyl phosphate-D- mannose:protein O-D-																													
YDL095W	PMT1	•	NA	NA	NA	. NA	NA	1	1	-0.02	TP	1	1 -(0.04 1	TP 1	.08).99 T	P 1.	.1 1	.02 TI	1.1	11 0.98	вТР	1.12	2 1.04	4 TP	1.11	1.03	TP	NA	NA NA
		Dolichyl phosphate-D-																													
YAL023C	DMT2	mannose:protein O-D- mannosyltransferase	NIA.	NA	. 1	6.2	FP	1	4	-0.01	TD	1	1 (CD 4	00 0) 04 T	D 4	1 0		1,1	11 0 0	, TD	1 10	0.00	e TD	1 11	0.06	TD	Oth	Mannosyntransferase activity not required in the model. NA
TALUZSC	FIVITZ	Dolichyl phosphate-D-	INA	INA	<u> </u>	6.3	FF	-	H	-0.01	IF		1 -(J.UZ 1	IFI	.00 (J.94 I	F 1.	.1 0	.94 11	11.1	11 0.94	+ 117	1.12	2 0.9	0 11	1.11	0.96	IF	Otti	INALIHOSYITTATISTETASE ACTIVITY HOLTEQUITED III THE HIODEL.
		mannose:protein O-D-																													
YOR321W	PMT3	mannosyltransferase Dolichyl phosphate-D-	NA	NA	NA	. NA	NA	1	1	-0.05	TP	1	1 -(0.05 1	TP 1	.08 1	1.01 T	P 1.	.1 1	.02 TI	1.1	11 1.02	2 TP	1.12	2 1.0	2 TP	1.11	1.03	TP	NA	NA NA
		mannose:protein O-D-																													
YDL093W	PMT5	mannosyltransferase	NA	NA	NA	. NA	NA	1	1	-0.06	TP	1	1 -0	0.06	ΓP 1	.08 1	1.02 T	P 1.	.1 1	.04 TI	1.1	11 1.04	4 TP	1.12	2 1.0	6 TP	1.11	1.03	TP	NA	NA NA
		Dolichyl phosphate-D- mannose:protein O-D-																													
YGR199W	РМТ6	mannosyltransferase	NA	NA	NA	. NA	NA	1	1	-0.01	TP	1	1 0	.03 1	TP 1							11 0.99									NA NA
		Nicotinamidase pyrazinamidase			NA				1	0.01		1			TP 1							11 1.0									
YLR209C	PNP1	Purine nucleoside phosphorylase	NA	NA	NA	. NA	NA	1	1	0	TP	1	1 (.04 7	IP 1	.08	1 1	P 1.	.1 1	.02 TI	1.0)5 1	IP	1.1	1.0	2 11	1.07	1.01	IP	NA	NA NA Does not grow well under aerobic conditions, because Pos5p
																															is the primary source of NADPH in mitochondria [Outten03].
YPL188W	DOS5	Involved in oxidative stress	NA	NA	1	02	FP	1	1	0.01	тр	1	1 (000	TD 1	00	0.7	D 1	1 0	92 5	1 1	11 0 5) ED	1 12	0.5	4 EB	1 11	0.6	ED	Mod	May need to change the model so that only Pos5p can provide NADPH in mitochondria.
YIL160C		3-oxoacyl CoA thiolase			NA				1	0.69		1		0.02			1.02 T					11 0.5									
YGL205W	POX1	Fatty-acyl coenzyme A oxidase	NA	NA	NA	. NA	NA	1	1	0.05	TP	1	1 -(0.01	ΓP 1	.08 1	1.01 T	P 1.	.1	1 TI	1.1	11 0.9	7 TP	1.12	2 1	TP	1.11	0.99	TP	NA	
YHR026W	PPΔ1	Proteolipid vacuolar ATPase V0 domain subunit c"	NΔ	NA	1	5.6	FP	1	1	0.03	тр	1	1 0	01 7	гр	08	0 8 F	D 1	1 0	65 FI	1 1	11 0 6	1 FD	1 12	0 0 6	FE	1 11	0.68	FD	Oth	See other vacuolar ATPase components. NA
1111(02011	IIAI	domain subunit c	INA	INA	<u> </u>	3.0	+	<u>'</u>	Ħ	0.03		_	1	.01	<u> </u>	.00	0.0	· · ·	.1 0	.03 11	1	0.0	' ' '	1.12	0.0	, 	1.11	0.00	H	Otti	occ other vacuolar ATT asc components.
																															PPA2 deletion strain has lost mitochondrial DNA apparently
																															because pyrophosphate produced during replication cannot be converted into phosphate [Lundin91]. The model does not
																															run any of the reactions producing ppi[m] in the ppa2 and
YMR267W	PPA2	Inorganic pyrophosphatase Phosphopantetheine:protein	NA	NA	1	3.4	FP	1	1	-0.04	TP	1	1 -(0.02 1	ΓP 1	.08 0).74 F	P 1.	.1 0	.67 FI	1.1	11 0.5	4 FP	1.12	0.49	9 FP	1.11	0.54	FP	Mod	utilizes the cytoplasmic forms of the reactions instead. NA
YPL148C	PPT2	transferase (PPTase)	NA	NA	1	7	FP	1	1	0.04	TP	1	1 -(0.03	TP 1	.08).64 F	P 1.	.1 0	.65 FI	1.1	11 0.5	2 FP	1.12	0.5	3 FP	1.11	0.51	FP	Oth	CoA biosynthesis not required in the model.
																															Should be a proline auxotroph, but should grow fine on rich
YDR300C	PR∩1	Gamma-glutamyl kinase	NΔ	NA	1	126	S FP	1	1	-0.01	тр	1	1	0 1	гр	08 0) 64 F	D 1	1 0	60 FI	1 1	11 0 0	5 ТР	1 12	0 0	, TD	1 11	1.06	тр	Unk	media. Model synthesizes proline from glutamate using ornithine as an intermediate.
1010000	i KOI	Gamma-glutamyl phosphate	IVA	INA	<u> </u>	12.0	1	<u> </u>	H	-0.01	"	_	+	0 1	<u> </u>	.00 0	7.04 1		.1 0	.03 11	1	0.5	J 11	1.12	0.3	, III	1.11	1.00	1	OTIK	Should be a proline auxotroph. Model synthesizes proline
YOR323C	PRO2	reductase	NA	NA	NA	. NA	NA	1	0	5.16	FP	1	1 -(0.03	TP 1	.08	1 T	P 1.	.1	1 TI	1.1	11 1.02	2 TP	1.12	2 1.0	2 TP	1.11	1.01	TP	Unk	from glutamate using ornithine as an intermediate.
		Delta 1-pyrroline-5-carboxylate																													Only deemed to be essential in one study [Giaever02]. The other study [Steinmetz02] shows normal growth on all
YER023W	PRO3		1	FP	NA	. NA	NA	NA	NA	NA	NA	NA	NA I	NA N	NA 1	.08 1	1.06 T	P 1.	.1 1	.05 TI	1.0	1.04	4 TP	1.11	1.1	1 TP	1.05	1.06	TP	Dis	substrates. FP
		Dihasa phasahata																													Prs3p has an unknown role in controlling cell growth. Its
YHL011C	PRS3	Ribose-phosphate pyrophosphokinase	NA	NA	1	7.6	FP	1	1	-0.02	TP	1	1	0 1	TP 1	.08).66 F	P 1	.1 0	.73 FI	1.1	1 1	TP	1.12	0.9	1 TP	1.11	0.92	TP	Oth	deletion causes a wide variety of phenotypes including small cell size.
		Ribose-phosphate																													
YBL068W	PRS4	pyrophosphokinase Phosphoribosylpyrophosphate	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	0 1	TP 1	.08 1	1.01 T	P 1.	.1 1	.03 TI	1.1	11 1.03	3 TP	1.12	2 1.0	5 TP	1.11	1.04	TP	NA	NA NA
		synthetase (ribose-phosphate																													
YOL061W	PRS5	pyrophosphokinase)	NA	NA	NA	. NA	NA	1	1	0.05	TP	1	1 -(0.02	TP 1	.08).99 T	P 1.	.1 1	.01 TI	1.1	11 1.03	3 TP	1.12	1.0	3 TP	1.11	1.02	TP	NA	NA NA

The control of the																															<u> </u>
Company Comp				_		Ε	9	=	Ε	9	e	=	mis ax	ave .	l=	۽	۵	_	sim	exp	5 2	_ a	_	ے	۵	l_l	_	۵ ا	_		
Company Comp	ш	ne		sin	cal	.s	e ×	W C2	D Si	D e	D a	Ö	Sal s	3al 8	3al o	Sir	ex	Ca	g	9 9	1 5	S S	3 ca	sir	ex	ca	is.	e l	2	SS	l e l
Property Property	O. R.	Naı		Ess	Ess	Slo	Slo	Slo	Σ	Σ	Σ	Σ	Y P(ΥP	ΥP(ΥPI	ΥPI	ΥPI	ΥPI	YPI	. ^	Y P	ΥP(γPi	γÞ	ΥPI	ΥPI	ΥPI		ဦ	Explanation [호
Part Description plant pla																															
Part Part	YDI 055C	PSA1		0	TN	NΔ	NΑ	NΔ	NΔ	NΔ	NΔ	NΔ	NA NA	NA	NΔ	NΔ	NΔ	NΑ	NΔ	NA N	ΔN	ΔΝΔ	NΔ	NΔ	NΑ	NΑ	NΑ	NA N	А	NΑ	NA NA
PROSESSON PROS					_		_	_	1			_	1 1																		
Fig. 12 Fig. 13 Fig. 14 Fig.				_	_		_	_	1			TP	1 1			1.08	1.03	TP	1.1	1.02 T	P 1.	11 1.01	_		_		.11	1.01 T	_		NA NA
Fig. Fig. Procedure of the product Section Sec				_	_			_	1	1		TP	1 1		_					1 T	_	_	_		_		.11	1.03 T	_		NA NA
PRIABET PRIA									1	1		_	1 1																		NA NA
Fig. Fig. Purity Purit							_	_	1	_	_	TP	1 1		_		_	_	_		_						.11	1.02 T			NA NA
Miles Mile	YLR142W	PUT1		NA	NA	NA	NA	NA	1	1 -	0.05	TP	1 1	-0.0	4 TP	1.08	1.01	TP 1	1.09	1 T	P 0.9	91 1	TP	1.1	1	TP ().99	1.01 T	РΙ	NA	NA NA
Vicinity Vicinity	VHD027W	חודים		NIA.	NI A	NIA.	NIA.	NI A	4		0.00	TD				4.00	4.04	TD		4 00 T	D 4	44 4 04	TD	4 40	0.07	TD	ا بيا			NI A	NA NA
ACC Camproper of knop-chain fally April Ap								_	1				1 1		8 TP													1.01 T			
WALFERSON WALF	7 0110 100					10.0	1.0.			Ť	0.00			0.0	<u> </u>	1100					Ť		<u> </u>		1102				Ť		
VEX. Psychological and provided and prov								NA	1	_		_	1 1															1.05 T			
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VPR327C PVR2 glotters				_	_		_	_	1	_		TP	1 1		_		_	_													
Ubiquind cytochrome c ubiquind cytochrome c ubiquind cytochrome c complex 8.5 kDa NA	12.12.00			10,		10.0	1.0.			Ť	00			0	Ť	1100					Ť		Ė		1101				Ť		
Ubigund cytochrome Complex 8.5 kDa Na Na Na Na Na Na Na Na Na Na Na Na Na	YOR347C	PYK2	isoform	NA	NA	NA	NA	NA	1	1 -	0.04	TP	1 1	-0.0	6 TP	1.08	1.01	TP	1.1	1.03 T	P 1.	11 1.04	TP	1.12	1.04	TP 1	.11	1.02 T	PΙ	NA	
Ubiquinol-cytochrome C oxidereductase complex & S. Na. Na. Na. Na. Na. Na. Na. Na. Na. Na																															Deletion of QCR10 does not impair growth on non-
Ubiquario-lypochrome c doubleway we have modeled the complex. This subunit should be made a non-assertal part of the MA NA																															
94R091WA QCR1 (aubumit			Ubiqunol-cytochrome c																												
40 kDa ubiquinol cytochrome-c VPR191W QCR2 reductase core protein 2 NA NA 03 44 TN 030 1 -0.01 TP 032 1 -0.05 TP 030 152 TP 0.24 0.87 FN 0.14 0.49 TN 0.08 0.39 TN 0.17 0.6 TN Med consider increasing maximum glu cytosher in PVGE medium. NA Ubiquinol cytochrome C Ubiquinol cy																															
9R191W QCR2 eductase core protein 2	YHR001WA	QCR1	subunit	NA	NA	NA	NA	NA	0.89	1 -	0.03	TP ().82 1	0	TP	0.98	1.01	TP (0.24	1.02 F	N 0.	14 1.02	FN	0.08	1.01	FN C).17	1.03 F	N	Iso	complex since it only plays structural role. NA
9R191W QCR2 eductase core protein 2																															This is probably due to excessive respiration under the
Deletion of QCR8 does not have significant effect on the formation or stability of cytochrome C Ubiquinol cytochrome C GUBiquinol Cytochrome C GuBiqui			40 kDa ubiquinol cytochrome-c																												
Exercise Ubiquind cytochrome C Ubiquind cytochro	YPR191W	QCR2	reductase core protein 2	NA	NA	0.9	4.4	TN	0.89	1 -	0.01	TP ().82 1	-0.0	5 TP	0.98	0.92	TP (0.24	0.87 F	N 0.	14 0.49	TN	0.08	0.39	TN C	0.17	0.6 T	ΝN	Лed	consider increasing maximum glc uptake in YPDGE medium. NA
Exercise Ubiquind cytochrome C Ubiquind cytochro																															Dalatina of OCDC dans and house significant affect on the
Ubiquinol cytochrome C CR7 Code of addreductases subunit 6 (17 kBa) NA NA NA NA NA NA NA NA NA NA NA NA NA																															
YER032C CCR6 oxdoreductase subunit 6 (17 kDa) Na Na Na Na Na Na Na			Ubiquinol cytochrome C																												
YR183C QCR7 oxidoreductase subunit 7 (14 kDa)	YFR033C	QCR6	oxidoreductase subunit 6 (17 kDa)	NA	NA	NA	NA	NA	0.89	1 -	0.02	TP ().82 1	0.1	TP	0.98	1.02	TP (0.24	0.98 F	N 0.	14 0.87	FN.	0.08	0.82	FN C).17	0.92 F	N	Iso	indicated by the gene-protein-reaction associations currently. NA
Ubiquinol cytochrome C reductase PyLL166W OCRS subunit 8 (11 kDa) NA NA 0.9 6.3 TN 0.89 1 0.05 TP 0.82 1 0.15 TP 0.88 0.93 TP 0.24 0.86 FN 0.14 0.6 TN 0.08 0.52 TN 0.17 0.54 TN Med consider increasing maximum glc uptake in YPDGE medium. NA NA NA NA NA NA NA NA NA NA NA NA NA	VDDEOOC	0007		١			- 0		0.00		0.00	TD (0.00		0.00	0.07		204	0.05				0.00	0.54					~ 4L	
Value Valu	YDR529C	QCR7	oxidoreductase subunit 7 (14 kDa)	NA	NA	0.9	5.3	IN	0.89	1 -	0.02	IP ().82 1	-0.0	2 11	0.98	0.67	FP (J.24	0.65 1	N 0.	14 0.53	IIN	0.08	0.51	INC).17 (0.59 1	N	Jtn	primarily fermentative conditions.
Value Valu																															This is probably due to excessive respiration under the
Ublquinol cytochrome c oxidoreductase complex 7.3 kDa subunit 9																															simulation conditions - glucose vs oxygen limitation, may
VRR183C QCR9 subunit 9	YJL166W	QCR8		NA	NA	0.9	6.3	TN	0.89	1	0.05	TP ().82 1	0.15	5 TP	0.98	0.93	TP (0.24	0.86 F	N 0.	14 0.6	TN	0.08	0.52	TN C).17 (0.54 T	ΝN	Лed	consider increasing maximum glc uptake in YPDGE medium. NA
YER183C CCR Subunit 9																															
FP FP FP FP FP FP FP FP	YGR183C	QCR9	-	NA	NA	NA	NA	NA	0.89	1	0.13	TP (0.82 1	0.2	1 TP	0.98	0.96	TP (0.24	0.85 T	N 0.	14 0.6	TN	0.08	0.58	TN C).17	0.63 T	N I	NA	NA NA
UDP-N-acetylglucosamine			Glutamine-dependent NAD																												
\(\) \\ \(\) \\ \(\) \\ \(\) \\ \(\) \\ \(\) \\ \(\) \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\	YHR074W	QNS1		1	FP	NA	NA	NA	NA	NA	NA	NA	NA N	NA	NA	NA	NA	NA	NA	NA N	A N	A NA	NA	NA	NA	NA	NA	NA N	IA I	Bio	
\(\begin{array}{c c c c c c c c c c c c c c c c c c c	YDI 103C	ORI1	, ,	1	FP	NΔ	NΑ	NΔ	NΔ	NΔ	NΔ	ΝΔ	NA NA	NA	NΔ	NΔ	NΔ	NΔ	NΔ	NA N	ΔN	ΔΝΔ	NΔ	NΔ	NΑ	NΑ	NΔ	NA N	Δ	Rio	
CAAX farnesyltransferase alpha YKL019W RAM2 Subunit 1 FP NA NA NA NA NA NA NA N				NA		1	7						1 1																		
YCR036W RBK1 Ribokinase NA			CAAX farnesyltransferase alpha																												
YBR002C RER2 Cis-prenyltransferase 1 FP NA NA <t< td=""><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td>Quinone biosynthesis is not required in the model. NA</td></t<>																															Quinone biosynthesis is not required in the model. NA
YIL053W RHR2 DL-glycerol-3-phosphatase NA																															NA Ouinone biosynthesis is not required in the model ED
YBL033C RIB1 GTP cyclohydrolase II NA NA 1 10.3 FP 1 1 -0.04 TP 1 1 -0.04 TP 1 1 -0.01 TP 1.10 0.67 FP 1.11 0.67 FP Bio FAD biosynthesis not required in the model NA YOL143C RIB4 synthase (DMRL synthase) NA NA 1 4.5 FP 1 1 -0.01 TP NA								_																							NA NA
YOL143C RIB4 synthase) NA NA 1 4.5 FP 1 1 -0.01 TP NA NA NA NA NA NA NA NA NA NA NA NA NA			GTP cyclohydrolase II																												
YBR256C RIB5 Riboflavin biosynthesis 1 FP NA NA NA NA NA NA NA NA NA NA NA NA NA	VOL 4 := 5	D.F.																											I		
Protein involved in the biosynthesis of riboflavin, second step in the riboflavin biosynthesis pathway YBR153W RIB7 riboflavin biosynthesis pathway 1 FP NA NA NA NA NA NA NA NA NA NA NA NA NA													1 1	-0.0	1 TP	NA	NA NA	NA	NA	NA N	A N	A NA	NA	NA	NA	NA	NA NA	NA N	A I	Bio	
YBR153W RIB7 riboflavin biosynthesis pathway 1 FP NA NA NA NA NA NA NA NA NA NA NA NA NA	TBR250C	COIN	Tribonaviii biosyntilesis	_	FP	INA	INA	INA	NA	INA	IVA	NA	INA IN	1 IVA	INA	INA	NA	INA	INA	INA IN	A IN	AINA	INA	NA	IVA	INA	INA	INA IN	A	טוט	Tribonaviii biosynthesis is not required in the model
YBR153W RIB7 riboflavin biosynthesis pathway 1 FP NA NA NA NA NA NA NA NA NA NA NA NA NA			Protein involved in the biosynthesis																												
Rieske iron-sulfur protein of the mitochondrial cytochrome bc1																															
mitochondrial cytochrome bc1	YBR153W	RIB7		1	FP	NA	NA	NA	NA	NA	NA	NA	NA N	NA	NA	NA	NA	NA	NA	NA N	A N	A NA	NA	NA	NA	NA	NA	NA N	A I	Bio	Riboflavin biosynthesis is not required in the model. NA
YEL024W RIP1 complex NA NA NA NA NA NA NA NA NA NA NA NA NA			·																												
	YEL024W	RIP1		NA	NA	NA	NA	NA	0.89	1	0.36	TP (0.82 1	0.46	3 ТР	0.98	0.9	TP (0.24	0.82 T	N 0.	14 0.54	TN	0.08	0.42	TN).17	0.55 T	N	NA	NA NA

ORF	ıme		s sim	Ess call	Slow sim	Slow exp	ow call	MMD sim	MMD exp	MMD ave	MMD call	/PGal sim	Gal exp	YPGal ave	'PGal call	YPD sim	YPD exp		rPDGE SIM	YPDGE exp	/PG sim	YPG exp	/PG call	/PE sim	YPE exp	rPE call			Class		rster et al
Ö	Na	Annotation Ribose-5-phosphate ketol-	Es	Es	Š	Š	š	Σ	Σ	Σ	Ź	7	7	7	} ;	<u> </u>	<u>}</u>	: 5	÷	¥ ¥	7	<u>}</u>	Y	7	7	<u>}</u>	>	7	ਠ	Explanation	Ľ.
YOR095C	RKI1	isomerase	0.81	TN	NA	NA	NA	NA I	NA	NA	NA	NA	NA	NA I	NA N	NA I	NA N	A N	ΙA	NA NA	N/	NA NA	. NA	NA	NA	NA NA	N/	NA	NA	In silico slow growth.	NA
YER070W	RNR1	Ribonucleotide reductase, large (R1) subunit	NA	NΙΔ	1	22.3	FD	1	1 -	0.04	тр	1	1 -	.0 04	тр	JΔ	NA N	ΔΝ	IΔ	ΝΑ ΝΑ	NI/	ΔINA	NΙΔ	ΝΔ	NΔ	NA NA	. NZ	NIA	Oth	DNA synthesis not required in the model.	NA
TEIROTOVV	IXIVIXI	Ribonucleotide reductase	INA	INA		22.5	-	-	-	0.04		_		0.04		NA I	INA IN	A IN	*/^	IN/A IN/	14/	11/7	INC	INA	INA	IVA IVA	147	111/	Our	DIAA Synthosis not required in the model.	IVA
YJL026W	DNID2	subunit ribonucleotide reductase, small (R2) subunit	1	ED	NΙΛ	NΙΛ	NIA	NIA I	NIA	NΙΛ	NIA	NΙΛ	NIA	NIA I	NA N		NIA NI	٨٨	10	NIA NIA	NI/	NIA	NIA	NΙΛ	NIA	NA NA	l NI	NIA.	Oth	DNA synthesis not required in the model.	NA
13L02644	KINKZ	Ribonucleotide reductase, large	_	FF	INA	INA	INA	INA I	NA	INA	INA	INA	INA	INA	NA I	NA I	INA IN	A IV	N/A	INA INA	INA	A INA	INA	INA	INA	INA INA	INA	INA	Oth	DIVA synthesis not required in the model.	INA
YIL066C	RNR3	(R1) subunit	NA	NA	NA	NA	NA	1	1 -	0.01	TP	1	1 -	0.05	TP 1	.08	1 TI	P 1	.1	1.02 TP	1.1	1 1.03	3 TP	1.12	1.03	TP 1.1	1 1.0	3 TF	NA	NA	NA
YGR180C	RNR4	Ribonucleotide reductase, small (R2) subunit	NA	NA	1	8.5	FP	1	1 -	0.03	TP	1	1 -	0.02	TP 1	.08).81 FI	P 1	.1 (0.69 FP	1.1	1 0.59	FP	1.12	0.62	FP 1.1	1 0.6	S FF	Oth	DNA synthesis not required in the model.	NA
		D-ribulose-5-Phosphate 3-																												The PPP is only used at a low level on glycerol. The effect of	
YJL121C	RPE1	epimerase S-adenosyl-L-homocysteine	NA	NA	NA	NA	NA	0.97	1 (0.67	TP	1	1	0.22	TP 1.	.08 0	0.92 TI	P 1	.1 (0.84 FP	1.0	6 0.78	3 FP	1.11	0.78	TP 1.0	8 0.9	2 TF	Unk	this deletion is small in vivo anyway.	NA
		hydrolase (putative)	0	_	_	NA		NA I												NA NA											NA
		S-adenosylmethionine synthetase Methionine biosynthesis regulation			NA NA			1		0.02							0.98 TI			0.96 TP 1.02 TP											NA NA
1010020	OAIVIZ	High affinity S-adenosylmethionine	INA	INA	INA	INA	IVA	-	_	0.03		_	1	0.01		.00 1	1.01	+	-	1.02 11	 '''	1 1.02	- 11	1.12	1.03		1 1.0	3 11	14/4	101	IVA
YPL274W	SAM3	permease AdoMet-homocysteine	NA	NA	NA	NA	NA	1	1	0	TP	1	1	0	TP 1.	.08 1	1.02 TI	P 1	.1	1.05 TP	1.1	1 1.05	5 TP	1.12	1.07	TP 1.1	1 1.0	6 TF	NA	NA	NA
YPL273W	SAM4	methyltransferase	NA	NA	NA	NA	NA	1	1	0	TP	1	1 -	0.05	TP 1	.08 1	1.01 TI	P 1	.1	1.04 TP	1.1	1 1.05	5 TP	1.12	1.05	TP 1.1	1 1.0	4 TF	NA	NA	NA
YMR272C		Desaturase hydroxylase	NA	NA	NA	NA	NA	1	1 :	2.17	TP	1	1	0	TP 1	.08 0).99 TI	P 1	.1	1.01 TP	1.1	1 1.01	1 TP	1.12	0.99	TP 1.1	1 0.9	8 TF	NA		NA
YKL148C		Succinate dehydrogenase flavoprotein subunit	NA	NA	NA	NA	NA	1	1 -	0.01	TP	1	1	0.06	TP 1	.08	1 TI	P 1	.1	0.97 TP	1.1	1 0.69) FP	1.12	0.79	TP 1.1	1 0.6	1 FF	Iso	Sdh1p is not considered to be an essential part of the succinate dehydrogenase complex.	NA
		Succinate dehydrogenase																													
YLL041C	SDH3	(ubiquinone) iron-sulfur protein subunit	NIA	NIA	NΙΛ	NA	NΙΛ	1	1 (0.01	тр	1	1	0.07	TD 1	00 0	07 T	D 1	01	0 07 TE	0.0	0.67	7 TN	0.50	0.75	TNIOO	2 0 5	0 55	Mod	With a lower lactate uptake rate the model shows slow growth on lactate.	NA
TLL041C	3DI IZ	Suburiit	INA	INA	INA	INA	INA	-		0.01	15	_	-	0.07	IF I	.00 0	0.97 11	1.	.01	0.57 11	0.0	5 0.07	IIN	0.56	0.73	110 0.9	3 0.3	9 1 1	IVIEC	The model has an isozyme that includes an alternate subunit	INA
V/// 4 44\\\		Succinate dehydrogenase cytochrome b																			١						1		11-1	with high imilarity to Sdh3p, but even if this is removed the	NIA.
YKL141W	SDH3	Succinate dehydrogenase	1	FP	NA	NA	NA	NA I	NA	NA	NA	NA	NA	NA I	NA P	NA I	NA N	AN	NA.	NA NA	N/	A NA	. NA	NA	NA	NA NA	N/	N/	Unk	mutation is non-lethal. Sdh4p is not considered to be an essential part of the	NA
		membrane anchor subunit				NA		1		0.07		1					1.02 TI							_						succinate dehydrogenase complex.	NA
YIL168W YFL045C	_	NA Phosphomannomutase		TN	NA NA			NA N	_	0.03 NA		1 NA			TP 1.		1.02 TI NA N			1.03 TP				1.12 NA		TP 1.1			NA NA		NA NA
		Membrane protein required for core																													
YMR013C	SEC59	glycosylation	1	FP	NA	NA	NA	NA I	NA	NA	NA	NA	NA	NA I	NA N	NA I	NA N	A N	1A	NA NA	N/	NA NA	. NA	NA	NA	NA NA	N/	NA	Der	Substrate in this reaction is a dead-end (dolichol).	FP
YOR184W	SER1	Phosphoserine transaminase	NA	NA	NA	NA	NA	1	0 :	28.8	FP (0.99	1 -	0.02	TP 1.	.07 1	1.03 TI	P 1.	.09	1.02 TP	1.1	1 1.02	2 TP	1.12	0.99	TP 1.1	1 1.0	4 TF	Unk	Removing AGT reaction (catalyzed by Agx1p) would fix this false positive. Agx1p is annotated as a alanine-glyoxylate aminotransferase and there is evidence that this enzymatic function is indeed found in yeast [Monschau97], but the pathway is only active on a non-fermentative carbon source.	NA
YGR208W	SER2	Phosphoserine phosphatase	NA	NA	NA	NA	NA	1	0 :	5.08	FP (0.99	1	0.03	TP 1.	.07 1	1.02 TI	P 1.	.09	0.99 TP	1.1	1 0.98	в тр	1.12	0.95	TP 1.1	1 1	TF	Unk	Removing AGT reaction (catalyzed by Agx1p) would fix this false positive. Agx1p is annotated as a alanine-glyoxylate aminotransferase and there is evidence that this enzymatic function is indeed found in yeast [Monschau97], but the pathway is only active on a non-fermentative carbon source.	NA
VED004W	CED3	3-phosphoglycerate dehydrogenase	NIA	NIA	NIA	NIA	NIA			0.00	TD		_	0.00	TD 4	00 4	. 04			1.01 TP		4 4 04	, , , ,	4.40	0.00	TD 4.4	1 0 0	0 TF	NIA	NA	NIA
TERUOTA	SEKS	3-priospriogrycerate derrydrogenase	INA	NA	NA	NA	NA	1	1 '	0.33	IP	1	1 -	0.08	IP I	.08 1	1.01 11	PI	.1	1.01 11	1.1	1 1.0	IIIP	1.12	0.98	IP 1.1	1 0.9	9 11	INA	IVA	NA
		3-phosphoglycerate dehydrogenase				NA				0.02		1	1 -	0.02	TP 1	.08 1	1.02 TI	P 1	.1	1.04 TP	1.1	1 1.04	4 TP	1.12	1.05	TP 1.1	1 1.0	5 TF	NA	NA Protein cynthosia not required in the model	NA
YDR023W		Serine-tRNA ligase Glutathione-dependent	1	FΡ	NA	NA	NA	NA I	NA	NA	ΝA	NA	NA	NA I	NA N	A	NA N	A N	ıΑ	NA NA	N/	A NA	. NA	NA	NA	NA NA	N/	NA	Oth	Protein synthesis not required in the model	NA
VD1 4		formaldehyde dehydrogenase long-																													
YDL168W		chain alcohol dehydrogenase Succinate-fumarate transport	NA	NA	NA	NA	NA	1	1 -	0.02	TP	1	1 -	0.02	TP 1.	.08 1	1.02 TI	P 1	.1	1.03 TP	1.1	1 1.02	2 TP	1.12	1.03	TP 1.1	1 1.0	3 TF	NA	NA .	NA
YJR095W		protein	NA	NA	NA	NA	NA	1	1 -	0.03	TP	1	1	0.01	TP 1	.08 1	1.02 TI	P 1	.1	1.04 TP	1.1	1 1.04	4 TP	1.12	1.08	TP 1.1	1 1.0	6 TF	NA	NA	NA
YBR263\M	SHM1	Serine hydroxymethyltransferase, mitochondrial	NΔ	NΙΔ	NΔ	NA	NΔ	1	1	0	TP	1	1	0.06	TP 1	08 4	1 03 TI	P 1	1	1.03 TP	1 1	1 1 0	тп	1 12	1 04	TP 1 1	1 1 0	2 TE	NΑ	NA	NA
DIVEOUV	JI IIVI I		IVA	1474	14/1	14/4	140		+	Ū				0.00		.55		T				. 1.02	1	1.12	1.04	1.1	1.0		14/1		
YLR058C	SHM2	Serine hydroxymethyltransferase	NA	NA	NA	NA	NA	1	0 4	4.29	FP	1	1	0	TP 1.	.08	1 TI	P 1	.1	1.01 TP	1.1	1 1.01	1 TP	1.12	1	TP 1.1	1 1.0	1 TF	Unk	Shm2p should not be required for growth in minimal media as even a shm1/shm2 double mutant is a glycine prototroph.	NA

	le le		sim	call	w sim	low exp	ilow call	MD exp	MMD ave	call	/PGal sim	al exp	al ave	al call		rPD exp	PDGE sim	'PDGE exp	PDGE call	/PG sim	PG exp	/PE sim	/PE exp	PEcall	YPL sim	exp	call	Sõ		ster et al
OR.	Nam	Annotation	Ess	Ess	Slow	Slow		¥	MM	MIMD	YPG	YPGal	YPGal	YPGal			YPD	YPD	YPD	YPG	YPG	YPE	YPE	YPE	YPL	YP.	YPL	Class	Explanation	Forster
		1-acyl-sn-gylcerol-3-phosphate acyl																											Two distinct enzymes are necessary for PA synthesis in lipid particles: the second step, acylation of lysophosphatidic acid is catalyzed by Slc1p; a specific point mutant allows cells to grow without making sphingolipids; this deletion is lethal	
YDL052C	SLC1	transferase (putative)	NA	NA	NA	NA N	IA () 1	0.1	FN	0	1 0	.02 I	FN (0.	99 FN	0	1	FN	0	0.99 FI	0	1.0	04 FN	0	1	FN	Bio	because PA is req'd in our biomass.	NA
	SOL1	Multicopy Suppressor Of los1	NA	_			_	1 1	-0.05		1			TP 1.	_	02 TF			TP		1 TI			99 TF	1.11	1	TP		NA	NA
YCR073WA	SOL2	Multicopy suppressor of los1-1	NA	NA	NA	NA N	IA 1	1 1	0.12	TP	1	1 -0	0.01	TP 1.	08	1 TF	1.1	1.01	TP	1.11	1.01 TI	1.1	2 1	TF	1.11	1	TP	NA	NA	NA
YHR163W	SOI 2	Weak multicopy suppressor of los1-	NA	NA	NA	NA N	10		0.31	TP	,	4	0	TD 4	08	1 TF	1 1 1	1.02	ТП	1.11	1 TI	1.1	2 1	TF	1.11	1.01	, 	NIA	NA NA	NA
YGR248W		6-phosphogluconolactonase		NA			IA 1	1 1	-0.01		1		0.06	_		02 TF				1.11	1.03 TI			06 TF					NA	NA
YKL184W		Ornithine decarboxylase	NA	_	NA		JA 1	1 1	-0.01		1		_	_	_	01 TF			TP			2 1.1			1.11	1.05			NA NA	NA
		S-adenosylmethionine		1																										
YOL052C	SPE2	decarboxylase	NA	NA	NA	NA N	IA 1	1 1	0	TP	1	1	0	TP 1.	08 1.	03 TF	1.1	1.06	TP	1.11	1.05 TI	1.1	2 1.0	08 TF	1.11	1.07	7 TP	NA	NA	NA
VDDaga		Putrescine aminopropyltransferase	١	l																							.		A1A	
YPR069C YLR146C	SPE3	(spermidine synthase) Spermine synthase	NA	NA	NA NA	NA N		1 1	0.01	TP	1			TP 1.		01 TF			TP		1.02 TI 1.04 TI				1.11				NA NA	NA NA
TEN 140C	SFE4	Exo-1,3-beta-glucanase,	INA	INA	INA	INA I	N/A	<u> </u>	U	IF	-	1 -0	J.U4	IF 1.	06 1.	02 11	1.1	1.03	IF	1.11	1.04 11	1.1.	2 1.0	J4 I F	1.11	1.03	3 11	INA	IVA	INA
YOR190W	SPR1	sporulation-specific	NA	NA	NA	NA N	IA 1	1 1	0.23	TP	1	1 -0	0.04	TP 1.	08 1.	02 TF	1.1	1.04	TP	1.11	1.04 TI	1.1	2 1.0	07 TF	1.11	1.05	5 TP	NA	NA	NA
		Cis-prenyltransferase		NA		NA N	IA 1	1 1	-0.01		1			TP 1.		01 TF					1.01 TI						1 TP		NA	NA
		Pyridoxal-5'phosphate-dependent enzyme homologous to mouse glial																												
YKL218C		serine racemase	NA	_	NA	NA N	IA 1	1 1	0	TP	1			TP 1.		04 TF					1.03 TI									NA
YDR536W		Sugar transporter-like protein	NA					1 1	-0.03		1			TP 1.		02 TF			TP			1.1			1.11				NA	NA
YJR130C	STR2	Cystathionine gamma-synthase	NA	NA	NA	NA N	JA 1	1	0.07	TP	1	1 0	0.01	TP 1.	08 1.	01 TF	1.1	1.04	TP	1.11	1.03 TI	2 1.1	2 1.0	05 TF	1.11	1.03	3 TP	NA	NA	NA
YLR305C	STT4	Phosphatidylinositol-4- kinase similar to VPC34	1	FP	NA	NA N	JA N	A NA	. NA	NA	NA I	NA I	1 AN	NA N	IA N	IA NA	NA NA	NA	NA	NA	NA N	A NA	A NA	A NA	NA NA	NA	. NA	Den	Phospholipid produced by this reaction leads to a dead-end (1D-myo-Inositol 1,4,5-trisphosphate). Also Pik1p is an isozyme.	FP
YMR054W	STV1	110 kDa subunit; not in vacuole membrane vacuolar H-ATPase	NA	NA	NA	NA N	JA 1	1 1	-0.06	TP	1	1 -0	0.05	TP 1.	08 0.	97 TF	1.1	0.97	TP	1.11	0.83 TI	1.1	2 0.8	36 TF	1.11	0.97	7 TP	NA	NA	NA
VIII 400\A/	01100	Invertase (sucrose hydrolyzing	l																											
YIL162W		enzyme) Sulfate uptake is mediated by specific sulfate transporters SUL1	NA	NA	NA	NA N	NA 1	1	0.02	TP	1	1 -(0.02	TP 1.	08 1.	02 TF	1.1	1	TP	1.11	0.98 TI	1.1	2 0.9	96 TF	1.11	0.97	7 TP	NA	NA .	NA
		and SUL2, which control the concentration of endogenous																												
YBR294W		activated sulfate intermediates.		NA		NA N	IA 1	1 1	0.08		1			TP 1.		01 TF					1.02 TI								NA	NA
YLR092W	SUL2	High affinity sulfate permease	NA	NA	NA	NA N	IA 1	1	0.1	TP	1	1 0	0.02	TP 1.	08 1.	01 TF	1.1	1.01	TP	1.11	1.01 TI	1.1	2 1	TF	1.11	1.01	1 TP	NA	NA	NA
YPL057C	SUR1	Integral membrane protein similar to YBR161w, Hoc1p, and Och1p	NA	NA	NA	NA N	JA 1	. 1	-0.03	TP	1	1 -0	0.02	TP 1.	08 1	01 TF	11	1 01	TP	1 11	1 TI	0 1 1	2 0 0	37 TE	1.11	0.00	9 ТР	ΝΔ	NA	NA
YDR297W		Sphingosine hydroxylase		NA		NA N		1	0.29		1			TP 1.							0.99 TI						TP		NA NA	NA
YLR372W		Elongase	NA		1		P 1		-0.01		1										0.89 TI								Involved in sphingolipid biosynthesis. These lipids are not currently required for growth by the model.	NA
		Transaldolase, enzyme in the																												
YLR354C	TAL1	pentose phosphate pathway	NA	NA	NA	NA N	IA 1	1	0	TP	1	1 -0	0.02	TP 1.	08 0.	99 TF	1.1	1.02	TP	1.11	0.92 TI	1.1	2 1.0	09 TF	1.11	0.95	5 TP	NA	NA	NA
YBR069C	TAT1	Amino acid transport protein for valine, leucine, isoleucine, and tyrosine	NA	NA	NA	NA N	JA 1	1 1	0.7	TP	1	1	0	TP 1.	08 0.	87 FF	1.1	0.98	ТР	1.11	1.01 TI	2 1.1	2 1	TE	1.11	1.01	1 TP	Iso	There are multiple alternative isozymes for amino acid transporters.	NA
YOL020W	TAT2	Tryptophan permease, high affinity Glyceraldehyde-3-phosphate	NA	NA	NA	NA N	JA 1	1	0.05	TP	1	1 -0	80.0	TP 1.	08	1 TF	1.1	1	TP	1.11	1.01 TI	1.1	2 1.0)2 TF	1.11	1.01	1 TP	NA	NA .	NA
YJL052W	TDH1	dehydrogenase 1 Glyceraldehyde 3-phosphate	NA	NA	NA	NA N	IA 1	1	-0.01	TP	1	1	0	TP 1.	08 0.	99 TF	1.1	1.02	TP	1.11	1.05 TI	1.1	2 1.0)5 TF	1.11	1.03	3 TP	NA	NA .	NA
YJR009C	TDH2	dehydrogenase	NA	NA	NA	NA N	IA 1	1	-0.03	TP	1	1 -0	0.02	TP 1.	08	1 TF	1.1	1	TP	1.11	1.02 TI	1.1	2 0.9	99 TF	1.11	1	TP	NA	NA	NA
YGR192C	TDH3	Glyceraldehyde-3-phosphate dehydrogenase 3	NA	NA	NA	NA N	JA 1	1 1	0.01	TP	1	1 -0	0.01	TP 1.	08 0.	97 TF	1.1	0.94	TP	1.11	0.98 TI	1.1	2 0.9	95 TF	1.11	0.98	в тр	NA	NA	NA

щ	me		Ess sim	Ess call	low sim	low exp	ow call	IMD sim	IMD exp		MD call	/PGal sim	PGal exp	YPGal ave	PGal call	/PD sim	YPD exp	PD call	PDGE sim	YPDGE exp	PDGE call	/PG sim	/PG exp	PG call	YPE sim	YPE exp	YPE call	YPL sim	L exp	YPL call	Class	Explanation
ORF	Sa	Annotation	Es	Es	Slo	Slo	Sic	2	Σ	ž	Σ	ΥP	Ϋ́	ΥP	ΥP	\	ΥP	ΥP	ΥP	ΥP	ΥP	\	Ϋ́	Ϋ́	ΥP	ΥP	Ϋ́	Ϋ́	YPL	Ϋ́	ਠੌ	Explanation
YDL185W		Site-specific endonuclease VDE (PI-Scel) vacuolar ATPase V1 domain subunit A (69 kDa) protein with three regions (ABC) that are spliced to yield the extein AC and the intein B; AC is a 69K vacuolar (H+)-ATPase, and B is a 50K site-specific endonuclease named VDE (PI-Scel) that is homologous to HO. Cleavage is meiosis-specific and induces ge		NA	1	12.2	: FP	1	1 .	-0.03	TP	1	1	-0.02	TP	1.08	0.7	FP	1.1	0.66	FP	1.11	0.49) FP	1.12	2 0.5	7 FP	1.11	0.5	9 FP	Oth	The tfp1 null mutant is viable but is calcium-sensitive, lacks vacuolar (H)-ATPase activity, and is defective in vacuolar acidification and assembly of the remaining V1 subunits [SGD]. pH balancing problem.
		Vacuolar ATPase V0 domain																														71 01
YPL234C	TED2	subunit c' (17 kDa) vacuolar H(+) ATPase 17 kDa subunit C	NIA	NA	1	71	ED	1	1	0.02	тр	1	,	0.04	TD	1 00	0.70	ED	11	0.66	ED	1 11	0.61	ED	1 10	١	ا	1 11	0.6	, ED	Oth	See other vacuolar ATPase components.
		THI for thiamine metabolism. Transcribed in the presence of low level of thiamine (10-8M) and turned off in the presence of high level (10-6M) of thiamine. Under the positive control of THI2 and THI3.			NA																										NA	
YPL258C		THI for thiamine metabolism. Transcribed in the presence of low level of thiamine (10-8M) and turned off in the presence of high level (10-6M) of thiamine. Under the positive control of THI2 and THI3.		NA	NA	NA	NA	1	1	-0.04	TP	1	1	-0.1	TP	1.08	1.01	TP	1.1	1.03	s TP	1.11	1.04	4 TP	1.12	2 1.0	4 TP	1.11	1.0	3 TP	NA	NA
		THI for thiamine metabolism. Transcribed in the presence of low level of thiamine (10-8M) and turned off in the presence of high level (10-6M) of thiamine. Under the																														
YPR121W	THI22	positive control of THI2 and THI3.	NA	NA	NA	NA	NA	1	1	0.02	TP	1	1	-0.02	TP	1.08	1.02	TP	1.1	0.99	TP	1.11	1	TP	1.12	1.0	1 TP	1.11	1.0	1 TP	NA	NA
		pyrophosphorylase hydroxyethylthia																														
		zole kinase	NA		NA			1		0.07		1																			NA	
YLR237W YOR143C	THI7	Thiamine transporter Thiamin pyrophosphokinase	NA 1	NA FP	NA NA		NΑ	1 NA		0.01 NA	TP NA	1 NA		0.01 NA		1.08 NA			1.1 NA			1.11 NA	1.07 NA		1.12 NA			1.11 NA		_		NA Thiamin biosynthesis not required in the model
		Homoserine kinase	NA	Ħ	NA		NA			6.34		1																				This should only be a threonine auxotroph [SGD]. May play some other uncharacterized role. Threonine can be synthesized by the model from glycine
VCDOEOW	TUDA	Thropping gypthage	N. A	N: A	N: A	NIA	N: A	4		7.67	ED	1	1	0.00	TO	1.00	1.04	TC	1.4	1.00		1 1 1	4	TL	1.40			1 4 4	14.0) TC	Lini	using Gly1p. If CYSTL (Cys1p) and AHCi (Sah1p) reactions are removed the false positive prediction is corrected and both of these have putative assignments, but neither can be removed from the model.
YIL078W		Threonine synthase Threonine-tRNA ligase	1 1	FP	NA NA			NA		NA		NA				1.08			1.1						1.12			1.11				removed from the model. Protein synthesis not required in the model
	TKL1	Transketolase 1	NA	NA	NA		NA		-		_	1		0.1		1.08			1.1						1.12			1.11		_		NA .
YJR066W	TOR1	Phosphatidylinositol kinase	NA	NΔ	NΔ	NΑ	NΙΔ	1		-0.01	тр	1	1	-0.04	TP	1 09	1.01	ТР	1 1	1.03	ТР	1 11	1.01	R TD	1 12	1 0	3 TE	1 11	1 1 0	тп	NA	NA
		Putative protein/phosphatidylinositol kinase involved in signaling activation of translation initiation, distribution of the actin cytoskeleton, and meiosis	I		NA					-0.01																						Phospholipid produced by this reaction leads to a dead end (phosphatidyl-10-myo-inositol 3,4-bisphosphate).
		Triosephosphate isomerase			NA			NA																								Mutant is unable to grow on glucose as sole carbon source. If ethanol or acetate is added to media containing glucose or galactose, cells are viable. Impaired growth probably due to NADH/energy shortage on glucose [Compagno01]. In one study this gene is found to be essential [Giaever02], wheras in the other one it has no phenotype [Steinmetz02].

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щ.	me		ssim	s call	Slow sim	w exp	w call	MMD sim	MMD exp	MMD ave	ID call	YPGal sim	YPGal exp	YPGal ave	/PGal call	YPD sim	YPD exp	(PD call	/PDGE sim	/PDGE exp	PDGE cal	YPG sim	YPG exp	rPG call	YPE sim	YPE exp	rre call	YPLexp	r call	Class	Explanation Explanation
ORF	Z Z	Annotation	Ess	Ess	Slo	Slow	Slow	Σ	Σ	Σ	MMD	Ϋ́Ρ	Σ	YP.	Ϋ́	<u>F</u>	ΥP	<u>F</u>	Σ	Ϋ́	<u>-</u>	Ž !	Ž į	<u>ا</u>	Δ	YPE		Ϋ́Ρ	YPL	C Sa	Explanation C
YBR126C	TPS1	Trehalose-6-phosphate synthase/phosphatase complex 56 kDa synthase subunit	NA	NA	1	6.8	FP	0	1	-0.06	TN	1	1 -(0.02	TP 1	08 0) 81 F	FP 1	1 1	0.83	-P 1	11 0	91 7	ΓP 1	12 0	86 1	P 1 1	1 0.8	9 TF	Med	Essential for growth on glucose and fructose [MIPS]. Deletion of TPS1 totally abolishes trehalose-6-phosphate synthase activity and measurable trehalose production, but YP media contains trehalose so TPS1 should not be required.
12111200		Trehalose-6-phosphate						Ŭ	Ť																						
YDR074W	TPS2	phosphatase	NA	NA	1	18	FP	0	1	0	TN	1	1 -(0.05	TP 1	.08	0.96	TP 1	1.1	0.95	TP 1	.11 1	.06 1	ΓP 1.	.12 1	.03 T	P 1.1	1 1.0	2 TF	Med	I See TPS1. NA
YMR261C	TPS3	Trehalose-6-phosphate synthase/phosphatase complex 115 kDa regulatory subunit		NA	NA	NA	NA	1	1	0.1	TP	1	1	0 -	TP 1	.08 0	0.99	TP 1	1.1	0.98	ГР 1	.11 0	.99 1	ΓP 1.	.12 0	.96 T	P 1.1	1 0.9	7 TF	NA	NA NA
YDR007W	TRP1	N-(5'-phosphoribosyl)-anthranilate isomerase	NA	NA	NA	NA	NA	0	0	5.83	TN	1	1 0	.02	TP 1	.08	1	TP 1	1.1	1.02	ГР 1	.11 1.	.03 1	TP 1.	.12 1	.05 T	P 1.1	1 1.0	3 TF	NA	NA NA
YER090W		Anthranilate synthase component			NA		NA	1		2.88	TP	1						TP 1				.11 1.								NA	
YKL211C	TRP3	Anthranilate synthase component II indole-3-phosphate	NA	NA	NA	NA	NA	0	0	7.77	TN	1	1 -(0.07	TP 1	.08 1	1.02	TP 1	1.1	1.03	ΓP 1	.11 1.	.03 1	ΓP 1.	.12 1	.06 T	P 1.1	1 1.0	4 TF	NA	NA NA
VDD054W	TDD4	Anthranilate phosphoribosyl						•		0.04		,			TD 4	00 0							04		40 4	00 7			ا	NIA.	Week folioe pegative
YDR354W YGL026C		transferase Tryptophan synthetase		NA	NA NA			0	1	2.64 1.4	TN TN	1			TP 1	.08 0	0.99					.11 1									Weak false negative NA Weak false negative NA
YDR353W		Thioredoxin reductase EC 1.6.4.5	0	TN	NA	NA	NA	NA	NA	NA	_	NA I		_	_		_	_			NA I			IA N			IA N		NA NA	NA	NA NA
YHR106W		Thioredoxin reductase	NA	_	NA		_	1	_		TP	1			_		_	TP 1		1.01			.01 T				P 1.1	_	_	_	NA NA
YBR265W		3-ketosphinganine reductase Similar to TPS3 gene	1	FP	NA	NA	NA	NA	NA	NA	NA	NA I	NA I	1 AV	1 AV	NA I	NA N	1 AN	NA	1 AN	NA I	NA N	NA N	IA N	1 AV	NA N	IA N	A N/	NA NA	Bio	Sphingolipid synthesis not required in the model FP
YML100W		product trehalose-6-phosphate synthase/phosphatase complex 123 kDa regulatory subunit		NA	NA	NA	NA	1	1	-0.02	TP	1	1 -(0.07	TP 1	.08 1	1.02	TP 1	1.1	1.05	ГР 1	.11 1	.04 1	ΓP 1.	.12 1	.08 T	P 1.1	1 1.0	6 TF	NA NA	
YBR166C	TVD1	Prephenate dehydrogenase (NADP+)	NA	NIA	1	3.5	FP	1	1	0	TP	1	1 (04	TD .	NIA I	NIA N	NA N	NIA.	NIA P	.1.0	NA N	.14	10 10		.14	IA N	A NI	NIA.	Unl	Should be a tyrosine auxotroph, but the media contains tyrosine. Also, the model has an alternative reaction with no gene association.
		Tyrosine-tRNA ligase			NA				NA	0 NA		NA I		1 AV				A A		I AN		NA N	NA N				IA N				Protein synthesis not required in the model NA
		Gamma-aminobutyrate (GABA) transaminase (4-aminobutyrate																													
YGR019W	UGA1	aminotransferase) Succinate semialdehyde	NA	NA	NA	NA	NA	1	1	-0.04	TP	1	1 -(0.04	TP 1	.08 1	1.01	TP 1	1.1	1.02	ГР 1	.11 1.	.01 7	ΓP 1.	.12 1	.03 T	P 1.1	1 1.0	2 TF	NA	NA NA
		dehydrogenase		NA			NA	1			TP	1	1	0.2	TP 1	.08			1.1			.11 0									
YDL210W	UGA4	GABA-specific transport protein	NA	NA	NA	NA	NA	1	1	0.11	TP	1	1 -(0.05	TP 1	.08 1	1.02	TP 1	1.1	1.02	TP 1	.11 1	.02 1	ΓP 1.	.12 1	.01 T	P 1.1	1 1.0	1 TF	NA	
YKL035W	UGP1	Uridinephosphoglucose pyrophosphorylase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA I	NA	1 AV	1 AV	NA I	NA N	1 AN	NA	NA I	JA	NA N	JA N	JA	1 AV	N AL	IA N	A N	NA	Bio	Reaction produces UDPglc, which is not required in our model.
		Dihydroorotate dehydrogenase	NA		NA		_		_	-0.02	TP	1	1 -(TP 1			TP 1				.11 0								NA	
\# 4D 0= 4 0		Orotate phosphoribosyltransferase																													
YMR271C	URA10	Aspartate transcarbamylase carbamoyl	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1 -(0.07	TP 1	.08 1	1.01	TP 1	1.1	1.03	TP 1	.11 1.	.02 1	ΓP 1.	.12	1 T	P 1.1	1 1	TF	NA	NA NA
YJL130C		phosphate synthetase glutamine amidotransferase	NIA	NA	NA	NA	NΙΛ	1	1	-0.06	тр	1	1	0	TP 1	08 4	1.01	тр	1 1	1.03	гр	.11 1	02 7	гр 1	12 4	02 7	D 1 4	1 1 0	3 TF	NIA	NA NA
		Dihydrooratase			NA			1	1	0	TP	1			TP 1		1.02					.11 1									
YML106W	URA5	Orotate phosphoribosyltransferase 1	NA	NA	NA	NA	NA	1	1	0.03	TP	1	1 0	.01	TP 1	.08	1	TP 1	1.1	1.01	ΓP 1	.11 1.	.02 T	ΓP 1.	.12 1	.03 T	P 1.1	1 1.0	1 TF	NA	NA NA
YKL024C	URA6	Uridine-monophosphate kinase (uridylate kinase)	1	FP	NA	NA	NA	NA	NA	NA	NA	NA I			1 AV	NA I													NA NA	Oth	RNA and protein synthesis not required in the model.
		CTP synthase	NA	_	1	3.2		_	_	-0.03	TP	1			TP 1																Model does not require ctp to grow on complex media.
YJR103W	URA8	CTP synthase	NA	NA	NA	NA	NA	1	1	0.01	TP	1	1 -(0.07	TP 1	.08 1	1.01	TP 1	1.1	1	ΓP 1	.11 1.	.01 1	ΓP 1.	.12	1 T	P 1.1	1 1	TF	NA	NA NA
YDR400W	URH1	Uridine nucleosidase (uridine ribohydrolase); EC 3.2.2.3	ΝΔ	NΔ	NΔ	NA	NΔ	1	1	-0.02	ТР	1	1 -0	0 01	TP 1	.08 1	1 01	TP 4	1 1	1	TP 1	.11 0	99 7	TP 1	12 0	99 T	P 1 1	1 1	ТС	NA	NA NA
		Uridine kinase				NA		1		0.02		1		0 -	TP 1	.08 0	0.97	TP 1	1.1	0.95	ΓP 1	.11 0	.99 1	ΓP 1.	.12 1	.01 T	P 1.1	1 1	TF		NA NA
YJR049C	UTR1	Associated with ferric reductase			NA			1	1	0.14	TP	1		0.07	TP 1	.08	0.95	TP 1	1.1	0.99	ΓP 1	.11 0	.98 1	ΓP 1.	.12 0	.95 T	P 1.1	1 0.9	7 TF	NA	NA NA
YGR094W	VAS1	Valine-tRNA ligase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA I	NA I	1 AV	1 AV	NA I	NA N	1 AN	NA	1 AN	NA I	NA N	NA N	IA N	1 AV	NA N	IA N	A NA	NA NA	Oth	Protein synthesis not required in the model NA
YGR065C	VHT1	H+-biotin symporter	1	FP	NΔ	NΔ	NΔ	NΔ	NΔ	NΔ	NΑ	NΔ	NΔ	NA A	1 40	NΔ	NA M	NA N	NΔ	NA I	JA I	NA N	ΔL	JA N	Δ. A.	ΔΔ.	IA N	Δ NA	NA	Ric	Biotin not required in our model, but bakers' yeast is auxotrophic for biotin (vitamin H) and depends on the efficient uptake of this compound from the environment [Stolz99].
. 0.13000		Vacuolar H(+) ATPase V1 sector		<u> </u>		,	,	, .	(
YPR036W	VMA13	54 kDa subunit Vacuolar ATPase V1 domain	NA	NA	1	5.9	FP	1	1	-0.04	TP	1	1 0	.03	TP 1	.08 0).73 F	FP 1	1.1	0.61 I	P 1	.11 0	.59 F	P 1.	.12 0	.62 F	P 1.1	1 0.6	8 FF	Oth	See other vacuolar ATPase components. NA
YBR127C	VMA2	subunit B (60 kDa)	NA	NA	1	10.6	FP	1	1	-0.03	TP	1	1 -0	0.02	TP 1	.08).86 F	FP 1	1.1	0.7 I	P 1	.11 0	.75 F	P 1.	.12 ().7 F	P 1.1	1 0.7	3 FF	Oth	See other vacuolar ATPase components. NA
YOR332W	VMA4	E subunit of V1 sector vacuolar H(+) ATPase 27 kDa subunit	NA	NA	1	5.2	FP	1	1	0.02	TP	1	1 -(0.03	TP 1	.08	0.9	TP 1	1.1	0.87	ΓP 1	.11 0	.65 F	P 1.	.12 0	.61 F	P 1.1	1 0.6	6 FF	Oth	See other vacuolar ATPase components. NA

					Ε	9	=	Ε	сb)e	=	mis	dxe	ave	, ,	=	۵ =	sim	a a	call	L L	۵	_	ء	a						et a
ORF	ame		ss sim	ss call	Slow sim	ow exp	ow ca	MMD sim	IMD exp	MMD ave	IMD call	PGal sim	Call Call		Poal call		PD call	PDGE sim	and 3000	PDGE call	PG sim	PG exp	PG call	'PE sim	PE exp	PEcall	PL sim	/PL exp	/PL call	Class	Explanation 2
		Annotation V1 sector hydrophilic subunit C vacuolar ATPase V1 domain subunit C (42 kDa) vacuolar H-	Ш	E	S	Ĭ,	S	Σ	Σ	Σ	Σ	<u> </u>	 	5	5		<u> </u>	<u> </u>	5	.	Ϋ́	>	Ϋ́	<u></u>	¥	>	=	,	Ϋ́	<u></u>	Explanation
YKL080W	VMA5	ATPase Vacuolar ATPase V0 domain	NA	NA	1	6.1	FP	1	1 -(0.02	ΓP	1	1 -0.	.02 T	P 1.	08 0.	.66 FI	P 1.1	1 0.	62 FF	1.1	1 0.5	7 FP	1.12	2 0.5	1 FI	P 1.1	0.5	7 FP	Oth	See other vacuolar ATPase components. NA
YLR447C	VMA6	subunit d (36 kDa) vacuolar H(+) ATPase 36 kDa subunit (D subunit of VO sector)	NA	NA	1	10.9	FP	1	1 -(0.03	ΤР	1	1 -0.	.02 T	P 1.	08 0.	.65 FI	P 1.1	1 0.	59 FF	1.1	1 0.58	8 FP	1.1	2 0.5	7 FI	P 1.1	0.6	5 FP	Oth	The vma6 null mutant is viable but shows a growth defect at neutral pH and is sensitive to calcium. pH balancing problem. NA
YGR020C	VMA7	Vacuolar ATPase V1 domain subunit F (14 kDa)	NA	NA	1	9.9	FP	1	1 -(0.01	ΓР	1	1 () Т	P 1.	08 0.	.72 FI	P 1.1	1 0.	62 FF	1.1	1 0.63	3 FP	1.12	2 0.6	4 FI	P 1.1	0.6	6 FP	Oth	See other vacuolar ATPase components. NA
YEL051W		V1 catalytic sector D subunit vacuolar H-ATPase	NA	NA	1	14.4	FP	1	1 -(0.02	ΤР	1	1 -0.	.01 T	P 1.	08 0.	.75 FI	P 1.1	1 0.	65 FF	1.1	1 0.5	7 FP	1.1:	2 0.5	8 FI	P 1.1	0.6	B FP	Oth	The vma8 null mutant is viable but lacks vacuolar (H)- ATPase activity, cannot grow at neutral pH or on nonfermentable carbon sources, and fails to accumulate quinacrine in the vacuole [SGD]. The slow growth phenotype is probably because of problems with pH balancing.
V0D2700	V/DLI4	V0 sector subunit essential for vacuolar acidification and vacuolar H-ATPase activity vacuolar ATPase V0 domain subunit a (100	NIA	NIA	4	2.4	ָב	4	4	04	TD.	4	4 0	00. T	TD 4.	00.0	00 7	D 4.	1 0	70 55		4 0 0			0.07	0 7			1 10	Oth	See other vacualar ATDage companyers
		kDa) vacuolar H-ATPase		NA		3.4				0.01																					See other vacuolar ATPase components. NA PI3 kinase activity involved in signaling processes - in the
		Phosphatidylinositol 3-kinase Tryptophan-tRNA ligase	NA 1		1 NA	18.9 NA	_	1 NA		0.01 NA I			1 -0. IA N		P 1.					56 FF		1 0.6									model this leads to a dead end. NA Protein synthesis not required in the model NA
YGR194C	XKS1	Xylulokinase Xanthine phosphoribosyl	NA	NA	NA	NA	NA	1	1 -0	0.03	ΤР	1	1 0.	14 T	P 1.	08 1.	.01 TI	P 1.1	1 1.0	01 TF	1.1	1 1	TP	1.12	2 1.0	1 TI	P 1.1	1.0	2 TP	NA	
		transferase			NA		NA	1			ΤР	1										1 1.04									
		Xylitol Dehydrogenase Carnitine acetyltransferase			NA NA		_	1	_	0.03	TP	1			P 1.			P 1.1				1 1.04 1 1.04							TP	NA NA	
		Hypothetical ORF	_	_	NA		_	1	_	_	TP	1	_		_	_		P 1.				1 0.9							3 TP		
		Hypothetical ORF	_	_	NA		NA	1	_	_	TP	1	_		_							1 1.04							_		NA NA
		Hypothetical ORF Hypothetical ORF			1 NA	5.2 NA		1 0.95			TP 0	1					73 FI					1 0.6								Oth	
		Protein required for cell viability				NA		NA I		0.02 T				.01 T								1 1.04 A NA									Protein synthesis not required in the model FP
		Pantothenate kinase (ATP:D- pantothenate 4'- phosphotransferase, EC 2.7.1.33) catalyzes the first committed step in the universal biosynthetic pathway leading to CoA.	1																												CoA biosynthesis not required in the model.
		Hypothetical ORF	NA			NA		1					1 -0.									1 1.00									NA NA
YEL047C	YEL04	Fumurate ReDuctase Soluble	NA	NA	NA	NA	NA	1	1 (0.01	ΤP	1	1 -0.	.03 T	P 1.	08 1.	.02 TI	P 1.	1 1.	03 TF	1.1	1 1.03	3 TP	1.12	2 1.0	3 TI	P 1.1	1.0	1 TP	NA	NA NA
	YER05	Sequence similarity to mitochondrial phosphate transporters	NA		NA).22				.06 T	P 1.	08 1.	.01 TI	P 1.1	1 1.0	03 TF	1.1	1 1.0	3 TP	1.1	2 1.0	1 TI	P 1.1	1.0	2 TP	NA	NA NA
YER087W	YER08	Hypothetical ORF	NA	NA	1	7.5	FP	1	1 -(0.02	ſΡ	1	1 () T	P 1.	08 0.	.97 TI	P 1.1	1 0.	89 TF	1.1	1 0.78	8 FP	1.12	2 0.7	2 FI	P 1.1	0.7	3 FP	Oth	Protein synthesis not required in the model NA Lower oxygen uptake rate would correct this false negative
YFL030W	YFL03	NA	NA	NA	NA	NA	NA	1	1 (0.08	ТР	1	1 -0.	.06 T	P 1.																prediction. NA
		Hypothetical ORF	_	_	NA		_			0.01		1		.07 T		08 1.	.03 TI	P 1.	1 1.0	02 TF	1.1	1 1.0	1 TP	1.13	2 1.0	3 TI	P 1.1	1.0	2 TP	NA	NA NA
		Protein required for cell viability Hypothetical ORF			NA NA		NA NA	NA I	NA 1		NA I	NA N										1 0.98									Protein synthesis not required in the model FP Model can't make cysteine without the rxn catalyzed by this gene. Might be able to bypass this by making cys from pyr using CYS1 [KEGG]. NA
YGR043C	YGR04	Hypothetical ORF	NA	NA	NA	NA	NA			0.02	TP	1	1 -0.	.01 T	P 1.	08 1.	.01 TI	P 1.1	1 1.0	01 TF	1.1	1 1	TP	1.12	2 1.0	4 TI	P 1.1	1.0	3 TP	NA	NA NA
		Hypothetical ORF			NA			1			TP	1								02 TF					2 1.0						NA NA
		Hypothetical ORF Hypothetical ORF			NA NA					0.05	ΓP	1			P 1.		.03 TI					1 1.0° 1 0.90									
		Protein required for cell viability			NA							NA N	IA N	IA N	IA N	A N	IA N	A NA	A N	A NA	N.A	A NA	NA	NA	NA NA	N,	A NA	NA	NA	Oth	Protein synthesis not required in the model NA
YJL045W		Similar to SDH1			NA							1				08 1.	.01 TI	P 1.1	1 1.0	03 TF	1.1	1 1.0	4 TP	1.12	2 1.0	3 TI	P 1.1	1.0	3 TP	NA	NA NA
		Hypothetical ORF Hypothetical ORF			NΑ	NA NA				0.04		1										1 1.0									
																															Aco1p acts as an isozyme for this reaction. For some reason
		Hypothetical ORF Hypothetical ORF				NA NA				i.69 i.01		1	1 -0.	.04 T	P 1.	08 1.	.02 TI	P 1.	1 1.0	01 TF	1.1	1 1.02	9 TP	1.12	2 1.0	1 TI	1.1°	1.0	2 TP	NA	YJL200C gene product is only required on minimal media. NA NA NA

ORF	Name	Annotation	Ess sim	Ess call	Slow sim	Slow exp	Slow call	MMD sim	ммр ехр	ММD ave	MMD call	r PGal SIM	r real exp	Y PGal ave	YPGal call	r PD SIM	YPD exp	Y PDGE eim	r PDGE SIM	YPDGE exp	YPDGE call	YPG sim	YPG exp	YPG call	YPE sim	YPEexp	YPE call	YPLsim	YPL exp	YPL call	Class	Explanation	Forster et al
YKL132C		Probable folyl-polyglutamate						,	,	0.00	j				,	00 4	00.7	,	,	4 04	TD		4 04	TD		4.00	-		4 00	1	NIA	NA	NIA
YLR089C		synthetase			NA NA					0.03					ΓΡ 1.																NA NA		NA NA
TLRUOSC		Hypothetical ORF	NA	INA	INA	IVA	INA	1	1	1.∠0	IP	1 ′	1 -0	1.05	IP 1.	08	1 1	P 1.	.1 1	1.03	IP	1.11	0.94	IP	1.12	0.99	IP	1.11	1.01	IP	INA	NA .	INA
YLR164W		YLR164Wp is homologous to	NIA	NIA	NA	NA	NIA	1	1 (0.09	TD	1 .		02	TD 4	00	, ,	D 1	1 0	0.00	TD.	1 11	0.00	TD	1 10	0.00	TD	1 11	0.00	тр	NA	NA	NA
		Hypothetical ORF					_	1	1 (TP																				NA		NA
		Hypothetical ORF					_	1	1	0.03																							NA
			_	_		_	_	1	_		_	1																			NA		NA
		Hypothetical ORF						1		0.04	TP	1																			NA		NA
		Hypothetical ORF	_	_		_	_	1	1 -																						NA		NA
YMRTI8C		Hypothetical ORF		NA	NA	NA	NA	1	1	0	TP	1 .	1 -0	1.02	IP 1.	08 1	.02 1	P 1.	.1 1	1.02	IP	1.11	1.02	IP	1.12	1.02	IP	1.11	1.02	IP	NA	NA .	NA
YMR293C		Protein similar to bacterial glutamyl- tRNA amidotransferases	NA	NA	1	3.1	FP	1	1 -	0.04	TP	, I.	1 -0	0.01	ΓP 1.	08 0).74 F	P 1.	.1	0.7	FP	1.11	0.63	FP	1.12	0.59	FP	1.11	0.63	FP	Den	This reaction is a dead end.	NA
																																Null mutant retains 10% of nucleoside diphosphate kinase activity. Sources of remaining enzyme activity are unknown, but possibilities are discussed in [Fukuchi93]. Reaction w/o gene associations could be added to the model to represent	
		Nucleoside diphosphate kinase	NA	NA																												these unidentified enzymes.	FN
		Protein required for cell viability																														Protein synthesis not required in the model	NA
YOR071C	YOR07	Hypothetical ORF	NA	NA	NA	NA	NA	1	1 (0.04	TP	1 1	1 -0	.07	ΓP 1.	08 1	.01 T	P 1.	.1 1	1.02	TP	1.11	1.01	TP	1.12	1.01	TP	1.11	1.01	TP	NA	NA NA	NA
YOR192C	YOR19	Hypothetical ORF	NA	NA	NA	NA	NA	1			TP	1 1																			NA		NA
YKR053C	YSR3	DHS-1-P phosphatase	NA	NA	NA	NA	NA	1	1 -	0.03	TP	1 1	1 -0	.07	ΓP 1.	08 1	.02 1	P 1.	.1 1	1.02	TP	1.11	1.02	TP	1.12	1.02	TP	1.11	1.01	TP	NA	NA	NA
YJL139C	YUR1	Mannosyltransferase	NA	NA	NA	NA	NA	1	1 (0.13	TP	1 1	1	0	ΓP 1.	08 0	.97 1	P 1.	.1 (0.99	TP	1.11	0.95	TP	1.12	0.98	TP	1.11	0.99	TP	NA	NA	NA