	ist of metabolic reactions in the				
Reaction name ACLDn	Metabolism Naphthalene degradation	Enzyme alcohol dehydrogenase	E.C. number 1.1.1.1	Locus(KOX) KOX_19595/KOX_20090/KOX_23025	Reaction (KOX) hmnapth + nad -> napthah + nadh
SALCH3	Naphthalene degradation	salicylate hydroxylase	1.14.13.1	KOX_25675	msalc + o2 + nadh -> dhtolen + nad + co2
SALCH4 ACLDnp	Naphthalene degradation Naphthalene degradation	salicylate hydroxylase alcohol dehydrogenase	1.14.13.1	KOX_25675 KOX_19595/KOX_20090/KOX_23025	msalc4 + o2 + nadh -> 4mctch + nad + co2 2napthm + nad -> 2napald + nadh
SALCH5	Naphthalene degradation	salicylate hydroxylase	1.14.13.1	KOX_19595/KOX_20090/KOX_25025 KOX_25675	4hmsalc + o2 + nadh -> 4hmcatech + nad + co2
ALHD15	1,2-Dichloroethane degradation	Chloroalkane and chloroalkene	1.2.1.3	KOX_00375	chacald + nad -> chac + nadh
	Chlorocyclohexane and chlorobenzene	degradation			
CMBLD3	degradation	carboxymethylenebutenolidase	3.1.1.45	KOX_02855/KOX_07760	c2ch4cmo -> 2chmac
CMBLD4	Chlorocyclohexane and chlorobenzene degradation	carboxymethylenebutenolidase	3.1.1.45	KOX_02855/KOX_07760	c4cmbo -> 2mac
CMBLD5	Chlorocyclohexane and chlorobenzene	carboxymethylenebutenolidase	21145	KOX_02855/KOX_07760	protmn -> cacac
	degradation Chloroalkane and chloroalkene				
ALCDt	degradation	alcohol dehydrogenase	1.1.1.1	KOX_19595/KOX_20090/KOX_23025	t3chp + nad -> 3chroald + nadh
ALHD13	Chloroalkane and chloroalkene	aldehyde dehydrogenase	1.2.1.3	KOX_00375	3chroald -> t3chc
	degradation Chloroalkane and chloroalkene	(NAD+)			
ACLDc	degradation	alcohol dehydrogenase	1.1.1.1	KOX_19595/KOX_20090/KOX_23025	c3chp + nad -> c3chroald + nadh
ALHD14	Chloroalkane and chloroalkene degradation	aldehyde dehydrogenase (NAD+)	1.2.1.3	KOX_00375	c3chroald -> c3chroc
DADH	Alanine and Aspartate Metabolism	D-Amino acid dehydrogenase	1.4.99.1	KOX_23495	dala + fad -> fadh2 + nh4 + pyr
ASPTA ALATA	Alanine and Aspartate Metabolism Alanine and Aspartate Metabolism	aspartate transaminase alanine transaminase	2.6.1.1 2.6.1.2	KOX_16370 KOX_26405	akg + asp <-> glu + oaa ala + akg <-> pyr + glu
ASNN	Alanine and Aspartate Metabolism	L-asparaginase	3.5.1.1	KOX_20403 KOX_17835/KOX_18055(ansA)	asn -> asp + nh4
ASPAML1	Alanine and Aspartate Metabolism	aspartateammonia ligase	6.3.1.1	KOX_06770	asp + atp + nh4 -> asn + amp + ppi
ALAR	D-Alanine Metabolism	alanine racemase asparagine synthase	5.1.1.1	KOX_08305(alr)/KOX_23490	ala <-> dala
ASNS	Alanine and Aspartate Metabolism	(glutamine-hydrolysing)	6.3.5.4	KOX_14335(asnB)	asp + atp + gln -> amp + asn + glu + ppi
ARGSUCS	Alanine and Aspartate Metabolism	argininosuccinate synthase 4-aminobutyrate	6.3.4.5	KOX_03675	asp + atp + citr -> amp + argsucc + ppi
4AMBUAT	Alanine and Aspartate Metabolism	aminotransferase	2.6.1.19	KOX_04875	bala + akg <-> 3opp + glu
T2AKGTA	beta-Alanine Metabolism	taurine2-oxoglutarate transaminase	2.6.1.55	KOX_13775	bala + akg <-> 3opp + glu
PRIAMOX	beta-Alanine Metabolism	primary-amine oxidase	1.4.3.21	KOX_19410(tynA)	13dapro + o2 -> bapa + nh4 + h2o2
ASPR	Alanine and Aspartate Metabolism	aspartate racemase	5.1.1.13 1.4.3.16	KOX_18745 KOX_27585	asp <-> asp-D
ASPOX1	Alanine and Aspartate Metabolism	L-aspartate oxidase succinate-semialdehyde			asp + o2 <-> oaa + nh4 + h2o2
SUCSD1	Alanine and Aspartate Metabolism	dehydrogenase (NADP)	1.2.1.16	KOX_09980/KOX_11825(gabD)/KOX_24465	nadp + sucsal <-> nadph + succ
ASP1DCB	Alanine and Aspartate Metabolism	aspartate 1-decarboxylase aspartyl-tRNA(Asn)/qlutamyl-	4.1.1.11	KOX_11205	asp -> bala + co2
GTADT2	Aminoacyl-tRNA biosynthesis	tRNA (Gln) amidotransferase	6.3.5.6	KOX_16785	asptrna + gln + atp -> asntrna + glu + pi + adp
ASPAML2	Alanine and aspartate metabolism	aspartate ammonia-lyase	4.3.1.1	KOX_08650(aspA)	asp -> fum + nh4
METTRFT	Aminoacyl-tRNA Biosynthesis	Methionyl-tRNA formyltransferase	2.1.2.9	KOX_04210(fmt)	fthf + mettrna -> fmettrna + thf
TYRTRS	Aminoacyl-tRNA Biosynthesis	tyrosyl-tRNA synthetase	6.1.1.1	KOX_22025	atp + trnatyr + tyr -> amp + ppi + tyrtrna
METTRS SERTRS	Aminoacyl-tRNA Biosynthesis Aminoacyl-tRNA Biosynthesis	Methionyl-tRNA synthetase Seryl-tRNA synthetase	6.1.1.10 6.1.1.11	KOX_25560(metG) KOX 15915	atp + met + trnamet -> amp + mettrna + ppi atp + ser + trnaser -> amp + ppi + sertrna
SECTRS	Aminoacyl-tRNA Biosynthesis	Seryl-tRNA synthetase	6.1.1.11	KOX_15915	atp + ser + trnasec -> amp + ppi + sectrna
ASPTRS	Aminoacyl-tRNA Biosynthesis	Aspartyl-tRNA synthetase	6.1.1.12	KOX_23945(aspS)	asp + atp + trnaasp -> amp + asptrna + ppi
ASNTRS GLYTRS	Aminoacyl-tRNA Biosynthesis Aminoacyl-tRNA Biosynthesis	Asparaginyl-tRNA synthetase Glycyl-tRNA synthetase	6.1.1.22	KOX_16105(asnC) KOX_05595(glyS)/KOX_05600(glyQ)	atp + asn + trnaasn -> amp + asntrna + ppi atp + gly + trnagly -> amp + glytrna + ppi
PROTRS	Aminoacyl-tRNA Biosynthesis	Prolyl-tRNA synthetase	6.1.1.15	KOX_11580	atp + pro + trnapro -> amp + ppi + protrna
CYSTRS GLNTRS	Aminoacyl-tRNA Biosynthesis Aminoacyl-tRNA Biosynthesis	Cysteinyl-tRNA synthetase Glutaminyl-tRNA synthetase	6.1.1.16 6.1.1.18	KOX_13215(cysS) KOX_14370	atp + cys + trnacys -> amp + cystrna + ppi atp + gln + trnagln -> amp + glntrna + ppi
ARGTRS	Aminoacyl-tRNA Biosynthesis	Arginyl-tRNA synthetase	6.1.1.19	KOX_23990(argS)	arg + atp + trnaarg -> amp + argtrna + ppi
TRPTRS PHETRS	Aminoacyl-tRNA Biosynthesis Aminoacyl-tRNA Biosynthesis	Tryptophanyl-tRNA synthetase Phenylalanyl-tRNA synthetase	6.1.1.2 6.1.1.20	KOX_04580/KOX_09720 KOX_22905(pheT)/KOX_22910(pheS)	atp + trnatrp + trp -> amp + ppi + trptrna
HISTRS	Aminoacyl-tRNA Biosynthesis	Histidyl-tRNA synthetase	6.1.1.21	KOX_222905(pile1)/KOX_22910(pile5) KOX_27270(his5)	atp + phe + trnaphe -> amp + phetrna + ppi atp + his + trnahis -> amp + histrna + ppi
THRTRS	Aminoacyl-tRNA Biosynthesis	Threonyl-tRNA synthetase	6.1.1.3	KOX_22930(thrS)	atp + thr + trnathr -> amp + ppi + thrtrna
LEUTRS ILETRS	Aminoacyl-tRNA Biosynthesis Aminoacyl-tRNA Biosynthesis	Leucyl-tRNA synthetase Isoleucyl-tRNA synthetase	6.1.1.4	KOX_14265(leuS) KOX_10530(ileS)	atp + leu + trnaleu -> amp + leutrna + ppi atp + ile + trnaile -> amp + iletrna + ppi
LYSTRS	Aminoacyl-tRNA Biosynthesis	Lysyl-tRNA synthetase	6.1.1.6	KOX_02370(lysS)	atp + lys + trnalys -> amp + lystrna + ppi
ALATRS	Aminoacyl-tRNA Biosynthesis	Alanyl-tRNA synthetase	6.1.1.7	KOX_00530(alaS)	ala + atp + trnaala -> alatrna + amp + ppi
VALTRS	Aminoacyl-tRNA Biosynthesis	Valyl-tRNA synthetase N-acetylglucosamine-6-	6.1.1.9	KOX_09325(valS)	atp + trnaval + val -> amp + ppi + valtrna
ACG6PD	Aminosugars metabolism	phosphate deacetylase	3.5.1.25	KOX_14355(nagA)	naga6p -> ac + ga6p
GM6PD	Aminosugars metabolism	glucosamine-6-phosphate deaminase	3.5.99.6	KOX_14360(nagB)	ga6p -> f6p + nh4
		UDP-N-			
UAEPGR	Aminosugars metabolism	acetylenolpyruvoylglucosamine reductase	1.1.1.158	KOX_07860(murB)	nadh + uaccg -> nad + udpnam
		UDP-N-			
UAEPGRp	Aminosugars metabolism	acetylenolpyruvoylglucosamine	1.1.1.158	KOX_07860(murB)	nadph + uaccg -> nadp + udpnam
		reductase glucosamine-1-phosphate N-			
GA1PACT	Aminosugars metabolism	acetyltransferase	2.3.1.157	KOX_06685(glmU)	accoa + galp -> nagalp + coa
UNAGCVT	Aminosugars metabolism	UDP-N-acetylglucosamine 1- carboxyvinyltransferase	2.5.1.7	KOX_03750	pep + udpnag -> pi + uaccg
GE6PT	Aminosugars metabolism	glutamine-fructose-6-	2.6.1.16	KOX 06680	f6p + gln -> ga6p + glu
GIOFI	Aminosugais metabolism	phosphate transaminase	2.0.1.10	KCX_00000	10p + giii -> gaop + gia
UNAGDP	Aminosugars metabolism	UDP-N-acetylglucosamine diphosphorylase	2.7.7.23	KOX_06685(glmU)	naga1p + utp -> ppi + udpnag
PGAMT	Aminosugars metabolism	phosphoglucosamine mutase	5.4.2.10	KOX_03685(glmM)	galp <-> ga6p
UDPACG	Aminosugars metabolism	UDP-N-acetylglucosamine 4- epimerase	5.1.3.7		udpnag <-> udpacgal
NADMA6PE	Aminosugars metabolism	N-acetylmannosamine-6-	5.1.3.9	KOX_03880	
NADIVIAOPE	Aminosugais metabolism	phosphate 2-epimerase	5.1.5.9	KOX_03660	nadma6p -> naga6p
NAMUR6PE	Aminosugars metabolism	N-acetylmuramic acid 6- phosphate etherase	4.2.1.126	KOX_06285	namur6p <-> naga6p + lac
NAHEXM	Aminosugars metabolism	beta-N-acetylhexosaminidase	3.5.1.52	KOX_17360	chitobiose -> 2 naga
NAGAK NADDAC	Aminosugars metabolism Aminosugars metabolism	N-acetylglucosamine kinase NAD-dependent deacetylase	2.7.1.59 3.5.1	KOX_17425 KOX_17430	naga + atp <-> naga6p + adp qa6p <-> f6p + nh4
NADDAC UDPNAGE1	Aminosugars metabolism  Aminosugars metabolism	NAD-dependent deacetylase UDP-N-acetylglucosamine 2-	5.1.3.14	KOX_17430 KOX_07565	
NADMAK		epimerase	2.7.1.60	KOX_07565 KOX_03875	udpnag -> nadma + udp
NADMAK NANEUL	Aminosugars metabolism Aminosugars metabolism	N-acylmannosamine kinase N-acetylneuraminate lyase	2.7.1.60 4.1.3.3	KOX_03875 KOX_03890	nadma + atp -> nadma6p + adp naneu -> nadma + pyr
UDPNAGE2	Aminosugars metabolism	UDP-N-acetylglucosamine 2-	5.1.3.14	KOX_07565	udpnag -> udpnadma
		epimerase		-	the state of the s
UDPNADMAD					
ODI TOTOTO	Aminosugars metabolism	UDP-N-acetyl-D-mannosamine dehydrogenase	1.1.1	KOX_07570(wecC)	udpnadma + 2 nad -> udpnadmarn + 2 nadh
00110101110	Aminosugars metabolism	UDP-N-acetyl-D-mannosamine dehydrogenase UDP-4-amino-4-deoxy-L-	1.1.1	KOX_07570(wecC)	udpnadma + 2 nad -> udpnadmarn + 2 nadh
		UDP-N-acetyl-D-mannosamine dehydrogenase UDP-4-amino-4-deoxy-L- arabinose formyltransferase /			
UDPGLCURD	Aminosugars metabolism  Aminosugars metabolism	UDP-N-acetyl-D-mannosamine dehydrogenase UDP-4-amino-4-deoxy-L- arabinose formyltransferase / UDP-glucuronic acid dehydrogenase (UDP-4-keto-	1.1.1	KOX_07570(wecC)  KOX_05070	udpnadma + 2 nad -> udpnadmam + 2 nadh udpglcur + nad -> udpara4o + co2 + nadh
		UDP-N-acetyl-D-mannosamine dehydrogenase UDP-4-amino-4-deoxy-L- arabinose formyltransferase / UDP-glucuronic acid dehydrogenase (UDP-4-keto- hexauronic acid			
UDPGLCURD	Aminosugars metabolism	UDP-N-acetyl-D-mannosamine dehydrogenase UDP-4-amino-d-deoxy-L-arabinose formyltransferase / UDP-glucuronic acid dehydrogenase (UDP-4-keto-hexauronic acid decarboxylating) UDP-4-amino-d-deoxy-L-uDP-4-amino-d-deoxy-L-	1.1.1.305	KOX_05070	
		UDP-N-acetyl-D-mannosamine dehydrogenase UDP-4-amino-4-deoxy-L- arabinose formyltransferase / UDP-glucuronic acid dehydrogenase (UDP-4-keto-hexauronic acid decarboxylating) UDP-4-amino-4-deoxy-L- arabinose-oxoglutarate			
UDPGLCURD	Aminosugars metabolism	UDP-N-acetyl-D-mannosamine dehydrogenase UDP-4-amino-d-deoxy-L-arabinose formyltransferase / UDP-glucuronic acid dehydrogenase (UDP-4-keto-hexauronic acid decarboxylating) UDP-4-amino-d-deoxy-L-uDP-4-amino-d-deoxy-L-	1.1.1.305	KOX_05070	
UDPGLCURD	Aminosugars metabolism	UDP-N-acetyl-D-mannosamine dehydrogenase UDP-4-amino-4-deoxy-L-arabinose formytransferase / UDP-9-lucuronic acid dehydrogenase (UDP-4-keto-hesuaronic acid decarboxylating) UDP-4-amino-4-deoxy-L-arabinose-oxoglutarate aminotransferase / arabinose formytransferase / uDP-4-amino-4-deoxy-L-arabinose formytransferase /	1.1.1.305	KOX_05070	
UDPGLCURD	Aminosugars metabolism	UDP-N-acetyl-D-mannosamine dehydrogenase UDP-4-amino-4-deoxy-L-arabinose formyttransferase / UDP-9-ducroinci acid dehydrogenase (UDP-4-keto-heazuroni; acid decarboxylating) UDP-4-amino-4-deoxy-L-arabinose-oxoglutarate aminotransferase aminotransferase / UDP-4-amino-4-deoxy-L-arabinose formyttransferase / UDP-4-amino-4-deoxy-L-arabinose formyttransferase / UDP-9-ducroinci acid	1.1.1.305	KOX_05070	
UDPGLCURD  UDPARAT	Aminosugars metabolism  Aminosugars metabolism	UDP-N-acetyl-D-mannosamine dehydrogenase UDP-4-amino-4-deoxy-L-arabinose formytransferase / UDP-9-lucuronic acid dehydrogenase (UDP-4-keto-hesuaronic acid decarboxylating) UDP-4-amino-4-deoxy-L-arabinose-oxoglutarate aminotransferase / arabinose formytransferase / uDP-4-amino-4-deoxy-L-arabinose formytransferase /	1.1.1.305	KOX_05070  KOX_05080	udpglcur + nad -> udpara4o + co2 + nadh udpara4o + glu -> udpara4n + akg
UDPGLCURD  UDPARAT	Aminosugars metabolism  Aminosugars metabolism	UDP-N-acetyl-D-mannosamine dehydrogenase UDP-4-amino-d-deoxyl-arabinose formyltransferase / UDP-glucuronic acid dehydrogenase (UDP-4-keto-heauronic acid decarboxylating) UDP-4-amino-d-deoxy-L-arabinose-oxoglutarate aminotransferase / UDP-4-amino-d-deoxy-L-arabinose-oxoglutarate aminotransferase / UDP-glucuronic acid dehydrogenase (UDP-4-keto-heauronic acid decarboxylating)	1.1.1.305	KOX_05070  KOX_05080	udpglcur + nad -> udpara4o + co2 + nadh udpara4o + glu -> udpara4n + akg
UDPGLCURD  UDPARAT	Aminosugars metabolism  Aminosugars metabolism  Aminosugars metabolism	UDP-N-acetyl-D-mannosamine dehydrogenase UDP-4-amino-4-deoxy-L-arabinose formyttransferase / UDP-9-ducroic acid dehydrogenase (UDP-4-keto-heazunoir, acid decarboy/ating) UDP-4-amino-4-deoxy-L-arabinose-oxoglutarate aminotransferase UDP-4-amino-4-deoxy-L-arabinose formyttransferase / UDP-9-ducronic acid dehydrogenase (UDP-4-keto-heazunoir, acid dehydrogenase (UDP-4	1.1.1.305	KOX_05070  KOX_05080	udpglcur + nad -> udpara4o + co2 + nadh  udpara4o + glu -> udpara4n + akg  fthf + udpara4n -> thf + udpara4fn
UDPARAT  UDPARAFT  UDPARAFNT	Aminosugars metabolism  Aminosugars metabolism  Aminosugars metabolism  Aminosugars metabolism	UDP-N-acety-ID-mannosamine dehydrogenase UDP-4-amino-4-deoxy-L- arabinose formyttransferase / UDP-3-durnion-i acid dehydrogenase (UDP-4-keto- heszuronia cid decarboxylating) UDP-4-amino-4-deoxy-L- arabinose-oxoglutarate aminotransferase UDP-4-amino-4-deoxy-L- arabinose formyttransferase / UDP-3-glucuronic acid decarboxylating) uDP-4-keto- heszuronic acid decarboxylating) undecaprenyi-phosphate 4-deoxy-4-formamido-1- arabinose transferase	11.1305 2.6.187 2.1.2.13 2.7.8.30	KOX_05070  KOX_05080  KOX_05070	udpgkur + nad -> udpara4o + co2 + nadh  udpara4o + glu -> udpara4n + akg  fthf + udpara4n -> thf + udpara4fn  udpara4fn + udcpp -> udcpara4fn + udp
UDPARAT  UDPARAFT  UDPARAFNT  MEL	Aminosugars metabolism  Aminosugars metabolism  Aminosugars metabolism  Aminosugars metabolism  Aminosugars metabolism	UDP-N-acetyl-D-mannosamine dehydrogenase UDP-4-amino-4-deoxy-L-arabinose formyttransferase / UDP-glucuronic acid dehydrogenase (UDP-4-keto-heauronic acid decarboxylating) UDP-4-amino-4-deoxy-L-arabinose-oxoglutarate aminotransferase / UDP-4-amino-4-deoxy-L-arabinose-oxoglutarate aminotransferase / UDP-glucuronic acid dehydrogenase (UDP-4-keto-heauronic acid decarboxylating) undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose transferase malic enzyme (NAD)	11.1305 2.61.87 2.12.13 2.7.8.30 11.138	KOX_05070  KOX_05080  KOX_05070  KOX_05075  KOX_05175/KOX_23885	udpglcur + nad -> udpara4o + co2 + nadh  udpara4o + glu -> udpara4n + akg  fthf + udpara4n -> thf + udpara4fn  udpara4fn + udcpp -> udcpara4fn + udp  mal + nad -> co2 + nadh + pyr
UDPARAT  UDPARAFT  UDPARAFNT	Aminosugars metabolism  Aminosugars metabolism  Aminosugars metabolism  Aminosugars metabolism	UDP-N-acety-ID-mannosamine dehydrogenase UDP-4-amino-4-deoxy-L- arabinose formyttransferase / UDP-3-durnion-i acid dehydrogenase (UDP-4-keto- heszuronia cid decarboxylating) UDP-4-amino-4-deoxy-L- arabinose-oxoglutarate aminotransferase UDP-4-amino-4-deoxy-L- arabinose formyttransferase / UDP-3-glucuronic acid decarboxylating) uDP-4-keto- heszuronic acid decarboxylating) undecaprenyi-phosphate 4-deoxy-4-formamido-1- arabinose transferase	11.1305 2.6.187 2.1.2.13 2.7.8.30	KOX_05070  KOX_05080  KOX_05070	udpglcur + nad -> udpara4o + co2 + nadh  udpara4o + glu -> udpara4n + akg  fthf + udpara4n -> thf + udpara4fn  udpara4fn + udcpp -> udcpara4fn + udp  mal + nad -> co2 + nadh + pyr  mal + nad -> co2 + nadh + pyr
UDPARAT  UDPARAFT  UDPARAFT  UDPARAFNT  MEL  ME2  OAAOC  PPA1	Aminosugars metabolism  Aminosugars metabolism  Aminosugars metabolism  Aminosugars metabolism  Anaplerotic Reactions Anaplerotic Reactions Anaplerotic Reactions Anaplerotic Reactions Anaplerotic Reactions	UDP-N-acetyl-D-mannosamine dehydrogenas UDP-4-amino-4-deoxy-L-arabinose formyttansferase / UDP-4-amino-6-deoxy-L-arabinose formyttansferase / UDP-glucuronic acid dehydrogenase (UDP-4-keto-hexauronic acid decarboxylating) UDP-4-amino-4-deoxy-L-arabinose-oxoglutarate aminotransferase vUDP-4-amino-4-deoxy-L-arabinose formyttransferase VUDP-glucuronic acid dehydrogenase (UDP-4-keto-hexauronic acid dehydrogenase (UDP-4-keto-hexauronic acid decarboxylating) undecaprenyl-phosphate 4-deoxy-4-formamido-1-arabinose transferase malic enzyme (NAD) malic enzyme (NAD) oxaloacetate decarboxylase inorganic diphosphatase	111305 26187 21213 27.830 11.138 11.140 4.113 3.611	KOX_05070  KOX_05070  KOX_05075  KOX_20115/KOX_23885  KOX_27030  KOX_03945/KOX_03970/KOX_10610/KOX_10615  KOX_050990/KOX_20095	udpgkur + nad -> udpara4o + co2 + nadh  udpara4o + glu -> udpara4n + akg  fthf + udpara4n -> thf + udpara4fn  udpara4fn + udcpp -> udcpara4fn + udp  mal + nad -> co2 + nadh + pyr  mal + nad -> co2 + nadh + pyr  oaa -> pyr + co2  ppi -> 2pi  ppi -> 2pi
UDPARAT  UDPARAFT  UDPARAFNT  MEI  ME2  OAADC  PPA1  PPA2	Aminosugars metabolism  Aminosugars metabolism  Aminosugars metabolism  Aminosugars metabolism  Aminosugars metabolism  Anaplerotic Reactions  Anaplerotic Reactions  Anaplerotic Reactions  Anaplerotic Reactions  Anaplerotic Reactions	UDP-N-acetyl-D-mannosamine dehydrogenas UDP-4-amino-4-deoxy-L-arabinose formyltransferase / UDP-glourronic acid dehydrogenase (UDP-4-keto-heavenay-latinose) udp-4-keto-heavenay-deoxy-L-arabinose-conglutariate aminotransferase / UDP-glourronic acid dehydrogenase (UDP-4-amino-4-deoxy-L-arabinose-conglutariate aminotransferase / UDP-glourronic acid dehydrogenase (UDP-4-keto-heavauronic acid decarboxy/asing) undecaprenyl-phosphate 4-deoxy-4-formamido-1-arabinose transferase malic enzyme (NADP) malic enzyme (NADP) malic enzyme (NADP) coaloacetate decarboxy/ase inorganic diphosphatase inorganic diphosphatase inorganic diphosphatase	11.1305 2.6.187 2.12.13 2.7.8.30 11.138 11.1140 4.113 3.6.11 3.6.11	KOX_05070  KOX_05080  KOX_05075  KOX_05075  KOX_20115/KOX_23885  KOX_02945/KOX_03970/KOX_10610/KOX_10615  KOX_05945/KOX_03970/KOX_10610/KOX_10615  KOX_05996/KOX_20995	udpglcur + nad -> udpara4n + co2 + nadh  udpara4n + glu -> udpara4n + akg  fthf + udpara4n -> thf + udpara4fn  udpara4fn + udcpa -> udcpara4fn + udp  mal + nad -> co2 + nadh + pyr  mal + nad -> co2 + nadh + pyr  nai - pyr + co2  ppi -> 2pi + pyr  ppi -> 2pi + pxr
UDPARAT  UDPARAFT  UDPARAFT  UDPARAFNT  MEL  ME2  OAAOC  PPA1	Aminosugars metabolism  Aminosugars metabolism  Aminosugars metabolism  Aminosugars metabolism  Anaplerotic Reactions Anaplerotic Reactions Anaplerotic Reactions Anaplerotic Reactions Anaplerotic Reactions	UDP-N-acetyl-D-mannosamine dehydrogenas UDP-4-amino-4-deoxy-L-arabinose formyltransferase / UDP-glourronic acid dehydrogenase (UDP-4-keto-hesartonic acid) UDP-4-amino-4-deoxy-L-arabinose-conglutariat aminotransferase / UDP-glourronic acid dehydrogenase (UDP-4-amino-4-deoxy-L-arabinose-conglutariat-arabinose formyltransferase / UDP-glourronic acid dehydrogenase (UDP-4-keto-hesauronic acid decarboxylating) undecaprenyl-phosphate 4-deoxy-4-formamido-1-arabinose transferase malic enzyme (NADP) malic enzyme (NADP) malic enzyme (NADP) coaloacetate decarboxylase inorganic diphosphatase inorganic diphosphatase phosphoenolpyruvate carboxylase	111305 26187 21213 27.830 11.138 11.140 4.113 3.611	KOX_05070  KOX_05070  KOX_05075  KOX_20115/KOX_23885  KOX_27030  KOX_03945/KOX_03970/KOX_10610/KOX_10615  KOX_050990/KOX_20095	udpglcur + nad -> udpara40 + co2 + nadh  udpara40 + glu -> udpara4n + akg  fthf + udpara4n -> thf + udpara4fn  udpara4fn + udcpp -> udcpara4fn + udp  mal + nad -> co2 + nadh + pyr  mal + nad -> co2 + nadh + pyr  oaa -> pyr + co2  ppi -> 2pi  ppi -> 2pi
UDPARAT  UDPARAFT  UDPARAFNT  MEI  ME2  OAADC  PPA1  PPA2	Aminosugars metabolism  Aminosugars metabolism  Aminosugars metabolism  Aminosugars metabolism  Aminosugars metabolism  Anaplerotic Reactions  Anaplerotic Reactions  Anaplerotic Reactions  Anaplerotic Reactions  Anaplerotic Reactions	UDP-N-acetyl-D-mannosamine dehydrogenase UDP-4-amino-4-deoxy-L-arabinose formytarnsferase / UDP-4-amino-4-deoxy-L-arabinose formytarnsferase / UDP-4-beto-heavenoria ded decadroxylating) UDP-4-amino-4-deoxy-L-arabinose-oxoglutarate aminotransferase (UDP-4-amino-4-deoxy-L-arabinose-oxylutarate aminotransferase (UDP-4-keto-heavenoria acid decadroxylating) undecaprenyl-phosphate 4-deoxy-4-foramanido-1-arabinose transferase malic enzyme (NAD) malic enzyme (NAD) oxaloacetate decadroxylase inorganic diphosphatase inorganic diphosphatase phosphosnolyzivuate carboxylase phosphosnolyzivuate	11.1305 2.6.187 2.12.13 2.7.8.30 11.138 11.1140 4.113 3.6.11 3.6.11	KOX_05070  KOX_05080  KOX_05075  KOX_05075  KOX_20115/KOX_23885  KOX_02945/KOX_03970/KOX_10610/KOX_10615  KOX_05945/KOX_03970/KOX_10610/KOX_10615  KOX_05996/KOX_20995	udpglcur + nad -> udpara4n + co2 + nadh  udpara4n + glu -> udpara4n + akg  fthf + udpara4n -> thf + udpara4fn  udpara4fn + udcpp -> udcpara4fn + udp  mal + nad -> co2 + nadh + pyr  mal + nad -> co2 + nadh + pyr  oaa -> pyr + co2  ppi -> 2pi ppi -> 2 pi ppi -> 2 pi pi -> 2 pi + bext
UDPARAT  UDPARAFT  UDPARAFNT  ME1  ME2  OAADC  PPA1  PPA2  PPC	Aminosugars metabolism  Aminosugars metabolism  Aminosugars metabolism  Aminosugars metabolism  Anaplerotic Reactions	UDP-N-acetyl-D-mannosamine dehydrogenas UDP-4-amino-4-deoxy-L-arabinose formyltransferase / UDP-glourronic acid dehydrogenase (UDP-4-keto-hesartonic acid) UDP-4-amino-4-deoxy-L-arabinose-conglutariat aminotransferase / UDP-glourronic acid dehydrogenase (UDP-4-amino-4-deoxy-L-arabinose-conglutariat-arabinose formyltransferase / UDP-glourronic acid dehydrogenase (UDP-4-keto-hesauronic acid decarboxylating) undecaprenyl-phosphate 4-deoxy-4-formamido-1-arabinose transferase malic enzyme (NADP) malic enzyme (NADP) malic enzyme (NADP) coaloacetate decarboxylase inorganic diphosphatase inorganic diphosphatase phosphoenolpyruvate carboxylase	111305 26187 21213 27.830 11138 11140 4113 3611 3611 41131	KOX_05070  KOX_05070  KOX_05075  KOX_20115/KOX_23885  KOX_27030  KOX_09990/KOX_20095  KOX_09990/KOX_20095  KOX_09990/KOX_20095  KOX_07360	udpglcur + nad -> udpara4o + co2 + nadh  udpara4o + glu -> udpara4n + akg  fthf + udpara4n -> thf + udpara4fn  udpara4fn + udcpp -> udcpara4fn + udp  mal + nad -> co2 + nadh + pyr  mal + nadp -> co2 + nadh + pyr  oaa -> pyr + co2  ppi -> 2 pi
UDPARAFT  UDPARAFT  UDPARAFT  ME1  ME2  OAADC  PPA1  PPA2  PPC  PPC	Aminosugars metabolism  Aminosugars metabolism  Aminosugars metabolism  Aminosugars metabolism  Amalerotic Reactions Anaplerotic Reactions	UDP-N-acetyl-D-mannosamine dehydrogenae UDP-4-amino-d-deoxy-L-arabinose formyttransferase / UDP-glucuronic acid dehydrogenae (UDP-4-keto-hezauronic acid dehydrogenaes (UDP-4-keto-hezauronic acid decarboxylating) UDP-4-amino-d-deoxy-L-arabinose-conglutarate aminostransferase UDP-4-amino-d-deoxy-L-arabinose formyttansferase / UDP-glucuronic acid dehydrogenaes (UDP-4-keto-hezauronic acid decarboxylating) undecaprenyl-phosphate d-deoxy-d-formamido-L-arabinose transferase malic enzyme (NADP) malic enzyme (NADP) malic enzyme (NADP) malic enzyme (NADP) coalacetate decarboxylase inorganic diphosphatase inorganic diphosphatase phosphoenolpyruvate carboxylase sociitate lyase malate symthase	2.6.187  2.1.2.13  2.7.8.30  1.1.1.38  1.1.1.40  4.1.1.3  3.6.1.1  4.1.1.31  4.1.1.31	KOX_05070  KOX_05070  KOX_05075  KOX_20115/KOX_23885  KOX_203945/KOX_03970/KOX_10610/KOX_10615  KOX_05960/KOX_20095  KOX_07360  KOX_07360  KOX_07360  KOX_07360	udpglcur + nad -> udpara4o + co2 + nadh  udpara4o + glu -> udpara4n + akg  fthf + udpara4n -> thf + udpara4fn  udpara4fn + udcpp -> udcpara4fn + udp  mal + nad -> co2 + nadh + pyr  mal + nad -> co2 + nadh + pyr  mal + nad -> co2 + nadh + pyr  ppi -> 2pi pj  ppi -> 2pi pj  ppi -> 2pi pj  ppi -> 2pi pi  ppi -> 2pi pi -> 2pi pi p
UDPARAT  UDPARAFT  UDPARAFNT  MEI  ME2  OAADC  PPA1  PPA2  PPC  PPC  PPCK  ICL	Aminosugars metabolism  Aminosugars metabolism  Aminosugars metabolism  Aminosugars metabolism  Amaplerotic Reactions Anaplerotic Reactions	UDP-N-acetyl-D-mannosamine dehydrogenase UDP-4-amino-4-deoxy-L-arabinose formytransferase / UDP-4-amino-4-deoxy-L-arabinose formytransferase / UDP-9-bucronic acid dehydrogenase (UDP-4-brown) (UDP-4-amino-4-deoxy-L-arabinose-oxoglutarate aminotransferase UDP-4-amino-4-deoxy-L-arabinose-oxoglutarate aminotransferase UDP-4-amino-4-deoxy-L-arabinose oxing transferase UDP-4-keto-hexauronic acid dehydrogenase (UDP-4-keto-hexauronic acid dehydrogenase (UDP-4-keto-hexauronic acid dehydrogenase (UDP-4-keto-hexauronic acid decarboxy/asting) undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose transferase malic enzyme (NADP) oxaloacetate decarboxy/aste inorganic diphosphatase inorganic diphosphatase phosphosenolypruvate carboxy/ase phosphosenolypruvate carboxy/ase phosphosenolypruvate Lacety-asia (UDP-4-carboxy/ase phosphosenolypruvate Lacety-oxy/ase) Lacety-asia (UDP-4-carboxy/ase) Lacety-asia (UDP-4-keto-hexauronic acid	2.6.187  2.6.187  2.1.2.13  2.7.8.30  1.1.1.80  1.1.1.40  4.1.1.3  4.1.1.41  4.1.1.49  4.1.3.1	KOX_05070  KOX_05070  KOX_05075  KOX_20115/KOX_23885  KOX_27030  KOX_0599/KOX_20095  KOX_0599/KOX_20095  KOX_07360  KOX_07360  KOX_06470/KOX_23370  KOX_068045	udpglcur + nad -> udpara4o + co2 + nadh  udpara4o + glu -> udpara4n + akg  fthf + udpara4n -> thf + udpara4fn  udpara4fn + udcpp -> udcpara4fn + udp  mal + nad -> co2 + nadh + pyr  mal + nadp -> co2 + nadh + pyr  oaa -> pyr + co2  ppi -> 2 pi
UDPARAT  UDPARAFT  UDPARAFT  WEI  ME2  OAAOC  PPC1  PPC2  PPC  PPCK  ICL  MALS	Aminosugars metabolism  Aminosugars metabolism  Aminosugars metabolism  Aminosugars metabolism  Aminosugars metabolism  Anaplerotic Reactions Arginine and Proline Metabolism	UDP-N-acetyl-D-mannosamine dehydrogenase UDP-4-amino-4-deoxy-L-arabinese formytransferase / UDP-4-amino-4-deoxy-L-arabinese formytransferase / UDP-9-bucronic acid dehydrogenase (UDP-4-brown) (UDP-4-amino-4-deoxy-L-arabinose-coxy) (UDP-4-amino-4-deoxy-L-arabinose-coxy) (UDP-4-amino-4-deoxy-L-arabinose-coxy) (UDP-4-amino-4-deoxy-L-arabinose-coxy) (UDP-4-brown) (UDP-4-keto-hexauronic acid dehydrogenase (UDP-4-keto-hexauronic acid dehydrogenase (UDP-4-keto-hexauronic acid decarboxy) (Auto-promaidio-L-arabinose transferase malic enzyme (NAD)) (NAD) (UDP-4-arabinose transferase malic enzyme (NAD)) (NAD) (UDP-4-arabinose transferase inorganic diphosphatase inorganic diphosphat	2.61.87  2.1.2.13  2.7.8.30  1.1.1.38  1.1.1.40  4.1.1.3  3.6.1.1  4.1.1.31  4.1.1.49  4.1.3.1  2.3.3.9	KOX_05070  KOX_05070  KOX_05075  KOX_20115/MOX_23885  KOX_0949/KOX_20095  KOX_07330  KOX_07330  KOX_07360  KOX_07360  KOX_0845/MOX_23370  KOX_0896/KOX_23370  KOX_0896/KOX_23370  KOX_0896/KOX_23370  KOX_08045  KOX_08045  KOX_08045  KOX_08045  KOX_08045  KOX_08045  KOX_08046  KOX_17015(putA)	udpglcur + nad -> udpara4n + co2 + nadh  udpara4n + glu -> udpara4n + akg  fthf + udpara4n -> thf + udpara4fn  udpara4fn + udcpp -> udcpara4fn + udp  mal + nad -> co2 + nadh + pyr  mal + nad -> co2 + nadh + pyr  oaa -> pyr + co2  ppi -> 2 pi
UDPARAT  UDPARAFT  UDPARAFT  ME1  ME2  OAAOC  PPC1  PPC2  PPC  PPC  LCL  MALS  PSCD1  PSCR1	Aminosugars metabolism  Aminosugars metabolism  Aminosugars metabolism  Aminosugars metabolism  Anaplerotic Reactions Arginine and Proline Metabolism Arginine and Proline Metabolism	UDP-N-acetyl-D-mannosamine dehydrogenae UDP-4-amino-d-deoxy-L-arabinose formyttransferase / UDP-glucuronic acid dehydrogenae (UDP-4-keto-hezauronic acid dehydrogenae (UDP-4-keto-hezauronic acid dehydrogenae (UDP-4-amino-d-deoxy-L-arabinose-orgolutrarte aminotransferase / UDP-glucuronic acid dehydrogenae (UDP-4-keto-hezauronic acid dehydrogenae (UDP-4-keto-hezauronic acid dehydrogenae (UDP-4-keto-hezauronic acid desponae) (UDP-4-manino-deoxy-4-formanido-1-arabinose transferase malic enzyme (NADP) malic	2.61.87  2.61.87  2.1.2.13  2.7.8.30  1.1.1.38  1.1.1.40  4.1.1.3  3.6.1.1  4.1.1.1  4.1.1.1  2.3.3.9  1.5.1.1.2  1.5.1.2	KOX_05070  KOX_05070  KOX_05075  KOX_2030  KOX_27030  KOX_05075  KOX_20115/MOX_23885  KOX_09345/KOX_0095  KOX_06945/KOX_20095  KOX_07360  KOX_0676/KOX_23370  KOX_0676/KOX_23370  KOX_0686/KOX_2056  KOX_0667/KOX_23370  KOX_0686/KOX_056/KOX_2370  KOX_0686/KOX_056/K	udpglcur + nad -> udpara4n + co2 + nadh  udpara4n + glu -> udpara4n + akg  fthf + udpara4n -> thf + udpara4fn  udpara4fn + udcpp -> udcpara4fn + udp  mal + nad -> co2 + nadh + pyr  mal + nad -> co2 + nadh + pyr  oaa -> pyr + co2  ppi -> 2 pi
UDPARAFT  UDPARAFT  UDPARAFT  WEL  ME2  OAADC  PPA1  PPA2  PPC  PPC  PPC  RICL  MALS  PSCD1  PSCR1  PSCR3	Aminosugars metabolism  Aminosugars metabolism  Aminosugars metabolism  Aminosugars metabolism  Aminosugars metabolism  Anaplerotic Reactions Arginine and Proline Metabolism	UDP-N-acetyl-D-mannosamine dehydrogenase UDP-4-amino-4-deoxy-L-arabinese formytransferase / UDP-4-amino-4-deoxy-L-arabinese formytransferase / UDP-9-bucronic acid dehydrogenase (UDP-4-brown) (UDP-4-amino-4-deoxy-L-arabinose-coxy) (UDP-4-amino-4-deoxy-L-arabinose-coxy) (UDP-4-amino-4-deoxy-L-arabinose-coxy) (UDP-4-amino-4-deoxy-L-arabinose-coxy) (UDP-4-brown) (UDP-4-keto-hexauronic acid dehydrogenase (UDP-4-keto-hexauronic acid dehydrogenase (UDP-4-keto-hexauronic acid decarboxy) (Auto-promaidio-L-arabinose transferase malic enzyme (NAD)) (NAD) (UDP-4-arabinose transferase malic enzyme (NAD)) (NAD) (UDP-4-arabinose transferase inorganic diphosphatase inorganic diphosphat	2.61.87  2.1.2.13  2.7.8.30  1.1.1.38  1.1.1.40  4.1.1.3  3.6.1.1  4.1.1.31  4.1.1.49  4.1.3.1  2.3.3.9  1.5.1.1.2	KOX_05070  KOX_05070  KOX_05075  KOX_20115/MOX_23885  KOX_0949/KOX_20095  KOX_07330  KOX_07330  KOX_07360  KOX_07360  KOX_0845/MOX_23370  KOX_0896/KOX_23370  KOX_0896/KOX_23370  KOX_0896/KOX_23370  KOX_08045  KOX_08045  KOX_08045  KOX_08045  KOX_08045  KOX_08045  KOX_08046  KOX_17015(putA)	udpglcur + nad -> udpara4o + co2 + nadh  udpara4o + glu -> udpara4n + akg  fthf + udpara4n -> thf + udpara4fn  udpara4fn + udcpp -> udcpara4fn + udp  mal + nad -> co2 + nadh + pyr  mal + nad -> co2 + nadh + pyr  mal + nad -> co2 + nadh + pyr  ppi -> 2pi pi  ppi -> 2pi pi  ppi -> 2pi + pox  ppi -> 2pi pi  ppi -> 2pi + pox  ppi -> 2pi pi  ppi -> 2pi + bext  pep + co2 -> coa + pi  atp + oaa -> adp + co2 + pep  icit -> glx + succ  accoa + glx -> coa + mal  p5c + nadh -> glu + nadh  p5c + nadh -> nadh + pro
UDPARAT  UDPARAFT  UDPARAFT  ME1  ME2  OAAOC  PPC1  PPC2  PPC  PPC  LCL  MALS  PSCD1  PSCR1	Aminosugars metabolism  Aminosugars metabolism  Aminosugars metabolism  Aminosugars metabolism  Anaplerotic Reactions Arginine and Proline Metabolism Arginine and Proline Metabolism	UDP-N-acetyl-D-mannosamine dehydrogenase UDP-4-amino-4-deoxy-L-arabinose formytransferase / UDP-4-amino-4-deoxy-L-arabinose formytransferase / UDP-9-bucronic acid dehydrogenase (UDP-4-seto-heavaronic acid decarboxylating) UDP-4-amino-4-deoxy-L-arabinose-conglutarate aminotransferase UDP-4-amino-4-deoxy-L-arabinose-conglutarate aminotransferase UDP-4-amino-4-deoxy-L-arabinose-complytransferase / UDP-glucuronic acid dehydrogenase (UDP-4-keto-heavaronic acid dehydrogenase (UDP-4-keto-heavaronic acid dearboxylating) undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose transferase malic enzyme (NADP) covaloacetate decarboxylase inorganic diphosphatase inorganic diphosphatase inorganic diphosphatase phosphosenolypruvate carboxykase phosphosenolypruvate	2.6.187  2.6.187  2.7.8.30  1.1.1.38  1.1.1.40  4.1.13  3.6.11  3.6.11  4.1.1.31  4.1.1.31  4.1.1.31  4.1.1.31  4.1.1.31  4.1.3.1  2.3.3.9  1.5.1.12  1.5.1.2  1.5.1.2  1.5.1.9.8	KOX_05070  KOX_05070  KOX_05075  KOX_2030  KOX_27030  KOX_05075  KOX_20115/MOX_23885  KOX_09345/KOX_0095  KOX_06945/KOX_20095  KOX_07360  KOX_0676/KOX_23370  KOX_0676/KOX_23370  KOX_0686/KOX_2056  KOX_0667/KOX_23370  KOX_0686/KOX_056/KOX_2370  KOX_0686/KOX_056/K	udpglcur + nad -> udpara4n + co2 + nadh  udpara4n + glu -> udpara4n + akg  fthf + udpara4n -> thf + udpara4fn  udpara4fn + udcpp -> udcpara4fn + udp  mal + nad -> co2 + nadh + pyr  mal + nad -> co2 + nadh + pyr  oaa -> pyr + co2  ppl -> 2 pi  ppl -> 2

ARGSCL	Arginine and Proline Metabolism	argininosuccinate lyase	4.3.2.1	KOX 07380	argsucc <-> arg + fum
GLUSSDT	Arginine and Proline Metabolism	L-glutamate 5-semialdehyde	spontaneous	KOA_0/360	glugsal -> p5c
GLUDH4	Arginine and Proline metabolism	dehydratase (spontaneous) glutamate dehydrogenase	1.4.1.3	KOX_19525	glu + nadp <-> akg + nh4 + nadph
P5CD2	Arginine and Proline metabolism	1-pyrroline-5-carboxylate	1.5.1.12	KOX_17015(putA)	glugsal + nad <-> glu + nadh
DECD3		dehydrogenase 1-pyrroline-5-carboxylate	15112		
PSCD3 PROD3	Arginine and Proline metabolism  Arginine and Proline metabolism	dehydrogenase Proline dehydrogenase	1.5.1.12	KOX_17015(putA) KOX_17015(putA)	4hglusa + nad -> e4hglu + nadh 4hglusa + nad -> e4hglu + nadh
P5CR2	Arginine and Proline metabolism	pyrroline-5-carboxylate	1.5.1.2	KOX 12395/KOX 21070	I1p3h5c + nadh -> 4hpro + nad
		reductase 1-pyrroline-5-carboxylate			
P5CD4	Arginine and Proline metabolism	dehydrogenase	1.5.1.12	KOX_17015(putA)	I1p3h5c + nad -> e4hglu + nadh
P5CD6	Arginine and Proline metabolism	1-pyrroline-5-carboxylate dehydrogenase	1.5.1.12	KOX_17015(putA)	l1p3h5c + nadp -> e4hglu + nadph
PTO4H	Arginine and Proline metabolism	1-pyrroline-5-carboxylate			l1p3h5c <-> 4hglusa
P5CD5	Arginine and Proline metabolism	dehydrogenase	1.5.1.12	KOX_17015(putA)	4hglusa + nadh -> e4hglu + nad
PROD4 ASPAM4	Arginine and Proline metabolism Arginine and Proline metabolism	Proline dehydrogenase aspartate aminotransferase	1.5.99.8 2.6.1.1	KOX_17015(putA) KOX_16370	4hglusa + nadh -> e4hglu + nad e4hglu + akg -> hydroxyakg + glu
HOGAD	Arginine and Proline metabolism	4-hydroxy-2-oxoglutarate	4.1.2.14	KOX 23850	hydroxyakg <-> pyr + glx
OAADC2	Arginine and Proline metabolism	aldolase oxaloacetate decarboxylase	4.1.1.3	KOX_03945/KOX_03970/KOX_10610/KOX_10615	
CREAH	Arginine and Proline metabolism	creatinine amidohydrolase 1-pyrroline-5-carboxylate	3.5.2.10	KOX_20850	cretn <-> creatine
P5CD1p	Arginine and Proline Metabolism	dehydrogenase	1.5.1.12	KOX_17015(putA)	p5c + nadp <-> glu + nadph
P5CR2p	Arginine and Proline metabolism	pyrroline-5-carboxylate reductase	1.5.1.2	KOX_12395/KOX_21070	l1p3h5c + nadph -> 4hpro + nadp
ACORND2	Arginine and Proline metabolism	acetylornithine deacetylase	3.5.1.16	KOX_07365/KOX_16395/KOX_19240	accitr -> ac + citr
UREAC ARGSUCCT	Arginine and Proline metabolism Arginine and Proline metabolism	urea carboxylase arginine N-succinyltransferase	6.3.4.6 2.3.1.109	KOX_20285 KOX_18145	atp + urea + hco3 <-> adp + pi + u1car succoa + arg -> coa + succarg
SUCCARGD	Arginine and Proline metabolism	succinylarginine dihydrolase	3.5.3.23	KOX_18155	succarg -> succorn + co2 + 2 nh4
SUCCORNAT	Arginine and Proline metabolism	succinylornithine aminotransferase	2.6.1.81	KOX_18140	succorn + akg -> succglusa + glu
SUCCGLUSAD	Arginine and Proline metabolism	succinylglutamic semialdehyde dehydrogenase	1.2.1.71	KOX_18150	succglusa + nad -> succglu + nadh
SUCCGLUDS	Arginine and Proline metabolism	succinylglutamate	3.5.1.96	KOX_18160	succglu -> glu + succ
PTRCAT	Arginine and Proline metabolism	desuccinylase putrescine aminotransferase	2.6.1.82	KOX_03220	akq + ptrc -> 4ab + qlu
DIAMACT	Arginine and Proline metabolism	diamine N-acetyltransferase	2.3.1.57	KOX_21535	accoa + ptrc -> coa + acputs
SPRMDAT1 SPRMDAT2	Arginine and Proline metabolism Arginine and Proline metabolism	Spermidine acetyltransferase Spermidine acetyltransferase	2.3.1.57	KOX_21535 KOX_21535	accoa + sprmd -> n1acsprmd + coa accoa + sprmd -> n8acsprmd + coa
GLUPTRCS	Arginine and Proline metabolism	gamma-glutamylputrescine	6.3.1.11	KOX_16935	atp + glu + ptrc -> adp + pi + gluptrc
GLUPTRCOX	Arginine and Proline metabolism	synthase gamma-glutamylputrescine	1.4.3	KOX_16915	gluptrc + o2 -> gluamibut + nh4 + h2o2
JEUT INCUA	Augmine and Promie metabolism	oxidase gamma-glutamyl-gamma-	2.9.3.*	NON_10313	gropers + oz -> gradinibus + nin4 + NZOZ
GLUAMIBUTD	Arginine and Proline metabolism	aminobutyraldehyde	1.2.1	KOX_16920	gluamibut + nad -> gluamibutr + nadh
		dehydrogenase gamma-glutamyl-gamma-			
GLUAMIBUTRH	Arginine and Proline metabolism	aminobutyrate hydrolase	3.5.1.94	KOX_16930(puuD)	gluamibutr -> gaba + glu
ORNDC	Arginine and Proline metabolism	ornithine decarboxylase L-glutamate 5-semialdehyde	4.1.1.17	KOX_02775	orn -> ptrc + co2
GLUGSALD	Arginine and Proline metabolism	dehydratase (spontaneous)			glugsal <-> p5c
GLCRD1 GALCTDH	Ascorbate and Aldarate metabolism Ascorbate and Aldarate metabolism	glucarate dehydratase galactarate dehydratase	4.2.1.40 4.2.1.42	KOX_01175 KOX_03480	dgluca <-> d4dg dgal -> d4dg
DGLUCAL1	Ascorbate and Aldarate metabolism	2-dehydro-3-deoxyglucarate	4.1.2.20	KOX_03470	d4dg <-> pyr + h3op
ADLD	Ascorbate and Aldarate metabolism	aldolase aldehyde dehydrogenase	1.2.1.3	KOX_00375	dglucl + nad <-> dgluca + nadh
GLCRD2	Ascorbate and Aldarate metabolism	(NAD+) glucarate dehydratase	4.2.1.40	KOX_00375 KOX 01175	dgluca <-> d3dq
DGLUCAL2	Ascorbate and Aldarate metabolism	2-dehydro-3-deoxyglucarate	4.1.2.20	KOX_03470	d3dg <-> pyr + h3op
		aldolase L-ascorbate 6-phosphate		_	
ASCB6PL	Ascorbate and Aldarate metabolism	lactonase	3.1.1	KOX_08920	ascb6p -> 3dhg6p
LRIB5P4E2	Ascorbate and Aldarate metabolism	L-ribulose-5-phosphate 4- epimerase	5.1.3.4	KOX_08950(sgaE)	Irl5p <-> xu5p
ARABNLAC	Ascorbate and Aldarate metabolism	L-arabinonolactonase	3.1.1.15	KOX_24440	arabnlac <-> arabn
AMDS6 APPS3	Benzoate degradation via CoA ligation Benzoate degradation via CoA ligation	amidase acylphosphatase	3.5.1.4 3.6.1.7	KOX_09850/KOX_13720/KOX_2051 KOX_16295	bzamid -> benzot + nh4 bzop -> benzot + pi
NITRH VANMOX	Benzoate degradation via CoA ligation Benzoate degradation via CoA ligation	nitrile hydratase vanillate monooxygenase	4.2.1.84 1.14.13.82	KOX_20500 KOX_16720	bzonit -> bzamid vanillate + o2 + nadh -> 34dhb + nad + formald
	benzoate degradation via COA ligation				
	Benzoate degradation via CoA ligation	3-hydroxybutyryl-CoA		KOX 19455	3hbcna + nadn -> aacna + nadnh
3HBCDH	Benzoate degradation via CoA ligation	dehydrogenase	1.1.1.157	KOX_19455	3hbcoa + nadp -> aacoa + nadph
	Benzoate degradation via CoA ligation  Benzoate degradation via Hydroxylation	dehydrogenase p-hydroxybenzoate 3- monooxygenase		KOX_19455 KOX_10205	3hbcoa + nadp -> aacoa + nadph 4hb + o2 + nadph -> 34dhb + nadp
3HBCDH		dehydrogenase p-hydroxybenzoate 3- monooxygenase protocatechuate 3,4-	1.1.1.157		
3HBCDH PHBZMN PROTCC1 4OXCTT	Benzoate degradation via Hydroxylation Benzoate degradation via Hydroxylation Benzoate degradation via Hydroxylation	dehydrogenase p-hydroxybenzoate 3- monooxygenase protocatechuate 3,4- dioxygenase 4-oxalocrotonate tautomerase	1.1.1.157 1.14.13.2 1.13.11.3 5.3.2	KOX_10205 KOX_19615/KOX_19620 KOX_02090/KOX_19920/KOX_20805	4hb + o2 + nadph -> 34dhb + nadp 34dhb + o2 -> carccm 2hmuc -> zoe
3HBCDH PHBZMN PROTCC1 40XCTT 30XAPLC 30XAPT	Benzoate degradation via Hydroxylation Benzoate degradation via Hydroxylation Benzoate degradation via Hydroxylation Benzoate degradation via Hydroxylation Benzoate degradation via Hydroxylation	dehydrogenase p-hydroxybenzoate 3- monoxygenase protocatechuate 3,4- dioxygenase 4-oxalocrotonate tautomerase 3-oxoadipate enol-lactonase 3-oxoadipate CoA-transferase	1.1.1.157 1.14.13.2 1.13.11.3 5.3.2- 3.1.1.24 2.8.3.6	KOX_10205 KOX_19615/KOX_19620 KOX_02090/KOX_19920/KOX_20805 KOX_21740 KOX_2175/KOX_21760	4hb + o2 + nadph -> 34dhb + nadp  34dhb + o2 -> carccm  2hmuc -> zoe 2odhfac -> oadip succa + oadip -> succ + ooadpcoa
3HBCDH PHBZMN PROTCC1 40XCTT 30XAPLC 30XAPT 30XADCT	Benzoate degradation via Hydroxylation Benzoate degradation via Hydroxylation	dehydrogenase p-hydroxybenzoate 3- monoxygenase protocatechuate 3,4- dioxygenase 4-oxalocrotonate tautomerase 3-oxoadipate enol-lactonase 3-oxoadipate CoA-transferase 3-oxoadipyl-CoA thiolase	111.157 114.132 113.113 5.3.2- 3.1.124 2.8.3.6 2.3.1.16	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_19920/KOX_20805  KOX_21740  KOX_21755/KOX_21760  KOX_07830(fadA)/KOX_26660(fadI)	4hb + o2 + nadph -> 34dhb + nadp 34dhb + o2 -> carccm 2hmuc -> zoe 2odhfac -> oadip succa + oadip -> succ + ooadpcoa ooadpcoa + coa -> succoa + accoa
3HBCDH PHBZMN PROTCC1 40XCTT 30XAPLC 30XAPT	Benzoate degradation via Hydroxylation Benzoate degradation via Hydroxylation Benzoate degradation via Hydroxylation Benzoate degradation via Hydroxylation Benzoate degradation via Hydroxylation	dehydrogenase p-hydroxybenzoate 3- monoxygenase protocatechuate 3,4- dioxygenase 4-oxalocrotonate tautomerase 3-oxoadipate enol-lactonase 3-oxoadipate CoA-transferase	1.1.1.157 1.14.13.2 1.13.11.3 5.3.2- 3.1.1.24 2.8.3.6	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_19920/KOX_20805  KOX_21740  KOX_21755/KOX_21760  KOX_07830(fad4)/KOX_26660(fad1)  KOX_21745	4hb + o2 + nadph -> 34dhb + nadp  34dhb + o2 -> carccm  2hmuc -> zoe 2odhfac -> oadip succoa + oadip -> succ + ooadpcoa ooadpoa + coa -> succoa + accoa carccm <-> gcarmclc
3HBCDH PHBZMN PROTCC1 40XCTT 30XAPLC 30XAPT 30XADCT	Benzoate degradation via Hydroxylation Benzoate degradation via Hydroxylation	dehydrogenase p-hydroxybenzoate 3-monoxygenase protocatechuate 3,4-dioxygenase 4-oxalocrotonate tautomerase 3-oxoadipate CoA-transferase 3-oxoadipate CoA-transferase 3-acaboxy-Csc,6:s-muconate cycloisomerase 4-carboxymuconolactone	111.157 114.132 113.113 5.3.2- 3.1.124 2.8.3.6 2.3.1.16	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_19920/KOX_20805  KOX_21740  KOX_21755/KOX_21760  KOX_07830(fadA)/KOX_26660(fadI)	4hb + o2 + nadph -> 34dhb + nadp  34dhb + o2 -> carccm  2hmuc -> zoe 2odhfac -> oadip succoa + oadip -> succ + ooadpcoa ooadpoa + coa -> succoa + accoa carccm <-> gcarmclc
3HBCDH PHBZMN PROTCC1 40XCTT 30XAPIC 30XAPT 30XADCT 3CMUCC	Benzoate degradation via Hydroxylation Benzoate degradation via Hydroxylation	dehydrogenase p-hydroxybenzoate 3- monoxygenase protocatechuate 3,4- dioxygenase 4-oxalocrotonate tautomerase 3-oxoadipate end-lactonase 3-oxoadipate end-lactonase 3-oxoadipate CoA trionase 3-carboxy-cis,cis-muconate cycloisomerase 4-carboxymuconolactone decarboxylase protocatechuate 3,4-	111157 114132 113113 532- 31124 283.6 23116 55512	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_19920/KOX_20805  KOX_2175/KOX_21760  KOX_02175/KOX_21760  KOX_07380/(64A)/KOX_26660(fadl)  KOX_2175/KOX_21765  KOX_21745  KOX_02105/KOX_07320/KOX_20565/KOX_20900	4hb + o2 + nadph -> 34dhb + nadp 34dhb + o2 -> carccm 2hmuc -> zoe 2odhfac -> oadip succa + oadip -> succ + ooadpcoa ooadpcoa + coa -> succoa + accoa carccm <-> gcarmclc
3HBCDH PHBZMN PROTCC1 4OXCTT 3OXAPIC 3OXAPT 3OXADCT 3CMUCC 4CBMCLC PROTCC2	Benzoate degradation via Hydroxylation	dehydrogenase p-hydroxybernoate 3- moncoxygenase protocatechuate 3,4- dioxygenase 4-oxalocrotonate tautomerase 3-oxoadipate end-lactonase 3-oxoadipate CoA-transferase 3-oxoadipy-CoA thiolase 3-carboxy-cis,Gis-muconate cycloisomerase 4-carboxymuconolactone decarboxylase	11.1157 114132 113113 53.2- 31124 2.83.6 2.3116 5.512 41144 113113	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_19920/KOX_20805  KOX_21740  KOX_21755/KOX_21760  KOX_21758/KOX_21760  KOX_217545  KOX_02105/KOX_07320/KOX_20565/KOX_20900  KOX_21755/KOX_24470  KOX_19615/KOX_19620	4hb + o2 + nadph -> 34dhb + nadp 34dhb + o2 -> carccm 2hmuc -> zoe 2odhfac -> oadip succa + oadip -> succ + ooadpcoa ooadpcoa + coa -> succoa + accoa carccm <-> gcarmclc gcarmclc <-> 2odhfac + co2 gallate + o2 -> 2py46dc
3HBCDH PHBZMN PROTCC1 40XCTT 30XAPL 30XAPL 30XAPCT 30XAPCT 3CMUCC 4CBMCLC PROTCC2 CARHM2	Benzoate degradation via Hydroxylation	dehydrogenase p-hydroxybenzoate 3-moncoxygenase protocatechuate 34-dioxygenase and 4-oxalorotonate tautomerase 3-oxoadipate enot-lactonase 3-oxoadipate coA-transferase 3-oxoadipate CoA-tronsferase 3-carboxy-cis,cis-muconate cycloisomerase 4-carboxymuconolactone decarboxylase protocatechuate 3-carboxymethyl-2-hydroxymuconate isomerase 5-carboxymethyl-2-hydroxymuconate isomerase	1.1.1157 1.14.132 1.13.113 5.3.2- 3.1.124 2.8.36 2.3.116 5.5.12 4.1.144 1.13.113 5.3.3.10	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_19920/KOX_20805  KOX_21740  KOX_21755/KOX_21760  KOX_07830(fada)/KOX_26660(fad)  KOX_21745  KOX_02105/KOX_07320/KOX_20565/KOX_20900  KOX_2175/KOX_2470  KOX_19615/KOX_19620  KOX_10404	4hb + o2 + nadph -> 34dhb + nadp  34dhb + o2 -> carccm  2hmuc -> zoe 2odhfac -> oadip succa + oadip -> succ + ooadpcoa ooadpcoa + coa -> succoa + accoa carcm <-> gcarmclc  gcarmclc <-> 2odhfac + co2 gallate + o2 -> 2py46dc  4c2hbd <-> 4obtc
SHBCDH PHBZMN PROTCC1 40XCTT 30XAPLC 30XAPL 30XAPCT 30XADCT 3CMUCC 4CBMCLC PROTCC2 CARHM2 DMRATT	Benzoate degradation via Hydroxylation Terpenoid backbone bioxynthesis	dehydrogenase p-hydroxybenzoate 3- monoxygenase protocatechuate 34- dioxygenase 4-osalcrotonate tautomerase 3-osadipate enol-lactonase 3-osadipate coA-transferase 3-osadipate CoA-transferase 3-osadipate CoA-transferase 3-osadipate CoA-transferase 4-carboxy-cis,cis-muconate cycloisomerase 4-carboxymuconalectone decarboxygenase protocatechuate 3,4- dioxygenase 5-carboxymethyl-2- hydroxymuconate isomerase geranyltranstransferase geranyltranstransferase	1.1.1157 1.14.13.2 1.13.113 5.3.2- 3.1.124 2.8.3.6 2.3.1.16 5.5.1.2 4.1.1.44 1.13.113 5.3.3.10 2.5.1.1	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_19920/KOX_20805  KOX_21740  KOX_2175/KOX_21760  KOX_07830(fadA)/KOX_26660(fad1)  KOX_21745  KOX_02105/KOX_07320/KOX_20565/KOX_20900  KOX_19615/KOX_19620  KOX_1040  KOX_1040  KOX_1040  KOX_1040  KOX_1040  KOX_1040  KOX_1040	4hb + o2 + nadph -> 34dhb + nadp  34dhb + o2 -> carccm  2hmuc -> zoe 2odhfac -> oadip succa + oadip -> succ + oadpcoa ooadpcoa + coa -> succoa + accoa carccm <-> gcarmclc  gcarmclc <-> zodhfac + co2 gallate + o2 -> zpy46dc 4c2hd <-> 4obtc dmpp + ipp -> gpp + ppi
3HBCDH PHBZMN PROTCC1 40XCTT 30XAPL 30XAPL 30XAPCT 30XAPCT 3CMUCC 4CBMCLC PROTCC2 CARHM2	Benzoate degradation via Hydroxylation	dehydrogenase p-hydroxybenzoate 3- monooxygenase protocatechuate 3,4- dioxygenase 4-oxalocrotonate tautomerase 3-oxoadipate end-lactonase 3-oxoadipate end-lactonase 3-oxoadipate CoA-transferase 3-oxoadipate CoA-transferase 3-carboxy-cis.cis-muconate cycloisomerase 4-carboxymuconolactone decarboxylase protocatechuate 3,4- dioxygenase 5-carboxymuconate isomerase geranyftranstransferase	1.1.1157 1.14.132 1.13.113 5.3.2- 3.1.124 2.8.36 2.3.116 5.5.12 4.1.144 1.13.113 5.3.3.10	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_19920/KOX_20805  KOX_21756  KOX_21756  KOX_021760  KOX_021765  KOX_02105/KOX_07320/KOX_20565/KOX_20900  KOX_1735/KOX_24470  KOX_19615/KOX_19620  KOX_10400  KOX_10565	4hb + o2 + nadph -> 34dhb + nadp 34dhb + o2 -> carccm 2hmuc -> zoe 2odhfac -> oadip succa + oadip -> succ + ooadpcoa ooadpcoa + coa -> succoa + accoa carccm <-> gcarmclc  gcarmclc <-> Zodhfac + co2 gallate + o2 -> Zpy46dc 4/2hbd <-> 4obtc dmp + ipp -> gpp + ppi ipp <-> dmpp
3HBCDH PHBZMN PROTCC1 40XCTT 30XAPLC 30XAPLC 30XAPLC 30XADCT 3CXMUCC 4CBMCLC PROTCC2 CARHM2 DMRATT LPPDI	Benzoate degradation via Hydroxylation Terpensiod backbone biosynthesis Terpensiod backbone biosynthesis	dehydrogenase p-hydronybenzoate 3- monooxygenase protocatechuate 3,4- dioxygenase 4-oxalocrotonate tautomerase 3-oxoadipate coA-transferase 3-oxoadipate CoA-transferase 3-oxoadipate CoA-tronsferase 3-carboxy-cis,cis-muconate cycloisomerase 4-carboxymuconolactone decarboxylase protocatechuate 3,4- dioxygenase 5-carboxymuconate isomerase geranyftranstransferase sicopentenyl-ciphosphate delta- isomerase geranyftranstransferase geranyftranstransferase geranyftranstransferase	1.1.1157 1.14.13.2 1.13.11.3 5.3.2. 3.1.124 2.8.3.6 2.3.1.16 5.5.1.2 4.1.1.44 1.13.11.3 5.3.3.10 2.5.1.1 5.3.3.2	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_19920/KOX_20805  KOX_21740  KOX_2175/KOX_21760  KOX_07830(fadA)/KOX_26660(fad1)  KOX_21745  KOX_02105/KOX_07320/KOX_20565/KOX_20900  KOX_19615/KOX_19620  KOX_1040  KOX_1040  KOX_1040  KOX_1040  KOX_1040  KOX_1040  KOX_1040	4hb + o2 + nadph -> 34dhb + nadp  34dhb + o2 -> carccm  2hmuc -> zoe 2odhfac -> oadip succa + oadip -> succ + oadpcoa ooadpcoa + coa -> succoa + accoa carccm <-> gcarmclc  gcarmclc <-> zodhfac + co2 gallate + o2 -> zpy46dc 4c2hd <-> 4obtc dmpp + ipp -> gpp + ppi
3HBCDH PHBZMN PROTCC1 40XCTT 30XAPLC 30XAPL 30XAPL 30XADCT 3CXMUCC 4CBMCLC PROTCC2 CARHM2 DMRATT IPPDI GRATT CDPMDEK	Benzoate degradation via Hydroxylation Terpenoid backbone biosynthesis Terpenoid backbone biosynthesis Terpenoid backbone biosynthesis	dehydrogenase p-hydroxybenzoate 3- monoxygenase protocatechuate 34- dioxygenase 4-osalocrotonate lautomerase 3-osoadipate enol-lactonase 3-osoadipate CoA-transferase 3-osoadipate CoA-transferase 3-osoadipate CoA-transferase 3-carboxy-cis,cis-muconate cycloisomerase 4-carboxymuconolactone decarboxygenase protocatechuate 3,4- dioxygenase 5-carboxymethyl-2- hydroxymuconate somerase geranytranstransferase	11.1157 1.14132 1.13113 5.3.2. 3.1.1.24 2.8.3.6 2.3.1.1.6 5.5.1.2 4.1.1.44 1.13113 5.3.3.10 2.5.1.1 5.3.3.2 2.5.1.10 2.7.1.148	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_19920/KOX_20805  KOX_21740  KOX_2175/KOX_21760  KOX_02105/KOX_21760  KOX_02105/KOX_07320/KOX_20565/KOX_20900  KOX_21745  KOX_02105/KOX_07320/KOX_20565/KOX_20900  KOX_21745  KOX_10400  KOX_19615/KOX_19620  KOX_10400  KOX_12610  KOX_02365  KOX_12610  KOX_02300(pk)	4hb + o2 + nadph -> 34dhb + nadp 34dhb + o2 -> carccm 2hmuc -> zoe 2odhfac -> oadip succa + oadip -> succ + ooadpcoa ooadpcoa + coa -> succoa + accoa carccm <-> gcarmclc  gramplc <-> zodhfac + co2 gallate + o2 -> 2py46dc  4/2hbd <-> 4obbt dmp + ipp -> gpp + ppi ipp <-> dmpp gpp + ipp -> frdp + ppi cdpmde + atp -> 2pcdpmde + adp
SHBCDH PHBZMN PROTCC1 40XCTT SOXAPIC S	Benzoate degradation via Hydroxylation Terpenoid backbone biosynthesis Terpenoid backbone biosynthesis Terpenoid backbone biosynthesis	dehydrogenase p-hydroxybenzoate 3- monoxygenase protocatechute 34- dioxygenase 4-osalocrotonate tautomerase 3-osoadipate enol-lactonase 3-osoadipate enol-lactonase 3-osoadipate CoA-transferase 3-osoadipate CoA-transferase 3-carboxy-CaS, 6-muconate cycloisomerase 4-carboxymuconolactone decarboxylase protocatechuate 3,4- dioxygenase protocatechuate 3,4- dioxygenase geranytranstransferase geranytranstransferase geranytranstransferase 4-(cytidine 5'-diphoxpho')-2-C- methyl-D-eythriol kinase 1-hydroxy-2-methyl-2-(C)- butenyl 4-diphoxphate	11.1157 114132 113113 532- 31124 2836 23116 55.12 41.144 113113 53310 25111 5332 25110	KOX_10205  KOX_19615/KOX_19620  KOX_02690/KOX_19920/KOX_20805  KOX_2175/KOX_21760  KOX_02175/KOX_21760  KOX_02175/KOX_21760  KOX_02175/KOX_21760  KOX_17145  KOX_02105/KOX_07320/KOX_20565/KOX_20900  KOX_17175/KOX_24470  KOX_1040  KOX_1040  KOX_1040  KOX_10565  KOX_10565  KOX_02365	4hb + o2 + nadph -> 34dhb + nadp 34dhb + o2 -> carccm 2hmuc -> zoe 2odhfac -> oadip succa + oadip -> succ + ooadpcoa ooadpcoa + coa -> succoa + accoa carccm <> ycarmcle  gcarmcl <> 2odhfac + co2 gallate + o2 -> 2py46dc 4c2hd <> 4obt dmp + ipp -> gpp + ppi ipp <> bright >> frdp + ppi
3HBCDH PHBZMN PROTCC1 40XCTT 30XAPLC 30XAPL 30XAPL 30XADCT 3CXMUCC 4CBMCLC PROTCC2 CARHM2 DMRATT IPPDI GRATT CDPMDEK	Benzoate degradation via Hydroxylation Terpenoid backbone biosynthesis Terpenoid backbone biosynthesis Terpenoid backbone biosynthesis Terpenoid backbone biosynthesis	dehydrogenase p-hydroxybenzoate 3- monoxygenase protocatechute 34- dioxygenase 4-osalocrotonate tautomerase 3-osoadipate enol-lactonase 3-osoadipate CoA-transferase 3-osoadipyt-CoA thiolase 3-carboxy-ciscis-muconate cyclotisomerase 4-carboxymethy-2- hydroxymuconate isomerase geranytranstransferase peranytranstransferase 4-(cytidine 5'-diphosphot)-2-Crenthyl-D-eythrol kinase 1-hydroxy-2-methyl-2-(C)- butenyl 4-diphosphate reductase (dmpp) 1-deosy-D-sylulose	11.1157 1.14132 1.13113 5.3.2. 3.1.1.24 2.8.3.6 2.3.1.1.6 5.5.1.2 4.1.1.44 1.13113 5.3.3.10 2.5.1.1 5.3.3.2 2.5.1.10 2.7.1.148	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_19920/KOX_20805  KOX_21740  KOX_2175/KOX_21760  KOX_02105/KOX_21760  KOX_02105/KOX_07320/KOX_20565/KOX_20900  KOX_21745  KOX_02105/KOX_07320/KOX_20565/KOX_20900  KOX_21745  KOX_10400  KOX_19615/KOX_19620  KOX_10400  KOX_12610  KOX_02365  KOX_12610  KOX_02300(pk)	4hb + o2 + nadph -> 34dhb + nadp  34dhb + o2 -> carccm  2hmuc -> zoe 2odhfac -> oadip succa + cadip  -> succ + ooadpcoa ooadpcoa + coa -> succoa + accoa carcm <-> gcarmclc  gcarmclc <-> 2odhfac + co2  gallate + o2 -> 2py46dc  4c2hhd <-> 4obtc dmpp + ipp -> gpp + ppi ipp <-> dmpp gpp + ipp -> frdp + ppi cdpmde + atp -> 2pcdpmde + adp  hmb4pp + nadh -> dmpp + nad
SHBCDH PHBZMN PROTCCI 40XCTT 30XAPLC 30XAPL 30XAPCT 30XADCT 3CMUCC 4CBMCLC PROTCC2 CARHM2 DMRATT JPPDI GRATT LPPDI GRATT CDPMDEK HMBAPPR DOXRII	Benzoate degradation via Hydroxylation Terpenoid backbone biosynthesis	dehydrogenase p-hydromydenzoate 3- monooygenase protocatechuate 34- dioxygenase 4-osalocrotonate tautomerase 3-osoadipate coA-transferase 3-osoadipate CoA-transferase 3-osoadipate CoA-transferase 3-carboxy-cis, cis-muconate cycloisomerase 4-carboxymuconolactone decarboxylase protocatechuate 3,4- dioxygenase protocatechuate protocatec	111157 114132 113113 5.32- 31124 2.836 2.3116 5.512 4.1144 113113 5.3310 2.511 5.332 2.5110 2.71148 11712	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_19920/KOX_20805  KOX_2175/KOX_21760  KOX_02195/KOX_21760  KOX_07380/(tadA)/KOX_26660(fadl)  KOX_07380/(tadA)/KOX_26660(fadl)  KOX_21745  KOX_21745  KOX_02105/KOX_07320/KOX_20565/KOX_20900  KOX_21735/KOX_24470  KOX_19615/KOX_19620  KOX_1040  KOX_12610  KOX_02306  KOX_12610  KOX_03045/(tabA)  KOX_10545/(tabA)  KOX_11645	4hb + o2 + nadph -> 34dhb + nadp  34dhb + o2 -> carccm  2hmuc -> zoe 2odhfac -> oadip succa + cadip -> succ + ooadpcoa ooadpcoa + coa -> succoa + accoa carcm <-> gcarmclc  gcarmclc <-> 2odhfac + co2  gallate + o2 -> 2py46dc  4c2hd <-> 4obtc dmp + ipp -> gpp + ppi ipp <-> ompp gpp + ipp -> frdp + ppi cdpmde + atp -> 2pcdpmde + adp  hmb4pp + nadh -> dmpp + nad  dx5p + nadph -> mde4p + nadp
SHBCDH PHBZMN PROTCCI 40XCTT 30XAPLC 30XAPL 30XAPCT 30XADCT 3CMUCC 4CBMCLC PROTCC2 CARHM2 DMRAIT JPPDI GRATT CDPMDEK HM84PPR	Benzoate degradation via Hydroxylation Terpenoid backbone biosynthesis Terpenoid backbone biosynthesis Terpenoid backbone biosynthesis Terpenoid backbone biosynthesis	dehydrogenase p-hydroxybenzoate 3- moncoxygenase protocatechuate 3,4- dioxygenase protocatechuate 3,4- dioxygenase 4-oxalocrotonate tautomerase 3-oxoadipate CoA-transferase 3-oxoadipate CoA-transferase 3-oxoadipate CoA-tronsferase 3-oxoadipate CoA-tronsferase 3-oxoadipate CoA-tronsferase 3-oxoadipate CoA-tronsferase 4-carboxym-ciscis-muconate cycloisomerase 4-carboxymeuthy-2- hydroxym-connate isomerase peranyltranstransferase sopentenyl-diphosphate delta- isomerase 4-(cytidine S-diphospho)-2-C- methyl-D-erythritol kinase 1-hydroxy"-armyli-2-(E)- buttenyl 4-diphosphate reductase (dimp) 1-deoxy-D-xylulore reductase (dimp) 1-deoxy-D-xylulore reductase (dimp) 1-deoxy-D-xylulore reductise (mpp)	111157 114132 113113 5.32 311124 2.8.36 2.3.116 5.5.12 4.1.144 113113 5.3.310 2.5.11 5.3.32 2.5.110 2.7.1.148	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_19920/KOX_20805  KOX_2175/KOX_21760  KOX_02195/KOX_21760  KOX_07380/(tadA)/KOX_26660(fadl)  KOX_07380/(tadA)/KOX_26660(fadl)  KOX_21745  KOX_02105/KOX_07320/KOX_20565/KOX_20900  KOX_21735/KOX_24470  KOX_19615/KOX_19620  KOX_10640  KOX_12610  KOX_12610  KOX_123200(ipk)  KOX_10545(ispH)	4hb + o2 + nadph -> 34dhb + nadp  34dhb + o2 -> carccm  2hmuc -> zoe 2odhfac -> oadip succa + cadip  -> succ + ooadpcoa ooadpcoa + coa -> succoa + accoa carcm <-> gcarmclc  gcarmclc <-> 2odhfac + co2  gallate + o2 -> 2py46dc  4c2hhd <-> 4obtc dmpp + ipp -> gpp + ppi ipp <-> dmpp gpp + ipp -> frdp + ppi cdpmde + atp -> 2pcdpmde + adp  hmb4pp + nadh -> dmpp + nad
SHBCDH PHBZMN PROTCCI 40XCTT 30XAPLC 30XAPL 30XAPCT 30XADCT 3CMUCC 4CBMCLC PROTCC2 CARHM2 DMRATT JPPDI GRATT LPPDI GRATT CDPMDEK HMBAPPR DOXRII	Benzoate degradation via Hydroxylation Terpenoid backbone biosynthesis	dehydrogenase p-hydroxybenzoate 3-monoxygenase protocatechuste 34-dioxygenase 4-ovalocrotonate tautomerase 3-oxoadipate enol-lactonase 3-oxoadipate col-transferase 3-oxoadipate CoA+transferase 3-oxoadipate CoA+transferase 3-oxoadipate CoA+transferase 3-oxoadipate CoA+transferase 3-oxoadipate CoA+transferase 3-oxoadipate CoA+transferase protocatechuate 3,4-dioxygenase protocatechuate 3,4-dioxygenase 5-carboxymethyl-2-hydroxymuconate isomerase geranyitransfransferase sepentenyl-dioxybenate delta-isomerase geranyitransfransferase 4-(cytidine 5'-diphospho')-2-Crenthyl-0-epthyl-0-bydroxyl-2-methyl-2-(E)-butenyl-4-diphosphate reductase (dmpp) 1-deoxyl-0-xylulose reductoisomerase 1-deoxyl-0-xylulose 5-deoxyl-0-xylulose 5-de	111157 114132 113113 5.32- 31124 2.836 2.3116 5.512 4.1144 113113 5.3310 2.511 5.332 2.5110 2.71148 11712	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_19920/KOX_20805  KOX_2175/KOX_21760  KOX_02195/KOX_21760  KOX_07380/(tadA)/KOX_26660(fadl)  KOX_07380/(tadA)/KOX_26660(fadl)  KOX_21745  KOX_21745  KOX_02105/KOX_07320/KOX_20565/KOX_20900  KOX_21735/KOX_24470  KOX_19615/KOX_19620  KOX_1040  KOX_12610  KOX_02306  KOX_12610  KOX_03045/(tabA)  KOX_10545/(tabA)  KOX_11645	4hb + o2 + nadph -> 34dhb + nadp  34dhb + o2 -> carccm  2hmuc -> zoe 2odhfac -> oadip succa + cadip -> succ + ooadpcoa ooadpcoa + coa -> succoa + accoa carcm <-> gcarmclc  gcarmclc <-> 2odhfac + co2  gallate + o2 -> 2py46dc  4c2hd <-> 4obtc dmp + ipp -> gpp + ppi ipp <-> ompp gpp + ipp -> frdp + ppi cdpmde + atp -> 2pcdpmde + adp  hmb4pp + nadh -> dmpp + nad  dx5p + nadph -> mde4p + nadp
SHBCDH PHBZMN PROTCC1 40XCTT 30XAPLC 30XAPLC 30XAPLC 30XADCT 30XADCT 30XADCT 30XADCT 30XADCT 30XADCT 30XADCT 4CBMCLC PROTCC2 CARHM2 DMRATT 1PPDI GRATT CDPMDEK HMB4PPR DOXRTI DOXPS HMB4DPR	Benzoate degradation via Hydroxylation Terpenoid backbone biosynthesis	dehydrogenase p-hydroxybenzoate 3- monoxygenase protocatechute 3-4- dioxygenase 4-ovalocrotonate tautomerase 3-owadipate enol-lactonase 3-owadipate enol-lactonase 3-owadipate Antiolase 4-captony-captonase 4-captonase 4-c	11.1157 1.14132 1.13113 5.3.2. 3.11.24 2.8.36 2.3.116 5.5.12 4.1.144 1.131.13 5.3.3.10 2.5.1.1 5.3.3.2 2.5.1.10 2.7.1.148 1.17.1.2 1.11.267 2.2.1.7	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_19920/KOX_20805  KOX_2175/KOX_21760  KOX_2175/KOX_21760  KOX_02105/KOX_21760  KOX_21745  KOX_02105/KOX_07320/KOX_20565/KOX_20900  KOX_21735/KOX_24470  KOX_10615/KOX_19620  KOX_10640  KOX_10640  KOX_10640  KOX_10640  KOX_10640  KOX_12610  KOX_02365  KOX_12610  KOX_02365  KOX_11645  KOX_11645  KOX_11645  KOX_11645  KOX_116455  KOX_11645  KOX_11645  KOX_116455  KOX_11645	4hb + o2 + nadph -> 34dhb + nadp  34dhb + o2 -> carccm  2hmuc -> zoe 2odhfac -> oadip succa + oadip -> succ + ooadpcoa ooadpcoa + coa -> succoa + accoa carccm <-> gcarmclc  gcarmclc <-> zodhfac + co2 gallate + o2 -> 2py46dc  4c2hhd <-> 4obtc dmpp + ipp -> gpp + ppi ipp <-> dmpp gpp + ipp -> frdp + ppi cdpmde + atp -> Zpcdpmde + adp  hmb4pp + nadh -> dmpp + nad  dxSp + nadph -> mde4p + nadp g3p + pyr -> co2 + dxSp  hmb4pp + nadh -> ipp + nad
3HBCDH PHBZMN PROTCCI 40XCTT 30XAPLC 30XAPL 30XAPCT 3CMUCC 4CBMCLC PROTCC2 CARHM2 DMRATT IDPDI IDRATT CDPMDEK HMB4PPR DOXRTI DOXPS	Benzoate degradation via Hydroxylation Terpenoid backbone biosynthesis	dehydrogenase p-hydroxybenzoate 3- monoxygenase protocatechute 3-4- dioxygenase 4-ovalocrotonate tautomerase 3-owadipate enol-lactonase 3-owadipate CoA-transferase 4-caboymetonate cycloisomerase 4-caboymetonate 4-caboymetonate 5-carboxymetonate 5-carboxymetonate soperansfuransferase sepranyfranstransferase sepranyfranstransferase sepranyfranstransferase sepranyfranstransferase sepranyfranstransferase 1-hydroxy-2-methyl-2-(E)- butenyl-4-diphosphate reductase 1-hydroxy-2-methyl-2-(E)- butenyl-4-diphosphate reductase 1-hydroxy-2-methyl-2-(E)- butenyl-4-diphosphate reductase 2-methyl-0-eyrhyl-12-(E)- butenyl-4-diphosphate reductase 2-methyl-0-eyrhylriol 2-4 cyclodiphosphate	11.1157 11413.2 113113 5.3.2- 3.11.24 2.8.36 2.3.1.16 5.5.1.2 4.1.1.44 113.113 5.3.3.10 2.5.1.1 5.3.3.2 2.5.1.1 2.7.1.148 1.7.1.2 1.1.1.267 2.2.1.7	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_19920/KOX_20805  KOX_21740  KOX_21755/KOX_21760  KOX_21755/KOX_21760  KOX_21745  KOX_21745  KOX_21745  KOX_21745  KOX_121610  KOX_10040  KOX_12665  KOX_12610  KOX_12610  KOX_12610  KOX_12610  KOX_11645  KOX_11645  KOX_11645  KOX_11655	4hb + o2 + nadph -> 34dhb + nadp  34dhb + o2 -> carccm  2hmuc -> zoe 2odhfac -> oadip succa + oadip -> succ + ooadpcoa ooadpcoa + coa -> succoa + accoa carccm <> ycarnclc  gcarmclc <> 2odhfac + co2 gallate + o2 -> 2py46dc  4c2hhd <> 4obtc dmp+ ipp -> gpp + ppi ipp <> odhmpp gpp + ipp -> frdp + ppi cdpmde + atp -> 2pcdpmde + adp hmb4pp + nadh -> dmpp + nad  dxSp + nadph -> mde4p + nadp g3p + pyr -> co2 + dxSp
SHBCDH PHBZMN PROTCC1 40XCTT 30XAPLC 30XAPLC 30XAPLC 30XADCT 30XADCT 30XADCT 30XADCT 30XADCT 30XADCT 30XADCT 4CBMCLC PROTCC2 CARHM2 DMRATT 1PPDI GRATT CDPMDEK HMB4PPR DOXRTI DOXPS HMB4DPR	Benzoate degradation via Hydroxylation Terpenoid backbone biosynthesis	dehydrogenase p-hydroxybenzoate 3- monoxygenase protocatechuate 3,4- dioxygenase protocatechuate 3,4- dioxygenase 4-oxalocrotonate tautomerase 3-oxoadipate coA-transferase 3-oxoadipate CoA-transferase 3-oxaodipy-CoA thiolase 3-carboxy-cis,cis-mucornate cycloisomerase 4-carboxymuconolactone decarboxylase protocatechuate 3,4- dioxygenase protocatechuates 1- pydroxy-2- methyl-2-(E)- butenyl 4- diphosphate reductase 1- pydroxy-2- methyl-2-(E)- butenyl 4- diphosphate reductase 1- pydroxy-2- methyl-2-(E)- butenyl 4- diphosphate reductase 2- C-methyl-D-eythritol 2,4	11.1157 1.14132 1.13113 5.3.2. 3.11.24 2.8.36 2.3.116 5.5.12 4.1.144 1.131.13 5.3.3.10 2.5.1.1 5.3.3.2 2.5.1.10 2.7.1.148 1.17.1.2 1.11.267 2.2.1.7	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_19920/KOX_20805  KOX_2175/KOX_21760  KOX_2175/KOX_21760  KOX_02105/KOX_21760  KOX_21745  KOX_02105/KOX_07320/KOX_20565/KOX_20900  KOX_21735/KOX_24470  KOX_10615/KOX_19620  KOX_10640  KOX_10640  KOX_10640  KOX_10640  KOX_10640  KOX_12610  KOX_02365  KOX_12610  KOX_02365  KOX_11645  KOX_11645  KOX_11645  KOX_11645  KOX_116455  KOX_11645  KOX_11645  KOX_116455  KOX_11645	4hb + o2 + nadph -> 34dhb + nadp  34dhb + o2 -> carccm  2hmuc -> zoe 2odhfac -> oadip succa + oadip -> succ + ooadpcoa ooadpcoa + coa -> succoa + accoa carccm <-> gcarmclc  gcarmclc <-> zodhfac + co2 gallate + o2 -> 2py46dc  4c2hhd <-> 4obtc dmpp + ipp -> gpp + ppi ipp <-> dmpp gpp + ipp -> frdp + ppi cdpmde + atp -> Zpcdpmde + adp  hmb4pp + nadh -> dmpp + nad  dxSp + nadph -> mde4p + nadp g3p + pyr -> co2 + dxSp  hmb4pp + nadh -> ipp + nad
SHBCDH PHBZMN PROTCCI 40XCTT 30XAPLC 30XAPL 30XAPL 30XADCT 3CXMUCC 4CBMCLC PROTCC2 CARHM2 DMRATT IPPOI GRATT ICDPMDEK HMB4PPR DOXRTI DOXPS HMB4DPR MECDPDHT	Benzoate degradation via Hydroxylation Terpenoid backbone biosynthesis	dehydrogenase p-hydroxybenzoate 3- monoxygenase protocatechuate 3-t- dioxygenase 4-osalorotonate tautomerase 3-osoadipate coA-transferase 4-carboxymiconolactone decarboxylase protocatechuate 3-4- dioxygenase 5-carboxymethyl-2- hydroxymiconate isomerase geranyltranstransferase 4-(cytidine 5'-diphosphate delta- isomerase geranyltranstransferase 1-hydroxy-2-methyl-2-(E)- butenyl 4-diphosphate reductase (dmpp) 1-deoxy-D-xylulose reductase 1-hydroxy-2-methyl-2-(E)- butenyl 4-diphosphate reductase 1-hydroxy-2-methyl-2-(E)- butenyl 4-diphosphate reductase 1-hydroxy-2-methyl-2-(E)- butenyl 4-diphosphate reductase 1-hydroxy-2-methyl-2-(E)- butenyl 4-diphosphate reductase 1-hydroxy-2-methyl-1-e-(F)- butenyl 4-diphosphate reductase 1-hydroxy-2-methyl-1-e-(F)- butenyl 4-diphosphate reductase 1-hydroxy-2-methyl-1-e-(F)- butenyl 4-diphosphate reductase 1-pydroxy-2-methyl-1-e-(F)- butenyl 4-diphosphate 1-pydroxy-2-methyl-1-	11.1157 1.14132 1.13113 5.3.2. 3.11.24 2.8.36 2.3.1.16 5.5.12 4.1.144 1.13113 5.3.3.10 2.5.1.1 5.3.3.2 2.5.1.1 5.3.3.2 2.5.1.1 2.7.1.148 1.17.1.2 1.11.267 2.2.17 1.17.1.2	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_19920/KOX_20805  KOX_21740  KOX_21740  KOX_21746  KOX_21746  KOX_21746  KOX_21746  KOX_21746  KOX_21746  KOX_21746  KOX_21746  KOX_21746  KOX_2105/KOX_17320/KOX_20565/KOX_20900  KOX_21735/KOX_24470  KOX_10404  KOX_10404  KOX_10404  KOX_12610  KOX_02365  KOX_12610  KOX_02365  KOX_12610  KOX_032300(jpk)  KOX_10545(sph)  KOX_11665  KOX_11665  KOX_12605  KOX_12605	4hb + o2 + nadph -> 34dhb + nadp  34dhb + o2 -> carccm  2hmuc -> zoe 2odhfac -> oadip succa + oadip -> succ + ooadpcoa ooadpcoa + coa -> succoa + actoa carccm <-> gcarmclc  gcarmclc <-> zodhfac + co2 gallate + o2 -> 2py46dc  4c2hhd <-> 4obtc dmpp + ipp -> gpp + ppi ipp <-> dmpp gpp + ipp -> frdp + ppi cdpmde + atp -> 2pcdpmde + adp hmb4pp + nadh -> dmpp + nad dx5p + nadph -> mde4p + nadp g3p + pyr -> co2 + dx5p hmb4pp + nadh -> ipp + nad mdecpp -> hmb4pp
SHBCDH PHBZMN PROTCCI 40XCTT 30XAPLC 30XAPL 30XAPL 30XADCT 3CXMUCC 4CBMCLC PROTCC2 CARHM2 DMRATT IJPDI GRATT CDPMDEK HMB4PPR DOXRTI DOXPS HMB4DPR MECDPDHT MECDPS ME4PCT	Benzoate degradation via Hydroxylation Terpenoid backbone biosynthesis	dehydrogenase p-hydroxybenzoate 3- monoxygenase protocatechuate 3-t- dioxygenase 4-osalorotonate tautomerase 3-osoadipate coA-transferase 4-carboxymiconolactone decarboxylase 4-carboxymiconolactone decarboxylase protocatechuate 3-4- dioxygenase 5-carboxymethyl-2- hydroxymiconate isomerase geranyltranstransferase 4-(cytidine 5'-diphosphate delta- isomerase geranyltranstransferase 1-hydroxy-2-methyl-2-(E)- butenyl 4-diphosphate reductase (dmpp) 1-deoxy-D-xylulose reductoisomerase 1-hydroxy-2-methyl-2-(E)- butenyl 4-diphosphate reductase 2-methyl-D-eythritol 2,4 cyclodiphosphate deltydratase 2-c-methyl-D-eythritol 2,4 cyclodiphosphate synthase 2-c-methyl-D-eythritol 2,4 cyclodiphosphate synthase 2-c-methyl-D-eythritol 2,4 cyclodiphosphate gynthase 2-c-methyl-D-eythritol 2,4 cyclodiphosphate	11.1157 1.14132 1.13113 5.3.2. 3.11.24 2.8.36 2.3.116 5.5.12 4.1.144 1.13113 5.3.310 2.5.11 5.3.32 2.5.110 2.7.1.148 1.17.12 1.11.267 2.2.17 1.17.12 1.17.12 4.6.112 2.7.7.60	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_1920/KOX_20805  KOX_21740  KOX_21740  KOX_21740  KOX_21746  KOX_104040  KOX_10416  KOX_104040  KOX_12610  KOX_23200(jpk)  KOX_10545(sph)	4hb + o2 + nadph -> 34dhb + nadp  34dhb + o2 -> carccm  2hmuc -> zoe  2odhfac -> oadip  succa + oadip -> succ + ooadpcoa ooadpcoa + coa -> succoa + actoa carccm <-> gcarmclc  gcarmclc <-> zodhfac + co2  gallate + o2 -> 2py46dc  4c2hhd <-> 4obtc  dmpp + ipp -> gpp + ppi ipp <-> dmpp  gpp + ipp -> frdp + ppi cdpmde + atp -> 2pcdpmde + adp  hmb4pp + nadh -> dmpp + nad  dxSp + nadph -> mde4p + nadp  g3p + pyr -> co2 + dxSp  hmb4pp + nadh -> ipp + nad  mdecpp -> hmb4pp  2pcdpmde -> mdecpp + cmp  mde4p + ctp -> cdpmde + ppi
SHBCDH PHBZMN PROTCCI 40XCTT 30XAPLC 30XAPL 30XAPL 30XADCT 3CXMUCC 4CBMCLC PROTCC2 CARHM2 DMRATT IPPOI GRATT ICDPMDEK HMB4PPR DOXRTI DOXPS HMB4DPR MECDPDHT MECDPS ME4PCT OCTPPS	Benzoate degradation via Hydroxylation Terpenoid backbone biosynthesis	dehydrogenase p-hydroxybenzoate 3- monoxygenase protocatechuate 3-4- dioxygenase 4-ovalocrotonate tautomerase 3-owadipate end-lactonase 3-owadipate CoA-transferase 4-corbonymaconolactone decatboxylase protocatechuate 3-4- droxymaconolactone decatboxylase protocatechuate 3-4- droxymaconolactone geranyfiranstransferase geranyfiranstransferase 4-(cytidine 5-diphosphate delta- isomerase geranyfiranstransferase 4-(cytidine 5-diphosphate)-2-C- methyl-D-erythritol kinase 1-hydroxy2-methyl-2-(E)- butenyl 4-diphosphate reductase 1-hydroxy2-methyl-2-(E)- butenyl 4-diphosphate reductase 2-C-methyl-D-erythritol 2-4 cyclodiphosphate synthase 1-hydroxy2-methyl-2-(E)- butenyl 4-diphosphate 2-C-methyl-D-erythritol 2-4 cyclodiphosphate synthase 2-C-methyl-D-erythritol 4- phosphate cytidylyttransferase C-taprenyl pyrophosphate synthase	11.1157 1.14132 1.13113 5.3.2. 3.11.24 2.8.36 2.3.116 5.5.12 4.1.144 1.13113 5.3.310 2.5.11 5.3.32 2.5.110 2.7.1148 1.17.12 1.11267 2.2.17 1.17.12 1.17.12 4.6.112 2.7.7.60 2.5.190	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_19920/KOX_20805  KOX_21740  KOX_21740  KOX_2175/KOX_21760  KOX_2175/KOX_21760  KOX_21745  KOX_02105/KOX_07320/KOX_20565/KOX_20900  KOX_21735/KOX_24470  KOX_1040  KOX_1040  KOX_105405/KOX_19620  KOX_105405/KOX_19620  KOX_105405  KOX_105405  KOX_105405  KOX_105405  KOX_10545(spH)	4hb + o2 + nadph -> 34dhb + nadp  34dhb + o2 -> carccm  2hmuc -> coe 2odhfac -> cadip  succa + coal -> succa + coadpcoa coadpcoa + coa -> succoa + actoa carccm <-> gcarmclc  gcarmclc <-> codhfac + co2  gallate + o2 -> 2py46dc  4c2hhd <-> 4obtc  dmpp + ipp -> fdpp + ppi ipp <-> dmpp  gpp + ipp -> fdpp + ppi cdpmde + atp -> 2pcdpmde + adp  hmb4pp + nadh -> dmpp + nad  dxSp + nadph -> mde4p + nadp  g3p + pyr -> co2 + dxSp  hmb4pp + nadh -> ipp + nad  mdecpp -> hmb4pp  2pcdpmde -> mdecpp + cmp  mde4p + ctp -> cdpmde + ppi  fdp + 5 ipp -> opp + 5 ppi
SHBCDH PHBZMN PROTCCI 40XCTT 30XAPLC 30XAPL 30XAPL 30XADCT 3CXMUCC 4CBMCLC PROTCC2 CARHM2 DMRATT IJPDI GRATT CDPMDEK HMB4PPR DOXRTI DOXPS HMB4DPR MECDPDHT MECDPS ME4PCT	Benzoate degradation via Hydroxylation Terpenoid backbone biosynthesis	dehydrogenase p-hydroxybenzoate 3- monoxygenase protocatechuse 3-4- dioxygenase 4-ovalocrotonate tautomerase 3-owadipate end-lactonase 3-owadipate CoA-transferase 4-corboxymuconolactone protocatechuate 3,4- dioxygenase 4-carboxymuconolactone protocatechuate 3,4- dioxygenase 4-coytimensterasferase peranytranstransferase querytranstransferase 4-(cytidine 5'-diphospho)-2-c- methyl-D-erythriol binase 1-hydroxy-2-methyl-2-(E)- butenyl 4-diphosphate reductase 1-hydroxy-2-methyl-2-(E)- butenyl 4-diphosphate reductase 2-c-methyl-D-erythriol 2,4- cyclodiphosphate synthase 1-hydroxy-2-methyl-2-cyclodiphosphate 2-c-methyl-D-erythriol 2,4- cyclodiphosphate synthase 2-c-methyl-D-erythriol 4- phosphate cytidylytransferase Ctaprenyl prophosphate synthase undecaprenyl diphosphate synthase undecaprenyl diphosphate synthase	11.1157 1.14132 1.13113 5.3.2. 3.11.24 2.8.36 2.3.116 5.5.12 4.1.144 1.13113 5.3.310 2.5.11 5.3.32 2.5.110 2.7.1.148 1.17.12 1.11.267 2.2.17 1.17.12 1.17.12 4.6.112 2.7.7.60	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_1920/KOX_20805  KOX_21740  KOX_21740  KOX_21740  KOX_21746  KOX_104040  KOX_10416  KOX_104040  KOX_12610  KOX_23200(jpk)  KOX_10545(sph)	4hb + o2 + nadph -> 34dhb + nadp  34dhb + o2 -> carccm  2hmuc -> zoe  2odhfac -> oadip  succa + oadip -> succ + ooadpcoa ooadpcoa + coa -> succoa + actoa carccm <-> gcarmclc  gcarmclc <-> zodhfac + co2  gallate + o2 -> 2py46dc  4c2hhd <-> 4obtc  dmpp + ipp -> gpp + ppi ipp <-> dmpp  gpp + ipp -> frdp + ppi cdpmde + atp -> 2pcdpmde + adp  hmb4pp + nadh -> dmpp + nad  dxSp + nadph -> mde4p + nadp  g3p + pyr -> co2 + dxSp  hmb4pp + nadh -> ipp + nad  mdecpp -> hmb4pp  2pcdpmde -> mdecpp + cmp  mde4p + ctp -> cdpmde + ppi
SHBCDH PHBZMN PROTCCI 40XCTT 30XAPLC 30XAPL 30XAPL 30XADCT 3CXMUCC 4CBMCLC PROTCC2 CARHM2 DMRATT IPPOI GRATT ICDPMDEK HMB4PPR DOXRTI DOXPS HMB4DPR MECDPDHT MECDPS ME4PCT OCTPPS	Benzoate degradation via Hydroxylation Terpenoid backbone biosynthesis	dehydrogenase p-hydroxybenzoate 3- monoxygenase protocatechute 3-4- dioxygenase 4-ovalocrotonate tautomerase 3-owadipate enol-lactonase 3-owadipate CoA+ transferase 2-carboxymethy-2- hydroxymuconate isomerase peranytranstransferase isopentenyl-diphosphate deltaisomerase geranytranstransferase isopentenyl-diphosphate deltaisomerase geranytranstransferase isopentenyl-diphosphate deltaisomerase 1-hydroxy2-methyl-2-(E)- buttenyl 4-diphosphate reductase 1-hydroxy2-methyl-2-(E)- buttenyl 4-diphosphate reductase 2-C-methyl-D-eythritol 2-A cyclodiphosphate synthase 1-hydroxy2-methyl-2-(E)- buttenyl 4-diphosphate ceductase 2-C-methyl-D-eythritol 2-A cyclodiphosphate synthase 2-C-methyl-D-eythritol 4- phosphate cytchyltransferase Ctaprenyl pryophosphate synthase undecaprenyl diphosphate synthase undecaprenyl diphosphate synthase undecaprenyl diphosphate synthase undecaprenyl diphosphate synthase	11.1157 1.14132 1.13113 5.3.2. 3.11.24 2.8.36 2.3.116 5.5.12 4.1.144 1.13113 5.3.310 2.5.11 5.3.32 2.5.110 2.7.1148 1.17.12 1.11267 2.2.17 1.17.12 1.17.12 4.6.112 2.7.7.60 2.5.190	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_19920/KOX_20805  KOX_21740  KOX_21740  KOX_2175/KOX_21760  KOX_2175/KOX_21760  KOX_21745  KOX_02105/KOX_07320/KOX_20565/KOX_20900  KOX_21735/KOX_24470  KOX_1040  KOX_1040  KOX_105405/KOX_19620  KOX_105405/KOX_19620  KOX_105405  KOX_105405  KOX_105405  KOX_105405  KOX_10545(spH)	4hb + o2 + nadph -> 34dhb + nadp  34dhb + o2 -> carccm  2hmuc -> coe 2odhfac -> cadip  succa + coal -> succa + coadpcoa coadpcoa + coa -> succoa + actoa carccm <-> gcarmclc  gcarmclc <-> codhfac + co2  gallate + o2 -> 2py46dc  4c2hhd <-> 4obtc  dmpp + ipp -> fdpp + ppi ipp <-> dmpp  gpp + ipp -> fdpp + ppi cdpmde + atp -> 2pcdpmde + adp  hmb4pp + nadh -> dmpp + nad  dxSp + nadph -> mde4p + nadp  g3p + pyr -> co2 + dxSp  hmb4pp + nadh -> ipp + nad  mdecpp -> hmb4pp  2pcdpmde -> mdecpp + cmp  mde4p + ctp -> cdpmde + ppi  fdp + 5 ipp -> opp + 5 ppi
SHBCDH PHBZMN PROTCCI 40XCIT 30XAPIC 30XAPIC 30XAPIC 30XADCT 30XADCT 30XADCT 3CMUCC 4CBMCLC PROTCC2 CARHM2 DMRATT IPPOI GRATT ICDPMDEK HMB4PPR DOXRII DOXPS HMB4DPR MECDPDHT MECDPS ME4PCT OCTPPS ALHD18	Benzoate degradation via Hydroxylation Terpenoid backbone biosynthesis	dehydrogenase p-hydroxybenzoate 3- monooxygenase protocatechuste 3-4- dioxygenase 4-ovalocrotonate tautomerase 3-owadipate coh-transferase 0-workpate 1-carboxylase protocatechuate 3-4- dioxygenase 5-carboxymuconalactone decarboxylase protocatechuate 3-4- dioxygenase 5-carboxymuconate isomerase geranyltranstransferase isopenateryl-diphosphate delta- isomerase geranyltranstransferase geranyltranstransferase geranyltranstransferase geranyltranstransferase peranyltranstransferase 1-hydroxy-2-methyl-2-(C)- butenyl 4-diphosphate reductase 1-hydroxy-2-methyl-2-(C)- butenyl 4-diphosphate reductase 2-c-methyl-0-erythritol 2-4 cyclodiphosphate dehydrospate reductase 2-c-methyl-0-erythritol 2-4 cyclodiphosphate synthase 1-hydroxy-2-methyl-1-0-prythritol 2-4 cyclodiphosphate synthase 1-hydroxy-2-methyl-1-0-prythritol 2-4 cyclodiphosphate synthase 1-hydroxy-2-methyl-1-0-prythritol 2-4 cyclodiphosphate synthase 1-hydroxy-2-methyl-1-0-prythritol 2-4 cyclodiphosphate synthase 1-hydroxy-2-methyl-1-prythritol 2-4 cyclodiphosphate synthase 1-hydroxy-2-prythritol 2-4 cyclodiphosphate synthase 1-bydroxy-2-prythritol 2-4 cyclodiphosphate synthase	11.1157 1.14132 1.13113 5.3.2. 3.11.24 2.8.36 2.3.1.16 5.5.12 4.1.144 1.13113 5.3.310 2.5.1.1 5.3.3.2 2.5.1.10 2.7.1.148 1.17.1.2 1.11.267 2.2.17 1.17.12 1.17.12 1.17.12 1.17.12 1.17.12 2.7.7.60 2.5.1.90 2.5.1.10	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_19920/KOX_20805  KOX_21740  KOX_21740  KOX_21740  KOX_21746  KOX_21745  KOX_21746  KOX_21745  KOX_21746  KOX_21746  KOX_1040  KOX_10545(sph)  KOX_10545(sph)  KOX_10545(sph)  KOX_10545(sph)  KOX_10545(sph)  KOX_10545(sph)  KOX_27275(spG)  KOX_01055(sph)	4hb + o2 + nadph -> 34dhb + nadp  34dhb + o2 -> carccm  2hmuc -> zoe 2odhfac -> oadip succa + oadip -> succ + ooadpcoa ooadpcoa + coa -> succoa + actoa carccm <-> gcarmclc  gcarmclc <-> zodhfac + co2 gallate + o2 -> 2py46dc  4c2hhd <-> 4obtc dmpp + ipp -> gpp + ppi ipp <-> dmpp gpp + ipp -> frdp + ppi cdpmde + atp -> 2pcdpmde + adp hmb4pp + nadh -> dmpp + nad dxSp + nadph -> mde4p + nadp g3p + pyr -> co2 + dxSp hmb4pp + nadh -> ipp + nad mdecpp -> hmb4pp 2pcdpmde -> mdecpp + cmp mde4p - ctp -> cdpmde + ppi frdp + 5 ipp -> opp + 5 ppi frdp + 8 ipp -> udcpdp + 8 ppi perflald + nad <-> perfl + nadh
SHBCDH PHBZMN PROTCCI 40XCTT 30XAPL 30XAPL 30XAPC 30XAPC 30XAPC 4GBMCLC PROTCC2 CARHM2 DMRATT IPPOI GRATT IPPOI GRATT IPPOI GRATT DOXPS HMB4PPR MECDPOHT MECDPS ME4PCT OCTPPS UDCPDPS ALHD18 CZMIPCH	Benzoate degradation via Hydroxylation Terpenoid backbone biosynthesis	dehydrogenase p-hydroxybenzoate 3- monoxygenase protocatechute 3-4- dioxygenase 4-osalocrotonate tautomerase 3-osoadipate enol-lactonase 3-osoadipate CoA-transferase 3-osoadipate CoA-transferase 3-osoadipate CoA-transferase 3-osoadipate CoA-transferase 3-osoadipate CoA-transferase 3-carboxy-cis,cis-mucornate cycloisomerase 4-carboxymeuty-2- hydroxymuconate isomerase geranyltranstransferase 5-carboxymethyl-2- hydroxymuconate isomerase geranyltranstransferase 4-(cytidine 5'-diphospho)-2-C- methyl-D-eythritol kinase 1-hydroxy-2-methyl-2-(E)- butenyl 4-diphosphate reductase 1-hydroxy-2-methyl-2-(C)- butenyl 4-diphosphate reductase 1-hydroxy-2-methyl-2-(C)- butenyl 4-diphosphate reductase 2-methyl-D-eythritol 2-d cyclodiphosphate synthase 1-hydroxy-2-methyl-2-(C)- butenyl 4-diphosphate reductase 2-methyl-D-eythritol 2-d cyclodiphosphate synthase 2-methyl-D-eythritol 2-d cyclodiphosphate synthase 2-methyl-D-eythritol 2-d cyclodiphosphate synthase 2-methyl-D-eythritol 2-d cyclodiphosphate synthase 3-c-methyl-D-eythritol 3-d cyclodiphosphate synthase 3-c-methyl-D-eythritol 3-d cyclodiphosphate synthase 3-c-methyl-D-eythritol 3-d cyclod	11.1157 114132 113113 5.32. 31.124 2.8.36 2.3.116 5.5.12 4.1.144 1.13113 5.3.310 2.5.11 5.3.32 2.5.1.10 2.7.1.148 1.17.12 1.17.12 1.17.12 1.17.71 4.6.112 2.7.760 2.5.190 2.5.131 1.2.13 4.2.117	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_19920/KOX_20805  KOX_21740  KOX_21740  KOX_21740  KOX_21746  KOX_02136/KOX_21660  KOX_102105/KOX_07320/KOX_20565/KOX_20900  KOX_21735/KOX_24470  KOX_1040  KOX_1040  KOX_1610  KOX_02365  KOX_12610  KOX_02365  KOX_12610  KOX_12650  KOX_12660  KOX_12660  KOX_10545(spH)  KOX_11465  KOX_10545(spH)  KOX_10545(spH)  KOX_10545(spH)  KOX_010545(spH)  KOX_010545(spH)  KOX_11470  KOX_017835(daB)/KOX_19445/KOX_26655(fad/)/  KOX_017835(daB)/KOX_19445/KOX_26655(fad/)/	4hb + o2 + nadph -> 34dhb + nadp  34dhb + o2 -> carccm  2hmuc -> zoe 2odhfac -> cadip succa + cadip -> succ + ooadpcoa ooadpcoa + coa -> succoa + accoa carcm <-> gcarmclc  gamlac + o2 -> 2py46dc  4c2hbd <-> 4obtc dmp + ipp -> gpp + ppi ipp <-> dmpp gpp + ipp -> frdp + ppi cdpmde + atp -> 2pcdpmde + adp hmb4pp + nadh -> dmpp + nad dx5p + nadph -> mde4p + nadp g3p + pyr -> co2 + dx5p hmb4pp + nadh -> ipp + nad mdecpp -> hmb4pp  2pcdpmde -> mdecpp + cmp mde4p + ctp -> cdpmde + ppi frdp + 5ipp -> opp + 5ppi frdp + 5ipp -> opp + 5ppi frdp + 5ipp -> opp + 5ppi frdp + 8 ipp -> udcpdp + 8 ppi perllald + nad <-> perll + nadh c2migdcoa -> 3hdmmhcoa
SHBCDH PHBZMN PROTCCI 40XCIT 30XAPIC 30XAPIC 30XAPIC 30XADCT 30XADCT 30XADCT 3CMUCC 4CBMCLC PROTCC2 CARHM2 DMRATT IPPOI GRATT ICDPMDEK HMB4PPR DOXRII DOXPS HMB4DPR MECDPDHT MECDPS ME4PCT OCTPPS ALHD18	Benzoate degradation via Hydroxylation Terpenoid backbone biosynthesis	dehydrogenase p-hydroxybenzoate 3- monoxygenase protocatechuate 3-4- dioxygenase 4-ovalocrotonate tautomerase 3-owadipate enol-lactonase 3-owadipate CoA-transferase protocatechuate 3-4- dioxygenase 5-carboxymuconolactone decarboxylase protocatechuate 3-4- dioxygenase 5-carboxymuconate isomerase geranyfitanstransferase geranyfitanstransferase geranyfitanstransferase decarboxylase peranyfitanstransferase decarboxylase peranyfitanstransferase 1-hydroxy-2-methyl-2-(E)- butenyl 4-diphosphate reductase (dmpp) 1-deoxy-D-xylulose phosphate synthase 1-hydroxy-2-methyl-2-(E)- butenyl 4-diphosphate reductase 2-C-methyl-D-erythriol 2-A cyclodiphosphate synthase 2-C-methyl-D-erythriol 4- phosphate cylidyltransferase Cxtprenyl pryophosphate synthase undecaprenyl diphosphate synthase undecaprenyl diphospha	11.1157 114132 113113 5.32. 31.124 2.8.36 2.3.116 5.5.12 4.1.144 1.13113 5.3.310 2.5.11 5.3.32 2.5.1.10 2.7.1.148 1.17.12 1.17.12 1.17.12 1.17.71 4.6.112 2.7.760 2.5.190 2.5.131 1.2.13 4.2.117	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_19920/KOX_20805  KOX_21740  KOX_21740  KOX_21740  KOX_21746  KOX_21745  KOX_21746  KOX_21745  KOX_21746  KOX_21746  KOX_1040  KOX_10545(sph)  KOX_10545(sph)  KOX_10545(sph)  KOX_10545(sph)  KOX_10545(sph)  KOX_10545(sph)  KOX_27275(spG)  KOX_01055(sph)	4hb + o2 + nadph -> 34dhb + nadp  34dhb + o2 -> carccm  2hmuc -> zoe 2odhfac -> cadip succa + cadip -> succ + ooadpcoa ooadpcoa + coa -> succoa + accoa carcm <-> gcarmclc  gamlac + o2 -> 2py46dc  4c2hbd <-> 4obtc dmp + ipp -> gpp + ppi ipp <-> dmpp gpp + ipp -> frdp + ppi cdpmde + atp -> 2pcdpmde + adp hmb4pp + nadh -> dmpp + nad dx5p + nadph -> mde4p + nadp g3p + pyr -> co2 + dx5p hmb4pp + nadh -> ipp + nad mdecpp -> hmb4pp  2pcdpmde -> mdecpp + cmp mde4p + ctp -> cdpmde + ppi frdp + 5ipp -> opp + 5ppi frdp + 5ipp -> opp + 5ppi frdp + 5ipp -> opp + 5ppi frdp + 8 ipp -> udcpdp + 8 ppi perllald + nad <-> perll + nadh c2migdcoa -> 3hdmmhcoa
SHBCDH PHBZMN PROTCCI 40XCTT 30XAPL 30XAPL 30XAPC 30XAPC 30XAPC 4GBMCLC PROTCC2 CARHM2 DMRATT IPPOI GRATT IPPOI GRATT IPPOI GRATT DOXPS HMB4PPR MECDPOHT MECDPS ME4PCT OCTPPS UDCPDPS ALHD18 CZMIPCH	Benzoate degradation via Hydroxylation Terpenoid backbone biosynthesis	dehydrogenase p-hydroxybenzoate 3- monoxygenase protocatechuate 3-4- dioxygenase 4-ovalocrotonate tautomerase 3-owadipate enol-lactonase 3-owadipate enol-lactonase 3-owadipate CoA+ transferase 3-owadipate CoA+ transferase 3-owadipate A-carboxy-tiscis-muconate cycloisomerase 4-carboxymetonate cycloisomerase 4-carboxymetonate 4-carboxymetonate 4-carboxymetonate 5-carboxymethy-2- hydroxymuconate isomerase geranyitranstransferase 4-(cytidine 5'-diphosphate delta- isomerase geranyitranstransferase 1-hydroxy-2-methyl-2-(E)- butenyl 4-diphosphate reductase (dmpp) 1-deoxy-D-xylutose reductoisomerase 1-hydroxy-2-methyl-2-(E)- butenyl 4-diphosphate reductase 2-c-methyl-D-erythritol 2,4 cyclodiphosphate synthase 1-hydroxy-2-methyl-2-(E)- butenyl 4-diphosphate reductase 2-c-methyl-D-erythritol 2,4 cyclodiphosphate synthase 2-c-methyl-D-erythritol 2,4 cyclodiphosphate synthase 2-c-methyl-D-erythritol 4- phosphate cytidyltransferase Ctaprenyl gyrophosphate synthase undecaprenyl diphosphate synthase aldehyde dehydrogenase (NAD-1) cis-2-Methyl-5-isopropylhexa-2,5-dienoyl-CoA hydro-lyase	11.1157 114132 113113 5.32. 31.124 2.8.36 2.3.116 5.5.12 4.1.144 1.13113 5.3.310 2.5.11 5.3.32 2.5.1.10 2.7.1.148 1.17.12 1.17.12 1.17.12 1.17.71 4.6.112 2.7.760 2.5.190 2.5.131 1.2.13 4.2.117	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_19920/KOX_20805  KOX_21740  KOX_21740  KOX_21740  KOX_21746  KOX_02136/KOX_21660  KOX_102105/KOX_07320/KOX_20565/KOX_20900  KOX_21735/KOX_24470  KOX_1040  KOX_1040  KOX_1610  KOX_02365  KOX_12610  KOX_02365  KOX_12610  KOX_12650  KOX_12660  KOX_12660  KOX_10545(spH)  KOX_11465  KOX_10545(spH)  KOX_10545(spH)  KOX_10545(spH)  KOX_010545(spH)  KOX_010545(spH)  KOX_11470  KOX_017835(daB)/KOX_19445/KOX_26655(fad/)/  KOX_017835(daB)/KOX_19445/KOX_26655(fad/)/	4hb + o2 + nadph -> 34dhb + nadp  34dhb + o2 -> carccm  2hmuc -> zoe 2odhfac -> cadip succa + cadip -> succ + ooadpcoa ooadpcoa + coa -> succoa + accoa carcm <-> gcarmclc  gamlac + o2 -> 2py46dc  4c2hbd <-> 4obtc dmp + ipp -> gpp + ppi ipp <-> dmpp gpp + ipp -> frdp + ppi cdpmde + atp -> 2pcdpmde + adp hmb4pp + nadh -> dmpp + nad dx5p + nadph -> mde4p + nadp g3p + pyr -> co2 + dx5p hmb4pp + nadh -> ipp + nad mdecpp -> hmb4pp  2pcdpmde -> mdecpp + cmp mde4p + ctp -> cdpmde + ppi frdp + 5ipp -> opp + 5ppi frdp + 5ipp -> opp + 5ppi frdp + 5ipp -> opp + 5ppi frdp + 8 ipp -> udcpdp + 8 ppi perllald + nad <-> perll + nadh c2migdcoa -> 3hdmmhcoa
SHBCDH PHBZMN PROTCCI 40XCTT 30XAPI 30XAPI 30XAPC 4GBMCLC PROTCC2 CARHM2 DMRATT IPPOI COPMDEK HMBAPPR DOXRTI DOXPS HMBADPR MECDPDHT MECDPS MEAPCT OCTPPS UDCPDPS ALHD18 CZMIPCH TZMIPCH ISOCHORPL	Benzoate degradation via Hydroxylation Terpenoid backbone biosynthesis	dehydrogenase p-hydroxybenzoate 3- monooxygenase protocatechuste 3-4- dioxygenase 4-ovalocrotonate tautomerase 3-owadipate coh-transferase 0-working coh-transferase 0-working coh-transferase 0-working coh-transferase 0-working coh-transferase 0-working coh-transferase 1-depth 2-depth-transferase 1-depth-transferase 1-depth-trans	111157 114132 113113 532- 31124 2836 23116 5512 41144 113113 53310 2511 5332 25116 25110 271148 11712 111267 2217 11712 11771 46112 27760 25190 25131 1213 42117 42117	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_19920/KOX_20805  KOX_2175/KOX_21760  KOX_02090/KOX_19920/KOX_20805  KOX_21740  KOX_175/KOX_21760  KOX_175/KOX_21760  KOX_175/KOX_21760  KOX_1040  KOX_1175/KOX_19620  KOX_10640  KOX_10640  KOX_10640  KOX_10640  KOX_10645  KOX_10645  KOX_11645  KOX_11465  KOX_11465  KOX_11665  KOX_11545(spH)  KOX_01055(ispH)  KOX_01055(ispH)  KOX_01055(ispH)  KOX_01055(ispH)  KOX_01055(ispH)  KOX_11470  KOX_00375  KOX_07835(fadB)/KOX_19445/KOX_26655(fadl)/  KOX_07835(fadB)/KOX_19445/KOX_26655(fadl)/  KOX_07835(fadB)/KOX_19445/KOX_26655(fadl)/  KOX_07835(fadB)/KOX_19445/KOX_26655(fadl)/  KOX_07835(fadB)/KOX_19445/KOX_26655(fadl)/  KOX_016850/KOX_20605	4hb + o2 + nadph -> 34dhb + nadp  34dhb + o2 -> carccm  2hmuc -> zoe 2odhfac -> oadip succa + oadip -> succ + ooadpcoa ooadpcoa + coa -> succoa + accoa carcm <>> gcarmclc  gramclc <>> 2odhfac + co2 gallate + o2 -> 2py46dc  4c2hbd <-> 4debtc dmp + ipp -> dpp + ppi ipp +> ipp -> frdp + ppi cdpmde + atp -> 2pcdpmde + adp hmb4pp + nadh -> dmpp + nad  dxSp + nadph -> mde4p + nadp g3p + pyr -> co2 + dxSp hmb4pp + nadh -> ipp + nad mdecpp -> hmb4pp 2pcdpmde -> mdecpp + cmp mde4p + ctp -> cdpmde + ppi frdp + 5 ipp -> opp + 5 ppi frdp + 5 ipp -> udcpdp + 8 ppi perflald + nadh c2mipdcoa -> 3hdmmhcoa  t2mipdcoa -> 3hdmmhcoa isochor -> salcyl + pyr
SHBCDH PHBZMN PROTCCI 40XCTT 30XAPI 30XAPI 30XAPI 30XADCT 3CMUCC 4GBMCLC PROTCC2 CARHM2 DMRATT IPPDI GRATT CDPMDEK HMBAPPR DOXRTI DOXPS HMBADPR MECDPDHT MECDPS ME4PCT OCTPPS UDCPDPS ALHD18 CZMIPCH TZMIPCH	Benzoate degradation via Hydroxylation Terpenoid backbone biosynthesis	dehydrogenase p-hydroxybenzoate 3- monooxygenase protocatechuste 3-4- dioxygenase 4-ovalocrotonate tautomerase 3-owadipate coh-transferase protocatechuate 3-4- dioxygenase 5-carboxymuconale isomerase geranytranstransferase isopenateryl-diphosphate delta- isomerase geranytranstransferase geranytranstransferase geranytranstransferase geranytranstransferase geranytranstransferase 1-hydroxy-2-methyl-2-(Co- huthyl-D-eythritol kinase 1-hydroxy-2-methyl-2-(Ci- butenyl 4-diphosphate reductase 1-hydroxy-2-methyl-2-(Ci- butenyl 4-diphosphate reductase 1-hydroxy-2-methyl-2-(Ci- butenyl 4-diphosphate reductase 1-hydroxy-2-methyl-2-(Ci- butenyl 4-diphosphate reductase 1-hydroxy-2-methyl-1-eythritol 2-4 cyclodiphosphate synthase 1-hydroxy-2-methyl-1-eythritol 2-methyl-1-epythritol 2-methyl-1-epythritol 2-methyl-1-epythritol 3-c-methyl-1-eythritol 3	111157 114132 113113 532- 31124 2836 23116 55512 41144 113113 53310 2511 5332 25110 271148 11712 111267 2217 11712 11771 46112 27760 25190 25131 1213 42117	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_19920/KOX_20805  KOX_21740  KOX_21740  KOX_21740  KOX_21746  KOX_21745  KOX_21745  KOX_21745  KOX_21745  KOX_21745  KOX_21746  KOX_1040  KOX_21745  KOX_1040  KOX_10456  KOX_10465  KOX_11465  KOX_11465  KOX_11465  KOX_11465  KOX_10545(spH)  KOX_27275(spG)  KOX_01055(spF)  KOX_01060(spD)  KOX_03740  KOX_107335(fadB)/KOX_19445/KOX_26655(fadJ)/  KOX_07835(fadB)/KOX_19445/KOX_26655(fadJ)/  KOX_07835(fadB)/KOX_19445/KOX_26655(fadJ)/  KOX_07835(fadB)/KOX_19445/KOX_26655(fadJ)/  KOX_07835(fadB)/KOX_19445/KOX_26655(fadJ)/  KOX_07835(fadB)/KOX_19445/KOX_26655(fadJ)/  KOX_07835(fadB)/KOX_19445/KOX_26655(fadJ)/	4hb + o2 + nadph -> 34dhb + nadp  34dhb + o2 -> carccm  2hmuc -> zoe 2odhfac -> cadip succa + cadip -> succ + coadpeoa ooadpoa + coa -> succoa + accoa carcm <-> pcarmclc  gramclc <-> 2odhfac + co2 gallate + o2 -> 2py46dc  4c2hhd <-> 4obtc dmp + ipp -> gpp + ppi ipp <-> ypp + ipp -> frdp + ppi cdpmde + atp -> 2pcdpmde + adp hmb4pp + nadh -> dmpp + nad  dxSp + nadph -> mde4p + nadp g3p + pyr >> co2 + dxSp hmb4pp + nadh -> ipp + nad  mdecpp -> hmb4pp 2pcdpmde -> mdecpp + cmp mde4p + ctp -> cdpmde + ppi frdp + 5 ipp -> opp + 5 ppi frdp + 8 ipp -> udcpdp + 8 ppi perflald + nad <-> perfl + nadh c2mipdcoa -> 3hdmmhcoa
SHBCDH PHBZMN PROTCCI 40XCTT 30XAPI 30XAPI 30XAPC 4GBMCLC PROTCC2 CARHM2 DMRATT IPPOI COPMDEK HMBAPPR DOXRTI DOXPS HMBADPR MECDPDHT MECDPS MEAPCT OCTPPS UDCPDPS ALHD18 CZMIPCH TZMIPCH ISOCHORPL	Benzoate degradation via Hydroxylation Terpenoid backbone biosynthesis	dehydrogenase p-hydroxybenzoate 3- monoxygenase protocatechuate 3-4- dioxygenase 4-ovalocrotonate tautomerase 3-owadipate GoA-transferase 4-carboxymuconate decarboxylase protocatechuate 3,4- dioxygenase 5-carboxymethyl-2- hydroxymuconate isomerase geranyfiranstransferase 4-(cytidine 5-diphospho)-2-c- methyl-0-gridine 5-diphosphopate gridine 5-diphos	111157 114132 113113 532- 31124 2836 23116 5512 41144 113113 53310 2511 5332 25116 25110 271148 11712 111267 2217 11712 11771 46112 27760 25190 25131 1213 42117 42117	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_19920/KOX_20805  KOX_2175/KOX_21760  KOX_02090/KOX_19920/KOX_20805  KOX_21740  KOX_175/KOX_21760  KOX_175/KOX_21760  KOX_175/KOX_21760  KOX_1040  KOX_1175/KOX_19620  KOX_10640  KOX_10640  KOX_10640  KOX_10640  KOX_10645  KOX_10645  KOX_11645  KOX_11465  KOX_11465  KOX_11665  KOX_11545(spH)  KOX_01055(ispH)  KOX_01055(ispH)  KOX_01055(ispH)  KOX_01055(ispH)  KOX_01055(ispH)  KOX_11470  KOX_00375  KOX_07835(fadB)/KOX_19445/KOX_26655(fadl)/  KOX_07835(fadB)/KOX_19445/KOX_26655(fadl)/  KOX_07835(fadB)/KOX_19445/KOX_26655(fadl)/  KOX_07835(fadB)/KOX_19445/KOX_26655(fadl)/  KOX_07835(fadB)/KOX_19445/KOX_26655(fadl)/  KOX_016850/KOX_20605	4hb + o2 + nadph -> 34dhb + nadp  34dhb + o2 -> carccm  2hmuc -> zoe 2odhfac -> oadip succa + oadip -> succ + ooadpcoa ooadpcoa + coa -> succoa + accoa carcm <>> gcarmclc  gramclc <>> 2odhfac + co2 gallate + o2 -> 2py46dc  4c2hbd <-> 4debtc dmp + ipp -> dpp + ppi ipp +> ipp -> frdp + ppi cdpmde + atp -> 2pcdpmde + adp hmb4pp + nadh -> dmpp + nad  dxSp + nadph -> mde4p + nadp g3p + pyr -> co2 + dxSp hmb4pp + nadh -> ipp + nad mdecpp -> hmb4pp 2pcdpmde -> mdecpp + cmp mde4p + ctp -> cdpmde + ppi frdp + 5 ipp -> opp + 5 ppi frdp + 5 ipp -> udcpdp + 8 ppi perflald + nadh c2mipdcoa -> 3hdmmhcoa  t2mipdcoa -> 3hdmmhcoa isochor -> salcyl + pyr
SHBCDH PHBZMN PROTCCI 40XCIT 30XAPIC 30XAPIC 30XAPIC 30XAPIC 30XADCT 3CMUCC 46BMCLC PROTCC2 CARHM2 DMRATT IPPOI GRATT IPPOI GRATT IPPOI GRATT IPPOI GRATT IPPOI GRATT ODPMDEK HMB4PPR DOXRII DOXPS HMB4DPR MECDPDHT MECDPS ME4PCT OCTPPS UDCPDPS ALHD18 CZMPCH TZMBPCH ISOCHORPL ISOCHORPL ISOCHORPL	Benzoate degradation via Hydroxylation Terpenoid backbone biosynthesis	dehydrogenase p-hydroxybenzoate 3- monoxygenase protocatechuate 3-4- dioxygenase 4-ovalocrotonate tautomerase 3-owadipate GoA-transferase protocatechuate 3-4- dioxygenase 5-carboxymuconolactone decarboxylase protocatechuate 3-4- dioxygenase 5-carboxymuconate isomerase geranyfitanstransferase geranyfitanstransferase geranyfitanstransferase 4-(cytidine 5'-diphosphate delta-isomerase 4-(cytidine 5'-diphosphate)-2-C- methyl-D-eythriot (biase 1-hydroxy-2-methyl-2-(E)- butenyl 4-diphosphate reductase 1-hydroxy-2-methyl-2-(E)- butenyl 4-diphosphate reductase 2-C-methyl-D-eythriot (2-4 cyclodiphosphate synthase 1-hydroxy-2-methyl-2-(E)- butenyl 4-diphosphate reductase 2-C-methyl-D-eythriot (2-4 cyclodiphosphate synthase 2-C-methyl-D-eythriot (2-4 cyclodiphosphate synthase 2-C-methyl-D-eythriot (3-4 cyclodiphosphate 3-4 cyclodiphosphate	111157 114132 113113 532- 31124 2836 23116 5512 41144 113113 53310 2511 5332 25110 271148 11712 111267 2217 117.12 117.12 117.11 46.112 27.760 25.130 25.131 12.13 42.117 42.99.21 33.21	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_19920/KOX_20805  KOX_2175/KOX_1920/KOX_20805  KOX_2175/KOX_1920/KOX_20606  KOX_02105/KOX_1720/KOX_20660(fadl)  KOX_1040  KOX_1040  KOX_1040  KOX_1040  KOX_10610  KOX_10640  KOX_10645(fispH)  KOX_10545(fispH)  KOX_11465  KOX_10545(fispH)  KOX_11465  KOX_10545(fispH)  KOX_11465  KOX_10545(fispH)  KOX_107835(fispH)  KOX_11470  KOX_107835(fispH)  KOX_11470  KOX_107835(fispH)  KOX_11470  KOX_107835(fispH)  KOX_107835(fispH)  KOX_11470  KOX_107835(fispH)  KOX_11470  KOX_107835(fispH)  KOX_11470  KOX_107835(fispH)  KOX_11470  KOX_11470  KOX_107835(fispH)  KOX_11470  KO	4hb + o2 + nadph -> 34dhb + nadp  34dhb + o2 -> carccm  2hmuc -> zoe 2odhfac -> oadip succa + oadip -> succ + ooadpcoa ooadpcoa + coa -> succoa + accoa carcm <-> garmclc  garmclc <-> zodhfac + co2 gallate + o2 -> 2py46dc  4c2hhd <-> 4obtc dmp + ipp -> gpp + ppi ipp <-> dmpp gpp + ipp -> frdp + ppi cdpmde + atp -> 2pcdpmde + adp hmb4pp + nadh -> dmpp + nad dx5p + nadph -> mde4p + nadp g3p + pyr -> co2 + dx5p hmb4pp + nadh -> ipp + nad mdecpp -> hmb4pp 2pcdpmde -> mdecpp + cmp mde4p - ttp -> cdpmde + ppi frdp + 5 ipp -> opp + 5 ppi frdp + 8 ipp -> udcpdp + 8 ppi perflaid + nad <-> perfl + nadh c2mipdcoa -> 3hdmmhcoa sochor -> salcyl + pyr sochor -> 23d23dhb + pyr  23d23dhb + nad -> 23dhb + nadh
3HBCDH PHBZMN PROTCCI 40XCTT 30XAPL 30XAPL 30XAPCT 3CMUCC 4CBMCLC PROTCC2 CARHM2 DMRATT IPPDI GRATT CDPMDEK HMB4DPR DOXRTI DOXPS HMB4DPR MECDPDHT MECDPS ME4PCT OCTPPS UDCPDPS ALHD18 CZMIPCH TZMIPCH ISOCHORPH	Benzoate degradation via Hydroxylation Terpenoid backbone biosynthesis	dehydrogenase p-hydroxybenzoate 3- monoxygenase protocatechuate 3-4- dioxygenase 4-ovalocrotonate tautomerase 3-owadipate GoA-transferase protocatechuate 3-4- dioxygenase 5-carboxymuconate isomerase geranyltranstransferase geranyltranstransferase geranyltranstransferase 4-(cytidine 5'-diphospho)-2-C- methyl-D-eythriot Diase 1-hydroxy-2-methyl-2-(E)- butenyl 4-diphosphate reductase 1-hydroxy-2-methyl-2-(E)- butenyl 4-diphosphate reductase 1-hydroxy-2-methyl-2-(E)- butenyl 4-diphosphate reductase 2-C-methyl-D-eythriot J- cytodiphosphate synthase 1-hydroxy-2-methyl-2-(E)- butenyl 4-diphosphate reductase 2-C-methyl-D-eythriot J- phosphate cytidyl-transferase C-C-methyl-D-eythriot J- phosphate cytidyl-transferase C-C-methyl-D-eythriot J- phosphate cytidyl-transferase C-C-methyl-D-eythriot J- cytodiphosphate synthase 1-decon-D-synthase C-C-methyl-D-eythriot J- cytodiphosphate synthase C-C-methyl-D-eythriot J- cytodiphosphate	111157 114132 113113 532- 31124 2836 23116 5512 41144 113113 53310 2511 5332 25110 271148 11712 111267 2217 117.12 117.12 117.11 46.112 27.760 25.130 25.131 12.13 42.117 42.99.21 33.21	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_19920/KOX_20805  KOX_2175/KOX_1760  KOX_2175/KOX_21760  KOX_02105/KOX_21760  KOX_2175/KOX_21760  KOX_1030/GAN_26660(fadl)  KOX_10346  KOX_10340  KOX_1040  KOX_10615/KOX_19620  KOX_10640  KOX_10640  KOX_10640  KOX_10640  KOX_10640  KOX_10640  KOX_10640  KOX_10640  KOX_10645(fspth)  KOX_10545(fspth)  KOX_1054	4hb + o2 + nadph -> 34dhb + nadp  34dhb + o2 -> carccm  2hmuc -> zoe 2odhfac -> oadip succa + oadip -> succ + ooadpcoa ooadpcoa + coa -> succoa + accoa carccm <-> gearmele grammle <-> zodhfac + co2 gallate + o2 -> 2py46dc  4c2hbd <-> 4obte dmpp + ipp -> frdp + ppi ipp <-> dmpp gpp + ipp -> frdp + ppi cdpmde + atp -> 2pcdpmde + adp  hmb4pp + nadh -> dmpp + nad  dx5p + nadph -> mde4p + nadp g3p + pyr -> co2 + dx5p  hmb4pp + nadh -> ipp + nad  mdecpp -> hmb4pp  2pcdpmde -> mdecpp + cmp mde4p + ctp -> cdpmde + ppi frdp + 5 ipp -> opp + 5 ppi frdp + 8 ipp -> udcpdp + 8 ppi perllald + nad <-> perll + nadh c2mipdcoa -> 3hdmmhcoa  tzmipdcoa -> 3hdmmhcoa isochor -> salcyl + pyr isochor -> 23d23dhb + pyr
SHBCDH PHBZMN PROTCCI 40XCIT 30XAPIC 30XAPIC 30XAPIC 30XAPIC 30XADCT 3CMUCC 46BMCLC PROTCC2 CARHM2 DMRATT IPPOI GRATT IPPOI GRATT IPPOI GRATT IPPOI GRATT IPPOI GRATT ODPMDEK HMB4PPR DOXRII DOXPS HMB4DPR MECDPDHT MECDPS ME4PCT OCTPPS UDCPDPS ALHD18 CZMPCH TZMBPCH ISOCHORPL ISOCHORPL ISOCHORPL	Benzoate degradation via Hydroxylation Terpenoid backbone biosynthesis	dehydrogenase p-hydroxybenzoate 3- monooxygenase protocatechuste 3-4- dioxygenase 4-oxalocrotonate tautomerase 3-oxoadipate col-transferase 0-xoadipyl-CoA thiolase 3-carboxy-Giscis-muconate cycloisomerase 4-carboxymuconalactone decarboxylase protocatechuate 3-4- dioxygenase 5-carboxymuconate isomerase geranyltranstransferase isopenateryl-diphosphate delta- isomerase geranyltranstransferase geranyltranstransferase geranyltranstransferase geranyltranstransferase 1-hydroxy-2-methyl-2-(Col- butenyl 4-diphosphate reductase 1-hydroxy-2-methyl-2-(Col- butenyl 4-diphosphate reductase 1-hydroxy-2-methyl-2-(Col- butenyl 4-diphosphate reductase 1-hydroxy-2-methyl-2-(Col- butenyl 4-diphosphate reductase 1-hydroxy-2-methyl-1-2-(Col- butenyl-1-0-prythritol 2,4 cyclodiphosphate dehydrospate synthase 1-hydroxy-2-methyl-1-2-(Col- butenyl-1-2-2-(Col- butenyl-1-2-2-2-2-2-2-2-2-2-2-2-2-2-2-2-2-2-2-	11.1157 114132 113113 53.2. 31.124 2.8.36 2.3.116 5.5.12 4.1.144 113.113 5.3.310 2.5.11 5.3.32 2.5.110 2.7.1.148 1.17.12 1.17.12 1.17.12 1.17.12 1.17.11 4.6.112 2.7.7.60 2.5.190 2.5.131 1.2.13 4.2.117 4.2.117 4.2.117 4.2.117 4.2.9.2.1 3.3.2.1 1.3.1.28	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_19920/KOX_20805  KOX_2175/KOX_1920/KOX_20805  KOX_2175/KOX_1920/KOX_20606  KOX_02105/KOX_1720/KOX_20660(fadl)  KOX_1040  KOX_1040  KOX_1040  KOX_1040  KOX_10610  KOX_10640  KOX_10645(fispH)  KOX_10545(fispH)  KOX_11465  KOX_10545(fispH)  KOX_11465  KOX_10545(fispH)  KOX_11465  KOX_10545(fispH)  KOX_107835(fispH)  KOX_11470  KOX_107835(fispH)  KOX_11470  KOX_107835(fispH)  KOX_11470  KOX_107835(fispH)  KOX_107835(fispH)  KOX_11470  KOX_107835(fispH)  KOX_11470  KOX_107835(fispH)  KOX_11470  KOX_107835(fispH)  KOX_11470  KOX_11470  KOX_107835(fispH)  KOX_11470  KO	4hb + o2 + nadph -> 34dhb + nadp  34dhb + o2 -> carccm  2hmuc -> zoe 2odhfac -> oadip succa + oadip -> succ + ooadpcoa ooadpcoa + coa -> succoa + accoa carcm <-> garmclc  garmclc <-> zodhfac + co2 gallate + o2 -> 2py46dc  4c2hhd <-> 4obtc dmp + ipp -> gpp + ppi ipp <-> dmpp gpp + ipp -> frdp + ppi cdpmde + atp -> 2pcdpmde + adp hmb4pp + nadh -> dmpp + nad dx5p + nadph -> mde4p + nadp g3p + pyr -> co2 + dx5p hmb4pp + nadh -> ipp + nad mdecpp -> hmb4pp 2pcdpmde -> mdecpp + cmp mde4p - ttp -> cdpmde + ppi frdp + 5 ipp -> opp + 5 ppi frdp + 8 ipp -> udcpdp + 8 ppi perflaid + nad <-> perfl + nadh c2mipdcoa -> 3hdmmhcoa sochor -> salcyl + pyr sochor -> 23d23dhb + pyr  23d23dhb + nad -> 23dhb + nadh
3HBCDH PHBZMN PROTCCI 40XCTT 30XAPIC 30XAPIC 30XAPIC 30XAPIC 30XADCT 3CMUCC 46BMCLC PROTCC2 CARHM2 DMRATT IPPOI GRATT IPPOI GRATT IPPOI GRATT IPPOI GRATT IPPOI GRATT CDPMDEK HMB4PPR DOXRII DOXPS HMB4DPR MECDPDHT MECDPS ALHD18 CZMPCH TZMIPCH ISOCHORPL ISOCHORPL 23D4BAS AOXNS	Benzoate degradation via Hydroxylation Terpenoid backbone biosynthesis Biosynthesis of siderophore group nonribosomal peptides	dehydrogenase p-hydroxybenzoate 3- monooxygenase protocatechuste 3-4- dioxygenase 4-ovalocrotonate tautomerase 3-owadipate coh-transferase 4-carboxymuconalactone decarboxylase protocatechuate 3-4- dioxygenase 5-carboxymuconate isomerase geranyltranstransferase isopenateryl-diphosphate delta- isomerase geranyltranstransferase geranyltranstransferase 4-(cytidine 5-qilhopspho)-2-c- methyl-D-erythritol 1- hydroxy-2-methyl-2-(E)- butenyl 4-diphosphate reductase 1-hydroxy-2-methyl-2-(E)- butenyl 4-diphosphate reductase 1-hydroxy-2-methyl-2-(E)- butenyl 4-diphosphate reductase 1-hydroxy-2-methyl-2-(E)- butenyl 4-diphosphate reductase 1-hydroxy-2-methyl-1-2-(E)- butenyl 4-diphosphate reductase 1-hydroxy-2-methyl-1-2-(E)- butenyl 4-diphosphate synthase 1-hydroxy-2-methyl-1-2-(E)- butenyl 4-diphosphate synthase synthase 1-hydroxy-2-methyl-1-2-(E)- butenyl-1-4-phosphate cytidylytrosphate synthase 1-hydroxy-2-methyl-1-2-(E)- butenyl-1-4-phosphate cytidylytrosphate synthase 1-hydroxy-2-methyl-1-2-(E)- butenyl-1-4-phosphate cytidylytrosphate synthase 1-hydroxy-2-methyl-2-(E)- butenyl-1-4-phosphate cytidylytrosphate synthase 1-hydroxy-2-methyl-1-2-(E)- butenyl-1-4-phosphate cytidylytrosphate synthase 1-hydroxy-2-methyl-1-2-(E)- butenyl-1-2-2-2-2-2-2-2-2-2-2-2-2-2-2-2-2-2-2-	11.1157 114132 113113 53.2. 31.124 2.8.36 2.3.116 5.5.12 4.1.144 113113 5.3.310 2.5.11 5.3.32 2.5.110 2.7.1.148 117.12 111.267 2.2.17 117.12 117.12 117.12 117.13 4.6.112 2.7.7.60 2.5.190 2.5.131 1.2.13 4.2.117 4.2.92.1 3.3.21 1.3.1.28 2.7.7.58	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_19920/KOX_20805  KOX_2175/KOX_119620  KOX_02090/KOX_11920/KOX_20805  KOX_12745  KOX_02105/KOX_12760  KOX_1040  KOX_1040  KOX_1040  KOX_1040  KOX_1040  KOX_1040  KOX_1040  KOX_1040  KOX_10540  KOX_10540  KOX_10545(ispH)  KOX_10540  KOX_10545(ispH)  KOX_11465  KOX_10545(ispH)  KOX_11465  KOX_10545(ispH)  KOX_11465  KOX_10545(ispH)  KOX_1055(ispF)  KOX_1055	4hb + o2 + nadph -> 34dhb + nadp  34dhb + o2 -> carccm  2hmuc -> zoe 2odhfac -> oadip succa + oadip -> succ + ooadpcoa ooadpcoa + coa -> succoa + accoa carcm <-> garmclc  garmclc <-> zodhfac + co2 gallate + o2 -> 2py46dc  4c2hhd <-> 4obtc dmp + ipp -> gpp + ppi ipp <-> dmpp gpp + ipp -> frdp + ppi cdpmde + atp -> 2pcdpmde + adp hmb4pp + nadh -> dmpp + nad dx5p + nadph -> mde4p + nadp g3p + pyr -> co2 + dx5p hmb4pp + nadh -> ipp + nad mdecpp -> hmb4pp 2pcdpmde -> mdecpp + cmp mde4p + ctp -> cdpmde + ppi frdp + 5 ipp -> opp + 5 ppi frdp + 8 ipp -> udcpdp + 8 ppi perilaid + nad <-> peril + nadh c2mipdcoa -> 3hdmmhcoa tzmipdcoa -> 3hdmmhcoa tzmipdcoa -> 3ddb + pyr 23d23dhb + nad -> 23dhb + nadh 23dhb + atp <-> 23dhba + ppi
3HBCDH PHBZMN PROTCCI 40XCTT 30XAPIC 30XAPIC 30XAPIC 30XAPIC 30XADCT 3CMUCC 46BMCLC PROTCC2 CARHM2 DMRATT IPPOI GRATT IPPOI GRATT IPPOI GRATT IPPOI GRATT IPPOI GRATT CDPMDEK HMB4PPR DOXRII DOXPS HMB4DPR MECDPDHT MECDPS ALHD18 CZMPCH TZMIPCH ISOCHORPL ISOCHORPL ISOCHORPL 23D13D3D3D3D3D3D3D3D3D3D3D3D3D3D3D3D3D3D	Benzoate degradation via Hydroxylation Terpenoid backbone biosynthesis Biosynthesis of siderophore group nonribosomal peptides Biosynthesis of siderophore group nonribosomal peptides Biosynthesis of siderophore group nonribosomal peptides	dehydrogenase p-hydroxybenzoate 3- monoxygenase protocatechuate 3-4- dioxygenase 4-ovalocrotonate tautomerase 3-owadipate GoA-transferase protocatechuate 3-4- dioxygenase 5-carboxymuconolactone decarboxylase protocatechuate 3-4- dioxygenase 5-carboxymuconate isomerase geranyfitanstransferase geranyfitanstransferase geranyfitanstransferase decarboxylase geranyfitanstransferase 4-(cytidine 5-diphospho)-2-c- methyl-0-gridyntol (shopping) 1-deoxy-0-xylulose polydione 5-diphospho)-2-c- methyl-0-gridyntol (shopping) 1-deoxy-0-xylulose reductise (dmpp) 1-deoxy-0-xylulose phosphate synthase 1-hydroxy-2-methyl-2-(E)- butenyl 4-diphosphate reductase 2-c-methyl-0-grythriol 2-A cyclodiphosphate synthase 2-c-methyl-0-grythriol 2-A cyclodiphosphate synthase 2-c-methyl-0-grythriol 2-Phosphate cythyl-1-grythriol 4- phosphate synthase 1-greynel grythriol 2-2- Cyclodiphosphate synthase 2-c-methyl-0-grythriol 4- phosphate synthase 1-grythyl-0-grythriol 4- phosphate synthase 1-grythyl-0-	11.1157 114132 113113 53.2. 31.124 2.8.36 2.3.116 5.5.12 4.1.144 113113 5.3.310 2.5.11 5.3.32 2.5.110 2.7.1148 117.12 11.1267 2.2.17 1.17.12 1.17.12 1.17.1 4.6.112 2.7.7.60 2.5.190 2.5.131 1.2.13 4.2.117 4.2.117 4.2.117 4.2.9.2.1 3.3.2.1 1.3.1.2.8 2.7.7.5.8 2.3.1.47	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_19920/KOX_20805  KOX_21756  KOX_21756  KOX_21756  KOX_21740  KOX_10216  KOX_102105/KOX_07320/KOX_20565/KOX_20900  KOX_1735/KOX_24470  KOX_1040  KOX_1040  KOX_10410  KOX_10540  KOX_10540  KOX_10540  KOX_12610  KOX_02365  KOX_12610  KOX_10540  KOX_10545/sipH)  KOX_11655  KOX_10540  KOX_10540  KOX_10545/sipH)  KOX_11465  KOX_10540  KOX_10545/sipH)  KOX_11465  KOX_10545/sipH)  KOX_11465  KOX_10545/sipH)	4hb + o2 + nadph -> 34dhb + nadp  34dhb + o2 -> carccm  2hmuc -> zoe 2odhfac -> oadip succa + oadip -> succ + ooadpcoa ooadpcoa + coa -> succoa + accoa carcm <-> pcarmclc  gramclc <-> zodhfac + co2 gallate + o2 -> 2py46dc  4c2hhd <-> 4obtc dmp + ipp -> gpp + ppi ipp <-> dmpp gpp + ipp -> frdp + ppi cdpmde + atp -> 2pcdpmde + adp hmb4pp + nadh -> dmpp + nad dx5p + nadph -> mde4p + nadp g3p + pyr -> co2 + dx5p hmb4pp + nadh -> ipp + nad mdecpp -> hmb4pp 2pcdpmde -> mdecpp + cmp mde4p + ctp -> cdpmde + ppi frdp + 8 ipp -> udcpdp + 8 ppi perilaid + nad <-> peril + nadh c2mipdcoa -> 3hdmmhcoa t2mipdcoa -> 3hdmmhcoa tsochor -> salcyl + pyr sochor -> 23d23dhb + pyr 23d23dhb + nad -> 23dhb + nadh 23dh + atp <-> 23dhba + ppi ala + pmcoa <-> anna + co2 + coa
3HBCDH PHBZMN PROTCCI 40XCTT 30XAPIC 30XAPIC 30XAPIC 30XAPIC 30XAPCT 3CMUCC 4CBMCLC PROTCC2 CARHM2 DMRATT IPPDI GRATT CDPMDEK HMB4DPR DOXRTI DOXPS HMB4DPR MECDPDHT MECDPS ME4PCT OCTPPS UDCPDPS ALHD18 CZMIPCH TZMIPCH ISOCHORPL ISOCHORPL 23023DHBD 23DHBAS AOXNIS AMAOXNIT	Benzoate degradation via Hydroxylation Terpenoid backbone biosynthesis	dehydrogenase p-hydroxybenzoate 3- monoxygenase protocatechuate 3-4- dioxygenase 4-ovalocrotonate tautomerase 3-owadipate GoA-transferase protocatechuate 3-4- dioxygenase 5-carboxymuconate isomerase geranyltranstransferase isopenteryl-1diphosphate delta- isomerase 4-(cytidine 5'-diphospha)-2-C- methyl-0-gythrot biase 1-hydroxy-2-methyl-2-(E)- butenyl 4-diphosphate reductase (dmpp) 1-deoxy-0-xylulose reductiosemerase 1-hydroxy-2-methyl-2-(E)- butenyl 4-diphosphate reductase 2-C-methyl-0-gythrot J- cytodiphosphate synthase 1-hydroxy-2-methyl-2-(E)- butenyl 4-diphosphate reductase 2-C-methyl-0-gythriot J- cytodiphosphate synthase 2-C-methyl-0-gythriot J- phosphate cytidyltransferase C-taprenyl pryophosphate synthase L-C-methyl-0-gythriot J- cis-2-Methyl-5-isopropylbexa- synthase aldehyde dehydrogenase (NAD-1) cis-2-Methyl-5-isopropylbexa- denydate synthase 3-a-dinydroxybenzoate adenydate synthase 3-a-dinydroxybenzoate adenydate synthase 3-a-dinydroxybenzoate adenydate synthase 3-a-dinydroxybenzoate adenydate synthase 3-denion-7-oxonoanaoate synthase 3-denion-7-oxonoanaoate synthase 3-denion-7-oxonoanaoate sitotin synthase 3-denion-1	111157 114132 113113 532- 311124 2836 23116 5512 41144 113113 53310 2511 5332 25110 27.1148 117.12 117.12 117.12 117.12 117.11 46.112 27.760 25.130 25.131 12.13 42.117 42.99.21 33.21 13.128 27.758 23.147 26.162	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_19920/KOX_20805  KOX_21740  KOX_21740  KOX_21740  KOX_21746  KOX_21746  KOX_21746  KOX_21746  KOX_21746  KOX_21746  KOX_21746  KOX_1040  KOX_1040  KOX_1040  KOX_1040  KOX_1040  KOX_10545(spH)  KOX_01055(spF)  KOX_01055(spF)  KOX_01055(spF)  KOX_01055(spF)  KOX_01055(spF)  KOX_01470  KOX_03740  KOX_07835(sdB)/KOX_19445/KOX_26655(sdJ)/  KOX_13965  KOX_13965  KOX_13965  KOX_13965  KOX_14920  KOX_14910	4hb + o2 + nadph -> 34dhb + nadp  34dhb + o2 -> carccm  2hmuc -> zoe 2odhfac -> oadip succa + oadip -> succ + ooadpcoa ooadpcoa + coa -> succoa + actoa carccm <-> gcarmclc  gcarmclc <-> zodhfac + co2 gallate + o2 -> 2py46dc  4c2hhd <-> 4obtc dmpp + ipp -> gpp + ppi ipp <-> dmpp gpp + ipp -> frdp + ppi cdpmde + atp -> 2pcdpmde + adp hmb4pp + nadh -> dmpp + nad dx5p + nadph -> mde4p + nadp g3p + pyr -> co2 + dx5p hmb4pp + nadh -> ipp + nad mdecpp -> hmb4pp 2pcdpmde -> mdecpp + cmp mde4p + ctp -> cdpmde + ppi frdp + 5 ipp -> opp + 5 ppi frdp + 5 ipp -> opp + 5 ppi frdp + 5 ipp -> odp+ 8 ppi perllald + nad <-> perll + nadh c2mipdcoa -> 3hdmmhcoa sischor -> salcyl + pyr sischor -> z3ddbh + pyr 23d23dhb + nad -> 23dhb + nadh 23dhb + atp <-> 23dhba + ppi ala + pmcoa <-> aona + co2 + coa aona + sam <-> samob + danna
SHBCDH PHBZMN PROTCCI 40XCTT 30XAPIC 30XAPIC 30XAPIC 30XAPIC 30XAPCT 3CMUCC 4GBMCLC PROTCC2 CARHM2 DMRATT IPPOI GRATT CDPMDEK HMB4PPR DOXRTI DOXPS HMB4DPR MECDPDHT MECDPS ME4PCT OCTPPS UDCPDPS ALHD18 CZMIPCH TZMIPCH ISOCHORPL ISOCHORPL 23D23DHBD 23DHBAS AOXNS AMAOXNT BIOTS1	Berzoate degradation via Hydroxylation Benzoate degradation via Hydroxylation Terpenoid backbone biosynthesis Terpenoid	dehydrogenase p-hydroxybenzoate 3- monooxygenase protocatechuste 3-4- dioxygenase 4-ovalocrotonate tautomerase 3-owadipate coh-transferase 4-carboxymuconale somerase geranytranstransferase isopenateryl-diphosphate delta-isomerase geranytranstransferase geranytranstransferase geranytranstransferase geranytranstransferase 1-hydroxy-2-methyl-2-(Coh-trentyl-10-prythritol kinase 1-hydroxy-2-methyl-2-(Coh-trentyl-10-prythritol Lyd-cytodiphosphate reductase 1-deoxy-D-xylulose 5-hoosphate synthase 1-hydroxy-2-methyl-2-(Coh-trentyl-10-prythritol 2-4 cytodiphosphate dehydrosphate productase 1-methyl-0-prythritol 2-4 cytodiphosphate synthase 1-hydroxy-2-methyl-1-prythritol 2-methyl-1-prythritol 2-methyl-1-prythritol 2-methyl-1-prythritol 2-methyl-1-prythritol 2-methyl-1-prythritol 3-c-methyl-1-prythritol 3-c-methyl-1-	111157 114132 113113 532- 311124 2836 233116 55512 41144 113113 53310 2511 5332 25110 271148 11712 111267 2217 11712 11771 46112 27760 25190 25131 1213 42117 429921 3321 13128 27758 23147 26162 2816	KOX_10205  KOX_19615/KOX_19620  KOX_02090/KOX_19920/KOX_20805  KOX_2175/KOX_21760  KOX_02090/KOX_19920/KOX_20805  KOX_21740  KOX_10740  KOX_10740  KOX_10740  KOX_10740  KOX_10740  KOX_10840  KOX_10845(spth)  KOX_10845(spth)  KOX_10845(spth)  KOX_01085(spth)  KOX_01086(spth)  KOX_11470  KOX_03750  KOX_07835(sdt8)/KOX_19445/KOX_26655(sdt)/  KOX_13960  KOX_13965  KOX_13965  KOX_14910  KOX_14910  KOX_14915	4hb + o2 + nadph -> 34dhb + nadp  34dhb + o2 -> carccm  2hmuc -> zoe 2odhfac -> oadip succa + oadip -> succ + ooadpcoa ooadpcoa + coa -> succoa + accoa carcm <>> gramcle  gamlac +> o2 -> 2dhfac + co2 gallate + o2 -> 2dhfac + co2 gallate + o2 -> 2dpfac  4c2hbd <-> 4obtc dmpp + ipp -> dppp + ppi ipp +> ipp -> ppr + ppi cdpmde + atp -> 2pcdpmde + adp hmb4pp + nadh -> dmpp + nad  dx5p + nadph -> mde4p + nadp g3p + pyr -> co2 + dx5p  hmb4pp + nadh -> ipp + nad  mdecpp -> hmb4pp 2pcdpmde -> mdecpp + cmp mde4p + ctp -> cdpmde + ppi frdp + 5 ipp -> udcpdp + 8 ppi perllald + nad <-> perll - nadh c2mipdcoa -> 3hdmmhcoa  t2mipdcoa -> 3hdmmhcoa  t2mipdcoa -> 3ddb + pyr 23d23dhb + nad -> 23dhb + nadh 23dbb + atp <-> 23dbb + nadh 23dbb + atp <-> 23dbb + nadh 23dbb + atp <-> 23dbb + nadh 2ana + sam <-> samob + danna sam + dtb + s -> bt + da-5 + met

BTNACL	Biotin metabolism	biotin-[acetyl-CoA-carboxylase]	6.3.4.15	KOX 07865	atp + bt -> ppi + b5amp
		ligase biotin-[acetyl-CoA-carboxylase]			
BTNACL2	Biotin metabolism	ligase (R)-Malate:NAD+	6.3.4.15	KOX_07865	b5amp + apoCAB -> amp + holoCAB
MALDO	Butanoate metabolism	oxidoreductase (decarboxylating)/D-malate	1.1.1.83	KOX_16905	dmal + nad -> co2 + nadh + pyr
ACALDb	Butanoate metabolism	, , , , , , , , , , , , , , , , , , , ,	1.2.1.10	KOX_22675/KOX_23025	butanal + coa + nad -> c040coa + nadh
AC4HB	Butanoate metabolism	acetyl-CoA: 4-hydroxybutanoate CoA transferase (two-step reaction, unclear reaction)			4hbt + accoa <-> 3btecoa + ac
		aldehyde dehydrogenase			
	Butanoate metabolism	(NAD+)	1.2.1.3	KOX_00375	3bla + nad -> 3but + nadh
	Butanoate metabolism	acetolactate decarboxylase	4.1.1.5	KOX_22365	alac-S -> acetoin + co2
ACETRD DIACTS	Butanoate metabolism Butanoate metabolism	acetoin reductase Spontaneous	1.1.1.4	KOX_01940/KOX_22375	acetoin + nadh <-> 23bdo + nad alac-S + o2 -> diacetyl + co2
	Butanoate metabolism	diacetyl reductase	1.1.1.303	KOX_01940/KOX_22375	diacetyl + nadh -> acetoin + nad
SUCCS	C5-Branched Dibasic acid metabolism	succinyl-CoA synthetase	6.2.1.5	KOX_14600(sucC)/KOX_14605	atp + itcn + coa <-> adp + pi + itcncoa
METASPAL	C5-Branched Dibasic acid metabolism	methylaspartate ammonia-lyase	4.3.1.2	KOX_14665	thr3masp -> mesacon + nh4
MDH1	Citric Acid Cycle	malate dehydrogenase	1.1.1.37	KOX_04000	mal + nad <-> nadh + oaa
	Citric Acid Cycle	isocitrate dehydrogenase	1.1.1.42	KOX_17560	icit + nadp <-> akg + co2 + nadph
		(NADP) Malate dehydrogenase			
MDH2	Citric Acid Cycle	(ubiquinone 8 as acceptor)	1.1.5.4	KOX_21685/KOX_26070	mal + uq -> oaa + uqh2
MDH3	Citric Acid Cycle	Malate dehydrogenase (menaquinone 8 as acceptor)	1.1.5.4	KOX_21685/KOX_26070	mal + mk -> oaa + mqn
CITL	Citric Acid Cycle	Citrate lyase	4.1.3.6	KOX_10630/KOX_10635/KOX_10640/KOX_16575/ KOX_16580	cit -> ac + oaa
FUMR	ent with t	,	4.2.1.2	KOX_16560 KOX_14640/KOX_21730/KOX_21890(fumC)/KOX_	
	Citric Acid Cycle	fumarase		21895	
ACONT1	Citric Acid Cycle		4.2.1.3	KOX_10580/KOX_11075/KOX_18415	cit <-> acon-C
ACONT2	Citric Acid Cycle	aconitase (isocitrate hydro- lyase)	4.2.1.3	KOX_10580/KOX_11075/KOX_18415	acon-C <-> icit
SUCOAS	Chair Anid Couls	succinyl-CoA synthetase (ADP-	6.2.1.5	VOV 14500/C/WOV 14505	atp + coa + succ -> succoa + adp + pi
SUCUAS	Citric Acid Cycle	forming)		KOX_14600(sucC)/KOX_14605	atp + coa + succ -> succoa + aup + pi
AKGDH	Citric Acid Cycle	2-Oxogluterate dehydrogenase	1.2.4.2/2.3.1.61/1.8.	KOX_14590(sucA)/KOX_14595/KOX_11055/KOX_ 20455	akg + coa + nad -> co2 + nadh + succoa
CITS	Citric Acid Cycle	citrate synthase	2.3.3.1	KOX_14565(gltA)/KOX_25260	accoa + oaa -> cit + coa
				KOX_08760/KOX_08765/KOX_08770/KOX_08775/	
SUCCDf	Citric Acid Cycle	succinate dehydrogenase (irreversible)	1.3.99.1	KOX_14570(sdhC)/KOX_14575(sdhD)/KOX_14580 (sdhA)/KOX_14585(sdhB)/KOX_21720	succ + fad -> fum + fadh2
SUCCDm	Citric Acid Cycle	succinate dehydrogenase (irreversible)	1.3.99.1	KOX_08760/KOX_08765/KOX_08770/KOX_08775/ KOX_14570(sdhC)/KOX_14575(sdhD)/KOX_14580	
		succinate dehydrogenase		(sdhA)/KOX_14585(sdhB)/KOX_21720 KOX_08760/KOX_08765/KOX_08770/KOX_08775/	
SUCCDd	Citric Acid Cycle	(irreversible)	1.3.99.1	KOX_14570(sdhC)/KOX_14575(sdhD)/KOX_14580 (sdhA)/KOX_14585(sdhB)/KOX_21720	fum + 2dmmql8 -> succ + 2dmmq8
GGMT1	Cyanoamino acid metabolism	gamma-glutamyltranspeptidase	2.3.2.2	KOX_04780(ggt)/KOX_16795	cyaala + glu -> ggbap + co2
GGMT2	Cyanoamino acid metabolism	gamma-glutamyltranspeptidase	2322	KOX_04780(ggt)/KOX_16795	cyaala + glu -> ggbcya
TSULSFT SEROAT	Cyanoamino acid metabolism Cysteine Metabolism	thiosulfate sulfurtransferase serine O-acetyltransferase	2.8.1.1 2.3.1.30	KOX_04705(glpE)/KOX_18100/KOX_27315(sseA) KOX_05805(cysE)/KOX_18685	cn + tsul -> so3 + tcynt accoa + ser <-> aser + coa
CYSST1	Cysteine Metabolism	cysteine synthase	2.5.1.47	KOX_18690/KOX_26885(cysM)	aser + h2s -> ac + cys
	Cysteine metabolism	cystathionine beta-lyase	4.4.1.8	KOX_02875/KOX_21920	cyst -> pyr + nh4 + tcys
	Cysteine metabolism	cystathionine beta-lyase	4.4.1.8	KOX_02875/KOX_21920	cys -> h2s + pyr + nh4
CYTTS6 CYSST2	Cysteine metabolism		2.5.1.48 2.5.1.47	KOX_07310 KOX_18690/KOX_26885(cysM)	aser + tsul -> sslcys + ac
SERDHT2	Cysteine metabolism Cysteine metabolism	cysteine synthase L-serine dehydratase	4.3.1.17	KOX_10090/KOX_20003(CysM) KOX_01230/KOX_23635	aser + tsul -> sslcys + ac ser -> 2aa
				KOX_12795/KOX_18690/KOX_26835/KOX_26885(	
CYSST3	Cysteine metabolism	cysteine synthase	2.5.1.47	cysM)	aser + tsul + rthio -> cys + so3 + othio + ac
ASPAM1	Cysteine metabolism	aspartate aminotransferase	2.6.1.1	KOX_16370	mpyr + glu <-> cys + akg
ASPAM2	Cysteine metabolism	aspartate aminotransferase	2.6.1.1	KOX_16370	3slala + akg -> 3sfpyr + glu
ASPAM3 L-LACD5	Cysteine metabolism Cysteine metabolism	aspartate aminotransferase	2.6.1.1 1.1.1.27	KOX_16370 KOX_21270	cysteate + akg -> 3spyr + glu
	Cysteine Metabolism	L-lactate dehydrogenase Sulfate adenyltransferase	2.7.7.4	KOX_01080(cysN)/KOX_01085	mpyr + nadh -> 3mlac + nad atp + selnt <-> ppi + aselnt
DCYSDS	Cysteine Metabolism	D-cysteine desulfhydrase	4.4.1.15	KOX_18740	dcys -> h2s + nh4 + pyr
MPYRST	Cysteine Metabolism	3-mercaptopyruvate	2.8.1.2	KOX 18100/KOX 27315(sseA)	mpyr + so3 -> tsul + pyr
MPYRST	Cysteine Metabolism	sulfurtransferase	2.8.1.2	KOX_18100/KOX_27315(sseA)	mpyr + so3 -> tsul + pyr
MPYRST	Cysteine Metabolism  Cysteine Metabolism	sulfurtransferase homoserine O-	2.8.1.2 2.3.1.46		mpyr + so3 -> tsul + pyr succoa + hser -> coa + oslhser
HSERST SRHCYSL	Cysteine Metabolism Cysteine Metabolism	sulfurtransferase		KOX_08035	
HSERST SRHCYSL ALAALAL	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism	sulfurtransferase homoserine O- succinyltransferase	2.3.1.46	KOX_08035 KOX_00500	succoa + hser -> coa + oslhser
HSERST SRHCYSL ALAALAL	Cysteine Metabolism Cysteine Metabolism	sulfurtransferase homoserine O- succinyltransferase S-ribosylhomocysteine lyase	2.3.1.46 4.4.1.21	KOX_08035 KOX_00500	succoa + hser -> coa + oslhser srlh -> 45dhpen + hcys
HSERST SRHCYSL ALAALAL	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-glutamine and D-glutamate	sulfurtransferase homoserine O- succinyltransferase S-ribosylhomocysteine lyase D-alanine-D-alanine ligase	2.3.1.46 4.4.1.21 6.3.2.4 3.5.1.2 2.3.1.41 AND	KOX_08035 KOX_00500 KOX_10935(ddl)/KOX_12350 KOX_14645/KOX_21250	succoa + hser -> coa + osihser srih -> 45chpen + hçys 2 dala + atp <-> adp + alaala + pi dgln -> dglu + nh4
HSERST SRHCYSL ALAALAL GLUN2	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-glutamine and D-glutamate metabolism	sulfurtransferase homoserine O- succinyltransferase S-ribosylhomocysteine lyase D-alanine-D-alanine ligase	2.3.1.46 4.4.1.21 6.3.2.4 3.5.1.2	KOX_08035 KOX_00500 KOX_10935(ddl)/KOX_12350	succoa + hser -> coa + oshser srih -> 45dhpen + hçys 2 dala + atp <-> adp + alaala + pi dgln -> dglu + nM
HSERST SRHCYSL ALAALAL	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-glutamine and D-glutamate	sulfurtansferase homoserine O- succinytransferase S-ribosylhomocysteine lyase D-alanine-D-alanine ligase glutaminase	2.3.1.46 4.4.1.21 6.3.2.4 3.5.1.2 2.3.1.41 AND 2.3.1.179 AND 2.3.1.180 AND 1.1.1.100 AND	KOX_08035  KOX_00500  KOX_10935(ddl)/KOX_12350  KOX_14645/KOX_21250  KOX_05025/KOX_26605/KOX_00905/KOX_05040/ KOX_17300/KOX_17280/KOX_00890/KOX_02015/ Labely/KOX_0935/Keb/KOX_12780/KOX_17300/KOX_1780/K	succoa + hser -> coa + osihser srih -> 45dhpen + hcys 2 dala + atp <-> adp + alaala + pi dgln -> dglu + nh4
HSERST SRHCYSL ALAALAL GLUN2	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-glutamine and D-glutamate metabolism	sulfurtransferase homoserine O- succinyltransferase S-ribosylhomocysteine lyase D-alanine-D-alanine ligase glutaminase	2.3.1.46 4.4.1.21 6.3.2.4 3.5.1.2 2.3.1.41 AND 2.3.1.179 AND 2.3.1.180 AND 1.1.1.100 AND 4.2.1. AND 1.3.1.9	KOX_08035 KOX_00500 KOX_10935(dd);KOX_12350 KOX_14645;KOX_21250 KOX_14645;KOX_2505;KOX_00905;KOX_050400;KOX_05040;KOX_050400;KOX_05040;KOX_050400;KOX_050400;KOX_05040	succoa + hser -> coa + osihser srih -> 45dhpen + hcys 2 dala + atp <-> adp + alaala + pi dgln -> dglu + nh4
HSERST SRHCYSL ALAALAL GLUN2	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-glutamine and D-glutamate metabolism	sulfurtransferase homoserine O- succinyltransferase S-ribosylhomocysteine lyase D-alanine-D-alanine ligase glutaminase	2.3.146 4.4.121 6.3.24 3.5.12 2.3.1.41 AND 2.3.1.179 AND 2.3.1.180 AND 1.1.100 AND 4.21. AND 1.3.1.9 AND 1.3.1 2.3.1.41 AND	KOX, 08035 KOX, 00500 KOX, 10935(ddl)/KOX_12350 KOX_13645K/COX_21250 KOX_05025/KOX_26605/KOX, 00905/KOX, 05040) KOX_05025/KOX, 26605/KOX, 00905/KOX, 05040/KOX, 17280/KOX, 17280/KOX, 17280/KOX, 17280/KOX, 17280/KOX, 18475/KOX, 18960	succoa + hser -> coa + osihser srih -> 45dhpen + hcys 2 dala + atp <-> adp + alaala + pi dgin -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP
HSERST SRHCYSL ALAALAL GLUNZ FABC120	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-glutamine and D-glutamate metabolism Fatty acid biosynthesis	sulfurtransferase homoserine O- succinytransferase S-ribosylhomosystenie lyase D-alanine-D-alanine ligase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)	23.146 44.121 63.24 35.12 23.141 AND 23.1179 AND 23.1180 AND 11.1100 AND 4.21- AND 13.1- AND 13.1- 23.141 AND 23.147 AND	KCX, 08035 KCX, 00500 KCX, 1095(ddl)/KCX, 12250 KCX, 1095(ddl)/KCX, 12250 KCX, 14645/KCX, 21250 KCX, 05025/KCX, 26605/KCX, 00905/KCX, 05040/KCX, 12200/KCX, 12200/KCX, 12200/KCX, 12200/KCX, 12405/KCX, 12200/KCX, 12500/KCX, 12500/KCX, 12500/KCX, 12500/KCX, 12500/KCX, 12500/KCX, 15005/KCX, 05040/KCX, 050505/KCX, 05050/KCX, 05050/KC	succoa + hser -> coa + oshser srih -> 45chpen + hcys 2 dala + atp <-> adp + alaala + pi dgln -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP
HSERST SRHCYSL ALAALAL GLUNZ FABC120	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-glutamine and D-glutamate metabolism	sulfurtransferase homoserine O- succinyltransferase S-ribosylhomocysteine lyase D-alanine-D-alanine ligase glutaminase	2.3.146 4.4.121 6.3.24 3.5.12 2.3.1.41 AND 2.3.1.179 AND 2.3.1.180 AND 1.1.100 AND 4.21. AND 1.3.1.9 AND 1.3.1 2.3.1.41 AND	KCX, 08035 KCX, 00500 KCX, 1095(ddl)/KCX, 12250 KCX, 1095(ddl)/KCX, 12250 KCX, 14645/KCX, 21250 KCX, 05025/KCX, 26605/KCX, 00905/KCX, 05040/KCX, 12200/KCX, 12200/KCX, 12200/KCX, 12200/KCX, 12405/KCX, 12200/KCX, 12500/KCX, 12500/KCX, 12500/KCX, 12500/KCX, 12500/KCX, 12500/KCX, 15005/KCX, 05040/KCX, 050505/KCX, 05050/KCX, 05050/KC	succoa + hser -> coa + oshser srih -> 45chpen + hcys 2 dala + atp <-> adp + alaala + pi dgln -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP
HSERST SRHCYSL ALAALAL GLUNZ FABC120	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-glutamine and D-glutamate metabolism Fatty acid biosynthesis	sulfurtransferase homoserine O- succinyltransferase S-ribosylhomocysteine lyase D-alanine-D-alanine ligase glutaminase Fatty acid biosynthesis (dodecanoic acid; c12:0)	2.3.1.46 4.4.1.21 6.3.2.4 3.5.1.2 2.3.1.41 AND 2.3.1.179 AND 1.3.1.00 AND 4.2.1. AND 1.3.1.9 AND 1.3.1. 2.3.1.41 AND 2.3.1.180 AND 1.3.1.0 AND 4.2.1.1.100 AND 4.2.1.100 AND	KCX, 08035 KCX, 00500 KCX, 1095(ddl)/KCX, 12250 KCX, 1095(ddl)/KCX, 12250 KCX, 14645/KCX, 21250 KCX, 05025/KCX, 26605/KCX, 00905/KCX, 05040/KCX, 12200/KCX, 12200/KCX, 12200/KCX, 12200/KCX, 12405/KCX, 12200/KCX, 12500/KCX, 12500/KCX, 12500/KCX, 12500/KCX, 12500/KCX, 12500/KCX, 15005/KCX, 05040/KCX, 050505/KCX, 05050/KCX, 05050/KC	succoa + hser -> coa + osihser srih -> 45dhpen + hcys 2 dala + atp <-> adp + alaala + pi dgin -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP
HSERST SRHCYSL ALAALAL GLUNZ FABC120	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-glutamine and D-glutamate metabolism Fatty acid biosynthesis	sulfurtransferase homoserine O- succinyltransferase S-ribosylhomocysteine lyase D-alanine-D-alanine ligase glutaminase Fatty acid biosynthesis (dodecanoic acid; c12:0)	23.146 44.121 63.24 35.12 23.1179 AND 23.1180 AND 11.1100 AND 4.21- AND 13.1- 23.1179 AND 23.1179 AND 23.1179 AND 11.1100 AND 4.21- AND 13.1- AND 13.1- AND 13.1-	KCX_08035 KCX_00500 KCX_10935(ddl)/KCX_12250 KCX_14645/KCX_21250 KCX_14645/KCX_21250 KCX_14645/KCX_21250 KCX_17280/KCX_0898/KCX_08540/KCX_17280/KC	succoa + hser -> coa + oshser srih -> 45chpen + hcys 2 dala + atp <-> adp + alaala + pi dgln -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP
HSERST SRHCYSL ALAALAL GLUNZ FABC120	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-glutamine and D-glutamate metabolism Fatty acid biosynthesis	sulfurtransferase homoserine O- succinyltransferase S-ribosylhomocysteine lyase D-alanine-D-alanine ligase glutaminase Fatty acid biosynthesis (dodecanoic acid; c12:0)	2.3.1.46 4.4.1.21 6.3.2.4 3.5.1.2 2.3.1.41 AND 2.3.1.179 AND 1.3.1.00 AND 4.2.1. AND 1.3.1.9 AND 1.3.1. 2.3.1.41 AND 2.3.1.180 AND 1.3.1.0 AND 4.2.1.1.100 AND 4.2.1.100 AND	KCX_08035 KCX_00500 KCX_10935(ddl)/KCX_12250 KCX_14645/KCX_21250 KCX_14645/KCX_21250 KCX_14645/KCX_21250 KCX_17280/KCX_0898/KCX_08540/KCX_17280/KC	succoa + bser -> coa + osihser srih -> 45dhpen + hcys 2 dala + atp <-> adop + alaala + pi dgin -> dglu + nb4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c130ACP + 5 co2 + 5 ACP
HSERST SRHCVSL ALAALAL GLUNZ FABC120	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-alanine metabolism D-glutamine and D-glutamate metabolism Fatty acid biosynthesis	sulfurtansferase homoserine O- succinyfitansferase S-ribosylthomosystenie lyase D-alanine-D-alanine ligase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)	23.146 4.4121 6.324 3.5.12 2.3.141 AND 2.3.1160 AND 1.11.100 AND 4.21 AND 1.3.1- 2.3.141 AND 2.3.1180 AND 1.3.1- 2.3.141 AND 2.3.1180 AND 1.11.1100 AND 4.21 AND 1.3.1- AND 1.3.1- 2.3.141 AND 2.3.119 AND 2.3.119 AND 2.3.119 AND 2.3.119 AND 2.3.119 AND	KOX, 08035 KOX, 00500 KOX, 10935(dd)/KOX,12350 KOX, 14645/KOX,21250 KOX, 14645/KOX,21250 KOX, 17300/KOX, 17280/KOX, 00905/KOX, 05040/KOX, 17300/KOX, 17300/KOX, 16725/KOX, 12720/KOX, 17300/KOX, 17300/KOX, 16725/KOX, 12720/KOX, 17300/KOX, 16725/KOX, 12720/KOX, 18650/KOX, 17300/KOX, 17300/KOX, 17280/KOX, 00890/KOX, 02015/fabGy/KOX, 17300/KOX, 17280/KOX, 16725/KOX, 12720/KOX, 17300/KOX, 18650/KOX,	succoa + bser -> coa + osihser srih -> 45dhpen + hcys 2 dala + atp <-> adp + alaala + pi dgln -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c130ACP + 5 co2 + 5 ACP
HSERST SRHCVSL ALAALAL GLUNZ FABC120	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-glutamine and D-glutamate metabolism Fatty acid biosynthesis	suflutransferase homoserine O- succinytransferase D-alanine-D-alanine ligase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c12:0)	23.146 44.121 63.24 35.12 23.141 AND 23.1179 AND 23.1179 AND 11.1100 AND 421- AND 13.19 AND 13.1- 23.141 AND 23.1180 AND 11.1100 AND 421- AND 13.19 AND 13.1- 23.141 AND 23.1179 AND 23.1179 AND 23.1179 AND 23.1180 AND 11.1100 AND 23.1180 AND 11.1100 AND 23.1180 AND 23.1180 AND	KCX, 08035 KCX, 00500 KCX, 10935(ddl),KCX, 12250 KCX, 14645,KCX, 21250 KCX, 14645,KCX, 21250 KCX, 14645,KCX, 21250 KCX, 17300/KCX, 17280,KCX, 00890,KCX, 05040,KCX, 17300/KCX, 17300/KCX, 16455,KCX, 17300/KCX, 16455,KCX, 17300/KCX, 15405,KCX, 15405,KCX, 17300/KCX, 15405,KCX, 15405,KCX, 15405,KCX, 17300,KCX, 17280,KCX, 00890,KCX, 05040,KCX, 17300,KCX, 17300,KCX, 17300,KCX, 17300,KCX, 17300,KCX, 17300,KCX, 17300,KCX, 00890,KCX, 05040,KCX, 17300/KCX, 17290,KCX, 17300,KCX, 17290,KCX, 17290,KCX, 17300/KCX, 17290,KCX, 17300/KCX, 17290,KCX, 17300/KCX, 17290,KCX, 17300/KCX, 17290,KCX, 17290,KCX, 17300/KCX, 17300/KCX, 17290,KCX, 17300/KCX, 17290,KCX, 17300/KCX, 17290,KCX, 17300/KCX, 17290,KCX, 17300/KCX, 1	succoa + bser -> coa + osihser srih -> 45dhpen + hcys 2 dala + atp <> adp + ataala + pi dgln -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c130ACP + 5 co2 + 5 ACP
HSERST SRHCVSL ALAALAL GLUNZ FABC120	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-alanine metabolism D-glutamine and D-glutamate metabolism Fatty acid biosynthesis	sulfurtansferase homoserine O- succinyfitansferase S-ribosylthomosystenie lyase D-alanine-D-alanine ligase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)	23.146 4.4121 6.324 3.5.12 2.3.141 AND 2.3.1160 AND 1.11.100 AND 4.21 AND 1.3.1- 2.3.141 AND 2.3.1180 AND 1.3.1- 2.3.141 AND 2.3.1180 AND 1.11.1100 AND 4.21 AND 1.3.1- AND 1.3.1- 2.3.141 AND 2.3.119 AND 2.3.119 AND 2.3.119 AND 2.3.119 AND 2.3.119 AND	KOX, 08035 KOX, 00500 KOX, 10935(dd)/KOX,12350 KOX, 14645/KOX,21250 KOX, 14645/KOX,21250 KOX, 17300/KOX, 17280/KOX, 00905/KOX, 05040/KOX, 17300/KOX, 17300/KOX, 16725/KOX, 12720/KOX, 17300/KOX, 17300/KOX, 16725/KOX, 12720/KOX, 17300/KOX, 16725/KOX, 12720/KOX, 18650/KOX, 17300/KOX, 17300/KOX, 17280/KOX, 00890/KOX, 02015/fabGy/KOX, 17300/KOX, 17280/KOX, 16725/KOX, 12720/KOX, 17300/KOX, 18650/KOX,	succoa + bser -> coa + osihser srih -> 45dhpen + hcys 2 dala + atp <-> adp + alaala + pi dgln -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c130ACP + 5 co2 + 5 ACP
HSERST SRHCVSL ALAALAL GLUNZ FABC120	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-alanine metabolism D-glutamine and D-glutamate metabolism Fatty acid biosynthesis	sulfurtansferase homoserine O- succinyfitansferase S-ribosylthomosystenie lyase D-alanine-D-alanine ligase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)	231.46 4.4.121 6.32.4 3.5.12 2.3.1.41 AND 2.3.1.179 AND 1.3.1.100 AND 4.21. AND 1.3.19 AND 1.3.1.02 AND 1.3.1.100 AND 4.21.4 NAD 2.3.1.179 AND 2.3.1.19 AND 2.3.1.100 AND 4.21.4 AND 1.3.1.00 AND 4.21.4 AND 1.3.1.2 2.3.1.41 AND	KOX, 08035 KOX, 00500 KOX, 10935(dd)/KOX,12350 KOX, 14645/KOX,21250 KOX, 14645/KOX,21250 KOX, 14645/KOX, 221250 KOX, 1500/KOX, 17280/KOX, 00905/KOX, 05040/KOX, 17200/KOX, 17200	succoa + hser -> coa + osihser  srih -> 45dhpen + hcys 2 data + atp <-> adop + altaala + pi dgin -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c130ACP + 5 co2 + 5 ACP
HSERST SRHCVSL ALAALAL GLUNZ FABC120 FABC130	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-alanine metabolism D-glutamine and D-glutamate metabolism Fatty acid biosynthesis Fatty acid biosynthesis	suflutransferase homoserine O- succinytransferase D-alanine-D-alanine ligase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)	23.146 44.121 63.24 35.12 23.141 AND 23.1179 AND 23.1179 AND 11.1100 AND 42.1- AND 13.19 AND 13.1- 23.141 AND 23.1179 AND 23.1179 AND 23.1179 AND 23.1180 AND 11.1100 AND 42.1- AND 13.19 AND 13.1- 23.141 AND 23.1180 AND 11.1100 AND 42.1- AND 13.19 AND 13.1- 11.1100 AND 42.1- AND 13.19 AND 13.1- 23.141 AND 23.1180 AND 13.1- 23.141 AND 23.1180 AND 23.1180 AND 23.1180 AND 23.1180 AND	KOX, 08035 KOX, 00500 KOX, 10935(ddl),KOX, 12250 KOX, 10935(ddl),KOX, 12250 KOX, 14645,KOX, 21250 KOX, 14645,KOX, 21250 KOX, 13600,KOX, 126805,KOX, 09809,KOX, 095040) KOX, 15000,KOX, 17280,KOX, 16425,KOX, 17290 fabG),KOX, 15150(fabZ),KOX, 18475,KOX, 18960 KOX, 17200,KOX, 17280,KOX, 10425,KOX, 17290 KOX, 17200,KOX, 17280,KOX, 10425,KOX, 17290 KOX, 17200,KOX, 17280,KOX, 00899,KOX, 025040) KOX, 17200,KOX, 17280,KOX, 00899,KOX, 025040 KOX, 17200,KOX, 17280,KOX, 108950,KOX, 17290 KOX, 17200,KOX, 17280,KOX, 108950,KOX, 02905,KOX, 02906,KOX, 02905,KOX, 0	succoa + bser -> coa + osihser  srih -> 45dhpen + hcys 2 dala + atp <-> adop + alaala + pi  dgln -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c130ACP + 5 co2 + 5 ACP  acACP + 6 malACP + 12 nadph -> 12 nadp + c140ACP + 6 co2 + 6 ACP
HSERST SRHCVSL ALAALAL GLUNZ FABC120 FABC130	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-alanine metabolism D-glutamine and D-glutamate metabolism Fatty acid biosynthesis	sulfurtansferase homoserine O- succinyfitansferase S-ribosylthomosystenie lyase D-alanine-D-alanine ligase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)	231.46 4.4.121 6.32.4 3.5.12 2.3.1.41 AND 2.3.1.179 AND 1.3.1.100 AND 4.21. AND 1.3.19 AND 1.3.1.02 AND 1.3.1.100 AND 4.21.4 NAD 2.3.1.179 AND 2.3.1.19 AND 2.3.1.100 AND 4.21.4 AND 1.3.1.00 AND 4.21.4 AND 1.3.1.2 2.3.1.41 AND	KOX, 08035 KOX, 00500 KOX, 10935(dd)/KOX,12350 KOX, 14645/KOX,21250 KOX, 14645/KOX,21250 KOX, 14645/KOX, 221250 KOX, 1500/KOX, 17280/KOX, 00905/KOX, 05040/KOX, 17200/KOX, 17200	succoa + bser -> coa + osihser  srih -> 45dhpen + hcys 2 data + atp <-> adop + altala + pi dgin -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c130ACP + 5 co2 + 5 ACP  acACP + 6 malACP + 12 nadph -> 12 nadp + c140ACP + 6 co2 + 6 ACP
HSERST SRHCVSL ALAALAL GLUNZ FABC120 FABC130	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-alanine metabolism D-glutamine and D-glutamate metabolism Fatty acid biosynthesis Fatty acid biosynthesis	suffurtansferase homoserine O- sucrinytransferase S-ribosylmonoysteine lyase D-alanine-D-alanine ligase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)  Fatty acid biosynthesis (terradecanoic acid; c14:0)	231.46 4.4.121 6.32.4 3.5.12 2.3.1.41 AND 2.3.1.179 AND 1.3.1.100 AND 4.21. AND 1.3.1.9 AND 1.3.1. 2.3.1.179 AND 2.3.1.170 AND 2	KOX, 08035 KOX, 00500 KOX, 10935(dd)/KOX,12350 KOX, 14645/KOX,21250 KOX,14645/KOX,21250 KOX,14645/KOX,21250 KOX,1520/KOX, 26605/KOX, 00905/KOX, 05040/KOX, 17300/KOX, 17300/KOX, 17425/KOX, 12456/KOX, 17300/KOX, 17456/KOX, 12456/KOX, 17400/KOX, 1500/4612/KOX, 18475/KOX, 18460/KOX, 17500/KOX, 18450/KOX, 18450/	succoa + bser -> coa + osihser  srih -> 45dhpen + hcys 2 data + atp <-> adop + altala + pi dgin -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c130ACP + 5 co2 + 5 ACP  acACP + 6 malACP + 12 nadph -> 12 nadp + c140ACP + 6 co2 + 6 ACP
HSERST SRHCVSL ALAALAL GLUNZ FABC120 FABC130	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-alanine metabolism D-glutamine and D-glutamate metabolism Fatty acid biosynthesis Fatty acid biosynthesis	suffurtansferase homoserine O- sucrinytransferase S-ribosylmonoysteine lyase D-alanine-D-alanine ligase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)  Fatty acid biosynthesis (terradecanoic acid; c14:0)	23.1.46 4.4.1.21 6.3.2.4 3.5.1.2 2.3.1.41 AND 2.3.1.179 AND 2.3.1.179 AND 1.1.1.100 AND 4.21. AND 1.3.1.9 AND 1.3.1. 2.3.1.41 AND 2.3.1.179 AND 2.3.1.179 AND 2.3.1.179 AND 2.3.1.180 AND 1.1.1.100 AND 4.21. AND 1.3.1.9 AND 1.3.1. 2.3.1.41 AND 2.3.1.180 AND 1.1.1.100 AND 4.21. AND 1.3.1.9 AND 1.3.1. 2.3.1.41 AND 2.3.1.80 AND 2.3.1.80 AND 4.2.1. AND 1.3.1.9 AND 1.3.1.	KCX, 08035 KCX, 00500 KCX, 10935(ddl),KCX, 12350 KCX, 10935(ddl),KCX, 12350 KCX, 14645,KCX, 21250 KCX, 14645,KCX, 21250 KCX, 14645,KCX, 21250 KCX, 05025,KCX, 26605,KCX, 00905,KCX, 05940,KCX, 13000,KCX, 130000,KCX, 130000,KCX, 13000	succoa + bser -> coa + osihser  srih -> 45dhpen + hcys 2 data + atp <-> adop + altala + pi dgin -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c130ACP + 5 co2 + 5 ACP  acACP + 6 malACP + 12 nadph -> 12 nadp + c140ACP + 6 co2 + 6 ACP
HSERST SRHCVSL ALAALAL GLUNZ FABC120 FABC130	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-alanine metabolism D-glutamine and D-glutamate metabolism Fatty acid biosynthesis Fatty acid biosynthesis	suffurtansferase homoserine O- sucrinytransferase S-ribosylmonoysteine lyase D-alanine-D-alanine ligase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)  Fatty acid biosynthesis (terradecanoic acid; c14:0)	231.46 4.4.121 6.32.4 2.3.1.179 AND 2.3.1.179 AND 2.3.1.179 AND 1.11.100 AND 4.21. AND 1.3.1.9 AND 1.3.1. 2.3.1.179 AND 2.3.1.180 AND 1.1.1.100 AND 4.2.1. AND 1.3.1.00 AND 4.2.1. AND 1.3.1.2. 2.3.1.41 AND 2.	KOX, 08035 KOX, 00500 KOX, 10935(dd)/KOX,12350 KOX,14645/KOX,21250 KOX,14645/KOX,21250 KOX,14645/KOX,21250 KOX,1520/KOX, 26605/KOX, 00905/KOX, 05040/KOX, 17300/KOX, 17300/KOX, 17425/KOX, 12405/KOX,	succoa + hser -> coa + osihser  srih -> 45dhpen + hcys 2 dafa + atp <-> adop + altaala + pi dgin -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c130ACP + 5 co2 + 5 ACP  acACP + 6 malACP + 12 nadph -> 12 nadp + c140ACP + 6 co2 + 6 ACP  acACP + 6 malACP + 11 nadph -> 11 nadp + c141ACP + 6 co2 + 6 ACP
HSERST SRHCYSL ALAALAL GLUNZ FABC120 FABC130 FABC140	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-alanine metabolism D-glutamine and D-glutamate metabolism Fatty acid biosynthesis  Fatty acid biosynthesis  Fatty acid biosynthesis	suffurtansferase homoserine O- sucrinytransferase S-ribosylmonoysteine lyase D-alanine-D-alanine ligase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)  Fatty acid biosynthesis (terradecanoic acid; c14:0)	231.46 4.4.121 6.32.4 2.3.1.179 AND 2.3.1.179 AND 2.3.1.179 AND 1.11.100 AND 4.21. AND 1.3.1.9 AND 1.3.1. 2.3.1.41 AND 2.3.1.179 AND	KOX, 08035 KOX, 00500 KOX, 10935(dd)/KOX,12350 KOX, 14645/KOX,21250 KOX, 14645/KOX,21250 KOX, 14645/KOX, 221250 KOX, 1520/KOX, 26605/KOX, 00905/KOX, 05040/KOX, 15100/KOX, 15100	succoa + hser -> coa + osihser  srih -> 45dhpen + hcys 2 data + atp <-> adop + altaala + pi  dgln -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c130ACP + 5 co2 + 5 ACP  acACP + 6 malACP + 12 nadph -> 12 nadp + c140ACP + 6 co2 + 6 ACP  acACP + 6 malACP + 11 nadph -> 11 nadp + c141ACP + 6 co2 + 6 ACP
HSERST SRHCYSL ALAALAL GLUNZ FABC120 FABC130 FABC140	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-alanine metabolism D-glutamine and D-glutamate metabolism Fatty acid biosynthesis Fatty acid biosynthesis	sulfurtansferase homoserine O- succinyfiransferase S-ribosylmonocysterie lyase D-alanine-D-alanine ligase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)  Fatty acid biosynthesis (tridecanoic acid; c14:0)  Fatty acid biosynthesis (tridecanoic acid; c14:0)  Fatty acid biosynthesis (tetradecanoic acid; c14:1)	23.1.46 4.4.1.21 6.3.2.4 3.5.1.2 2.3.1.41 AND 2.3.1.179 AND 2.3.1.179 AND 1.1.1.100 AND 4.2.1. AND 1.3.1.9 AND 1.3.1. 2.3.1.41 AND 2.3.1.179 AND 2.3.1.180 AND 1.1.1.100 AND 4.2.1. AND 1.3.1.9 AND 1.3.1. 2.3.1.41 AND 2.3.1.180 AND 1.1.1.100 AND 4.2.1. AND 1.3.1.9 AND 1.3.1. 2.3.1.41 AND 2.3.1.180 AND 1.3.1.2 3.1.41 AND 2.3.1.180 AND 1.3.1.3 2.3.1.41 AND 2.3.1.180 AND	KOX, 08035 KOX, 00500 KOX, 10935(ddl)/KOX,12350 KOX, 14645/KOX, 21250 KOX, 14645/KOX, 21250 KOX, 14645/KOX, 21250 KOX, 14645/KOX, 21250 KOX, 1500(KOX, 17280/KOX, 00905/KOX, 05040/KOX, 17280/KOX, 16025/KOX, 160	succoa + hser -> coa + osihser  srih -> 45dhpen + hcys 2 data + atp <-> adop + altaala + pi  dgln -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c130ACP + 5 co2 + 5 ACP  acACP + 6 malACP + 12 nadph -> 12 nadp + c140ACP + 6 co2 + 6 ACP  acACP + 6 malACP + 11 nadph -> 11 nadp + c141ACP + 6 co2 + 6 ACP
HSERST SRHCYSL ALAALAL GLUNZ FABC120 FABC130 FABC140	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-alanine metabolism D-glutamine and D-glutamate metabolism Fatty acid biosynthesis  Fatty acid biosynthesis  Fatty acid biosynthesis	suffurtansferase homoserine O- succinytransferase D- succinytransferase D- succinytransferase D- alanine Ilgase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)  Fatty acid biosynthesis (terradecanoic acid; c14:0)  Fatty acid biosynthesis (terradecanoic acid; c14:1)  Fatty acid biosynthesis (terradecanoic acid; c14:1)	231.46 4.4.121 6.32.4 2.31.179 AND 2.31.179 AND 2.31.179 AND 1.11.100 AND 4.21. AND 1.31.9 AND 1.31	KOX, 08035 KOX, 00500 KOX, 10935(dd)/KOX,12350 KOX, 14645/KOX,21250 KOX, 14645/KOX,21250 KOX, 14645/KOX, 221250 KOX, 1520/KOX, 26605/KOX, 00905/KOX, 05040/KOX, 15100/KOX, 15100	succoa + hser -> coa + osihser  srih -> 45dhpen + hcys 2 data + atp <-> adop + altaala + pi  dgln -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c130ACP + 5 co2 + 5 ACP  acACP + 6 malACP + 12 nadph -> 12 nadp + c140ACP + 6 co2 + 6 ACP  acACP + 6 malACP + 11 nadph -> 11 nadp + c141ACP + 6 co2 + 6 ACP
HSERST SRHCYSL ALAALAL GLUNZ FABC120 FABC130 FABC140	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-alanine metabolism D-glutamine and D-glutamate metabolism Fatty acid biosynthesis  Fatty acid biosynthesis  Fatty acid biosynthesis	suffurtansferase homoserine O- succinytransferase D- succinytransferase D- succinytransferase D- alanine Ilgase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)  Fatty acid biosynthesis (terradecanoic acid; c14:0)  Fatty acid biosynthesis (terradecanoic acid; c14:1)  Fatty acid biosynthesis (terradecanoic acid; c14:1)	231.46 4.4.121 6.32.4 2.31.41 AND 2.31.179 AND 1.31.100 AND 4.21. AND 1.31.9 AND 1.31.100 AND 4.21. AND 1.31.9 AND 2.31.179 AND 2.31.180 AND 1.11.100 AND 4.21. AND 2.31.180 AND 1.31.1.2.31.41 AND 2.31.179 AND 2.31.180 AND 1.31.2.31.41 AND	KOX, 08035 KOX, 00500 KOX, 10935(dd)/KOX,12350 KOX, 1045K/KOX,21250 KOX, 14645K/KOX,21250 KOX, 1520K/KOX, 256605/KOX, 00905/KOX, 05040/KOX, 11720K/KOX, 11720K/KOX	succoa + bser -> coa + osihser  srih -> 45dhpen + hcys 2 data + atp <-> adop + alaala + pi dgln -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c130ACP + 5 co2 + 5 ACP  acACP + 6 malACP + 12 nadph -> 12 nadp + c140ACP + 6 co2 + 6 ACP  ppacp + 6 malACP + 11 nadph -> 11 nadp + c141ACP + 6 co2 + 6 ACP
HSERST SRHCYSL ALAALAL GLUNZ FABC120 FABC130 FABC140	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-alanine metabolism D-glutamine and D-glutamate metabolism Fatty acid biosynthesis  Fatty acid biosynthesis  Fatty acid biosynthesis	sulfurtansferase homoserine O- succinytransferase S-ribosylmonocysterie lyase D-alanine-D-alanine ligase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)  Fatty acid biosynthesis (tridecanoic acid; c14:0)  Fatty acid biosynthesis (tetradecanoic acid; c14:1)  Fatty acid biosynthesis (tetradecanoic acid; c14:1)  Fatty acid biosynthesis (tetradecanoic acid; c14:1)	23.1.46 4.4.1.21 6.3.2.4 3.5.1.2 2.3.1.41 AND 2.3.1.179 AND 2.3.1.179 AND 1.1.1.100 AND 4.21- AND 1.3.1- 2.3.1.41 AND 2.3.1.179 AND 2.3.1.180 AND 1.1.1.100 AND 4.2.1- AND 1.3.1- 2.3.1.41 AND	KOX, 08035 KOX, 00500 KOX, 10935(ddl)/KOX,12350 KOX, 10935(ddl)/KOX,12350 KOX, 13645K/COX,21250 KOX, 13645K/COX,21250 KOX, 13600KCOX, 12780K/COX, 00905/KOX, 05040/KOX, 13605(KOX, 13700KCOX, 1370KCOX, 1	succoa + bser -> coa + osihser  srih -> 45dhpen + hcys 2 data + atp <-> adop + alaala + pi dgln -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c130ACP + 5 co2 + 5 ACP  acACP + 6 malACP + 12 nadph -> 12 nadp + c140ACP + 6 co2 + 6 ACP  ppacp + 6 malACP + 11 nadph -> 11 nadp + c141ACP + 6 co2 + 6 ACP
HSERST SRHCYSL ALAALAL GLUNZ FABC120 FABC130 FABC140 FABC141	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-alanine metabolism D-glutamine and D-glutamate metabolism Fatty acid biosynthesis  Fatty acid biosynthesis  Fatty acid biosynthesis	suffurtansferase homoserine O- succinytransferase Po- succinytransferase S-ribosylmonoysteine lyase D-alanine-D-alanine ligase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)  Fatty acid biosynthesis (tetradecanoic acid; c14:0)  Fatty acid biosynthesis (tetradecanoic acid; c14:1)  Fatty acid biosynthesis (tetradecanoic acid; c14:1)  Fatty acid biosynthesis (pentadecanoic acid; c15:0)	231.46 4.41.21 6.32.4 2.31.41 AND 2.31.179 AND 1.31.100 AND 4.21. AND 1.31.9 AND 1.31.100 AND 4.21.4 NAD 1.31.9 AND 2.31.179 AND	KOX_08035 KOX_00500 KOX_10935(dd);KOX_12350 KOX_10935(dd);KOX_12350 KOX_14645;KOX_21250 KOX_14645;KOX_21250 KOX_1520;KOX_26605;KOX_00905;KOX_05040;KOX_17300;KOX_17280;KOX_16450;KOX_17280;KOX_17280;KOX_16450;KOX_17280;KOX_17280;KOX_16450;KOX_17280;KOX_17280;KOX_16450;KOX_17280;KOX_17280;KOX_16450;KOX_17280;KOX_17280;KOX_16450;KOX_17280;KOX_17280;KOX_17280;KOX_16450;KOX_17280;KOX_17280;KOX_17280;KOX_17280;KOX_17280;KOX_17280;KOX_17280;KOX_18450;KOX_17280;KOX_17280;KOX_16450;KOX_18450;KOX_17280;KOX_17280;KOX_18450	succoa + hser -> coa + osihser  srih -> 45dhpen + hcys 2 data + atp <-> adop + alaala + pi dgln -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  acACP + 6 malACP + 12 nadph -> 12 nadp + c140ACP + 6 co2 + 6 ACP  acACP + 6 malACP + 11 nadph -> 11 nadp + c141ACP + 6 co2 + 6 ACP  ppacp + 6 malACP + 12 nadph -> 12 nadp + 6 co2 + 6 ACP + c150ACP
HSERST SRHCYSL ALAALAL GLUNZ FABC120 FABC130 FABC140 FABC141	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-alanine metabolism D-glutamine and D-glutamate metabolism Fatty acid biosynthesis  Fatty acid biosynthesis  Fatty acid biosynthesis	sulfurtansferase homoserine O- succinytransferase S-ribosylmonocysterie lyase D-alanine-D-alanine ligase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)  Fatty acid biosynthesis (tridecanoic acid; c14:0)  Fatty acid biosynthesis (tetradecanoic acid; c14:1)  Fatty acid biosynthesis (tetradecanoic acid; c14:1)  Fatty acid biosynthesis (tetradecanoic acid; c14:1)	23.1.46 4.4.1.21 6.3.2.4 3.5.1.2 2.3.1.41 AND 2.3.1.179 AND 2.3.1.179 AND 1.1.1.100 AND 4.21- AND 1.3.1- 2.3.1.41 AND 2.3.1.179 AND 2.3.1.180 AND 1.1.1.100 AND 4.2.1- AND 1.3.1- 2.3.1.41 AND 2.	KOX, 08035 KOX, 00500 KOX, 10935(ddl)/KOX,12350 KOX, 10935(ddl)/KOX,12350 KOX, 13645K/COX,21250 KOX, 13645K/COX,21250 KOX, 13600KCOX, 12780K/COX, 00905/KOX, 05040/KOX, 13605(KOX, 13700KCOX, 1370KCOX, 1	succoa + hser -> coa + osihser  srih -> 45dhpen + hcys 2 data + atp <-> adop + alaala + pi dgln -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  acACP + 6 malACP + 12 nadph -> 12 nadp + c140ACP + 6 co2 + 6 ACP  acACP + 6 malACP + 11 nadph -> 11 nadp + c141ACP + 6 co2 + 6 ACP  ppacp + 6 malACP + 12 nadph -> 12 nadp + 6 co2 + 6 ACP + c150ACP
HSERST SRHCYSL ALAALAL GLUNZ FABC120 FABC130 FABC140 FABC141	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-alanine metabolism D-glutamine and D-glutamate metabolism Fatty acid biosynthesis  Fatty acid biosynthesis  Fatty acid biosynthesis	suffurtansferase homoserine O- succinytransferase Po- succinytransferase S-ribosylmonoysteine lyase D-alanine-D-alanine ligase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)  Fatty acid biosynthesis (tetradecanoic acid; c14:0)  Fatty acid biosynthesis (tetradecanoic acid; c14:1)  Fatty acid biosynthesis (tetradecanoic acid; c14:1)  Fatty acid biosynthesis (pentadecanoic acid; c15:0)	23.1.46 4.4.1.21 6.3.2.4 3.5.1.2 2.3.1.41 AND 2.3.1.179 AND 2.3.1.179 AND 1.11.100 AND 4.21- AND 1.3.1- 2.3.1.41 AND 2.3.1.179 AND 2.3.1.180 AND 1.1.1.100 AND 4.2.1- AND 1.3.1- 2.3.1.41 AND 2.3.1.180 AND 1.1.1.2 2.3.1.41 AND 2.3.1.180 AND 1.3.1- 2.3.1.41 AND 2.3.1.180 AND	KOX, 08035 KOX, 00500 KOX, 10935(ddl);KOX, 12350 KOX, 13645;KOX, 21250 KOX, 14645;KOX, 21250 KOX, 14645;KOX, 21250 KOX, 14645;KOX, 21250 KOX, 15007(xx), 2780;KOX, 00905;KOX, 05040;KOX, 12015(fabc);KOX, 11500(fabc);KOX, 14475;KOX, 148960 KOX, 05025;KOX, 26665;KOX, 00905;KOX, 05040;KOX, 1500(fabc);KOX, 14475;KOX, 18960 KOX, 05025;KOX, 26665;KOX, 00905;KOX, 05040;KOX, 1500(fabc);KOX, 14475;KOX, 18960 KOX, 05025;KOX, 26605;KOX, 00905;KOX, 05040;KOX, 17300;KOX, 17320;KOX, 1500(fabc);KOX, 14475;KOX, 12900;KOX, 17300;KOX, 17320;KOX, 1500(fabc);KOX, 1500;KOX, 1500;KOX	succoa + hser -> coa + osihser  srih -> 45dhpen + hcys 2 data + atp <-> adop + alaala + pi dgln -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  acACP + 6 malACP + 12 nadph -> 12 nadp + c140ACP + 6 co2 + 6 ACP  acACP + 6 malACP + 11 nadph -> 11 nadp + c141ACP + 6 co2 + 6 ACP  ppacp + 6 malACP + 12 nadph -> 12 nadp + 6 co2 + 6 ACP + c150ACP
HSERST SRHCYSL ALAALAL GLUNZ FABC120 FABC130 FABC140 FABC141	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-alanine metabolism D-glutamine and D-glutamate metabolism Fatty acid biosynthesis  Fatty acid biosynthesis  Fatty acid biosynthesis	suffurtansferase homoserine O- succinytransferase Po- succinytransferase S-ribosylmonoysteine lyase D-alanine-D-alanine ligase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)  Fatty acid biosynthesis (tetradecanoic acid; c14:0)  Fatty acid biosynthesis (tetradecanoic acid; c14:1)  Fatty acid biosynthesis (tetradecanoic acid; c14:1)  Fatty acid biosynthesis (pentadecanoic acid; c15:0)	231.46 4.41.21 6.32.4 2.31.41 AND 2.31.179 AND 1.31.100 AND 4.21. AND 1.31.9 AND 1.31.100 AND 4.21. AND 1.31.9 AND 2.31.179 AND 2.31.180 AND 1.11.100 AND 4.21. AND 2.31.179 AND 2.31.170 A	KOX, 08035 KOX, 00500 KOX, 10935(dd)/KOX,12350 KOX, 10935(dd)/KOX,12350 KOX,14645/KOX,21250 KOX,14645/KOX,21250 KOX,14645/KOX,21250 KOX, 1520/KOX, 15265/KOX, 00905/KOX, 05040/KOX, 1520/KOX, 1520/K	succoa + hser -> coa + oshser  srh -> 45dhpen + hcys 2 dafa + atp <-> adop + alaala + pi dgln -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c130ACP + 5 co2 + 5 ACP  acACP + 6 malACP + 12 nadph -> 12 nadp + c140ACP + 6 co2 + 6 ACP  acACP + 6 malACP + 11 nadph -> 11 nadp + c141ACP + 6 co2 + 6 ACP  ppacp + 6 malACP + 12 nadph -> 12 nadp + 6 co2 + 6 ACP + c150ACP
HSERST SRHCYSL ALAALAL GLUNZ FABC120 FABC130 FABC140 FABC141	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-alanine metabolism D-alanine metabolism Fatty acid biosynthesis Fatty acid biosynthesis Fatty acid biosynthesis Fatty acid biosynthesis	suffurtansferase homoserine O- succinytransferase S-ribosylmonosysteine lyase D-alanine-D-alanine ligase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)  Fatty acid biosynthesis (terradecanoic acid; c14:0)  Fatty acid biosynthesis (terradecanoic acid; c14:1)  Fatty acid biosynthesis (terradecanoic acid; c15:0)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)	231.46 4.41.21 6.32.4 3.5.12 2.3.1.41 AND 2.3.1.179 AND 1.3.11.00 AND 4.21. AND 1.3.19 AND 1.3.1.00 AND 4.21. AND 1.3.19 AND 2.3.1.179 AND 2.3.1.180 AND 1.1.1.100 AND 4.2.1. AND 2.3.1.179 AND	KOX, 08035 KOX, 00500 KOX, 10935(dd)/KOX,12350 KOX, 10935(dd)/KOX,12350 KOX, 14645/KOX,21250 KOX, 14645/KOX,21250 KOX, 14645/KOX, 12250 KOX, 15000KOX, 127280/KOX, 00905/KOX, 05040/KOX, 127280/KOX, 127280/KOX, 10095/KOX, 12015(da5)/KOX, 11500(da52/KOX, 14645/KOX, 13800 KOX, 05025/KOX, 26605/KOX, 00905/KOX, 05040/KOX, 127300/KOX, 127280/KOX, 10095/KOX, 127280/KOX, 1	succoa + bser -> coa + osihser  srih -> 45dhpen + hcys 2 dala + atp <-> adop + alaala + pi dgin -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c130ACP + 5 co2 + 5 ACP  acACP + 6 malACP + 12 nadph -> 12 nadp + c140ACP + 6 co2 + 6 ACP  ppacp + 6 malACP + 11 nadph -> 11 nadp + c141ACP + 6 co2 + 6 ACP  ppacp + 6 malACP + 11 nadph -> 12 nadp + 6 co2 + 6 ACP + c150ACP
HSERST SRHCYSL ALAALAL GGUN2 FABC120 FABC130 FABC141 FABC151	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-alanine metabolism D-glutamine and D-glutamate metabolism Fatty acid biosynthesis  Fatty acid biosynthesis  Fatty acid biosynthesis	sulfurtansferase homoserine O- succinytransferase S-ribosylmonocysterie lyase D-alanine-D-alanine ligase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)  Fatty acid biosynthesis (tetradecanoic acid; c14:0)  Fatty acid biosynthesis (tetradecanoic acid; c14:1)  Fatty acid biosynthesis (tetradecanoic acid; c15:0)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)	23.1.46 4.4.1.21 6.3.2.4 3.5.1.2 2.3.1.41 AND 2.3.1.179 AND 2.3.1.179 AND 1.11.100 AND 4.21. AND 1.3.1.9 AND 1.3.1	KOX, 08035 KOX, 00500 KOX, 10935(ddl);KOX, 12350 KOX, 13645;KOX, 221250 KOX, 13645;KOX, 221250 KOX, 13645;KOX, 226605;KOX, 00905;KOX, 05904) KOX, 13600;KOX, 127280;KOX, 00905;KOX, 05904) KOX, 13700(KOX, 137280;KOX, 16425;KOX, 12720) KOX, 13500(KOX, 137280;KOX, 16425;KOX, 12720) KOX, 05025;KOX, 26605;KOX, 00905;KOX, 05904) KOX, 05025;KOX, 26605;KOX, 00905;KOX, 05904) KOX, 13700(KOX, 137280;KOX, 16425;KOX, 12720) KOX, 05025;KOX, 26605;KOX, 00905;KOX, 05904) KOX, 13700(KOX, 137280;KOX, 16425;KOX, 13720) KOX, 05025;KOX, 26605;KOX, 00905;KOX, 05904) KOX, 13700(KOX, 137280;KOX, 00905;KOX, 12720) KOX, 13700(KOX, 137280;KOX, 00905;KOX, 12720) KOX, 13700(KOX, 137280;KOX, 00905;KOX, 12720) KOX, 13700(KOX, 137280;KOX, 00905;KOX, 13906) KOX, 13700(KOX, 137280;KOX, 00905;KOX, 05904) KOX, 13700(KOX, 137280;KOX, 0	succoa + hser -> coa + oshser  srh -> 45dhpen + hcys 2 dafa + atp <-> adop + alaala + pi dgln -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c130ACP + 5 co2 + 5 ACP  acACP + 6 malACP + 12 nadph -> 12 nadp + c140ACP + 6 co2 + 6 ACP  acACP + 6 malACP + 11 nadph -> 11 nadp + c141ACP + 6 co2 + 6 ACP  ppacp + 6 malACP + 12 nadph -> 12 nadp + 6 co2 + 6 ACP + c150ACP
HSERST SRHCYSL ALAALAL GLUNZ FABC120 FABC130 FABC140 FABC141	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-alanine metabolism D-alanine metabolism Fatty acid biosynthesis Fatty acid biosynthesis Fatty acid biosynthesis Fatty acid biosynthesis	suffurtansferase homoserine O- succinytransferase S-ribosylmonosysteine lyase D-alanine-D-alanine ligase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)  Fatty acid biosynthesis (terradecanoic acid; c14:0)  Fatty acid biosynthesis (terradecanoic acid; c14:1)  Fatty acid biosynthesis (terradecanoic acid; c15:0)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)	23.1.46 4.4.1.21 6.3.2.4 3.5.1.2 2.3.1.41 AND 2.3.1.179 AND 2.3.1.179 AND 1.11.100 AND 4.21. AND 1.3.1.9 AND 1.3.1	KOX, 08035 KOX, 00500 KOX, 10935(dd)/KOX,12350 KOX, 10935(dd)/KOX,12350 KOX, 14645/KOX,21250 KOX, 14645/KOX,21250 KOX, 14645/KOX, 12250 KOX, 15000KOX, 127280/KOX, 00905/KOX, 05040/KOX, 127280/KOX, 127280/KOX, 10095/KOX, 12015(da5)/KOX, 11500(da52/KOX, 14645/KOX, 13800 KOX, 05025/KOX, 26605/KOX, 00905/KOX, 05040/KOX, 127300/KOX, 127280/KOX, 10095/KOX, 127280/KOX, 1	succoa + bser -> coa + osihser  srih -> 45dhpen + hcys 2 dala + atp <-> adop + alaala + pi dgin -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c130ACP + 5 co2 + 5 ACP  acACP + 6 malACP + 12 nadph -> 12 nadp + c140ACP + 6 co2 + 6 ACP  ppacp + 6 malACP + 11 nadph -> 11 nadp + c141ACP + 6 co2 + 6 ACP  ppacp + 6 malACP + 11 nadph -> 12 nadp + 6 co2 + 6 ACP + c150ACP
HSERST SRHCYSL ALAALAL GLUNZ FABC120 FABC130 FABC140 FABC141	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-alanine metabolism D-alanine metabolism Fatty acid biosynthesis Fatty acid biosynthesis Fatty acid biosynthesis Fatty acid biosynthesis	suffurtansferase homoserine O- succinytransferase S-ribosylmonosysteine lyase D-alanine-D-alanine ligase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)  Fatty acid biosynthesis (terradecanoic acid; c14:0)  Fatty acid biosynthesis (terradecanoic acid; c14:1)  Fatty acid biosynthesis (terradecanoic acid; c15:0)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)	231.16 4.41.21 6.32.4 3.5.12 2.3.1.41 AND 2.3.1.179 AND 1.3.11.00 AND 4.21. AND 1.3.19 AND 1.3.1.00 AND 4.21. AND 1.3.19 AND 2.3.1.179 AND 2.3.1.170 AND 2.3	KOX, 08035 KOX, 00500 KOX, 10935(dd)/KOX, 12350 KOX, 10935(dd)/KOX, 12350 KOX, 124645/KOX, 21250 KOX, 124645/KOX, 21250 KOX, 124645/KOX, 21250 KOX, 12500/KOX, 12625/KOX, 00905/KOX, 05040/KOX, 127300/KOX, 127300	succoa + bser -> coa + osihser  srih -> 45dhpen + hcys 2 dala + atp <-> adop + alaala + pi dgin -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c130ACP + 5 co2 + 5 ACP  acACP + 6 malACP + 12 nadph -> 12 nadp + c140ACP + 6 co2 + 6 ACP  ppacp + 6 malACP + 11 nadph -> 11 nadp + c141ACP + 6 co2 + 6 ACP  ppacp + 6 malACP + 11 nadph -> 12 nadp + 6 co2 + 6 ACP + c150ACP
HSERST SRHCYSL ALAALAL GLUNZ FABC120 FABC130 FABC140 FABC141	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-alanine metabolism D-alanine metabolism Fatty acid biosynthesis Fatty acid biosynthesis Fatty acid biosynthesis Fatty acid biosynthesis	sulfurtansferase homoserine O- succinytransferase S-ribosylmonocysteine lyase D-alanine-D-alanine ligase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)  Fatty acid biosynthesis (tetradecanoic acid; c14:0)  Fatty acid biosynthesis (tetradecanoic acid; c14:1)  Fatty acid biosynthesis (tetradecanoic acid; c15:0)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)	23.1.46 4.4.1.21 6.3.2.4 3.5.1.2 2.3.1.41 AND 2.3.1.179 AND 2.3.1.179 AND 1.11.100 AND 4.21. AND 1.3.1.9 AND 1.3.1	KOX, 08035 KOX, 00500 KOX, 10935(ddl)/KOX, 12350 KOX, 10935(ddl)/KOX, 12350 KOX, 13645/KOX, 221250 KOX, 13645/KOX, 221250 KOX, 13600/KOX, 127280/KOX, 00905/KOX, 05904/KOX, 127280/KOX, 100905/KOX, 05904/KOX, 127280/KOX, 100905/KOX, 12905/KOX,	succoa + bser -> coa + osihser  srih -> 45dhpen + hcys 2 dals + atp <-> adop + alaala + pi dgin -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c130ACP + 5 co2 + 5 ACP  acACP + 6 malACP + 12 nadph -> 12 nadp + c140ACP + 6 co2 + 6 ACP  acACP + 6 malACP + 11 nadph -> 11 nadp + c141ACP + 6 co2 + 6 ACP  ppacp + 6 malACP + 11 nadph -> 12 nadp + 6 co2 + 6 ACP + c150ACP  acACP + 6 malACP + 11 nadph -> 11 nadp + 6 co2 + 6 ACP + c151ACP
HSERST SRHCYSL ALAALAL GGUN2 FABC120 FABC130 FABC140 FABC151 FABC151	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-alanine metabolism D-alanine metabolism Fatty acid biosynthesis Fatty acid biosynthesis Fatty acid biosynthesis Fatty acid biosynthesis	suffurtransferase homoserine O- succinytransferase S-ribosylmonosysteine lyase D-alanine-D-alanine ligase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)  Fatty acid biosynthesis (tetradecanoic acid; c14:0)  Fatty acid biosynthesis (tetradecanoic acid; c14:1)  Fatty acid biosynthesis (tetradecanoic acid; c15:1)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)	231.146 4.41.21 6.32.4 3.5.12 2.3.1.41 AND 2.3.1.179 AND 1.3.1100 AND 4.21. AND 1.3.1.9 AND 1.3.1.0 AND 1.3.1.1 AND 2.3.1.179 AND 2.3.1.17	KOX, 08035 KOX, 00500 KOX, 10935(ddl)/KOX, 12350 KOX, 10935(ddl)/KOX, 12350 KOX, 126465/KOX, 221250 KOX, 14645/KOX, 221250 KOX, 15000KOX, 127280/KOX, 00905/KOX, 05040/KOX, 127280/KOX, 127280/KOX, 10095/KOX, 12015(da5)/KOX, 12130/KOX, 12015(da5)/KOX, 12130/KOX, 12015(da5)/KOX, 12130/KOX, 12015(da5)/KOX, 12130/KOX, 12015(da5)/KOX, 12130/KOX, 12015(da5)/KOX, 12130/KOX, 121280/KOX, 12015(da5)/KOX, 1	succoa + hser -> coa + osihser  srih -> 45dhpen + hcys 2 dala + atp <-> adop + alaala + pi dgln -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c130ACP + 5 co2 + 5 ACP  acACP + 6 malACP + 12 nadph -> 12 nadp + c140ACP + 6 co2 + 6 ACP  acACP + 6 malACP + 11 nadph -> 11 nadp + c141ACP + 6 co2 + 6 ACP  ppacp + 6 malACP + 12 nadph -> 12 nadp + c140ACP + 6 co2 + 6 ACP  acACP + 7 malACP + 11 nadph -> 11 nadp + 6 co2 + 6 ACP + c150ACP  acACP + 7 malACP + 14 nadph -> 14 nadp + c160ACP + 7 co2 + 7 ACP
HSERST SRHCYSL ALAALAL GGUN2 FABC120 FABC130 FABC140 FABC151 FABC151	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-alanine metabolism D-alanine metabolism Fatty acid biosynthesis	sulfurtansferase homoserine O- succinytransferase S-ribosylmonocysteine lyase D-alanine-D-alanine ligase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)  Fatty acid biosynthesis (tetradecanoic acid; c14:0)  Fatty acid biosynthesis (tetradecanoic acid; c14:1)  Fatty acid biosynthesis (tetradecanoic acid; c15:0)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)	23.1.46 4.4.1.21 6.3.2.4 3.5.1.2 2.3.1.41 AND 2.3.1.179 AND 2.3.1.179 AND 1.1.1.100 AND 4.21. AND 1.3.1.9 AND 1.3.1. 2.3.1.41 AND 2.3.1.179 AND 2.3.1.180 AND 1.3.1. 2.3.1.41 AND 2.3.1.180 AND 1.3.1. 2.3.1.41 AND 2.3.1.180 AND 1.3.1.0 AND 1.3.1.0 AND 1.3.1.0 AND 1.3.1.0 AND 1.3.1.0 AND 1.3.1.1 AND 2.3.1.180 AND 2.3.1.1100 AND 2.3.1.180 AND	KOX, 08035 KOX, 00500 KOX, 10353(ddl)/KOX,12350 KOX, 10353(ddl)/KOX,12350 KOX, 13645/KOX, 21250 KOX, 13645/KOX, 21250 KOX, 13645/KOX, 21250 KOX, 13600/KOX, 127280/KOX, 00905/KOX, 05040/KOX, 13615/KOX, 13705/KOX, 13615/KOX, 13615/KOX, 13615/KOX, 13605/KOX, 13605/KO	succoa + hser -> coa + osihser  srih -> 45dhpen + hcys 2 dala + atp <-> adop + alaala + pi dgln -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c130ACP + 5 co2 + 5 ACP  acACP + 6 malACP + 12 nadph -> 12 nadp + c140ACP + 6 co2 + 6 ACP  acACP + 6 malACP + 11 nadph -> 11 nadp + c141ACP + 6 co2 + 6 ACP  ppacp + 6 malACP + 12 nadph -> 12 nadp + c140ACP + 6 co2 + 6 ACP  acACP + 7 malACP + 11 nadph -> 11 nadp + 6 co2 + 6 ACP + c150ACP  acACP + 7 malACP + 14 nadph -> 14 nadp + c160ACP + 7 co2 + 7 ACP
HSERST SRHCYSL ALAALAL GGUN2 FABC120 FABC130 FABC140 FABC151 FABC151	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-alanine metabolism D-alanine metabolism Fatty acid biosynthesis	suffurtransferase homoserine O- succinytransferase S-ribosylmonosysteine lyase D-alanine-D-alanine ligase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)  Fatty acid biosynthesis (tetradecanoic acid; c14:0)  Fatty acid biosynthesis (tetradecanoic acid; c14:1)  Fatty acid biosynthesis (tetradecanoic acid; c15:1)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)	23.1.46 4.4.1.21 6.3.2.4 3.5.1.2 2.3.1.41 AND 2.3.1.179 AND 2.3.1.179 AND 1.11.100 AND 4.21. AND 1.3.1.9 AND 1.3.1	KOX, 08035 KOX, 00500 KOX, 10935(ddl)/KOX, 12350 KOX, 10935(ddl)/KOX, 12350 KOX, 126465/KOX, 221250 KOX, 14645/KOX, 221250 KOX, 15000KOX, 127280/KOX, 00905/KOX, 05040/KOX, 127280/KOX, 127280/KOX, 10095/KOX, 12015(da5)/KOX, 12130/KOX, 12015(da5)/KOX, 12130/KOX, 12015(da5)/KOX, 12130/KOX, 12015(da5)/KOX, 12130/KOX, 12015(da5)/KOX, 12130/KOX, 12015(da5)/KOX, 12130/KOX, 121280/KOX, 12015(da5)/KOX, 1	succoa + hser -> coa + osihser  srih -> 45dhpen + hcys 2 dala + atp <-> adop + alaala + pi dgln -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c130ACP + 5 co2 + 5 ACP  acACP + 6 malACP + 12 nadph -> 12 nadp + c140ACP + 6 co2 + 6 ACP  acACP + 6 malACP + 11 nadph -> 11 nadp + c141ACP + 6 co2 + 6 ACP  ppacp + 6 malACP + 12 nadph -> 12 nadp + c140ACP + 6 co2 + 6 ACP  acACP + 7 malACP + 11 nadph -> 11 nadp + 6 co2 + 6 ACP + c150ACP  acACP + 7 malACP + 14 nadph -> 14 nadp + c160ACP + 7 co2 + 7 ACP
HSERST SRHCYSL ALAALAL GGUN2 FABC120 FABC130 FABC140 FABC151 FABC151	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-alanine metabolism D-alanine metabolism Fatty acid biosynthesis	suffurtransferase homoserine O- succinytransferase S-ribosylmonosysteine lyase D-alanine-D-alanine ligase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)  Fatty acid biosynthesis (tetradecanoic acid; c14:0)  Fatty acid biosynthesis (tetradecanoic acid; c14:1)  Fatty acid biosynthesis (tetradecanoic acid; c15:1)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)	231.146 4.41.21 6.32.4 4.31.17 4.35.12 2.31.181 AND 2.31.179 AND 1.31.100 AND 4.21. AND 1.31.9 AND 1.31.2 3.31.180 AND 1.31.2 3.31.2 3.31.2 AND 2.31.2 AND 3.31.2 AND 3.31.2 AND 3.31.2 AND 3.31.2 AND 3.31.2 AND 3.31.2 AND	KOX, 08035 KOX, 00500 KOX, 10353(dd)/KOX,12350 KOX, 104645/KOX,21250 KOX, 14645/KOX,21250 KOX, 14645/KOX,21250 KOX, 150000, 150000, 150000, 150000, 150000, 150000, 150000, 150000, 1500000, 1500000, 1500000, 15000000, 150000000000	succoa + hser -> coa + osihser  srih -> 45dhpen + hcys 2 dala + atp <-> adop + alaala + pi dgln -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c130ACP + 5 co2 + 5 ACP  acACP + 6 malACP + 12 nadph -> 12 nadp + c140ACP + 6 co2 + 6 ACP  acACP + 6 malACP + 11 nadph -> 11 nadp + c141ACP + 6 co2 + 6 ACP  ppacp + 6 malACP + 12 nadph -> 12 nadp + c co2 + 6 ACP + c150ACP  ppacp + 6 malACP + 11 nadph -> 11 nadp + 6 co2 + 6 ACP + c150ACP  acACP + 7 malACP + 14 nadph -> 14 nadp + c160ACP + 7 co2 + 7 ACP  acACP + 7 malACP + 13 nadph -> 13 nadp + c160ACP + 7 co2 + 7 ACP
HSERST SRHCYSL ALAALAL GGUN2 FABC120 FABC130 FABC140 FABC151 FABC151	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-alanine metabolism D-alanine metabolism Fatty acid biosynthesis	sulfurtansferase homoserine O- succinytransferase S-ribosylmonycsteine lyase D-alanine-D-alanine ligase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)  Fatty acid biosynthesis (tridecanoic acid; c14:0)  Fatty acid biosynthesis (tetradecanoic acid; c14:1)  Fatty acid biosynthesis (tetradecanoic acid; c14:1)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)  Fatty acid biosynthesis (pentadecanoic acid; c16:0)	23.1.46 4.4.1.21 6.3.2.4 3.5.1.2 2.3.1.41 AND 2.3.1.179 AND 2.3.1.179 AND 1.1.1.100 AND 4.2.1. AND 1.3.1.9 AND 1.3	KOX, 08035 KOX, 00500 KOX, 10353(ddl)/KOX, 12350 KOX, 10353(ddl)/KOX, 12350 KOX, 13645K/COX, 21250 KOX, 13645K/COX, 21250 KOX, 13645K/COX, 21250 KOX, 13600KOX, 127280KOX, 00905K/COX, 05040K KOX, 13600KOX, 127280KOX, 00905K/COX, 12015(fabcl)/KOX, 11500(fabcl)/KOX, 136475KOX, 13690K KOX, 05025KOX, 26605KOX, 00905K/COX, 05040K KOX, 13700KOX, 127280KOX, 00909K/COX, 05040K KOX, 13700KOX, 137280KOX, 00909K/COX, 05040K KOX, 05025KOX, 26605KOX, 00909K/COX, 02015(fabcl)/KOX, 13700KOX,	succoa + hser -> coa + osihser  srih -> 45dhpen + hcys 2 dala + atp <-> adop + alaala + pi dgln -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c130ACP + 5 co2 + 5 ACP  acACP + 6 malACP + 12 nadph -> 12 nadp + c140ACP + 6 co2 + 6 ACP  acACP + 6 malACP + 11 nadph -> 11 nadp + c141ACP + 6 co2 + 6 ACP  ppacp + 6 malACP + 12 nadph -> 12 nadp + c co2 + 6 ACP + c150ACP  ppacp + 6 malACP + 11 nadph -> 11 nadp + 6 co2 + 6 ACP + c150ACP  acACP + 7 malACP + 14 nadph -> 14 nadp + c160ACP + 7 co2 + 7 ACP  acACP + 7 malACP + 13 nadph -> 13 nadp + c160ACP + 7 co2 + 7 ACP
HSERST SRHCYSL ALAALAL GGUN2 FABC120 FABC130 FABC140 FABC151 FABC151	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-alanine metabolism D-alanine metabolism Fatty acid biosynthesis	suffurtransferase homoserine O- succinytransferase S-ribosylmonosysteine lyase D-alanine-D-alanine ligase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)  Fatty acid biosynthesis (tetradecanoic acid; c14:0)  Fatty acid biosynthesis (tetradecanoic acid; c14:1)  Fatty acid biosynthesis (tetradecanoic acid; c15:0)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)  Fatty acid biosynthesis (pentadecanoic acid; c16:0)  Fatty acid biosynthesis (hexadecanoic acid; c16:0)  Fatty acid biosynthesis (hexadecanoic acid; c16:1)	231.146 4.41.21 6.32.4 4.31.17 4.35.12 2.31.181 AND 2.31.179 AND 1.31.100 AND 4.21. AND 1.31.9 AND 1.31.100 AND 4.21. AND 1.31.9 AND 1.31.100 AND 4.21. AND 1.31.100 AND 4.21.100 AND 4.21.1100 AND 4.21.11100 AND 4.21.1100 AND 4.21.11100 AND 4.21.111100 AND 4.21.11100 AND 4.21.111100 AND 4.21.1111	KOX, 08035 KOX, 00500 KOX, 10935(dd)/KOX, 12350 KOX, 10650, ACC, 123	succoa + hser -> coa + osihser  srih -> 45dhpen + hcys 2 dala + atp <-> adop + alaala + pi dgln -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c130ACP + 5 co2 + 5 ACP  acACP + 6 malACP + 12 nadph -> 12 nadp + c140ACP + 6 co2 + 6 ACP  acACP + 6 malACP + 11 nadph -> 11 nadp + c141ACP + 6 co2 + 6 ACP  ppacp + 6 malACP + 12 nadph -> 12 nadp + c6 co2 + 6 ACP + c150ACP  ppacp + 6 malACP + 11 nadph -> 11 nadp + 6 co2 + 6 ACP + c150ACP  acACP + 7 malACP + 14 nadph -> 14 nadp + c160ACP + 7 co2 + 7 ACP  acACP + 7 malACP + 14 nadph -> 14 nadp + c160ACP + 7 co2 + 7 ACP
HSERST SRHCYSL ALAALAL GIUNZ FABC120 FABC130 FABC140 FABC151 FABC151 FABC161	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-alanine metabolism D-alanine metabolism Fatty acid biosynthesis	sulfurtansferase homoserine O- succinytransferase S-ribosylmonycsteine lyase D-alanine-D-alanine ligase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)  Fatty acid biosynthesis (tridecanoic acid; c14:0)  Fatty acid biosynthesis (tetradecanoic acid; c14:1)  Fatty acid biosynthesis (tetradecanoic acid; c14:1)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)  Fatty acid biosynthesis (pentadecanoic acid; c16:0)	23.1.46 4.4.1.21 6.3.2.4 3.5.1.2 2.3.1.41 AND 2.3.1.179 AND 2.3.1.179 AND 1.1.1.100 AND 4.21. AND 1.3.1.9 AND 1.3.	KOX, 08035 KOX, 00500 KOX, 10353(dd)/KOX, 12350 KOX, 10353(dd)/KOX, 12350 KOX, 13645K/COX, 21250 KOX, 13645K/COX, 21250 KOX, 13645K/COX, 21250 KOX, 13600KOX, 127280KOX, 00905/KOX, 05904/KOX, 12615K/COX, 12705K/COX, 12705K/	succoa + hser -> coa + osihser  srih -> 45dhpen + hcys 2 dala + atp <-> adop + alaala + pi dgln -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c130ACP + 5 co2 + 5 ACP  acACP + 6 malACP + 12 nadph -> 12 nadp + c140ACP + 6 co2 + 6 ACP  acACP + 6 malACP + 11 nadph -> 11 nadp + c141ACP + 6 co2 + 6 ACP  ppacp + 6 malACP + 12 nadph -> 12 nadp + c6 co2 + 6 ACP + c150ACP  ppacp + 6 malACP + 11 nadph -> 11 nadp + 6 co2 + 6 ACP + c150ACP  acACP + 7 malACP + 14 nadph -> 14 nadp + c160ACP + 7 co2 + 7 ACP  acACP + 7 malACP + 14 nadph -> 14 nadp + c160ACP + 7 co2 + 7 ACP
HSERST SRHCYSL ALAALAL GIUNZ FABC120 FABC130 FABC140 FABC151 FABC151 FABC161	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-alanine metabolism D-alanine metabolism Fatty acid biosynthesis	suffurtransferase homoserine O- succinytransferase S-ribosylmonosysteine lyase D-alanine-D-alanine ligase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)  Fatty acid biosynthesis (tetradecanoic acid; c14:0)  Fatty acid biosynthesis (tetradecanoic acid; c14:1)  Fatty acid biosynthesis (tetradecanoic acid; c15:0)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)  Fatty acid biosynthesis (pentadecanoic acid; c16:0)  Fatty acid biosynthesis (hexadecanoic acid; c16:0)  Fatty acid biosynthesis (hexadecanoic acid; c16:1)	23.1.46 4.4.1.21 6.3.2.4 3.5.1.2 2.3.1.41 AND 2.3.1.179 AND 1.3.1.100 AND 4.21. AND 1.3.1.9 AND 1.3.1.100 AND 4.21.4 AND 1.3.1.9 AND 1.3.1.100 AND 1.3.1.1	KOX, 08035 KOX, 00500 KOX, 10935(dd)/KOX, 12350 KOX, 10650, ACC, 123	succoa + hser -> coa + osihser  srih -> 45dhpen + hcys 2 dala + atp <-> adop + alaala + pi dgln -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c130ACP + 5 co2 + 5 ACP  acACP + 6 malACP + 12 nadph -> 12 nadp + c140ACP + 6 co2 + 6 ACP  acACP + 6 malACP + 11 nadph -> 11 nadp + c141ACP + 6 co2 + 6 ACP  ppacp + 6 malACP + 12 nadph -> 12 nadp + c6 co2 + 6 ACP + c150ACP  ppacp + 6 malACP + 11 nadph -> 11 nadp + 6 co2 + 6 ACP + c150ACP  acACP + 7 malACP + 14 nadph -> 14 nadp + c160ACP + 7 co2 + 7 ACP  acACP + 7 malACP + 14 nadph -> 14 nadp + c160ACP + 7 co2 + 7 ACP
HSERST SRHCYSL ALAALAL GIUNZ FABC120 FABC130 FABC140 FABC151 FABC151 FABC161	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-alanine metabolism D-alanine metabolism Fatty acid biosynthesis	suffurtransferase homoserine O- succinytransferase S-ribosylmonosysteine lyase D-alanine-D-alanine ligase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)  Fatty acid biosynthesis (tetradecanoic acid; c14:0)  Fatty acid biosynthesis (tetradecanoic acid; c14:1)  Fatty acid biosynthesis (tetradecanoic acid; c15:0)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)  Fatty acid biosynthesis (pentadecanoic acid; c16:0)  Fatty acid biosynthesis (hexadecanoic acid; c16:0)  Fatty acid biosynthesis (hexadecanoic acid; c16:1)	231.16 4.41.21 6.32.4 4.41.21 6.32.4 2.31.18 AND 2.31.179 AND 2.31.179 AND 1.11.100 AND 4.21. AND 1.31.9 AND 1.31.4 AL21. AND 1.31.9 AND 1.31.9 AND 1.31.4 AL21.1 AND 1.31.9 AND 1.31.9 AND 1.31.4 AL21.1 AND 1.31.9 AND 1.31.2 AL21.1 AND 1.31.9 AND 1.31.4 AL21.1 AND 1.31.9 AND 1.31.4 AL21.1 AND 1.31.9 AND 1.31.2 AND 1.31.	KOX, 08035 KOX, 00500 KOX, 10353(dd)/KOX,12350 KOX, 10505(dd)/KOX,12350 KOX, 10505(dd)/KOX,12350 KOX, 10505(dd)/KOX,12350 KOX, 10505(dd)/KOX,12350 KOX, 10505(dd)/KOX,12350(dd)/KOX,12350(dd)/KOX,1250(dd)/KOX,1250(dd)/KOX,1250(KOX	succoa + hser -> coa + osihser  srih -> 45dhpen + hcys 2 dala + atp <-> adop + alaala + pi dgln -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c130ACP + 5 co2 + 5 ACP  acACP + 6 malACP + 12 nadph -> 12 nadp + c140ACP + 6 co2 + 6 ACP  acACP + 6 malACP + 11 nadph -> 11 nadp + c141ACP + 6 co2 + 6 ACP  ppacp + 6 malACP + 12 nadph -> 12 nadp + c co2 + 6 ACP + c150ACP  ppacp + 6 malACP + 11 nadph -> 11 nadp + 6 co2 + 6 ACP + c151ACP  acACP + 7 malACP + 14 nadph -> 14 nadp + c co2 + 6 ACP + c151ACP  acACP + 7 malACP + 14 nadph -> 14 nadp + c co2 + 6 ACP + c151ACP  ppacp + 7 malACP + 14 nadph -> 14 nadp + c co2 + 6 ACP + c151ACP
HSERST SRHCYSL ALAALAL GIUNZ FABC120 FABC130 FABC140 FABC151 FABC151 FABC161	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-alanine metabolism D-alanine metabolism Fatty acid biosynthesis	sulfurtansferase homoserine O- succinytransferase S-ribosylmonocysteine lyase D-alanine-D-alanine ligase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)  Fatty acid biosynthesis (tridecanoic acid; c14:0)  Fatty acid biosynthesis (tetradecanoic acid; c14:1)  Fatty acid biosynthesis (tetradecanoic acid; c14:1)  Fatty acid biosynthesis (tetradecanoic acid; c15:1)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)  Fatty acid biosynthesis (hexadecanoic acid; c16:1)  Fatty acid biosynthesis (hexadecanoic acid; c16:1)  Fatty acid biosynthesis (hexadecanoic acid; c16:1)	23.1.46 4.4.121 6.32.4 3.5.12 2.3.1.41 AND 2.3.1.179 AND 1.3.1.100 AND 4.2.1. AND 1.3.1.9 AND 1.3.1.100 AND 4.2.1. AND 1.3.1.9 AND 1.3.1.100 AND 4.2.1. AND 1.3.1.100 AND 4.2.1.100 AND	KOX, 08035 KOX, 00500 KOX, 10353(dd)/KOX, 12350 KOX, 10353(dd)/KOX, 12350 KOX, 13645/KOX, 21250 KOX, 13645/KOX, 21250 KOX, 13645/KOX, 21250 KOX, 13600/KOX, 12780/KOX, 00905/KOX, 05904/KOX, 12015(fabc)/KOX, 13700/KOX, 137	succoa + hser -> coa + oshser  srh -> 45dhpen + hcys 2 dafa + atp <-> adop + alaala + pi dgln -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c130ACP + 5 co2 + 5 ACP  acACP + 6 malACP + 12 nadph -> 12 nadp + c140ACP + 6 co2 + 6 ACP  acACP + 6 malACP + 11 nadph -> 11 nadp + c141ACP + 6 co2 + 6 ACP  ppacp + 6 malACP + 11 nadph -> 12 nadp + 6 co2 + 6 ACP + c150ACP  acACP + 7 malACP + 14 nadph -> 14 nadp + c160ACP + 7 co2 + 7 ACP  acACP + 7 malACP + 13 nadph -> 13 nadp + c160ACP + 7 co2 + 7 ACP  ppacp + 7 malACP + 14 nadph -> 14 nadp + 7 co2 + 7 ACP + c170ACP
HSERST SRHCYSL ALAALAL GIUNZ FABC120 FABC130 FABC140 FABC151 FABC151 FABC161	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-alanine metabolism D-alanine metabolism Fatty acid biosynthesis	suffurtransferase homoserine O- succinytransferase S-ribosylmonocysteine lyase D-alanine-D-alanine ligase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)  Fatty acid biosynthesis (tetradecanoic acid; c14:0)  Fatty acid biosynthesis (tetradecanoic acid; c14:1)  Fatty acid biosynthesis (tetradecanoic acid; c15:0)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)  Fatty acid biosynthesis (hexadecanoic acid; c16:0)  Fatty acid biosynthesis (hexadecanoic acid; c16:1)  Fatty acid biosynthesis (hexadecanoic acid; c16:1)  Fatty acid biosynthesis (hexadecanoic acid; c17:0)	231.146 4.41.21 6.32.4 4.41.21 6.32.4 2.31.187 AND 2.31.179 AND 1.31.100 AND 4.21. AND 1.31.9 AND 1.31.100 AND 4.21. AND 1.31.9 AND 1.31.100 AND 4.21. AND 1.31.100 AND 4.21.100 AND 4.21.1100 AND 4.	KOX, 08035 KOX, 00500 KOX, 10353(dd)/KOX,12350 KOX, 104645/KOX,21250 KOX, 16465/KOX,21250 KOX, 16465/KOX,21250 KOX, 16465/KOX, 12280/KOX, 00905/KOX, 05040/KOX, 17300/KOX, 17280/KOX, 10095/KOX, 05040/KOX, 17300/KOX, 17280/KOX, 10095/KOX, 16465/KOX, 1200006/KOX, 17280/KOX, 16465/KOX, 120006/KOX, 120005/KOX, 165040/KOX, 17300/KOX, 17280/KOX, 10095/KOX, 16250/KOX, 17300/KOX, 17280/KOX, 16465/KOX, 17300/KOX, 17280/KOX, 16465/KOX, 17300/KOX, 17280/KOX, 16465/KOX, 17300/KOX, 17280/KOX, 10095/KOX, 16465/KOX, 17300/KOX, 17280/KOX, 10095/KOX, 16465/KOX, 17300/KOX, 17280/KOX, 10095/KOX, 16465/KOX, 17300/KOX, 17280/KOX, 10095/KOX, 16465/KOX, 17300/KOX, 17280/KOX, 16465/KOX, 17300/KOX, 17300/KOX, 17280/KOX, 16465/KOX, 17300/KOX,	succoa + hser -> coa + osihser  srih -> 45dhpen + hcys 2 dala + atp <-> adop + alaala + pi dgln -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c130ACP + 5 co2 + 5 ACP  acACP + 6 malACP + 12 nadph -> 12 nadp + c140ACP + 6 co2 + 6 ACP  acACP + 6 malACP + 11 nadph -> 11 nadp + c141ACP + 6 co2 + 6 ACP  ppacp + 6 malACP + 12 nadph -> 12 nadp + c6 co2 + 6 ACP + c150ACP  ppacp + 6 malACP + 11 nadph -> 11 nadp + 6 co2 + 6 ACP + c151ACP  acACP + 7 malACP + 14 nadph -> 14 nadp + c160ACP + 7 co2 + 7 ACP  acACP + 7 malACP + 14 nadph -> 13 nadp + c160ACP + 7 co2 + 7 ACP  ppacp + 7 malACP + 14 nadph -> 13 nadp + c160ACP + 7 co2 + 7 ACP
HSERST SRHCYSL ALAALAL GGUN2 FABC120 FABC130 FABC140 FABC151 FABC151 FABC151 FABC160 FABC161	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-alanine metabolism D-alanine metabolism Fatty acid biosynthesis  Fatty acid biosynthesis	sulfurtransferase homoserine O- succinytransferase S-ribosylmonocysteine lyase D-alanine-D-alanine ligase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)  Fatty acid biosynthesis (tridecanoic acid; c14:0)  Fatty acid biosynthesis (tetradecanoic acid; c14:1)  Fatty acid biosynthesis (tetradecanoic acid; c14:1)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)  Fatty acid biosynthesis (hexadecanoic acid; c16:1)  Fatty acid biosynthesis (hexadecanoic acid; c16:1)  Fatty acid biosynthesis (hexadecanoic acid; c16:1)	23.1.46 4.4.121 6.32.4 3.5.12 2.3.1.41 AND 2.3.1.179 AND 1.3.1.100 AND 4.2.1. AND 1.3.1.9 AND 1.3.1.100 AND 4.2.1. AND 1.3.1.100 AND 4.2.1.41 AND 2.3.1.179 AND 2.3.1.180 AND 1.1.1.100 AND 4.1. AND 1.3.1. 2.3.1.41 AND 2.3.1.179 AND 2.3.1.179 AND 2.3.1.179 AND 2.3.1.179 AND 2.3.1.180 AND 1.1.1.100 AND 4.1. AND 1.3.1. 2.3.1.41 AND 2.3.1.180 AND 1.1.1.100 AND 4.2.1. AND 1.3.1. 2.3.1.41 AND 2.3.1.180 AND 1.1.1.100 AND 4.2.1. AND 1.3.1. 2.3.1.41 AND 2.3.1.180 AND 1.1.1.100 AND 4.2.1. AND 1.3.1. 2.3.1.41 AND 2.3.1.180 AND 1.1.1.100 AND 4.2.1. AND 1.3.1. 2.3.1.14 AND 2.3.1.180 AND 1.1.1.100 AND 4.2.1. AND 1.3.1. 2.3.1.14 AND 2.3.1.180 AND 1.1.1.100 AND 4.2.1. AND 1.3.1. 2.3.1.14 AND 2.3.1.180 AND	KOX, 08035 KOX, 00500 KOX, 10353(dd)/KOX, 12350 KOX, 10353(dd)/KOX, 12350 KOX, 13645/KOX, 21250 KOX, 13645/KOX, 21250 KOX, 13645/KOX, 21250 KOX, 13600/KOX, 127280/KOX, 00905/KOX, 05904/KOX, 12015(fabc)/KOX, 13700/KOX, 13	succoa + hser -> coa + osihser  srih -> 45dhpen + hcys 2 dala + atp <-> adop + alaala + pi dgln -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c130ACP + 5 co2 + 5 ACP  acACP + 6 malACP + 12 nadph -> 12 nadp + c140ACP + 6 co2 + 6 ACP  acACP + 6 malACP + 11 nadph -> 11 nadp + c141ACP + 6 co2 + 6 ACP  ppacp + 6 malACP + 12 nadph -> 12 nadp + c6 co2 + 6 ACP + c150ACP  ppacp + 6 malACP + 11 nadph -> 11 nadp + 6 co2 + 6 ACP + c151ACP  acACP + 7 malACP + 14 nadph -> 14 nadp + c160ACP + 7 co2 + 7 ACP  acACP + 7 malACP + 14 nadph -> 13 nadp + c160ACP + 7 co2 + 7 ACP  ppacp + 7 malACP + 14 nadph -> 13 nadp + c160ACP + 7 co2 + 7 ACP
HSERST SRHCYSL ALAALAL GGUN2 FABC120 FABC130 FABC140 FABC151 FABC151 FABC151 FABC160 FABC161	Cysteine Metabolism Cysteine Metabolism D-alanine metabolism D-alanine metabolism D-alanine metabolism Fatty acid biosynthesis  Fatty acid biosynthesis	suffurtransferase homoserine O- succinytransferase S-ribosylmonocysteine lyase D-alanine-D-alanine ligase glutaminase  Fatty acid biosynthesis (dodecanoic acid; c12:0)  Fatty acid biosynthesis (tridecanoic acid; c13:0)  Fatty acid biosynthesis (tetradecanoic acid; c14:0)  Fatty acid biosynthesis (tetradecanoic acid; c14:1)  Fatty acid biosynthesis (tetradecanoic acid; c15:0)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)  Fatty acid biosynthesis (pentadecanoic acid; c15:1)  Fatty acid biosynthesis (hexadecanoic acid; c16:0)  Fatty acid biosynthesis (hexadecanoic acid; c16:1)  Fatty acid biosynthesis (hexadecanoic acid; c16:1)  Fatty acid biosynthesis (hexadecanoic acid; c17:0)	23.1.46 4.4.121 6.32.4 3.5.12 2.3.1.41 AND 2.3.1.179 AND 1.3.1.100 AND 4.2.1. AND 1.3.1.9 AND 1.3.1.100 AND 4.2.1. AND 1.3.1.100 AND 4.2.1.41 AND 2.3.1.179 AND 2.3.1.180 AND 1.1.1.100 AND 4.1. AND 1.3.1. 2.3.1.41 AND 2.3.1.179 AND 2.3.1.179 AND 2.3.1.179 AND 2.3.1.179 AND 2.3.1.180 AND 1.1.1.100 AND 4.1. AND 1.3.1. 2.3.1.41 AND 2.3.1.180 AND 1.1.1.100 AND 4.2.1. AND 1.3.1. 2.3.1.41 AND 2.3.1.180 AND 1.1.1.100 AND 4.2.1. AND 1.3.1. 2.3.1.41 AND 2.3.1.180 AND 1.1.1.100 AND 4.2.1. AND 1.3.1. 2.3.1.41 AND 2.3.1.180 AND 1.1.1.100 AND 4.2.1. AND 1.3.1. 2.3.1.14 AND 2.3.1.180 AND 1.1.1.100 AND 4.2.1. AND 1.3.1. 2.3.1.14 AND 2.3.1.180 AND 1.1.1.100 AND 4.2.1. AND 1.3.1. 2.3.1.14 AND 2.3.1.180 AND	KOX, 08035 KOX, 00500 KOX, 10353(dd)/KOX,12350 KOX, 104645/KOX,21250 KOX, 16465/KOX,21250 KOX, 16465/KOX,21250 KOX, 16465/KOX, 12280/KOX, 00905/KOX, 05040/KOX, 17300/KOX, 17280/KOX, 10095/KOX, 05040/KOX, 17300/KOX, 17280/KOX, 10095/KOX, 16465/KOX, 1200006/KOX, 17280/KOX, 16465/KOX, 120006/KOX, 120005/KOX, 165040/KOX, 17300/KOX, 17280/KOX, 10095/KOX, 16250/KOX, 17300/KOX, 17280/KOX, 16465/KOX, 17300/KOX, 17280/KOX, 16465/KOX, 17300/KOX, 17280/KOX, 16465/KOX, 17300/KOX, 17280/KOX, 10095/KOX, 16465/KOX, 17300/KOX, 17280/KOX, 10095/KOX, 16465/KOX, 17300/KOX, 17280/KOX, 10095/KOX, 16465/KOX, 17300/KOX, 17280/KOX, 10095/KOX, 16465/KOX, 17300/KOX, 17280/KOX, 16465/KOX, 17300/KOX, 17300/KOX, 17280/KOX, 16465/KOX, 17300/KOX,	succoa + hser -> coa + osihser  srih -> 45dhpen + hcys 2 dala + atp <-> adop + alaala + pi dgln -> dglu + nh4  acACP + 5 malACP + 10 nadph -> 10 nadp + c120ACP + 5 co2 + 5 ACP  ppacp + 5 malACP + 10 nadph -> 10 nadp + c130ACP + 5 co2 + 5 ACP  acACP + 6 malACP + 12 nadph -> 12 nadp + c140ACP + 6 co2 + 6 ACP  acACP + 6 malACP + 11 nadph -> 11 nadp + c141ACP + 6 co2 + 6 ACP  ppacp + 6 malACP + 12 nadph -> 12 nadp + c6 co2 + 6 ACP + c150ACP  ppacp + 6 malACP + 11 nadph -> 11 nadp + 6 co2 + 6 ACP + c151ACP  acACP + 7 malACP + 14 nadph -> 14 nadp + c160ACP + 7 co2 + 7 ACP  acACP + 7 malACP + 14 nadph -> 13 nadp + c160ACP + 7 co2 + 7 ACP  ppacp + 7 malACP + 14 nadph -> 13 nadp + c160ACP + 7 co2 + 7 ACP

		Fatty acid biosynthesis	2.3.1.41 AND 2.3.1.179 AND 2.3.1.180 AND	KOX_05025/KOX_26605/KOX_00905/KOX_05040/ KOX_17300/KOX_17280/KOX_00890/KOX_02015(	
FABC180	Fatty acid biosynthesis	(octadecanoic acid; c18:0)	1.1.1.100 AND	fabG)/KOX_05035(fabG)/KOX_16425/KOX_17290( fabG)/KOX_1500(fabZ)/KOX_18475/KOX_18960	
			AND 1.3.1 2.3.1.41 AND	1850// NOX_11500(1882// NOX_10475/ NOX_10500	
FABC181	Fatty acid biosynthesis	Fatty acid biosynthesis	2.3.1.179 AND 2.3.1.180 AND	KOX_05025/KOX_26605/KOX_00905/KOX_05040/ KOX_17300/KOX_17280/KOX_00890/KOX_02015(	
TABCIOI	ratty acid biosynthesis	(octadecanoic acid; c18:1)		fabG)/KOX_05035(fabG)/KOX_16425/KOX_17290( fabG)/KOX_11500(fabZ)/KOX_18475/KOX_18960	, accer + a mancer + 15 manhii -> 15 manhi + 1202cer + a coz + a cer
			AND 1.3.1 2.3.1.41 AND	NOV GEODE WON DECOUNTY OF DATE WON GED AN	
FABC190	Fatty acid biosynthesis	Fatty acid biosynthesis	2.3.1.179 AND 2.3.1.180 AND	KOX_05025/KOX_26605/KOX_00905/KOX_05040/ KOX_17300/KOX_17280/KOX_0890/KOX_02015(	nnacn + 8 malACP + 16 nadnh -> 16 nadn + 8 co2 + 8 ACP + c190ACP
		(nonadecanoic acid; c19:0)	1.1.1.100 AND 4.2.1 AND 1.3.1.9 AND 1.3.1	fabG)/KOX_05035(fabG)/KOX_16425/KOX_17290( fabG)/KOX_11500(fabZ)/KOX_18475/KOX_18960	
MALADC ACCOAT	Fatty acid biosynthesis Fatty acid biosynthesis	Malonyl-ACP decarboxylase Acetyl-CoA ACP transacylase	4.1.1.87 2.3.1.180	KOX 17280	malACP -> acACP + co2 ACP + accoa <-> acACP + coa
PPCOAT	Fatty acid biosynthesis	Propionyl-CoA ACP transacylas	2.3.1.180	KOX_17280	ACP + ppcoa <-> coa + ppacp
MALCOAT	Fatty acid biosynthesis	Malonyl-CoA-ACP transacylase	2.3.1.39 2.3.1.41/2.3.1.179/2	KOX_17285/KOX_21675 KOX_05025/KOX_26605/KOX_00905/KOX_05040/	
BKACPS1	Fatty acid biosynthesis	beta-ketoacyl-ACP synthase	3.1.180	bZ)/KOX_18475/KOX_18960	
ACCOACB BITCB	Fatty acid biosynthesis Fatty acid biosynthesis	acetyl-CoA carboxylase biotin carboxylase	6.4.1.2 6.3.4.14	KOX_04110/KOX_04115/KOX_11525/KOX_26570 KOX_04115 KOX_05025/KOX_26605/KOX_00905/KOX_05040/	accoa + atp + hco3 -> adp + malcoa + pi
BKACPS2	Fatty acid biosynthesis	beta-ketoacyl-ACP synthase	2.3.1.41/2.3.1.179/2 3.1.180	KOX_USUZS/KOX_28805/KOX_00905/KOX_USU40/ KOX_17300/KOX_17280290(fabG)/KOX_11500(fa bZ)/KOX_18475/KOX_18960	
UDPGALPF	Fatty acid biosynthesis	UDP-D-galactopyranose furanomutase	5.4.99.9	KOX_25085	udpgal -> udpgalfur
		UDP-N-acetyl-D- glucosamine:undecaprenyl-			
UAGUPAGP	Fatty acid biosynthesis	phosphate N-acetyl-D- glucosamine	2.7.8.33	KOX_07555	udpnag + udcpp -> ump + acglcmpdp
		phosphotransferase		- KOX_23560/KOX_11675(fadE)/KOX_07835(fadB)/	
FAMC120	Fatty acid metabolism	Fatty acid metabolism (dodecanoic acid; c12:0)	AND 4.2.1.17 AND 1.1.1.35 AND 2.3.1.16	KOX_19445/KOX_26655(fadJ)/KOX_07835(fadB)/ KOX_26655(fadJ)/KOX_07830(fadA)/KOX_26660(fadI)	c120 + 6 coa + 5 fad + 5 nad + atp -> 6 accoa + 5 fadh2 + 5 nadh + amp + ppi
		Fatty acid metabolism	6.2.1.3 AND 1.3.99.	- KOX_23560/KOX_11675(fadE)/KOX_07835(fadB)/	
FAMC130	Fatty acid metabolism	(tridecanoic acid; c13:0)	1.1.1.35 AND 2.3.1.16	KOX_26655(fadJ)/KOX_07830(fadA)/KOX_26660(f adl)	c130 + 6 coa + 5 fad + 5 nad + atp -> 5 accoa + ppcoa + 5 fadh2 + 5 nadh + amp + ppi
FAMC140	Fath and matchedian	Fatty acid metabolism		<ul> <li>KOX_23560/KOX_11675(fadE)/KOX_07835(fadB)/</li> <li>KOX_19445/KOX_26655(fadJ)/KOX_07835(fadB)/</li> </ul>	210 . 7 6 frd . 6dd 7 6 frdb2 . 6db
FAMC140	Fatty acid metabolism	(tetradecanoic acid; c14:0)	1.1.1.35 AND 2.3.1.16	adī)	c140 + 7 coa + 6 fad + 6 nad + atp -> 7 accoa + 6 fadh2 + 6 nadh + amp + ppi
FAMC141	Fatty acid metabolism	Fatty acid metabolism	AND 4.2.1.17 AND	<ul> <li>KOX_23560/KOX_11675(fadE)/KOX_07835(fadB)/KOX_19445/KOX_26655(fadJ)/KOX_07835(fadB)/</li> </ul>	c141 + 7 coa + 6 fad + 6 nad + atp -> 7 accoa + 6 fadh2 + 6 nadh + amp + ppi
	,	(tetradecanoic acid; c14:1)	1.1.1.35 AND 2.3.1.16	adī)	
FAMC150	Fatty acid metabolism	Fatty acid metabolism (pentadecanoic acid; c15:0)		<ul> <li>KOX_23560/KOX_11675(fadE)/KOX_07835(fadB)/</li> <li>KOX_19445/KOX_26655(fadJ)/KOX_07835(fadB)/</li> <li>KOX_36655(fadJ)/KOX_07830(fadA)/KOX_36660(fadB)/</li> </ul>	c150 + 7 coa + 6 fad + 6 nad + atp -> 6 accoa + ppcoa + 6 fadh2 + 6 nadh + amp + ppi
		(pernadecarioic acid, c13.0)	2.3.1.16	adI)  - KOX_23560/KOX_11675(fadE)/KOX_07835(fadB)/	
FAMC151	Fatty acid metabolism	Fatty acid metabolism (pentadecanoic acid; c15:1)			c151 + 7 coa + 6 fad + 6 nad + atp -> 6 accoa + ppcoa + 6 fadh2 + 6 nadh + amp + ppi
				adI) - KOX_23560/KOX_11675(fadE)/KOX_07835(fadB)/	
FAMC160	Fatty acid metabolism	Fatty acid metabolism (hexadecanoic acid; c16:0)	1.1.1.35 AND	KOX_19445/KOX_26655(fadJ)/KOX_07835(fadB)/ KOX_26655(fadJ)/KOX_07830(fadA)/KOX_26660(f	c160 + 8 coa + 7 fad + 7 nad + atp -> 8 accoa + 7 fadh2 + 7 nadh + amp + ppi
		Fath and make diam		adl) - KOX_23560/KOX_11675(fadE)/KOX_07835(fadB)/	
FAMC161	Fatty acid metabolism	Fatty acid metabolism (hexadecanoic acid; c16:1)	1.1.1.35 AND 2.3.1.16	KOX_19445/KOX_26655(fadJ)/KOX_07835(fadB)/ KOX_26655(fadJ)/KOX_07830(fadA)/KOX_26660(f adI)	c161 + 8 coa + 7 fad + 7 nad + atp -> 8 accoa + 7 fadh2 + 7 nadh + amp + ppi
5445770	50 1 1 1	Fatty acid metabolism	6.2.1.3 AND 1.3.99.	<ul> <li>KOX_23560/KOX_11675(fadE)/KOX_07835(fadB)/</li> <li>KOX_19445/KOX_26655(fadJ)/KOX_07835(fadB)/</li> </ul>	370 0 7(1 7 1 4 7 7 7 7 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7
FAMC170	Fatty acid metabolism	(heptadecanoic acid; c17:0)	1.1.1.35 AND 2.3.1.16	KOX_26655(fadJ)/KOX_07830(fadA)/KOX_26660(f adI)	c170 + 8 coa + 7 fad + 7 nad + atp -> 7 accoa + ppcoa + 7 fadh2 + 7 nadh + amp + ppi
FAMC171	Fatty acid metabolism	Fatty acid metabolism	AND 4.2.1.17 AND	- KOX_23560/KOX_11675(fadE)/KOX_07835(fadB)/ KOX_19445/KOX_26655(fadJ)/KOX_07835(fadB)/	c171 + 8 coa + 7 fad + 7 nad + atp -> 7 accoa + ppcoa + 7 fadh2 + 7 nadh + amp + ppi
		(heptadecanoic acid; c17:1)	1.1.1.35 AND 2.3.1.16	KOX_26655(tadJ)/KOX_0/830(tadA)/KOX_26660(t adI) - KOX_23560/KOX_11675(fadE)/KOX_07835(fadB)/	
FAMC180	Fatty acid metabolism	Fatty acid metabolism (octadecanoic acid; c18:0)		KOX_25560/KOX_11075(fadb)/KOX_07835(fadb)/ KOX_19445/KOX_26655(fadJ)/KOX_07835(fadb)/ KOX_26655(fadJ)/KOX_07830(fadA)/KOX_26660(f	c180 + 9 coa + 8 fad + 8 nad + atp -> 9 accoa + 8 fadh2 + 8 nadh + amp + ppi
		(,	2.3.1.16	adI) - KOX_23560/KOX_11675(fadE)/KOX_07835(fadB)/	
FAMC181	Fatty acid metabolism	Fatty acid metabolism (octadecanoic acid; c18:1)	AND 4.2.1.17 AND 1.1.1.35 AND	KOX_19445/KOX_26655(fadJ)/KOX_07835(fadB)/ KOX_26655(fadJ)/KOX_07830(fadA)/KOX_26660(f	c181 + 9 coa + 8 fad + 8 nad + atp -> 9 accoa + 8 fadh2 + 8 nadh + amp + ppi
				adI) - KOX_23560/KOX_11675(fadE)/KOX_07835(fadB)/	
FAMC190	Fatty acid metabolism	Fatty acid metabolism (nonadecanoic acid; c19:0)	1.1.1.35 AND	KOX_19445/KOX_26655(fadJ)/KOX_07835(fadB)/ KOX_26655(fadJ)/KOX_07830(fadA)/KOX_26660(fadI)	c190 + 9 coa + 8 fad + 8 nad + atp -> 8 accoa + ppcoa + 8 fadh2 + 8 nadh + amp + ppi
FAOb	Fatty acid metabolism	fatty acid oxidation (Butanoyl- CoA )	2.3.1.16	adi)	c040coa + fad + nad -> aacoa + fadh2 + nadh
AACPS1	Fatty acid metabolism	acyl-[acyl-carrier-protein] synthetase (n-C12:0)	6.2.1.20	KOX_01650	ACP + atp + c120 -> amp + c120ACP + ppi
AACPS2	Fatty acid metabolism	acyl-[acyl-carrier-protein] synthetase (n-C14:0)	6.2.1.20	KOX_01650	ACP + atp + c140 -> amp + c140ACP + ppi
AACPS3	Fatty acid metabolism	acyl-[acyl-carrier-protein] synthetase (n-C14:1)	6.2.1.20	KOX_01650	ACP + atp + c141 -> amp + c141ACP + ppi
AACPS4	Fatty acid metabolism	acyl-[acyl-carrier-protein] synthetase (n-C15:0)	6.2.1.20	KOX_01650	ACP + atp + c150 -> amp + c150ACP + ppi
AACPS5	Fatty acid metabolism	acyl-[acyl-carrier-protein] synthetase (n-C15:1) acyl-[acyl-carrier-protein]	6.2.1.20	KOX_01650	ACP + atp + c151 -> amp + c151ACP + ppi
AACPS6	Fatty acid metabolism	synthetase (n-C16:0) acyl-[acyl-carrier-protein]	6.2.1.20	KOX_01650	ACP + atp + c160 -> amp + c160ACP + ppi
AACPS8	Fatty acid metabolism	synthetase (n-C16:1) acyl-[acyl-carrier-protein]	6.2.1.20	KOX_01650	ACP + atp + c161 -> amp + c161ACP + ppi
AACPS8 AACPS9	Fatty acid metabolism  Fatty acid metabolism	synthetase (n-C17:0) acyl-[acyl-carrier-protein]	6.2.1.20	KOX_01650 KOX_01650	ACP + atp + $c170$ -> amp + $c170$ ACP + ppi ACP + atp + $c171$ -> amp + $c171$ ACP + ppi
AACPS10	Fatty acid metabolism	synthetase (n-C17:1) acyl-[acyl-carrier-protein]	6.2.1.20	KOX_01650	ACP + atp + c180 -> amp + c180ACP + ppi
AACPS11	Fatty acid metabolism	synthetase (n-C18:0) acyl-[acyl-carrier-protein] synthetase (n-C18:1)	6.2.1.20	KOX_01650	ACP + atp + c181 -> amp + c181ACP + ppi
AACPS12	Fatty acid metabolism	acyl-[acyl-carrier-protein] synthetase (n-C19:0)	6.2.1.20	KOX_01650	ACP + atp + c190 -> amp + c190ACP + ppi
AACPS13	Fatty acid metabolism	acyl-[acyl-carrier-protein] synthetase (n-C13:0)	6.2.1.20	KOX_01650	ACP + atp + c130 -> amp + c130ACP + ppi
HACOAD1	Fatty acid metabolism	3-hydroxyacyl-CoA dehydrogenase (acetoacetyl-	1.1.1.35/1.1.1.157	KOX_07835(fadB)/KOX_26655(fadJ)/KOX_19455	3hbcoa + nad -> aacoa + nadh
ACOADH1	Fatty acid metabolism	CoA) acyl-CoA dehydrogenase	1.3.99	KOX 11675(fadE)	c040coa + fad <-> ccoa + fadh2
ACCOAAT1	Fatty acid metabolism	(butanoyl-CoA) acetyl-CoA C-acetyltransferase	2.3.1.9	KOX_01800/KOX_02020/KOX_02110/	2 accoa <-> aacoa + coa
ENCOAH1	Fatty acid metabolism	enoyl-CoA hydratase 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA	4.2.1.17	KOX_07835(fadB)/KOX_19445/KOX_26655(fadJ)/	auring <-> ccog
3HBCOADH	Fatty acid metabolism	hydratase / 3-hydroxybutyryl- CoA epimerase / enoyl-CoA	5.1.2.3	KOX_07835(fadB)/KOX_26655(fadJ)/	3hbcoa <-> r3hbcoa
CMBLD6	Fluorobenzoate degradation	isomerase carboxymethylenebutenolidase		KOX_02855/KOX_07760	4fmuclac -> 2mac + hf
CMBLD7	Fluorobenzoate degradation	carboxymethylenebutenolidase 3,5-dibromo-4-	3.1.1.45	KOX_02855/KOX_07760	5fmuclac -> 2mac + hf
35DB4HBH DHFR1	Fluorobenzoate degradation	hydroxybenzamide hydro-lyase (nitrile-forming)	4.2.1.84 1.5.1.3	KOX_20500/KOX_20505	bromox -> 35dbr4hb  dhf + nadh <-> nad + thf
DHFR1p DHFS2	Folate Biosynthesis Folate Biosynthesis Folate Biosynthesis	dihydrofolate reductase dihydrofolate reductase dihydropteroate synthase	1.5.1.3 1.5.1.3 2.5.1.15	KOX_10680(folA)/KOX_21840 KOX_10680(folA)/KOX_21840 KOX_03690(folP)	dhf + nadh <-> nad + thf dhf + nadph <-> nadp + thf paba + ahhmd -> dhpt + ppi
GTPCHI FPGLUS1	Folate Biosynthesis Folate Biosynthesis Folate Biosynthesis	GTP cyclohydrolase I folylpolyglutamate synthase	2.5.1.15 3.5.4.16 6.3.2.17/6.3.2.12	KOX_03690(folir) KOX_25750(folic) KOX_26565	paba + annma -> cmpt + ppi gtp -> ahdt + formate atp + dhpt + glu -> adp + dhf + pi
	•	11.12			

ABZS	Folate Biosynthesis	4-aminobenzoate synthase	4.1.3.38	KOX_17305	adchor -> paba + pyr
ADCMS	Folate Biosynthesis	4-amino-4-deoxychorismate	2.6.1.85	KOX_04530/KOX_04530(pabB)	chor + gln -> adchor + glu
DHNPTA	Folate Biosynthesis	synthase dihydroneopterin aldolase	4.1.2.25	KOX 03070(folB)	dhnpt -> ahhmp + glal
HMDPPK	Folate Biosynthesis	6-hydroxymethyl-dihydropterin	2.7.6.3	KOX 11220	ahhmo + ato -> ahhmd + amo
HMDPPK	Folate Biosynthesis	pyrophosphokinase	2.7.6.3	KOX_11220	annmp + atp -> annmd + amp
6PYRTP	Folate Biosynthesis	6-pyruvoyl tetrahydrobiopterin synthase	4.2.3.12	KOX_01125	ahdt -> pythp + pppi
AKLPP	Folate Biosynthesis	alkaline phosphatase	3.1.3.1	KOX_12385	ahdt -> dhnpt + 3 pi
DHPS1	Folate Biosynthesis	dihydropteroate synthase	2.5.1.15	KOX_03690(folP)	ahhmp + paba -> dhpt
DHFR2 DHFR3	Folate Biosynthesis Folate Biosynthesis	dihydrofolate reductase dihydrofolate reductase	1.5.1.3 1.5.1.3	KOX_10680(foIA)/KOX_21840 KOX_10680(foIA)/KOX_21840	dhf + nad <-> fl + nadh fl + 2 nadh -> thf + 2 nad
FPGLUS2	Folate Biosynthesis	folylpolyglutamate synthase	6.3.2.17	KOX_26565	atp + thf + glu <-> adp + pi + thfglu
DHFR2p	Folate Biosynthesis	dihydrofolate reductase	1.5.1.3	KOX_10680(folA)/KOX_21840	dhf + nadp <-> fl + nadph
DHFR3p	Folate Biosynthesis	dihydrofolate reductase methylenetetrahydrofolate	1.5.1.3	KOX_10680(folA)/KOX_21840	fl + 2 nadph -> thf + 2 nadp
METTHFD	Folate Metabolism	dehydrogenase (NADP)	1.5.1.5	KOX_13225	metthf + nadp <-> methf + nadph
FTHFDF	Folate Metabolism	formyltetrahydrofolate	3.5.1.10	KOX_23060(purU)	fthf -> formate + thf
GLYAMT	Folate Metabolism	deformylase aminomethyltransferase	2.1.2.10	KOX_02485	gly + nad + thf -> co2 + metthf + nadh + nh4
METTHER	Folate Metabolism	5,10-methylenetetrahydrofolate	1.5.1.20	KOX_07330(metF)	metthf + nadh -> mthf + nad
METITIER	rolate Metabolishi	reductase (NADH)		KOX_U/33U(ffetr)	mettii + naun -> mtii + nau
METTHFRp	Folate Metabolism	5,10-methylenetetrahydrofolate reductase (NADH)	1.5.1.20	KOX_07330(metF)	metthf + nadph -> mthf + nadp
FRUK	Fructose and Mannose metabolism	fructokinase	2.7.1.4	KOX_00775/KOX_06115/KOX_12435/KOX_13375	/ atp + fru -> adp + f6p
FRUK	rructose and Mannose metabolism		2.7.1.4	KOX_20965/KOX_27450	atp + iiu -> aup + iop
MAN6PI	Fructose and Mannose metabolism	mannose-6-phosphate isomerase	5.3.1.8	KOX_21900	man6p <-> f6p
SBT6PD	Fructose and Mannose metabolism	sorbitol-6-phosphate	1.1.1.140	KOX_00590/KOX_08120	sbt6p + nad <-> f6p + nadh
SDIOPD	rructose and Mannose metabolism	dehydrogenase	1.1.1.140	KOX_00390/KOX_08120	sutop + nau <-> top + naun
MNT1PD	Fructose and Mannose metabolism	mannitol-1-phosphate 5- dehydrogenase	1.1.1.17	KOX_05765	mnt1p + nad <-> f6p + nadh
RMNI	Fructose and Mannose metabolism	L-rhamnose isomerase	5.3.1.14	KOX_07205	rmn <-> rml
RMLK	Fructose and Mannose metabolism	rhamnulokinase	2.7.1.5	KOX_07210(rhaB)	rml + atp -> rml1p + adp
RM1PA	Fructose and Mannose metabolism	rhamnulose-1-phosphate aldolase	4.1.2.19	KOX_07200	rml1p <-> dhap + llald
F1PK	Fructose and Mannose metabolism	6-phosphofructokinase	2.7.1.56	KOX_03500/KOX_25815(fruK)	f1p + atp <-> fdp + adp
FUCI	Fructose and Mannose metabolism	L-fucose isomerase	5.3.1.25	KOX_01280(fucI)	fuc <-> fucul
FCL1PA	Fructose and Mannose metabolism	L-fuculose phosphate aldolase 2-keto-3-deoxy-L-rhamnonate		KOX_01270	fucul1p -> dhap + llald
2K3DRMNA	Fructose and Mannose metabolism	aldolase	4.1.2	KOX_26185	llald + pyr <-> 2d3drmn
RMNND	Fructose and Mannose metabolism	L-rhamnonate dehydratase	4.2.1.90	KOX_26195	2d3drmn <-> rmnn
FUCLK UDPG4E	Fructose and Mannose metabolism Galactose metabolism	L-fuculokinase UDPglucose 4-epimerase	2.7.1.51 5.1.3.2	KOX_01285 KOX_14785	fucul + atp -> fucul1p + adp udpg <-> udpgal
GALT1PD	Galactose metabolism	Galactitol-1-phosphate	1.1.1.251		
		dehydrogenase		KOX_03535	galt1p + nad <-> nadh + t6p
GALCTND	Galactose metabolism	galactonate dehydratase 2-dehydro-3-	4.2.1.6	KOX_06525	dgalctn -> 2d3dgalctn
2D3DOXGALK	Galactose metabolism	deoxygalactonokinase	2.7.1.58	KOX_06535	2d3dgalctn + atp -> 2d3dgalctn6p + adp
2D3D6PGA	Galactose metabolism	2-dehydro-3-deoxy-6-	4.1.2.21	KOX_06530/KOX_10095	2d3dqalctn6p -> q3p + pyr
200001011	diactose metabolism	phosphogalactonate aldolase tagatose 1,6-diphosphate	7.4.4.4.4	NON_UUSSUNON_IUUSS	2000guictiop - g.p., pyi
TAG16PA	Galactose metabolism	aldolase	4.1.2.40	KOX_03495(gatY)	dhap + g3p <-> t16p
PFK2	Galactose metabolism	phosphofructokinase		KOX_06965/KOX_07260/KOX_22945/KOX_03515	
GLACK	Galactose metabolism	galactokinase UDPglucose-hexose-1-	2.7.1.6	KOX_14775	glac + atp -> glac1p + adp
UDPGHPU	Galactose metabolism	phosphate uridylyltransferase	2.7.7.12	KOX_14780	glac1p + udpg <-> g1p + udpgal
GALCTS	Galactose metabolism	beta-D-galactosidase	3.2.1.23	KOX_03235(edgA)/KOX_03240(ebgC)	lactose -> glac + glc
GALACTAN AGALCTS1	Galactose metabolism Galactose metabolism	beta-D-galactosidase alpha-galactosidase	3.2.1.23 3.2.1.22	KOX_09055/KOX_12915 KOX_07045/KOX_16445	galactan -> galactan_1 + glac stachyose -> raffinose + glac
AGALCTS2	Galactose metabolism	alpha-galactosidase	3.2.1.22	KOX_07045/KOX_16445 KOX_07045/KOX_16445	qalactinol <-> mi + qlac
AGALCTS3	Galactose metabolism	alpha-galactosidase	3.2.1.22	KOX_07045/KOX_16445	melibt <-> sot + glac
AGALCTS4 AGALCTS5	Galactose metabolism Galactose metabolism	alpha-galactosidase alpha-galactosidase	3.2.1.22 3.2.1.22	KOX_07045/KOX_16445 KOX_07045/KOX_16445	epimelib <-> man + glac glacgly <-> gl + glac
AGALCTS6	Galactose metabolism	alpha-galactosidase	3.2.1.22	KOX 07045/KOX 16445	meli <-> glac + glc
AGALCTS7	Galactose metabolism	alpha-galactosidase	3.2.1.22	KOX_07045/KOX_16445	mannot <-> meli + glac
AGALCTS8 FRUFUS1	Galactose metabolism Galactose metabolism	alpha-galactosidase beta-fructofuranosidase	3.2.1.22 3.2.1.26	KOX_07045/KOX_16445 KOX_01765/KOX_07150/KOX_13360	raffinose <-> suc + glac stachyose -> mannot + fru
FRUFUS2	Galactose metabolism	beta-fructofuranosidase	3.2.1.26	KOX_01765/KOX_07150/KOX_13360 KOX_01765/KOX_07150/KOX_13360	raffinose -> meli + fru
GLUCSD1	Galactose metabolism	alpha-glucosidase	3.2.1.20	KOX_12475/KOX_15200	suc -> glc + fru
GLUCSD2	Starch and sucrose metabolism	beta-fructofuranosidase	3.2.1.26	KOX_01765/KOX_07150/KOX_13360	suc -> glc + fru
	Chlorocyclohexane and chlorobenzene	beta-fructofuranosidase carboxymethylenebutenolidase	3.2.1.26	KOX_01765/KOX_07150/KOX_13360 KOX_02855/KOX_07760	
GLUCSD2 CMBLD1		carboxymethylenebutenolidase	3.2.1.26 3.1.1.45	KOX_02855/KOX_07760	suc -> glc + fru dchrocmo -> dchrooe
GLUCSD2	Chlorocyclohexane and chlorobenzene degradation Chlorocyclohexane and chlorobenzene degradation		3.2.1.26 3.1.1.45		suc -> glc + fru
GLUCSD2 CMBLD1	Chlorocyclohexane and chlorobenzene degradation Chlorocyclohexane and chlorobenzene degradation gamma-Hexachlorocyclohexane	carboxymethylenebutenolidase	3.2.1.26 3.1.1.45	KOX_02855/KOX_07760	suc -> glc + fru dchrocmo -> dchrooe
GLUCSD2 CMBLD1 CMBLD2 4NPHP1	Chlorocyclohexane and chlorobenzene degradation Chlorocyclohexane and chlorobenzene degradation	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase	3.2.1.26 3.1.1.45 3.1.1.45 3.1.3.2	KOX_02855/KOX_07760 KOX_02855/KOX_07760 KOX_08315(aphA)/KOX_14030/KOX_18070	suc -> g(c - fru dchrocmo -> dchroce tcmbo -> 2mac ntphp -> pnp + pi
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP2	Chlorocydohexane and chlorobenzene degradation Chlorocydohexane and chlorobenzene degradation gamma-Hexachlorocydohexane degradation gamma-Hexachlorocydohexane degradation gamma-Hexachlorocydohexane degradation	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase	3.2126 3.1145 3.1145 3.132 3.131	KOX_02855/KOX_07760  KOX_02855/KOX_07760  KOX_08315(aphA)/KOX_14030/KOX_18070  KOX_12385	suc -> glc + fru dchrocmo -> dchroce tcmbo -> Zmac ntphp -> pnp + pi ntphp -> pnp + pi
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP2 ACCOAA2	Chlorocyclohexane and chlorobenzene degradation Chlorocyclohexane and chlorobenzene degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation Geraniol degradation	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-CoA acyltransferase	32.1.26 3.1.1.45 3.1.1.45 3.1.3.2 3.1.3.1 2.3.1.16	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_08315(aphA)/KCX_14030/KCX_18070  KCX_12385  KCX_07830(fadA)/KCX_26660(fadI)	suc -> glc + fru dchrocmo -> dchrooe  tcmbo -> Zmac  ntphp -> pnp + pi  ntphp -> pnp + pi  7m366ccoa + coa -> 5mh4ecoa + accoa
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3	Chlorocyclohexane and chlorobenzene degradation Chlorocyclohexane and chlorobenzene degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation Geraniol degradation Geraniol degradation Geraniol degradation	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-CoA acyltransferase acetyl-CoA acyltransferase succinate-semialethyde	32.1.26 3.1.1.45 3.1.1.45 3.1.3.2 3.1.3.1 2.3.1.16 2.3.1.16	KOX_02855/KOX_07760  KOX_02855/KOX_07760  KOX_08315(aphA)/KOX_14030/KOX_18070  KOX_12385  KOX_07830(fadA)/KOX_26660(fadI)  KOX_07830(fadA)/KOX_26660(fadI)	suc -> g(c + fru dchrocmo -> dchrooe tcmbo -> Zmac ntphp -> pnp + pi ntphp -> pnp + pi 7m366cca + cca -> 5mb4eca + acca 5m3o4bca + cca -> 3mccan + acca
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2	Chloroydohexane and chlorobenzene degradation Chloroydohexane and chlorobenzene degradation gamma-Hexachloroydohexane degradation gamma-Hexachloroydohexane degradation gamma-Hexachloroydohexane degradation Geraniol degr	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-CoA acyltransferase acetyl-CoA acyltransferase succinate-semialdehyde dehydrogenase (NAD)	32.1.26 3.1.1.45 3.1.1.45 3.1.3.2 3.1.3.1 2.3.1.16 2.3.1.16 1.2.1.16	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_08315(aphA)/KCX_14030/KCX_18070  KCX_12385  KCX_07830(fadA)/KCX_26660(fadI)  KCX_07830(fadA)/KCX_26660(fadI)  KCX_07830(fadA)/KCX_26660(fadI)  KCX_07830(fadA)/KCX_26660(fadI)	suc -> glc + fru dchrocmo -> dchroce tcmbo -> 2mac ntphp -> pnp + pi ntphp -> pnp + pi 7m3666coa + coa -> 5mh4ecoa + accoa 5m364hcoa + coa -> 3mccoa + accoa nad + sucsal <> nadh + succ
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1	Chioroydohexane and chlorobenzene degradation Chioroydohexane and chlorobenzene degradation gamma-Hexachloroxydohexane degradation gamma-Hexachloroxydohexane degradation gamma-Hexachloroxydohexane degradation Geraniol deg	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-CoA acyltransferase acetyl-CoA acyltransferase succinate-semialethyde dehydrogenase (NAD) 4-aminobutynate transaminase	32126 31145 31145 3132 3131 23116 23116 12116 26119	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_08315(apha)/KCX_14030/KCX_18070  KCX_12385  KCX_07830(fadA)/KCX_26660(fadl)  KCX_07830(fadA)/KCX_26660(fadl)  KCX_09880/KCX_11825(gabD)/KCX_24465  KCX_09887	suc -> glc + fru dchrocmo -> dchroce tcmbo -> Zmac ntphp -> pnp + pi ntphp -> pnp + pi 7/m366coa + coa -> 5mh4ecoa + accoa 5m364hcoa + coa -> 5mcoa + accoa and + sucsal <-> nadh + succ gaba + akg -> glu + sucsal
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS	Chloroydohexane and chlorobenzene degradation Chloroydohexane and chlorobenzene degradation gamma-Hexachloroydohexane degradation gamma-Hexachloroydohexane degradation gamma-Hexachloroydohexane degradation Geraniol degr	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-CoA acyltransferase acetyl-CoA acyltransferase succinate-semialdehyde dehydrogenase (NAD)	32126 31145 31145 3132 3131 23116 23116 12116 26119 6355	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_08315(aphA)/KCX_14030/KCX_18070  KCX_12385  KCX_07830(fadA)/KCX_26660(fadl)  KCX_07830(fadA)/KCX_26660(fadl)  KCX_07830(fadA)/KCX_26660(fadl)  KCX_07830(fadA)/KCX_26660(fadl)  KCX_07830(KCX_11825(gabD)/KCX_24465  KCX_04875  KCX_04875  KCX_10685/KCX_10660(car8)	suc -> glc + fru dchrocmo -> dchroce tcmbo -> 2mac ntphp -> pnp + pi ntphp -> pnp + pi 7m3666coa + coa -> 5mh4ecoa + accoa 5m364hcoa + coa -> 3mccoa + accoa nad + sucsal <> nadh + succ
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1	Chioroydohexane and chlorobenzene degradation Chioroydohexane and chlorobenzene degradation gamma-Hexachloroxydohexane degradation gamma-Hexachloroxydohexane degradation gamma-Hexachloroxydohexane degradation Geraniol deg	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-CoA acyltransferase acetyl-CoA acyltransferase succinate-semialdehyde dehydrogenase (NAD) 4-aminobutyrate transaminase carbamoyl-phosphate synthase (glutamine-hydrolysing) glutamate racemase	32126 31145 31145 3132 3131 23116 23116 12116 26119	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_08315(apha)/KCX_14030/KCX_18070  KCX_12385  KCX_07830(fadA)/KCX_26660(fadl)  KCX_07830(fadA)/KCX_26660(fadl)  KCX_09880/KCX_11825(gabD)/KCX_24465  KCX_09887	suc -> glc + fru dchrocmo -> dchroce tcmbo -> Zmac ntphp -> pnp + pi ntphp -> pnp + pi 7/m366coa + coa -> 5mh4ecoa + accoa 5m364hcoa + coa -> 5mcoa + accoa and + sucsal <-> nadh + succ gaba + akg -> glu + sucsal
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS	Chlorocydohexane and chlorobenzene degradation Chlorocydohexane and chlorobenzene degradation pamma-Hexachlorocydohexane degradation gamma-Hexachlorocydohexane degradation Geraniol degradation Geraniol degradation Glutamate metabolism Glutamate metabolism Glutamate metabolism	carbosymethylenebutenolidase carbosymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-CoA acyltransferase acetyl-CoA acyltransferase accinate-semiadelyide dehydrogenase (NA) 4-aminobutyar(Na) (glutamine-hydrobysing)	32126 31145 31145 3132 3131 23116 23116 12116 26119 6355	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_08315(aphA)/KCX_14030/KCX_18070  KCX_12385  KCX_07830(fadA)/KCX_26660(fadl)  KCX_07830(fadA)/KCX_26660(fadl)  KCX_07830(fadA)/KCX_26660(fadl)  KCX_07830(fadA)/KCX_26660(fadl)  KCX_07830(KCX_11825(gabD)/KCX_24465  KCX_04875  KCX_04875  KCX_10685/KCX_10660(car8)	suc -> glc + fru dchromo -> dchrone  tcmbo -> 2mac  ntphp -> pnp + pi  ntphp -> pnp + pi  7m366coa + coa -> 5mh4ecoa + accoa 5m304hcoa + coa -> 3mcoa + accoa  nad + sucal <> nadh + succ gaba + akg -> glu + sucal  2 atp + gln + hco3 -> 2 adp + cap + glu + pi
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS GLUR GGLUCYSS GTHRDS	Chloroydohexane and chlorobenzene degradation Chloroydohexane and chlorobenzene degradation Chloroydohexane and chlorobenzene degradation gamma-Hexachloroydohexane degradation gamma-Hexachloroydohexane degradation Geraniol degradation Geraniol degradation Glutamate metabolism	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-CoA acyltransferase acetyl-roba phate phylopate transaminase carbannyl-phosphate synthase (glutamine-hydrobysing) glutamate racemase gamma-glutamylcysteine synthetase glutathione synthetase	32126 31145 31145 31145 3132 3131 23116 23116 26119 6355 5113 6322 6323	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_08315(aphA)/KCX_14030/KCX_18070  KCX_12385  KCX_07830(fadA)/KCX_26660(fadI)  KCX_07830(fadA)/KCX_26660(fadI)  KCX_07830(fadA)/KCX_26660(fadI)  KCX_07830(KCX_11825(gabD)/KCX_24465  KCX_04875  KCX_04875  KCX_07855/KCX_10660(carl8)  KCX_07425  KCX_070555  KCX_070555  KCX_070575	suc -> glc + fru dchromo -> dchroee  tcmbo -> 2mac  ntphp -> pnp + pi  ntphp -> pnp + pi  7m366coa + coa -> 5mh4ecoa + accoa 5m364hcoa + coa -> 5mcoa + accoa nad + sucsal <-> nadh + succ gaba + akg -> glu + sucsal 2 atp + gln + hco3 -> 2 adp + cap + glu + pi dglu <-> glu atp + oys + glu -> adp + gsys + pi atp + gys + gly -> adp + gst + pi atp + gys + gly -> adp + gst + pi atp + gys + gly -> adp + gst + pi
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS GLUR GGLUCYSS GTHRDS GLUS1	Chlorocyclohexane and chlorobenzene degradation Chlorocyclohexane and chlorobenzene degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation Geraniol degradation Geraniol degradation Glutamate metabolism	carbosymethylenebutenolidase carbosymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-CoA acyltransferase acetyl-CoA acyltransferase acetyl-CoA acyltransferase acetyl-CoA pacyltransferase succinate-semialethyde dehydrogenase (NAD) 4-aminobutyrate transaminase carbannyl-phosphate synthase (glutamine-hydrobysing) glutamate racemase gamma-glutamylcysteine synthetase glutamitone synthase glutamitone synthase glutamate synthase	32126 31145 31145 3132 3131 23116 23116 23116 26119 6335 5113 6322 6323 6321 6321 6321 6321 6321	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_08315(aphA)/KCX_14030/KCX_18070  KCX_12385  KCX_07830(tadA)/KCX_26660(fad)  KCX_07830(tadA)/KCX_26660(fad)  KCX_07830(tadA)/KCX_26660(fad)  KCX_0980/KCX_11825(gabD)/KCX_24465  KCX_0980/KCX_11825(gabD)/KCX_24465  KCX_0475  KCX_0655/KCX_10660(car8)  KCX_07425  KCX_00505  KCX_06575  KCX_03656(giB)/KCX_03865(gifD)	suc -> g(c + fru dchrocmo -> dchrooe  tcmbo -> Zmac  ntphp -> pnp + pi  7m266coa + coa -> 5m34ecoa + accoa  5m364kcoa + coa -> 3mccoa + accoa  5m364kcoa + coa -> 3mccoa + accoa  smad + sucsal <> -> ada + succ  gaba + akg -> glu + succal  2 atp + gln + hoc3 -> 2 adp + cap + glu + pi  dglu <-> glu  atp + cys + glu -> adp + gcys + pi  atp + cys + glu -> adp + rgt + pi  akg + gln + nadaph -> 2 glu + nadp
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS GLUR GGLUCYSS GTHRDS	Chloroydohexane and chlorobenzene degradation Chloroydohexane and chlorobenzene degradation Chloroydohexane and chlorobenzene degradation gamma-Hexachloroydohexane degradation gamma-Hexachloroydohexane degradation Geraniol degradation Geraniol degradation Glutamate metabolism	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-CoA acyltransferase acetyl-roba phate phylopate transaminase carbannyl-phosphate synthase (glutamine-hydrobysing) glutamate racemase gamma-glutamylcysteine synthetase glutathione synthetase	32126 31145 31145 31145 3132 3131 23116 23116 26119 6355 5113 6322 6323	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_08315(aphA)/KCX_14030/KCX_18070  KCX_12385  KCX_07830(fadA)/KCX_26660(fadI)  KCX_07830(fadA)/KCX_26660(fadI)  KCX_07830(fadA)/KCX_26660(fadI)  KCX_07830(KCX_11825(gabD)/KCX_24465  KCX_04875  KCX_04875  KCX_07855/KCX_10660(carl8)  KCX_07425  KCX_070555  KCX_070555  KCX_070575	suc -> glc + fru dchrocmo -> dchrooe  tcmbo -> 2mac  ntphp -> pnp + pi  ntphp -> pnp + pi  7m366coa + coa -> 5mh4ecoa + accoa  5m364hcoa + coa -> 5mcoa + accoa  nad + sucal <> nadh + succ  gaba + akg -> glu + sucal  2 atp + gln + hco3 -> 2 adp + cap + glu + pi  dglu <-> glu  atp + 9s + glu -> adp + gsys + pi  atp + gsys + gly -> adp + rgt + pi  akg + gln + nadph -> 2 glu + nadp  akg + gln + nadph -> 2 glu + nadp  akg + gln + nadh -> 2 glu + nadp
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS GLUR GGLUCYSS GTHRDS GLUS1 GLUS1 GLUS2 GLUDH2 GLUDH2 GLUDH2	Chirocyclohexane and chlorobenzene degradation Chirocyclohexane and chlorobenzene degradation Chirocyclohexane and chlorobenzene degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation Geraniol degradation Geraniol degradation Gutamate metabolism Glutamate detabolism Glutamate Metabolism Glutamate Metabolism Glutamate Metabolism Glutamate Metabolism	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acepl-CoA ayltransferase acepl-CoA ayltransferase acetyl-CoA ayltransferase succinate-semialdehyde dehydrogenase (NAD) 4-aminobutyvate transaminase carbamyl-phosphate synthase (glutamine-hydrobysing) glutamate racemase synthase glutamate synthase glutamate synthase glutamate synthase glutamate synthase glutamate dehydrogenase glutamate dehydrogenase glutamate dehydrogenase	32126 31145 31145 3131 3131 23116 23116 23116 12116 63.55 5113 63.22 63.23 14.113 14.114 14.14	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_08315(aphA)/KCX_14030/KCX_18070  KCX_12385  KCX_07830(fadA)/KCX_26660(fadl)  KCX_07830(fadA)/KCX_126660(fadl)  KCX_07830(fadA)/KCX_11825(gabD)/KCX_24465  KCX_04875  KCX_04875  KCX_04875  KCX_02655/KCX_10660(car8)  KCX_02675  KCX_03865(glb)/KCX_03865(gltD)  KCX_03865(glb)/KCX_03865(gltD)  KCX_13255  KCX_13	suc - g(c + fru dchrocmo -> dchroce  tcmbo -> 2mac  ntphp -> pnp + pi  ntphp -> pnp + pi  7m3e6cca + cac -> 5mh4eca + acca 5m3e4hca + cac -> 5mca + acca and + sucsal <-> nadh + succ gaba + akg -> glu + sucsal  2 atp + gln + hca3 -> 2 adp + cap + glu + pi  dglu <-> glu atp + gys + glu -> adp + rgt + pi akg + gln + nadp -> 2 glu + nadp akg + gln + nadp -> 2 glu + nadp glu + nadq -> akg + nadh + bid  glu + nadq -> akg + nadh + hid  glu + nadq -> akg + nadh + hid
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS GLUR GGLUCYSS GTHRDS GLUS2 GLUDH1 GLUDH1 GLUDH1 GLUDH1 GLUDH1	Chlorocyclohexane and chlorobenzene degradation Chlorocyclohexane and chlorobenzene degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation Gamma-Hexachlorocyclohexane degradation Geraniol degradation Geraniol degradation Gutamate metabolism Glutamate destabolism Glutamate metabolism	carbosymethylenebutenolidase carbosymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-CoA acyltransferase acetyl-ToA acyltransferase acetyl-ToA acyltransferase acetyl-ToA acyltransferase (plutamine typtops) glutamine acynthase glutamine synthase glutamines glutamines glutamines delydrogenase glutamines glutamines	32126 31145 31145 3132 3131 23116 23116 23116 12116 26119 6335 5113 6322 6323 14113 14114 1414 1413 3512	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_02815(aphA)/KCX_14030/KCX_18070  KCX_12385  KCX_07830(fadA)/KCX_26660(fad1)  KCX_07830(fadA)/KCX_26660(fad1)  KCX_07830(fadA)/KCX_26660(fad1)  KCX_0980/KCX_11825(gabD)/KCX_24465  KCX_0980/KCX_11825(gabD)/KCX_24465  KCX_00505  KCX_07425  KCX_00505  KCX_00505  KCX_03860(gl8)/KCX_03865(gltD)  KCX_03860(gl8)/KCX_03865(gltD)  KCX_18085  KCX_18085  KCX_18085  KCX_18085  KCX_18085	suc -> g(c + fru dchrocmo -> dchrooe  tcmbo -> Zmac  ntphp -> pnp + pi  7m366ccas + cas -> Smh4ecas + accas 5m3o4hcas + cas -> 3mccas + accas 5m3o4hcas + cas -> 3mccas + accas  sm3o4hcas + ca
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS GLUR GGLUCYSS GTHRDS GLUS1 GLUS1 GLUS2 GLUDH2 GLUDH2 GLUDH2	Chirocyclohexane and chlorobenzene degradation Chirocyclohexane and chlorobenzene degradation Chirocyclohexane and chlorobenzene degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation Geraniol degradation Geraniol degradation Gutamate metabolism Glutamate detabolism Glutamate Metabolism Glutamate Metabolism Glutamate Metabolism Glutamate Metabolism	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acepl-CoA ayltransferase acepl-CoA ayltransferase acetyl-CoA ayltransferase succinate-semialdehyde dehydrogenase (NAD) 4-aminobutyvate transaminase carbamyl-phosphate synthase (glutamine-hydrobysing) glutamate racemase synthase glutamate synthase glutamate synthase glutamate synthase glutamate synthase glutamate dehydrogenase glutamate dehydrogenase glutamate dehydrogenase	32126 31145 31145 31145 3131 23116 23116 23116 12116 63.55 5113 63.22 63.23 14.114 14.14 14.14 14.14 14.13 35.12 63.12	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_08315(aphA)/KCX_14030/KCX_18070  KCX_12385  KCX_07830(fadA)/KCX_26660(fadl)  KCX_07830(fadA)/KCX_126660(fadl)  KCX_07830(fadA)/KCX_11825(gabD)/KCX_24465  KCX_04875  KCX_04875  KCX_04875  KCX_02655/KCX_10660(car8)  KCX_02675  KCX_03865(glb)/KCX_03865(gltD)  KCX_03865(glb)/KCX_03865(gltD)  KCX_13255  KCX_13	suc - g(c + fru dchrocmo -> dchroce  tcmbo -> 2mac  ntphp -> pnp + pi  ntphp -> pnp + pi  7m3e6coa + coa -> 5mMecoa + accoa 5m3ed4coa + coa -> 5mMecoa + accoa  nad + sucsal <> nadh + succ gaba + akg -> glu + sucsal  2 atp + gln + hco3 -> 2 adp + cap + glu + pi  dglu <<> plu  atp + gys + gly -> adp + rgt + pi  atp + gys + gly -> adp + rgt + pi  atp + gys + gly -> adp + rgt + pi  atp + gys + gly -> adp + rgt + pi  atp + gys + gly -> adp + rgt + pi  atp + gys + gly -> adp + rgt + pi  atp + gys + gly -> adp + rgt + pi  atp + gys + gly -> adp + rgt + pi  atp + gys + gly -> adp + rgt + pi  atp + gys + gly -> adp + rgt + pi  atp + gys + adp +> 2 glu + nadp  glu + nadf ->> 2 glu + nadf  glu + nadf ->> atg + nadf + rbf  glu -> glu + rh4  glu -> glu + rh4  atp + glu + rh4 -> adp + gln + pi
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS GLUR GGLUCYSS GTHRDS GLUS1 GLUS1 GLUS2 GLUDH2 GLUDH2 GLUDH1 GLUN1 GLUN1 GLUN1 GLUN1 GLUN1	Chirocyclohexane and chlorobenzene degradation Chirocyclohexane and chlorobenzene degradation Chirocyclohexane and chlorobenzene degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation Geraniol degrdation Geraniol degrdation Glutamate metabolism Glutamate detabolism Glutamate Metabolism	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acepl-CoA ayltransferase acepl-CoA ayltransferase acetyl-CoA ayltransferase succinate-semialdehyde dehydrogenase (NAD) 4-aminobutyrate transaminase carbamoyl-phosphate synthase glutamate racemase gutamate aylthase glutamate synthase glutamate synthase glutamate synthase glutamate dehydrogenase glutaminase glutamate dehydrogenase glutaminase glutaminase glutaminase glutaminase glutaminase glutaminase glutaminase glutaminase glutaminase	32126 31145 31145 31145 3131 23116 23116 23116 12116 63.55 5113 63.22 63.23 14.114 14.14 14.14 14.14 14.13 35.12 63.12	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_08315(aphA)/KCX_14030/KCX_18070  KCX_12385  KCX_07830(adA)/KCX_26660(fadl)  KCX_07830(fadA)/KCX_26660(fadl)  KCX_09880/KCX_11825(gabD)/KCX_24465  KCX_04875  KCX_04875  KCX_04875  KCX_04875  KCX_0559(KCX_10660(car8))  KCX_07425  KCX_05050  KCX_02675  KCX_02675  KCX_02675  KCX_03860(ghB)/KCX_03865(ghD)  KCX_13825  KCX_14645  KCX_14645  KCX_06895(ghA)	suc -> g(c + fru dchrocmo -> dchrooe  tcmbo -> Zmac  ntphp -> pnp + pi  7m366ccas + cas -> Smh4ecas + accas 5m3o4hcas + cas -> 3mccas + accas 5m3o4hcas + cas -> 3mccas + accas  sm3o4hcas + ca
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS GLUR GGLUCYSS GTHRDS GLUS1 GLUS1 GLUS2 GLUDH2 GLUDH1 GLUS1 GLUN1 GABAT2 GRADT1	Chlorocyclohexane and chlorobenzene degradation Chlorocyclohexane and chlorobenzene degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation Geraniol degradion Geraniol degradion Geraniol degradion Glutamate metabolism Aminoacyl-tRNA biosynthesis	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-CoA aryltransferase acetyl-CoA aryltransferase succinate-semialdehyde dehydrogenase (NAD) 4-aminobutyrate transaminase carbamoryl-phosphate synthase (glutamine-hydrolysing) glutamate races gamma-glutamylcysteine synthetase glutamate synthase glutamate synthase glutamate dehydrogenase glutamate dehydrogenase glutamine synthetase glutamine synthetase glutamine synthetase glutamine synthase glutamines glutamine synthase glutamines g	32126 31145 31145 3132 3131 23116 23116 23116 12116 63.55 5113 63.22 14.113 14.114 14.14 14.14 14.14 14.14 14.14 14.14 14.14 14.14 14.15 63.12 63.12 63.15	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_08315(aphA)/KCX_14030/KCX_18070  KCX_12385  KCX_07830(fudA)/KCX_26660(fud)  KCX_07830(fudA)/KCX_26660(fud)  KCX_07830(fudA)/KCX_26660(fud)  KCX_07830(fudA)/KCX_26660(fud)  KCX_07830(fudA)/KCX_26660(fud)  KCX_04875  KCX_04875  KCX_04875  KCX_04875  KCX_02655/KCX_10660(car8)  KCX_0675  KCX_03665(glb)/KCX_03865(glt)  KCX_18055  KCX_14645  KCX_04675  KCX_16785	suc-s gfc + fru  dchrocmo >> dchrooe  tcmbo >> Zmac  ntphp >> pnp + pi  7m366ccaa + coa >> Smh4ecaa + accaa  5m364hcaa + coa >> Smcoa + accaa  5m364hcaa + coa >> 3mcoa + accaa  and + sucal <> nath + succ  gaba + akg -> glu + sucal  2 atp + gln + hoa3 -> Z adp + cap + glu + pi  dglu <-> glu  atp + (sys + glu -> adp + gsys + pi  atp + (sys + glu -> adp + gsys + pi  akg + gln + naadph >> Z glu + naadp  akg + gln + naadph >> Z glu + nadp  glu + nad <-> skg + nadph + nbd  glu + nad <-> skg + nadph + nbd  glu + adc <-> skg + nadph + nbd  glu + adc <-> skg + nadph + nbd  glu + adc <-> skg + nadph + nbd  glu + adc <-> skg + nadph + nbd  glu + adc <-> skg + nadph + nbd  glu + adc <-> skg + nadph + nbd  glu + adc <-> skg + nadph + nbd  glu + adc <-> skg + nadph + nbd  glu + adc <-> skg + nadph + nbd  glu + adc <-> skg + nadph + nbd  glu + adc <-> skg + nadph + nbd  glu + adc <-> skg + nadph + nbd  glu + adc <-> skg + nadph + nbd  glu + adc <-> skg + nadph + nbd  glu + pdu + nbd >> adp + gln + pi  gaba + akg <-> glu + sucsal  glutrna + gln + atp >> glntrna + glu + pi + adp
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS GLUR GGLUCYSS GTHRDS GLUS1 GLU	Chloroydoheane and chlorobenzene degradation Chloroydoheane and chlorobenzene degradation gamma-Heachloroydoheane degradation gamma-Heachloroydoheane degradation Gamma-Heachloroydoheane degradation Geraniol degradion Geraniol degradion Geraniol degradion Geraniol degradion Glutamate metabolism	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acepl-CoA ayltransferase acepl-CoA ayltransferase acetyl-CoA ayltransferase succinate-semialdehyde dehydrogenase (NAD) 4-aminobutyrate transaminase carbamoyl-phosphate synthase glutamate racemase gutamate aylthase glutamate synthase glutamate synthase glutamate synthase glutamate dehydrogenase glutaminase glutamate dehydrogenase glutaminase glutaminase glutaminase glutaminase glutaminase glutaminase glutaminase glutaminase glutaminase	32126 31145 31145 31145 3132 3131 23116 23116 12116 6315 5113 6322 14113 14114 1414 1414 1414 1414 1415 3512 6312 26119	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_08315(aphA)/KCX_14030/KCX_18070  KCX_12385  KCX_07830(fadA)/KCX_26660(fadI)  KCX_07830(fadA)/KCX_26660(fadI)  KCX_07830(fadA)/KCX_26660(fadI)  KCX_07830(fadA)/KCX_26660(fadI)  KCX_07830(fadA)/KCX_26660(fadI)  KCX_04875  KCX_04875  KCX_04875  KCX_04875  KCX_02655/KCX_10660(car8)  KCX_02675  KCX_03860(fgl8)/KCX_03865(ght)  KCX_18058  KCX_18058  KCX_14645  KCX_04675  KCX_16465  KCX_04675  KCX_16465  KCX_06859(glax)  KCX_06857	suc-s gfc + fru dchrocmo >> dchrooe tcmbo >> Zmac ntphp >> pnp + pi 7m366ccaa + coa >> Smh4ecaa + accaa 5m3o4hcaa + coa >> Smcoa + accaa and + sucal <>> nadh + succ gaba + akg >> glu + sucal 2 atp + gln + hoa3 >> 2 adp + cap + glu + pi dglu <>> glu atp + (sy + glu >> adp + gys + pi atp + (sy + glu >> adp + gys + pi akg + gln + nadph >> 2 glu + nadp akg + gln + nadph >> 2 glu + nadp akg + gln + nadph >> 2 glu + nadp akg + gln + nadph >> 2 glu + nadp akg + gln + nadph >> 2 glu + nadp glu + nadc >> akg + nadph + nbd glu + nbd >> akg + co ylu + yucsal
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS GLUR GGLUCYSS GTHRDS GLUS1 GLUS1 GLUS2 GLUDH2 GLUDH1 GLUS1 GLUN1 GABAT2 GRADT1	Chlorocyclohexane and chlorobenzene degradation Chlorocyclohexane and chlorobenzene degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation Geraniol degradion Geraniol degradion Geraniol degradion Glutamate metabolism Aminoacyl-tRNA biosynthesis	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-Coa aryttransferase acetyl-Coa aryttransferase succinate-semialdehyde dehydrogenase (NAD) 4-aminobutyrate transaminase cutamonyl-shosphate synthase (glutamine-hydrolysing) glutamate racemase gutamate synthase glutamite synthetase glutamite synthase d-aminobritysate formite aminobritysate formite glutamite synthase d-aminobritysate formite glutamite synthase d-aminobritysate formite glutamite synthase d-aminobritysate formite glutamite synthase d-aminobritysate glutamite synthase d-aminobritysate glutamite g	32126 31145 31145 3132 3131 23116 23116 23116 12116 63.55 5113 63.22 14.113 14.114 14.14 14.14 14.14 14.14 14.14 14.14 14.14 14.14 14.15 63.12 63.12 63.15	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_08315(aphA)/KCX_14030/KCX_18070  KCX_12385  KCX_07830(fudA)/KCX_26660(fud)  KCX_07830(fudA)/KCX_26660(fud)  KCX_07830(fudA)/KCX_26660(fud)  KCX_07830(fudA)/KCX_26660(fud)  KCX_07830(fudA)/KCX_26660(fud)  KCX_04875  KCX_04875  KCX_04875  KCX_04875  KCX_02655/KCX_10660(car8)  KCX_0675  KCX_03665(glb)/KCX_03865(glt)  KCX_18055  KCX_14645  KCX_04675  KCX_16785	suc-s gfc + fru  dchrocmo >> dchrooe  tcmbo >> Zmac  ntphp >> pnp + pi  7m366ccaa + coa >> Smh4ecaa + accaa  5m364hcaa + coa >> Smcoa + accaa  5m364hcaa + coa >> 3mcoa + accaa  and + sucal <> nath + succ  gaba + akg -> glu + sucal  2 atp + gln + hoa3 -> Z adp + cap + glu + pi  dglu <-> glu  atp + (sys + glu -> adp + gsys + pi  atp + (sys + glu -> adp + gsys + pi  akg + gln + naadph >> Z glu + naadp  akg + gln + naadph >> Z glu + nadp  glu + nad <-> skg + nadph + nbd  glu + nad <-> skg + nadph + nbd  glu + adc <-> skg + nadph + nbd  glu + adc <-> skg + nadph + nbd  glu + adc <-> skg + nadph + nbd  glu + adc <-> skg + nadph + nbd  glu + adc <-> skg + nadph + nbd  glu + adc <-> skg + nadph + nbd  glu + adc <-> skg + nadph + nbd  glu + adc <-> skg + nadph + nbd  glu + adc <-> skg + nadph + nbd  glu + adc <-> skg + nadph + nbd  glu + adc <-> skg + nadph + nbd  glu + adc <-> skg + nadph + nbd  glu + adc <-> skg + nadph + nbd  glu + adc <-> skg + nadph + nbd  glu + pdu + nbd >> adp + gln + pi  gaba + akg <-> glu + sucsal  glutrna + gln + atp >> glntrna + glu + pi + adp
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS GLUR GGLUCYSS GTHRDS GLUS1 GLUS1 GLUS2 GLUDH2 GLUDH1 GLUS1 GLUNT GABAT2 GRAD71 MAAMPT	Chlorocyclohexane and chlorobenzene degradation Chlorocyclohexane and chlorobenzene degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation Geraniol degradation Geraniol degradation Geraniol degradation Glutamate metabolism	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-CoA aryltransferase acetyl-CoA aryltransferase succinate-semialdehyde dehydrogenase (NAD) 4-aminobutyrate transaminase carbamoryl-phosphate synthase (glutamine-hydrolysing) glutamate races gamma-glutamylcysteine synthetase glutamate synthase glutamate synthase glutamate dehydrogenase glutamate dehydrogenase glutamate dehydrogenase glutamine synthetase uptamine synthetase alutamine synthase glutamine synthase glutamines glutamine synthase glutamine synthas	32126 31145 31145 3132 3131 23116 23116 23116 12116 63.55 5113 63.22 14.113 14.114 14.14 14.14 14.14 14.14 14.14 14.14 14.14 14.14 14.15 35.12 63.12 26.119 63.357 34.112	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_028515(aphA)/KCX_14030/KCX_18070  KCX_12385  KCX_07830(fadA)/KCX_26660(fad)  KCX_07830(fadA)/KCX_26660(fad)  KCX_07830(fadA)/KCX_26660(fad)  KCX_0980/KCX_11825(gabD)/KCX_24465  KCX_0980/KCX_11825(gabD)/KCX_24465  KCX_00505  KCX_0655/KCX_10660(car8)  KCX_00505  KCX_14645  KCX_00505  KCX_14645  KCX_16785  KCX_16785  KCX_16785  KCX_16785	suc -> gic + fru dchrocmo -> dchrooe tcmbo -> Zmac ntphp -> pnp + pi 7m366ccna + coa -> Smh4ecna + accna 5m364bcna + coa -> 3mccna + accna 5m364bcna + coa -> 3mccna + accna nad + sucal <> -> nadh + succ gaba + akg -> glu + sucal 2 atp + gin + hcn3 -> 2 adp + cap + glu + pi dglu <>> glu atp + yos + glu -> adp + gsys + pi atp + yos + glu -> adp + grys + pi akg + gin + nadph -> 2 glu + nadp akg + gin + nadph -> 2 glu + nadp glu + nadp -> 3kg + nadph + nhd glu + nad <>> akg + nadph + nhd glu + nad <>> akg + nadph + nhd glu + nad <>> glu + nadph atp + yos + glu +> adp + gln + pi atp + yos + glu +> adp + gln + pi atp + glu + nhd -> 2 glu + nadp glu + nadp -> glu + hhd atp + glu + nhd -> adp + gln + pi atp + glu + nhd -> gln + pi atp + glu + nhd -> gln + pi atp + glu + nhd -> gln + pi atp + glu + nhd -> gln + pi atp + glu + pi + adp progly -> gly + pro atp + rgt + sprmd -> adp + gtspmd + pi
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS GLUR GGLUCYSS GTHRDS GLUS1 GLUS2 GLUDH1 GLUDH1 GLUN1 GLNST11 GABAT2 GTADT1 MAAMPT GTSPMDS GTHIR	Chirocyclohexane and chlorobenzene degradation Chirocyclohexane and chlorobenzene degradation Chirocyclohexane and chlorobenzene degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation Geraniol degrdation Geraniol degrdation Glutamate metabolism	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-CoA aryltransferase acetyl-CoA aryltransferase succinate-semialdehyde dehydrogenase (NAD) 4-aminobutyrate transaminase carbamoyl-phosphate synthase (glutamine-hydrolysing) glutamate racemase gamma-glutamylcysteine synthetase glutamate synthase glutamate synthase glutamate dehydrogenase glutamate dehydrogenase glutamine synthetase alvamine byrutate transaminase aspartyl-rRNA/Acstylgutamyl- transimate synthetase aspartyl-rRNA/Acstylgutamyl- transimate aspartyl-rRNA/Acstylgutamyl- transimate aspartyl-rRNA/Acstylgutamyl- transimate aspartyl-rRNA/Acstylgutamyl- transimate aspartyl-rRNA/Acstylgutamyl- transimate glutaminopeptidase glutathionylspermidine synthetase glutathionylspermidine synthetase glutathione hydralase	32126 31145 31145 3132 3131 23116 23116 23116 12116 26119 6355 5113 6322 63123 14113 14114 1413 3512 6312 6315 6323 34112 6316 6323 44112 6318 2322	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_02815(aphA)/KCX_14030/KCX_18070  KCX_12385  KCX_07830(fadA)/KCX_26660(fad1)  KCX_07830(fadA)/KCX_26660(fad1)  KCX_0980/KCX_11825(gabD)/KCX_24465  KCX_04875  KCX_04875  KCX_06565  KCX_06565  KCX_06565  KCX_06565  KCX_06565  KCX_08660(fal8)/KCX_03865(gltD)  KCX_03860(glt8)/KCX_03865(gltD)  KCX_18685  KCX_1525  KCX_14645  KCX_16785  KCX_02835  KCX_16785  KCX_16785  KCX_16785  KCX_02835  KCX_16785  KCX_02835  KCX_16785  KCX_02835  KCX_16785  KCX_02835  KCX_16785  KCX_02835  KCX_16785  KCX_0835/KCX_16795  KCX_07838/KCX_21655/KCX_16115(pepN)/KCX	suc -> gic + fru dchrocmo -> dchrooe  tcmbo -> Zmac  ntphp -> pnpp + pi  ntphp -> pnp + pi  sucal <-> nadh + succ  gaba + akg -> glu + sucal  2 atp + gln + ho3 -> 2 adp + cap + glu + pi  dglu <-> glu  atp - (ys + glu -> adp - gcys + pi  atp - (ys + glu -> adp + grys + pi  atp - (ys + glu -> adp + grys + pi  atp - (ys + glu -> adp + nadp  akg + gln + nadph -> 2 glu + nadp  akg + gln + nadph -> 2 glu + nadp  glu + nadp -> akg + nadph + nhd  glu + nadp -> akg + nadh + nhd  glu -> glu + nhd -> adp + gln + pi  glu -> glu + nhd -> adp + gln + pi  glu + progly -> gly + pro  atp + rgt + sprmd -> adp + gtspmd + pi  rgt -> cysgly + glu
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS GLUR GGLUCYSS GTHRDS GLUS1 GLUS1 GLUS2 GLUDH2 GLUDH2 GLUN1 GLNS1 GLAST GABAT2 GABAT2 GTADT1 MAAMPT GTSPMDS GTHHR ALAAPT	Chirocyclohexane and chlorobenzene degradation Chirocyclohexane and chlorobenzene degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation Geranicol degradation Geranicol degradation Geranicol degradation Gutamate metabolism Glutamate destabolism Glutamate destabolism Glutamate Metabolism Glutathione Metabolism	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-Coa aryttransferase acetyl-Coa aryttransferase succinate-semialdehyde dehydrogenase (NAD) 4-aminobutyrate transaminase carbamoyl-phosphate synthase (glutamine-hydrolysing) glutamiter acetylase gutamite synthase glutamite synthase glutathionylspermidine synthase glutathionylspermidine synthase glutathionylspermidine synthase alanyl aminopeptidase	32126 31145 31145 31145 3132 3131 23116 23116 23116 23116 63.55 5113 63.22 63.23 14.113 14.114 14.14 14.14 14.14 14.14 14.15 63.17 26.119 63.57 3.4112 63.18 2.32 3.4111,16.4112/3.413.	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_08315(aphA)/KCX_14030/KCX_18070  KCX_12385  KCX_07830(fadA)/KCX_26660(fad1)  KCX_09880/KCX_11825(gabc)/KCX_24465  KCX_09880/KCX_11825(gabc)/KCX_24465  KCX_04875  KCX_10655/KCX_10660(car8)  KCX_04875  KCX_05056  KCX_02656  KCX_12657  KCX_14656  KCX_16765  KCX_16765  KCX_16765  KCX_16765  KCX_16765  KCX_16765  KCX_16765  KCX_04780(ggtl/KCX_16795  KCX_04780(g	suc - s glc + fru dchrocmo -> dchrooe tcmbo -> Zmac ntphp -> pnp + pi 7m366ccaa + cca -> Smh4ecaa + accaa 5m34hcaa + cca -> Smccaa + accaa nad + sucsal <-> nadh + succa gaba + akg -> glu + succal gaba + akg -> glu + succal 2 atp + gln + hca3 -> 2 adp + cap + glu + pi dglu <-> glu atp + cys + glu -> adp + gcys + pi atp + gys + gly -> adp + rgt + pi akg + gln + nadph -> 2 glu + nadp akg + gln + nadph -> 2 glu + nadp akg + gln + nadph -> 2 glu + nadp akg + gln + nadph -> 2 glu + nad glu + nad <-> skg + nadph + nh4 glu -> glu + nh4 sln -> glu + nh4 -> adp + gln + pi gaba + akg <-> glu + succal glutrna + gln + atp -> glntrna + glu + pi + adp progly -> gly + pro atp + rgt + sprmd -> adp + gtspmd + pi rgt -> cysgly -> cys + gly
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS GLUR GGLUCYSS GTHRDS GLUS1 GL	Chlorocyclohexane and chlorobenzene degradation Chlorocyclohexane and chlorobenzene degradation Chlorocyclohexane and chlorobenzene degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation Geraniol degradation Geraniol degradation Glutamate metabolism Glutathione Metabolism Glutathione Metabolism Glutathione Metabolism Glutathione Metabolism Glutathione Metabolism	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-CoA aryltransferase acetyl-CoA aryltransferase succinate-semialdehyde dehydrogenase (NAD) 4-aminobutyrate transaminase carbamoryl-phosphate synthase (glutamine-hydrolysing) glutamate races gamma-glutamylcysteine synthetase glutamate synthase glutamate synthase glutamate dehydrogenase glutamate dehydrogenase glutamate dehydrogenase glutamine synthetase uptamine synthetase dlutamine synthase glutamine	32126 31145 31145 31145 3132 3131 23116 23116 23116 12116 63.55 5113 63.22 63.23 14.113 14.114 14.14 14.14 14.14 14.14 14.14 14.14 14.15 63.17 63.57 34.112 63.18 23.22 34.11.174.11.2/3.4 11.12/3.4 11.12/3.4 11.12/3.4 11.12/3.4 11.12/3.4 11.12/3.4 11.11.9	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_08315(aphA)/KCX_14030/KCX_18070  KCX_12385  KCX_07830(fadA)/KCX_26660(fadI)  KCX_07830(fadA)/KCX_126660(fadI)  KCX_09880/KCX_11825(gabD)/KCX_24465  KCX_04875  KCX_01655/KCX_10660(car8)  KCX_07425  KCX_07425  KCX_07425  KCX_07425  KCX_0366(glb)/KCX_03865(gltD)  KCX_08675  KCX_08685  KCX_08675  KCX_08695(glb)/KCX_03865(gltD)  KCX_18585  KCX_14585  KCX	suc-s gfc + fru dchrocmo >> dchrooe tcmbo >> Zmac ntphp >> pnp + pi 7m366ccaa + coa >> Smh4ecaa + accaa 5m364hcaa + coa >> Smcoa + accaa 5m364hcaa + coa >> 3mcoa + accaa and + sucsid <> nada + succ gabaa + akg -> gfu + succal 2 atp + gfn + hca3 -> Z adp + cap + gfu + pi dgfu <-> gfu atp +> gy +> gfu -> adp + gy +> pi atp +> gy +> gfu -> adp + gy +> pi akg +> gfn + nadph >> Z gfu + nadp akg +> gfn + nadph >> Z gfu + nadp algu += nad <-> akg += nadph += nbd gfu += nad <-> gfu += nbd gfu += nbd <-> akg += nadph += nbd gfu += nbd <-> akg += nadph += nbd gfu += nbd <-> akg += nadph += nbd gfu += nbd <-> adp += gy += pi aga +> gfu += nbd <-> adp += gy += pi aga +> gfu += nbd <-> adp += gy += pi aga += gfu += pi += pi += pi += pi gaba += akg <-> gfu += sucsal gfurma += gfu += pi += pi += pi += pi y -> y y y +> y y +> pro atp += gy += y y += pi y -> y y y +> y y += y y += pi y += y y y += y y += y y += pi y -> y y y y -> y y += y y += y y += pi y -> y y y -> y y += y y += y y += pi y -> y y y y -> y y += y y += y y += pi y -> y y y y -> y y += y y += pi y -> y y y y -> y y += y y += pi y -> y y y y -> y y += y y += pi y -> y y y y y y y y y y y y y y y y y y
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS GLUR GGLUCYSS GTHRDS GLUS1 GLUS1 GLUS2 GLUDH2 GLUDH2 GLUN1 GLNS1 GLAST GABAT2 GABAT2 GTADT1 MAAMPT GTSPMDS GTHHR ALAAPT	Chirocyclohexane and chlorobenzene degradation Chirocyclohexane and chlorobenzene degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation Geranicol degradation Geranicol degradation Geranicol degradation Gutamate metabolism Glutamate destabolism Glutamate destabolism Glutamate Metabolism Glutathione Metabolism	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-Coa aryttransferase acetyl-Coa aryttransferase succinate-semialdehyde dehydrogenase (NAD) 4-aminobutyrate transaminase carbamoyl-phosphate synthase (glutamine-hydrolysing) glutamiter acetylase gutamite synthase glutamite synthase glutathionylspermidine synthase glutathionylspermidine synthase glutathionylspermidine synthase alanyl aminopeptidase	32126 31145 31145 31145 3132 3131 23116 23116 23116 23116 63.55 5113 63.22 63.23 14.113 14.114 14.14 14.14 14.14 14.14 14.15 63.17 26.119 63.57 3.4112 63.18 2.32 3.4111,16.4112/3.413.	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_08315(aphA)/KCX_14030/KCX_18070  KCX_12385  KCX_07830(fadA)/KCX_26660(fad1)  KCX_09880/KCX_11825(gabc)/KCX_24465  KCX_09880/KCX_11825(gabc)/KCX_24465  KCX_04875  KCX_10655/KCX_10660(car8)  KCX_04875  KCX_05056  KCX_02656  KCX_12657  KCX_14656  KCX_16765  KCX_16765  KCX_16765  KCX_16765  KCX_16765  KCX_16765  KCX_16765  KCX_04780(ggtl/KCX_16795  KCX_04780(g	suc - s glc + fru dchrocmo -> dchrooe tcmbo -> Zmac ntphp -> pnp + pi 7m366ccaa + cca -> Smh4ecaa + accaa 5m34hcaa + cca -> Smccaa + accaa nad + sucsal <-> nadh + succa gaba + akg -> glu + succal gaba + akg -> glu + succal 2 atp + gln + hca3 -> 2 adp + cap + glu + pi dglu <-> glu atp + cys + glu -> adp + gcys + pi atp + gys + gly -> adp + rgt + pi akg + gln + nadph -> 2 glu + nadp akg + gln + nadph -> 2 glu + nadp akg + gln + nadph -> 2 glu + nadp akg + gln + nadph -> 2 glu + nad glu + nad <-> skg + nadph + nh4 glu -> glu + nh4 sln -> glu + nh4 -> adp + gln + pi gaba + akg <-> glu + succal glutrna + gln + atp -> glntrna + glu + pi + adp progly -> gly + pro atp + rgt + sprmd -> adp + gtspmd + pi rgt -> cysgly -> cys + gly
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS GLUR GGLUCYSS GTHRDS GLUS1 GL	Chlorocyclohexane and chlorobenzene degradation Chlorocyclohexane and chlorobenzene degradation Chlorocyclohexane and chlorobenzene degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation Geraniol degradation Geraniol degradation Glutamate metabolism Glutathione Metabolism Glutathione Metabolism Glutathione Metabolism Glutathione Metabolism Glutathione Metabolism	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-Coa aryttransferase acetyl-Coa aryttransferase acetyl-Coa aryttransferase succinate-semialdehyde dehydrogenase (NAD) 4-aminobutyrate transaminase carbamoyl-phosphate synthase (glutamine-hydrolysing) glutamate racemase gamma-glutamylcysteine synthetase glutamate synthase glutamate synthase glutamate synthase glutamate synthase glutamate synthase glutamate synthase glutaminase g	32126 31145 31145 31145 3132 3131 23116 23116 23116 12116 63.55 5113 63.22 63.23 14.113 14.114 14.14 14.14 14.14 14.14 14.14 14.14 14.15 63.17 63.57 34.112 63.18 23.22 34.11.174.11.2/3.4 11.12/3.4 11.12/3.4 11.12/3.4 11.12/3.4 11.12/3.4 11.12/3.4 11.11.9	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_08315(aphA)/KCX_14030/KCX_18070  KCX_12385  KCX_07830(fadA)/KCX_26660(fadI)  KCX_07830(fadA)/KCX_126660(fadI)  KCX_09880/KCX_11825(gabD)/KCX_24465  KCX_04875  KCX_01655/KCX_10660(car8)  KCX_07425  KCX_07425  KCX_07425  KCX_07425  KCX_0366(glb)/KCX_03865(gltD)  KCX_08675  KCX_08685  KCX_08675  KCX_08695(glb)/KCX_03865(gltD)  KCX_18585  KCX_14585  KCX	suc-s gfc + fru dchrocmo >> dchrooe tcmbo >> Zmac ntphp >> pnp + pi 7m366ccaa + coa >> Smh4ecaa + accaa 5m364hcaa + coa >> Smcoa + accaa 5m364hcaa + coa >> 3mcoa + accaa and + sucsid <> nada + succ gabaa + akg -> gfu + succal 2 atp + gfn + hca3 -> Z adp + cap + gfu + pi dgfu <-> gfu atp +> gy +> gfu -> adp + gy +> pi atp +> gy +> gfu -> adp + gy +> pi akg +> gfn + nadph >> Z gfu + nadp akg +> gfn + nadph >> Z gfu + nadp algu += nad <-> akg += nadph += nbd gfu += nad <-> gfu += nbd gfu += nbd <-> akg += nadph += nbd gfu += nbd <-> akg += nadph += nbd gfu += nbd <-> akg += nadph += nbd gfu += nbd <-> adp += gy += pi aga +> gfu += nbd <-> adp += gy += pi aga +> gfu += nbd <-> adp += gy += pi aga += gfu += pi += pi += pi += pi gaba += akg <-> gfu += sucsal gfurma += gfu += pi += pi += pi += pi y -> y y y +> y y +> pro atp += gy += y y += pi y -> y y y +> y y += y y += pi y += y y y += y y += y y += pi y -> y y y y -> y y += y y += y y += pi y -> y y y -> y y += y y += y y += pi y -> y y y y -> y y += y y += y y += pi y -> y y y y -> y y += y y += pi y -> y y y y -> y y += y y += pi y -> y y y y -> y y += y y += pi y -> y y y y y y y y y y y y y y y y y y
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS GLUR GGLUCYSS GTHRDS GLUS1 GL	Chlorocyclohexane and chlorobenzene degradation Chlorocyclohexane and chlorobenzene degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation Geraniol degradation Geraniol degradation Geraniol degradation Gutamate metabolism Glutamate Metabolism Glutathione Metabolism	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-CoA aryltransferase acetyl-CoA aryltransferase succinate-semialdehyde dehydrogenase (NAD) 4-aminobutyrate transaminase carbamoryl-phosphate synthase (glutamine-hydrolysing) glutamate racess gamma-glutamylcysteine synthetase glutamate synthase glutamate synthase glutamate dehydrogenase glutamate dehydrogenase glutamate dehydrogenase glutamate dehydrogenase glutamine synthase glutathione fyndalase glutathione peroxidase glutathione midase/grythetase	32126 31145 31145 31145 3132 3131 23116 23116 23116 12116 63.55 5113 63.22 63.23 14.113 14.114 14.14 14.14 14.14 14.14 14.14 14.14 14.15 63.17 63.57 34.112 63.18 23.23 24.11.18,41.12,4.11.21,4.11.19 11.119 18.17	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_028515(aphA)/KCX_14030/KCX_18070  KCX_07830(fadA)/KCX_26660(fad)  KCX_07830(fadA)/KCX_26660(fad)  KCX_0980/KCX_11825(gabD)/KCX_24465  KCX_0980/KCX_11825(gabD)/KCX_24465  KCX_0980/KCX_11825(gabD)/KCX_24465  KCX_00505  KCX_00505  KCX_00505  KCX_00505  KCX_00505  KCX_00505  KCX_03860(giB)/KCX_03865(gitD)  KCX_03860(giB)/KCX_03865(gitD)  KCX_14645  KCX_14645  KCX_14645  KCX_14645  KCX_14645  KCX_146785  KCX_146785  KCX_146785  KCX_146785  KCX_146785  KCX_146785  KCX_146785  KCX_146785  KCX_146785  KCX_02835  KCX_146785  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_02835	suc - s glc + fru  dchrocmo -> dchrooe  tcmbo -> Zmac  ntphp -> pnp + pi  7m366ccaa + coa -> Smh4ecaa + accaa  5m364hcaa + coa -> Smh4eca + accaa  5m364hcaa + coa -> 3mccaa + accaa  nad + sucal <>- nadh + succ  gaba + akg -> glu + sucsal  2 atp + gln + hca3 -> 2 adp + cap + glu + pi  dglu <>- yglu  atp + ygs + glu -> adp + gys + pi  atp + ygs + glu -> adp + gys + pi  atp + ygs + glu -> adp + rap + pi  akg + gln + nadph -> 2 glu + nadp  akg + gln + nadph -> 2 glu + nadp  glu + nadp -> alg + nagh + nbd  glu + nadp -> alg + nagh + nbd  glu + nadp -> glu + blu +
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS GLUR GGLUCYSS GTHRDS GLUS2 GLUDH1 GLUDH1 GLUN1 GLUN1 GLNST1 GABAT2 GTADT1 MAAMPT GTSPMDS GTHHR ALAAPT GTIPX GLUTHR GTSPMDAS GLYCK	Chirocyclohexane and chlorobenzene degradation Chirocyclohexane and chlorobenzene degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation Geraniol degrdation Geraniol degrdation Glutamate metabolism Glutamatione Metabolism Glutathione Metaboli	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-CoA aryltransferase acetyl-CoA aryltransferase succinate-semialdehyde dehydrogenase (NAD) 4-aminobutyrate transaminase carbamoryl-phosphate synthase (glutamine-hydrolysing) glutamate racemsas gamma-glutamylcysteine synthetase glutamate synthase glutamate synthase glutamate synthase glutamate dehydrogenase glutamate dehydrogenase glutamate dehydrogenase glutamate synthase glutamine synthase glutathione fyndralase glutathione peroxidase glutathione synthase glutathione syn	32126 31145 31145 31145 3132 3131 23116 23116 23116 12116 6315 6312 6312 14113 14114 1413 14112 6312 6319 63.57 34112 6318 232 34113 4114 1413 3517 34112 6318 3517 34112 6318 3517 34112 6318 3517 35178	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_02815(aphA)/KCX_14030/KCX_18070  KCX_12285  KCX_07830(adA)/KCX_26660(fad1)  KCX_07830(adA)/KCX_26660(fad1)  KCX_0980/KCX_11825(gabD)/KCX_24465  KCX_0980/KCX_11825(gabD)/KCX_24465  KCX_0980/KCX_11825(gabD)/KCX_24465  KCX_0980/KCX_11825(gabD)/KCX_24465  KCX_00505  KCX_07425  KCX_00505  KCX_00575  KCX_00575  KCX_03860(galB)/KCX_03865(ghD)  KCX_03860(galB)/KCX_03865(ghD)  KCX_18085  KCX_14645  KCX_16985(ghA)  KCX_16785  KCX_16785  KCX_16785  KCX_16785  KCX_16785  KCX_16785  KCX_16785  KCX_16785  KCX_16785  KCX_02835  KCX_08356KCX_11865	suc -> gic + fru dchrocmo -> dchrooe  tcmbo -> Zmac  ntphp -> pnpp + pi  7m366ccab -< cca -> Smh4ecab + accab 5m3o4hcoa + cca -> 3mccab + accab 5m3o4hcoa + cca -> 3mccab + accab sm3o4hcoa + cca -> 3mccab + accab sm3o4hcoa + cca -> 3mccab + accab sm3o4hcoa + ccab -> 3mccab + accab sm3o4bcoa +> 2adp + succ sabab - adp -> gys + gib -> adp + gys + pi adp + gys + gib -> adp + gys + pi adp + gib + nadph -> 2 gib + nadp adg + gin + nadph -> 2 gib + nadp adg + gin + nadph -> 2 gib + nadp gib -> gib + nhd gib + nadp -> 3dp + nhd gib + nadp -> 3dp + nhd adp - gib + nhd -> adp + gin + pi gaba + adg -> gib + succal glutma + gin + atp -> gintma + gib + pi + adp progly -> gly + pro atp + rgt + sprmd -> adp + gtspmd + pi rgt -> cysply + gib  cysply -> cys + gly hcc2 + 2 rgt -> cysply gtspmd -> rgt + sprmd atp + gl -> adp + glyc3p
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP1 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS GLUR GGLUCYSS GTHRDS GLUS1 GLUS1 GLUS2 GLUDH2 GLUS1 GL	Chirocyclohexane and chlorobenzene degradation Chirocyclohexane and chlorobenzene degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation Geranici degradation Geranici degradation Geranici degradation Gutamate metabolism Glutamate Metabolism Glutathione Metabolism Glycerolipid Metabolism Glycerolipid Metabolism Glycerolipid Metabolism Glycerolipid Metabolism Glycerolipid Metabolism	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-Coa aryttransferase acetyl-Coa aryttransferase acetyl-Coa aryttransferase succinate-semialdehyde dehydrogenase (NAD) 4-aminobutyrate transaminase carbamoyl-phosphate synthase (glutamine-hydrolysing) glutamate races gamma-glutamylcysteine synthetase glutamate synthase glutamate synthase glutamate synthase glutamate synthase glutamate synthase glutamate synthase glutaminase glutaminopeptidase glutathione peroxidase glutathione peroxidase glutathione reductase glutathionelyspermidine amidase/synthetase glycerol kinase glycerol kinase alcohol dehydrogenase (glycerol)	32126 31145 31145 31145 3132 3131 23116 23116 23116 23116 6355 5113 6322 6323 14113 14114 1414 1414 1414 1414 1414	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_02815(aphA)/KCX_14030/KCX_18070  KCX_08315(aphA)/KCX_14030/KCX_18070  KCX_07830(adA)/KCX_26660(fadl)  KCX_07830(adA)/KCX_26660(fadl)  KCX_09890/KCX_11825(gabD)/KCX_24465  KCX_04875  KCX_04875  KCX_04875  KCX_0455/KCX_10660(car8)  KCX_0475  KCX_05055  KCX_0675  KCX_0505  KCX_0675  KCX_03860(gl8)/KCX_03865(gltD)  KCX_03860(gl8)/KCX_03865(gltD)  KCX_03860(gl8)/KCX_03865(gltD)  KCX_1805  KCX_1525  KCX_16415(pepN)  KCX_04835  KCX_16115(pepN)  KCX_04835  KCX_04780(ggt)/KCX_16795  KCX_045225  KCX_050255  KCX_050255  KCX_0502255  KCX_0502255  KCX_0502256  KCX_05025/KCX_13865  KCX_06075/KCX_13865  KCX_06075/KCX_13865  KCX_06075/KCX_13865	suc - s glc + fru dchrocmo -> dchrooe tcmbo -> Zmac ntphp -> pnp + pi 7m366ccaa + coa -> Smh4ecaa + accaa 5m364kcaa + coa -> Smccaa + accaa nad + sucsal <> nadh + succa abaa + akg -> glu + succal abaa + akg -> glu + succal 2 atp + gln + hco3 -> 2 adp + cap + glu + pi dglu <-> glu atp + cys + glu -> adp + gcys + pi atp + gys + gly -> adp + rgt + pi akg + gln + nadph -> 2 glu + nadp akg + gln + nadph -> 2 glu + nadp akg + gln + nadph -> 2 glu + nadp akg + gln + nadph -> 2 glu + nadp akg + gln + nadph -> 2 glu + succal glu + nad <-> akg + nadh + nh4 gln -> glu + ph4 al + glu + ph4 -> adp + gln + pi gaba + akg <-> glu + succal glutma + gln + apt -> gln + pi gaba + akg <-> glu + succal glutma + gln + apt -> gln + pi gaba + akg -> gly + succal glutma + gln + apt -> glr + pi gaba + akg -> gly + succal glutma + gln + apt -> glr + pi gaba + akg -> gly + succal glutma + gln + apt -> glr + pi gaba + akg -> gly + succal glutma + gln + apt -> glr + andp eygly -> cys + gly hzo2 + 2 rgt <-> cys gt + nadph -> 2 rgt + nadp gtpmd -> rgt + sprmd atp + gl -> adp + glyC3p t3 + nad <-> gl + nadh
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS GLUR GGLUCYSS GTHRDS GLUS2 GLUDH1 GLUDH1 GLUN1 GLUN1 GLNST1 GABAT2 GTADT1 MAAMPT GTSPMDS GTHHR ALAAPT GTIPX GLUTHR GTSPMDAS GLYCK	Chirocyclohexane and chlorobenzene degradation Chirocyclohexane and chlorobenzene degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation Geraniol degrdation Geraniol degrdation Glutamate metabolism Glutamatione Metabolism Glutathione Metaboli	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-CoA aryltransferase acetyl-CoA aryltransferase succinate-semialdehyde dehydrogenase (NAD) 4-aminobutyrate transaminase carbamoryl-phosphate synthase (glutamine-hydrolysing) glutamate racemsas gamma-glutamylcysteine synthetase glutamate synthase glutamate synthase glutamate synthase glutamate dehydrogenase glutamate dehydrogenase glutamate dehydrogenase glutamate synthase glutamine synthase glutathione fyndralase glutathione peroxidase glutathione synthase glutathione syn	32126 31145 31145 3132 3131 23116 23116 23116 23116 23117 26119 6355 5113 6322 6323 14113 14114 1413 3512 6312 26119 6357 34112 6318 2322 6318 2322 6318 2322 6318 2323 6318 2323 6318 2323 6318 2323 6318 2323 6318 2323 6318 2323 6318 2323 6318 2323 6318 2323	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_02815(aphA)/KCX_14030/KCX_18070  KCX_07830(fadA)/KCX_26660(fad)  KCX_07830(fadA)/KCX_26660(fad)  KCX_07830(fadA)/KCX_26660(fad)  KCX_0785  KCX_0785  KCX_0856  KCX_0785  KCX_0785  KCX_0785  KCX_0785  KCX_0856(fall)/KCX_03865(ght)  KCX_0856(ght)/KCX_03865(ght)  KCX_0856(ght)/KCX_03865(ght)  KCX_14645  KCX_14645  KCX_16785  KCX_16785  KCX_16785  KCX_16785  KCX_16785  KCX_16785  KCX_02835  KCX_022835  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_03875/KCX_13865  KCX_19385/KCX_13865  KCX_02835  KCX_02835  KCX_02835  KCX_03875/KCX_13865  KCX_19385/KCX_13865  KCX_19385/KCX_13865  KCX_02835  KCX_02835  KCX_03157/KCX_13865  KCX_11956/KCX_13865	suc -> g(s + fru dchrocmo -> dchrooe tcmbo -> Zmac ntphp -> pnp + pi 7m366ccna + coa -> Smh4ecna + accna 5m364bcna + coa -> Smh4ecna + accna 5m364bcna + coa -> 3mcona + accna nad + sucal <> -> nadh + succ gaba + akg -> glu + sucsal 2 atp + gin + hcn3 -> 2 adp + cap + glu + pi dglu <-> glu atp + (ys + glu -> adp + gys + pi atp + (ys + glu -> adp + gys + pi akg + gin + nadph -> 2 glu + nadp akg + gin + nadph -> 2 glu + nadp glu + nadq -> akg + nadph + nh4 glu + nad <-> akg + nadph + nh4 atp - glu + sh4 -> glu + pi atp + gys + gly -> bi atp + gys + gly -> bi atp + gys + gly -> bi atp + gys + gly + bi atp + glu + nh4 -> adp + gln + pi atp + glu + nh4 -> adp + gln + pi atp + glu + nh4 -> adp + gln + pi atp + glu + sh4 -> adp + gln + pi atp + glu + sh4 -> adp + gln + pi atp + glu + sh4 -> adp + gls + pi atp + glu + sh4 -> adp + gls + pi atp + gl +> adp + grs + glu + pi atp + gl +> adp + grs + glu cysgly -> (ys + gly hco2 + 2 rgt +> cogt ogt + nadph -> 2 rgt + nadp gtspmd -> rgt + sprmd atp + gl -> adp + gyspa atp + gl -> adp + g
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS GLUR GGLUCYSS GTHRDS GLUS1 GLUS2 GLUDH2 GLUDH2 GLUDH1 GLUNT GLUDH1 GLUNT GABAT2 GTADT1 MAAMPT GTSPMD5 GTHRR ALAAPT GTIPX GLUTHR GTSPMDAS GLUCK ALDCg DHACK	Chlorocyclohexane and chlorobenzene degradation Chlorocyclohexane and chlorobenzene degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation Geraniol degradation Geraniol degradation Geraniol degradation Gutamate metabolism Glutamate to Metabolism Glutamate Metabolism Glutathione Metabolism Glycerolipid Metabolism	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-CoA aryltransferase acetyl-CoA aryltransferase succinate-semialdehyde dehydrogenase (NAD) 4-aminobutyrate transaminase carbamoryl-phosphate synthase (glutamine-hydrolysing) glutamate racemsas glutamate synthase glutamate synthase glutamate synthase glutamate dehydrogenase glutamate dehydrogenase glutamate dehydrogenase glutamate dehydrogenase glutamate synthase glutamine synthase	32126 31145 31145 31145 3132 3131 23116 23116 23116 12116 6315 6312 6312 14113 14114 1413 14112 6312 6312 6318 2311 6318 2318 2318 2318 2318 2318 2318 2318 2	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_02815(aphA)/KCX_14030/KCX_18070  KCX_08315(aphA)/KCX_14030/KCX_18070  KCX_07830(adA)/KCX_26660(fadl)  KCX_07830(adA)/KCX_26660(fadl)  KCX_09890/KCX_11825(gabD)/KCX_24465  KCX_04875  KCX_04875  KCX_04875  KCX_0455/KCX_10660(car8)  KCX_0475  KCX_05055  KCX_0675  KCX_0505  KCX_0675  KCX_03860(gl8)/KCX_03865(gltD)  KCX_03860(gl8)/KCX_03865(gltD)  KCX_03860(gl8)/KCX_03865(gltD)  KCX_1805  KCX_1525  KCX_16415(pepN)  KCX_04835  KCX_16115(pepN)  KCX_04835  KCX_04780(ggt)/KCX_16795  KCX_045225  KCX_050255  KCX_050255  KCX_0502255  KCX_0502255  KCX_0502256  KCX_05025/KCX_13865  KCX_06075/KCX_13865  KCX_06075/KCX_13865  KCX_06075/KCX_13865	suc -> g(s + fru dchrocmo -> dchrooe tcmbo -> Zmac ntphp -> pnp + pi 7m366ccna + coa -> Smh4ecna + accna 5m364bcna + coa -> Smh4ecna + accna 5m364bcna + coa -> 3mcona + accna nad + sucal <> -> nadh + succ gaba + akg -> glu + sucsal 2 atp + gin + hcn3 -> 2 adp + cap + glu + pi dglu <-> glu atp + (ys + glu -> adp + gys + pi atp + (ys + glu -> adp + gys + pi akg + gin + nadph -> 2 glu + nadp akg + gin + nadph -> 2 glu + nadp glu + nadq -> akg + nadph + nh4 glu + nad <-> akg + nadph + nh4 atp - glu + sh4 -> glu + pi atp + gys + gly -> bi atp + gys + gly -> bi atp + gys + gly -> bi atp + gys + gly + bi atp + glu + nh4 -> adp + gln + pi atp + glu + nh4 -> adp + gln + pi atp + glu + nh4 -> adp + gln + pi atp + glu + sh4 -> adp + gln + pi atp + glu + sh4 -> adp + gln + pi atp + glu + sh4 -> adp + gls + pi atp + glu + sh4 -> adp + gls + pi atp + gl +> adp + grs + glu + pi atp + gl +> adp + grs + glu cysgly -> (ys + gly hco2 + 2 rgt +> cogt ogt + nadph -> 2 rgt + nadp gtspmd -> rgt + sprmd atp + gl -> adp + gyspa atp + gl -> adp + g
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP1 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS GLUR GGLUCYSS GTHRDS GLUS1 GLUS1 GLUS2 GLUDH2 GLUS1 GL	Chloroyclohexane and chlorobenzene degradation Chloroyclohexane and chlorobenzene degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation Geraniol degrdation Geraniol degrdation Glutamate metabolism Glutathione Metabolism Glycerolipid Metabolism	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-Coa aryttransferase acetyl-Coa aryttransferase succinate-semialdehyde dehydrogenase (NAD) 4-aminobutyrate transaminase carbamoyl-phosphate synthase (glutamine-hydrolysing) glutamate racemase gamma-glutamylcysteine synthetase glutamate synthase glutamate dehydrogenase glutamate dehydrogenase glutamate synthase glutamate dehydrogenase glutaminase glutamate synthase glutaminase glutathione peroxidase glutathione peroxidase glutathione reductase glutathione reductase glutathione reductase glutathione reductase glutathione reductase glutathione reductase glutathione peroxidase glutathione reductase glutathione reductase glutathione reductase glutathione peroxidase glutathione reductase glutathione peroxidase glutathione reductase glutathione peroxidase glutathione reductase glutathione reductase glutathione peroxidase glutathione reductase glutathione peroxidase glutathione reductase glutathione peroxidase glutathione reductase glutathione peroxidase glutathione reductase	32126 31145 31145 31145 3132 3131 23116 23116 23116 12116 63.55 5113 63.22 63.18 14.114 14.14 14.14 14.14 14.14 14.14 14.14 14.14 14.14 14.14 14.14 14.14 14.15 15.12 63.17 26.119 63.57 34.11.2 63.18 23.22 34.11.174.11.2(3.4 11.27 11.11 11.11 27.1.30 11.11 27.1.30	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_02815(aphA)/KCX_14030/KCX_18070  KCX_07830(fadA)/KCX_26660(fad)  KCX_07830(fadA)/KCX_26660(fad)  KCX_07830(fadA)/KCX_26660(fad)  KCX_0785  KCX_0785  KCX_0856  KCX_0785  KCX_0785  KCX_0785  KCX_0785  KCX_0856(fall)/KCX_03865(ght)  KCX_0856(ght)/KCX_03865(ght)  KCX_0856(ght)/KCX_03865(ght)  KCX_14645  KCX_14645  KCX_16785  KCX_16785  KCX_16785  KCX_16785  KCX_16785  KCX_16785  KCX_02835  KCX_022835  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_03875/KCX_13865  KCX_19385/KCX_13865  KCX_02835  KCX_02835  KCX_02835  KCX_03875/KCX_13865  KCX_19385/KCX_13865  KCX_19385/KCX_13865  KCX_02835  KCX_02835  KCX_03157/KCX_13865  KCX_11956/KCX_13865	suc -> gid + fru  dchrocmo -> dchrooe  tcmbo -> Zmac  ntphp -> pnp + pi  7m366ccaa + cca -> Smh4ecaa + accaa  5m34hcaa + cca -> Smccaa + accaa  sm34hcaa + cca -> Smccaa + accaa  sm34hcaa + cca -> Smccaa + accaa  and + sucsal <-> nadh + succ  gaba + akg -> giu + succal  aba + akg -> giu + succal  2 atp + gin + hca3 -> 2 adp + cap + giu + pi  dgiu <-> giu  atp + cys + giu -> adp + gcys + pi  atp + gys + gy -> adp + rgt + pi  akg + gin + nadph -> 2 giu + nadp  akg + gin + nadph -> 2 giu + nadp  giu + nad <-> skg + nadh + nh4  gin -> giu + nh4  atp + giu + nh4 -> adp + gin + pi  gaba + akg <-> giu + succal  glutma + gin + adp +> gin + pi  paba + akg <-> giu + succal  glutma + gin + adp +> gin + pi  gaba + akg -> gy + succal  glutma + gin + adp +> gin + pi  gaba + akg -> gy + radh  yrgt -> cyspy + giu  cysgly -> cys + gly  hzo2 + 2 rgt <-> cys  gtpmd -> rgt + sprmd  atp + gi -> adp + adp  glyn + adr -> gip + nadh  glyn + atp -> dhap + adp  gl + nad -> gl + nadh  glyn + atp -> dhap + adp  gl + nad -> gl + nadh  glyn + atp -> gh + nadh
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS GLUR GGLUCYSS GTHRDS GLUS1 GL	Chlorocyclohexane and chlorobenzene degradation Chlorocyclohexane and chlorobenzene degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation Geraniol degradation Geraniol degradation Geraniol degradation Guttamate metabolism Glutamate Metabolism Glutathione Metabolism Glycerolipid M	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-Coa aryttransferase acetyl-Coa aryttransferase acetyl-Coa aryttransferase succinate-semialdehyde dehydrogenase succinate-semialdehyde dehydrogenase succinate-semialdehyde dehydrogenase glutamine-hydrolysing) glutamine-hydrolysing) glutamine-synthase d-aminobutyrate transaminase apartyl-tRNA (Gln) amidotransferase membrane alantyl aminopeptidase glutathione-peroxidase glutathione-peroxidase glutathione-peroxidase glutathione-peroxidase glutathione-peroxidase glutathione-growidase	32126 31145 31145 31145 31145 3132 3131 23116 23116 23116 23116 6355 5113 6322 6312 14114 1414 1414 1414 1414 1411 3512 6318 2321 34111/34112/34 1111 26119 1817 35178 27130 1111 27129 11116 42130 1111022	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_02815(aphA)/KCX_14030/KCX_18070  KCX_07830(fadA)/KCX_26660(fad)  KCX_07830(fadA)/KCX_26660(fad)  KCX_0980/KCX_11825(gabD)/KCX_24465  KCX_0980/KCX_11825(gabD)/KCX_24465  KCX_00505  KCX_00505  KCX_00505  KCX_00505  KCX_00505  KCX_03860(gl8)/KCX_03865(gltD)  KCX_03860(gl8)/KCX_03865(gltD)  KCX_10856(gl8)/KCX_03865(gltD)  KCX_14645  KCX_14645  KCX_14645  KCX_14645  KCX_16785  KCX_14785  KCX_146785  KCX_146785  KCX_146785  KCX_146785  KCX_146785  KCX_146785  KCX_146785  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_025295  KCX_02835  KCX_03150/KCX_13865  KCX_13170/KCX_03175  KCX_03160/KCX_03175  KCX_03160/KCX_03175  KCX_03160/KCX_03175  KCX_03160/KCX_03175	suc - s glc + fru dchrocmo -> dchrooe tcmbo -> Zmac ntphp -> pnp + pi 7m366ccaa - coa -> Smh4ecaa + accaa Sm364kcaa + coa -> Smcaa + accaa sm364kcaa + coa -> Smcaa + accaa nad + sucal <> nad + succ gabaa + akg -> glu + sucal 2 atp + gln + hca3 -> 2 adp + cap + glu + pi dglu <-> glu atp -> cys + glu -> adp + gsy + pi atp +> cys + gly -> adp + rgt + pi akg +> gln + nadph -> 2 glu + nadp akg +> gln + nadph -> 2 glu + nadp algu + nad <-> akg + nadh + nh4 gln -> glu + nh4 sln -> glu
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS GLUR GGLUCYSS GTHRDS GLUS1 GL	Chlorocyclohexane and chlorobenzene degradation Chlorocyclohexane and chlorobenzene degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation Geraniol degradation Geraniol degradation Geraniol degradation Guttamate metabolism Glutamate Metabolism Glutathione Metabolism Glycerolipid M	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acesly-CoA aryltransferase acesly-CoA aryltransferase succinate-semialdehyde dehydrogenase (NAD) 4-aminobutyrate transaminase carbamoryl-phosphate synthase (glutamine-hydrolysing) glutamate racemase gamma-glutamylcysteine synthetase glutamate synthase glutamate synthase glutamate synthase glutamate dehydrogenase glutamate dehydrogenase glutamate aryltransputation glutamyl-tRNA/Asni/glutamyl-trans- glutamione-proxidase glutathione-proxidase glutamione-proxidase glutamione-proxidase glutamione-proxida	32126 31145 31145 31145 3132 3131 23116 23116 23116 12116 63.55 5113 63.22 63.18 14.114 14.14 14.14 14.14 14.14 14.14 14.14 14.14 14.14 14.14 14.14 14.14 14.15 15.12 63.17 26.119 63.57 34.11.2 63.18 23.22 34.11.174.11.2(3.4 11.27 11.11 11.11 27.1.30 11.11 27.1.30	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_02815(aphA)/KCX_14030/KCX_18070  KCX_07830(fadA)/KCX_26660(fad)  KCX_07830(fadA)/KCX_26660(fad)  KCX_07830(fadA)/KCX_26660(fad)  KCX_0785  KCX_0785  KCX_0856  KCX_0785  KCX_0785  KCX_0785  KCX_0785  KCX_0856(fall)/KCX_03865(ght)  KCX_0856(ght)/KCX_03865(ght)  KCX_0856(ght)/KCX_03865(ght)  KCX_14645  KCX_14645  KCX_16785  KCX_16785  KCX_16785  KCX_16785  KCX_16785  KCX_16785  KCX_02835  KCX_022835  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_03875/KCX_13865  KCX_19385/KCX_13865  KCX_02835  KCX_02835  KCX_02835  KCX_03875/KCX_13865  KCX_19385/KCX_13865  KCX_19385/KCX_13865  KCX_02835  KCX_02835  KCX_03157/KCX_13865  KCX_11956/KCX_13865	suc -> gic + fru dchrocmo -> dchrooe  tcmbo -> Zmac  ntphp -> pnp + pi  7m366ccaa + coa -> Smh4ecaa + accaa  5m364hcaa + coa -> Smcoa + accaa  sm364hcaa + coa -> Smcoa + accaa  nad + sucal <>- nadh + succ  gaba + akg -> glu + sucsal  2 atp + gin + hca3 -> 2 adp + cap + glu + pi  dglu <>-> glu  atp + gys + glu -> adp + gys + pi  atp + gys + glu -> adp + gys + pi  akg + gln + nadph -> 2 glu + nadp  akg + gln + nadph -> 2 glu + nadp  akg + gln + nadph -> 2 glu + nadp  glu - nadp -> akg + nash + nbd  glu - nadq -> akg + nash + nbd  glu - nadq -> sig + nash + nbd  glu - glu + mh -> adp + gln + pi  atp + gys + glu +> succ  gaba + akg -> glu +> succ  glutma + gln + atp -> glntma + glu + pi + adp  progly -> gly + pro  atp + ggt + sprmd -> adp + gtspmd + pi  rgt -> cysgly - gys + gly  h2o2 + 2 rgt <>-> orgl +> orgl  ptspmd -> rgt +> sprmd  atp + gl -> adp + glyc3p  13 + nad <>-> glyc -> dhap + adp  gl + nadc <>-> glyn + nadh  glyn + atp -> dhap + adp  gl + nadc <>-> glyn + nadh  glyn + atp -> dhap + adp  gl + nadc <>-> glyn + nadh  glyn + atp -> dhap + adp  gl + nadc <>-> glyn + nadh  glyn + atp -> dhap + adp  gl + nadc <>-> glyn + nadh  glyn + atp -> dhap + adp  gl + nadc <>-> glyn + nadh  glyn + atp -> dhap + adp  gl + nadc <>-> glyn + nadh  glyn + atp -> dhap + adp  gl + nadc <>-> glyn + nadh  glyn + atp -> dhap + adp  gl + nadc <>-> glyn + nadh  glyn + atp -> dhap + adp  gl + nadc <>-> glyn + nadh  glyn + atp -> dhap + adp  gl + nadc <>-> glyn + nadh  glyn + atp -> dhap + adp  gl + nadc <>-> glyn + nadh  glyn + atp -> dhap + adp  gl + nadc <>-> glyn + nadh  glyn + atp -> dhap + adp  gl + nadc <>-> glyn + nadh  glyn + atp -> dhap + adp  gl + nadc <>-> glyn + nadh
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS GLUR GGLUCYSS GTHRDS GLUS1 GL	Chlorocyclohexane and chlorobenzene degradation Chlorocyclohexane and chlorobenzene degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation Geraniol degradation Geraniol degradation Geraniol degradation Guttamate metabolism Glutamate Metabolism Glutathione Metabolism Glycerolipid M	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-Coa acytransferase acetyl-Coa acytransferase acetyl-Coa acytransferase succinate-semialdehyde dehydrogenase (NAD) 4-aminobutyrate transaminase carbamoyl-phosphate synthase (glutamine-hydrolysing) glutamate racemase gamma-glutamylcysteine synthetase glutamate synthase glutamate synthase glutamate synthase glutamate dehydrogenase glutamate dehydrogenase glutamine synthetase glutamine synthetase d-aminobutyrate transaminase apartyl-RNA (Gin) amidotransferase membrane alanyl aminopeptidase glutathionelypermidine synthetase glutathione peroxidase glutathione peroxidase glutathione peroxidase glutathione reductase glutathione peroxidase glutathione peroxidase glutathione peroxidase glutathione reductase glutathione peroxidase	32126 31145 31145 31145 31145 3132 3131 23116 23116 23116 23116 6355 5113 6322 6312 14114 1414 1414 1414 1414 1411 3512 6318 2321 34111/34112/34 1111 26119 1817 35178 27130 1111 27129 11116 42130 1111022	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_02815(aphA)/KCX_14030/KCX_18070  KCX_12285  KCX_07830(adA)/KCX_26660(fad1)  KCX_07830(adA)/KCX_26660(fad1)  KCX_07830(adA)/KCX_26660(fad1)  KCX_07850  KCX_0785  KCX_0785  KCX_0785  KCX_0785  KCX_0785  KCX_0785  KCX_08675  KCX_08675  KCX_08675  KCX_08675  KCX_08675  KCX_08785  KCX_08675  KCX_16155  KCX_16155  KCX_16155(pepN)  KCX_08695(glt)/KCX_16795  KCX_07235/KCX_17157  KCX_167725(KCX_17157)  KCX_0835  KCX_0675/KCX_12858(phu)  KCX_06235  KCX_06235  KCX_06355  KCX_06355  KCX_06355  KCX_06355/KCX_033175  KCX_03170/KCX_033175  KCX_01465(pdu)/KCX_17465(gldA)  KCX_014655(pduC)/KCX_07460(pduD)/KCX_27465(gldA)	suc - s glc + fru dchrocmo -> dchrooe tcmbo -> Zmac ntphp -> pnp + pi 7m366ccaa - coa -> Smh4ecaa + accaa Sm364kcaa + coa -> Smcaa + accaa sm364kcaa + coa -> Smcaa + accaa nad + sucal <> nad + succ gabaa + akg -> glu + sucal 2 atp + gln + hca3 -> 2 adp + cap + glu + pi dglu <-> glu atp -> cys + glu -> adp + gsy + pi atp +> cys + gly -> adp + rgt + pi akg +> gln + nadph -> 2 glu + nadp akg +> gln + nadph -> 2 glu + nadp algu + nad <-> akg + nadh + nh4 gln -> glu + nh4 sln -> glu
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABATI CABPS GLUR GGLUCYSS GTHRDS GLUS1 GLUS1 GLUS2 GLUDH1 GLUS1 GLUS7 GLUPH2 GLUDH1 GLINN1 GABAT2 GTADT1 MAAMPT GTSPMDS GTHRR ALAAPT GTTPX GLUTHR GTSPMDAS GLUCK ALOCG GLUCK G	Chlorocyclohexane and chlorobenzene degradation Chlorocyclohexane and chlorobenzene degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation Geraniol degradation Geraniol degradation Geraniol degradation Gutamate metabolism Glutamate Metabolism Glutathione Metabolism Glycerolipid	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acesly-CoA aryltransferase acesly-CoA aryltransferase succinate-semialdehyde dehydrogenase (NAD) 4-aminobutyrate transaminase carbamoryl-phosphate synthase (glutamine-hydrolysing) glutamate racemsas glutamate synthase glutamate synthase glutamate synthase glutamate synthase glutamate dehydrogenase glutamate dehydrogenase glutamate synthase glutamine	32126 31145 31145 31145 31145 3132 3131 23116 23116 23116 12116 63.15 63.22 63.35 14.113 14.114 14.14 14.14 14.13 14.13 14.12 63.12 26.119 63.57 34.112 63.18 23.22 34.11,13,4,11,2,1,4,1,1,2,1,4,1,1,2,1,4,1,1,4,1,1,4,1,4	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_028515(aphA)/KCX_14030/KCX_18070  KCX_07830(fadA)/KCX_26660(fad)  KCX_07830(fadA)/KCX_26660(fad)  KCX_07830(fadA)/KCX_26660(fad)  KCX_0980/KCX_11825(gabD)/KCX_24465  KCX_0980/KCX_11825(gabD)/KCX_24465  KCX_0980/KCX_11825(gabD)/KCX_24465  KCX_00505  KCX_07425  KCX_00505  KCX_00505  KCX_00505  KCX_03866(gl8b)/KCX_03865(gltD)  KCX_03866(gl8b)/KCX_03865(gltD)  KCX_03866(gl8b)/KCX_03865(gltD)  KCX_14645  KCX_14645  KCX_14645  KCX_14645  KCX_146785  KCX_146785  KCX_14785  KCX_14785  KCX_14785  KCX_14785  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_03170/KCX_03175  KCX_03160/KCX_031460(pduD)/KCX_01466  KCX_01510	suc -> g(s + fru dchrocmo -> dchrooe tcmbo -> Zmac ntphp -> pnp + pi 7m366ccaa + coa -> Smh4ecaa + accaa 5m364hcaa + coa -> Smcoa + accaa 5m364hcaa + coa -> Smcoa + accaa and + sucal <> nadh + succ gaba + akg -> glu + sucal 2 atp + gln + hca3 -> 2 adp + cap + glu + pi dglu <>> glu atp + (ys + glu -> adp + gcys + pi atp + gys + glu -> adp + gys + pi akg + gln + nadph -> 2 glu + nadp akg + gln + nadph -> 2 glu + nadp akg + gln + nadph -> 2 glu + nadp akg + gln + nadph -> 2 glu + nadp glu - ndq -> akg + nadh + nbd glu - ndd -> akg + nadh + nbd glu - ndd -> glu + suc + adp glu + ndd -> glu + suc + adp glu + ndd -> akg + nadh + nbd glu - ndd -> glu + suc + adp glu + ndd -> adp + gln + pi akg + gln + atp -> glntma + glu + pi + adp progly -> glu + nbd -> adp + gls + pi atp + glu + nbd -> adp + gls + pi atp + glu + nbd -> adp + gls + pi atp + glu + nbd -> adp + gls + pi atp + glu + nbd -> adp + gls + pi atp + glu + nbd -> adp + gls + pi atp + glu + nbd -> adp + gls + pi atp + glu + nbd -> adp + gls + pi atp + glu + nbd -> adp + gls + pi atp + glu + nbd -> adp + gls + pi atp + glu + nbd -> adp + gls + pi atp -> gly -> gly + pro atp + glu + pid -> adp + gls + pid atp + gl -> adp + gly -3 pid atp + gl -> adp + gly -3 pid gls -> glp -> gl -> adp gls -> gl -> adp gl -> ad -> gl -> adp gl -> adp -> gl -> adp gls -> glp -> gl -> adp gl -> adp -> adp -> gl -> adp
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABATI CABPS GLUR GGLUCYSS GTHRDS GLUS1 GLUS2 GLUS1 GLUS1 GLUS1 GLUS1 GLUS1 GLUS1 GLUS1 GLUS2 GLUS1 GLUS1 GLUS2 GLUS1 GLUS3 GLUS3 GLUS3 GLUS3 GLUS3 GLUS3 GLUS3 GLUS3 GLUS4 GLUS1 GLU	Chirocyclohexane and chlorobenzene degradation Chirocyclohexane and chlorobenzene degradation Gamma-Heazchlorocyclohexane degradation gamma-Heazchlorocyclohexane degradation Gamma-Heazchlorocyclohexane degradation Geraniol degradation Geraniol degradation Glutamate metabolism Glutamate destabolism Glutamate destabolism Glutamate Metabolism Glutathione Metabolism Glycerolipid Metabolism	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-CoA aryltransferase acetyl-CoA aryltransferase succinate-semialdehyde dehydrogenase (NAD) 4-aminobutyrate transaminase carbamoryl-phosphate synthase (glutamine-hydrolysing) glutamate racemase gamma-glutamylcysteine synthetase glutamate synthase glutamate synthase glutamate synthase glutamate dehydrogenase glutamate dehydrogenase glutamate aryltransferase glutamine synthetase glutamine glutamytenase glutamine peroxidase glutathione peroxidase glutathio	32126 31145 31145 31145 31145 3132 3131 23116 23116 23116 12116 63.15 63.22 63.35 14.113 14.114 14.14 14.14 14.13 35.12 63.12 63.12 63.18 23.21 43.11 11.11 27.129	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_02815(aphA)/KCX_14030/KCX_18070  KCX_12385  KCX_07830(adA)/KCX_26660(fad)  KCX_07830(adA)/KCX_26660(fad)  KCX_07830(adA)/KCX_26660(fad)  KCX_0980/KCX_11825(gabD)/KCX_24465  KCX_04875  KCX_04875  KCX_00505  KCX_0675  KCX_00505  KCX_0675  KCX_00505  KCX_0675  KCX_03860(gaB)/KCX_03865(ghD)  KCX_03860(gaB)/KCX_03865(ghD)  KCX_03860(gaB)/KCX_03865(ghD)  KCX_14645  KCX_14645  KCX_14645  KCX_14645  KCX_146785  KCX_146785  KCX_146785  KCX_146785  KCX_146785  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_03160/KCX_03175  KCX_03160/KCX_031460(pduD)/KCX_01466  KCX_01515  KCX_01515  KCX_01515  KCX_01515  KCX_01515	suc -> g(s + fru dchrocmo -> dchrooe  tcmbo -> Zmac  ntphp -> pnp + pi  7m366ccaa + coa -> Smh4ecaa + accaa  5m364hcaa + coa -> Smcoa + accoa  5m364hcaa + coa -> Smcoa + accoa  nad + sucal <> nadh + succ  gaba + akg -> glu + sucsal  2 atp + gln + hca3 -> 2 adp + cap + glu + pi  dglu <>> glu  atp + (ys + glu -> adp + gcys + pi  atp + gys + glu -> adp + gys + pi  akg + gln + nadph -> 2 glu + nadp  akg + gln + nadph -> 2 glu + nadp  akg + gln + nadh -> 2 glu + nad  glu - nadq -> akg + nadh + nbd  glu - nadq -> akg + nadh + nbd  glu - nadq -> glu + suc + nadp  akg + gln + nadh -> 2 glu + nad  glu - ydu + nbd -> adp + gln + pi  akg + gln + nadh -> 2 glu + nad  glu -> glu + nbd -> adp + gln + pi  akg + gln + sadh -> 2 glu + nad  glu -> glu + nbd -> adp + gln + pi  atp + glu + nbd -> adp + gln + pi  atp + glu + nbd -> adp + gln + pi  atp + glu + nbd -> adp + gls + pi  atp + glu + pi +> adp + gls + pi  atp + gl +> gln + nadh -> adp + gtspmd + pi  rgt -> crysgly + glu  crysgly -> gly + pro  atp + gl + sprmd -> adp + gtspmd + pi  rgt -> crysgly + gly  5ts -> ds -> gl + nadh  gtspmd -> rgt + sprmd  atp + gl -> adp + glyc3p  st + nad -<> gl -> nadh  gl + nad -<> gl -> nadh  gl + nad -<> gl -> nadh  gl + nadh -> 13pdo + nadh  12ppd-R -> propanal  propanal + nadh -> 2 propanal
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS GLUR GGLUCYSS GTHRDS GLUSS GLUDH2 GLUDH1 GLUN1 GLNST1 GABAT2 GTADT1 MAAMPT GTSPMDS GTHHR ALAAPT GTSPMDS GLUTHR GTSPMDS GLUTHR GTSPMDS GTHHR ALAAPT GTSPMDS GTHHR ALAAPT GTSPMDS GLUTHR GTSPMDDS GLUTHR GTSPMDAS GLUTHR GTGTMAS GLU	Chloroyclohexane and chlorobenzene degradation Chloroyclohexane and chlorobenzene degradation gamma-Hexachloroyclohexane degradation gamma-Hexachloroyclohexane degradation gamma-Hexachloroyclohexane degradation Geraniol degradation Geraniol degradation Glutamate metabolism Glutathione Metabolism Glutathione Metabolism Glutathione Metabolism Glutathione Metabolism Glutathione Metabolism Glutathione Metabolism Glycerolipid Meta	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-Coa acytransferase acetyl-Coa acytransferase acetyl-Coa acytransferase succinate-semialdehyde dehydrogenase (NAD) 4-aminobutyrate transaminase carbamoyl-phosphate synthase (glutamine-hydrolysing) glutamate racemase gamma-glutamylcysteine synthetase glutamate gynthase glutamate gynthase glutamate dehydrogenase glutamate dehydrogenase glutamate dehydrogenase glutamine synthetase d-aminobutyrate transaminase agartyl-iRNA(Asni)/glutamyl- triNA (gin) amiotransferase membrane Janyl amiopeptidase glutathione peroxidase glutathionylspermidine amidase/synthetase glycerol dehydrogenase glycerol dehydrogenase glycerol dehydrogenase glycerol dehydrogenase glycerol dehydrogenase prospanaliNAD+ oxidoreductase propanaliNAD+ oxidoreductase prospanalinable-glataciosidase	32126 31145 31145 31145 3132 3131 3131 23116 23116 23116 23116 23117 6312 6312 6312 6312 6312 6311 14114 1413 1413 14114 1413 3512 6312 6318 2322 341112 6318 2322 341117 11119 1817 35178 27130 1111 1817 35178 27130 11110 1110 1110 111	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_02815(aphA)/KCX_14030/KCX_18070  KCX_12385  KCX_07830(adA)/KCX_26660(fad1)  KCX_07830(adA)/KCX_26660(fad1)  KCX_0980/KCX_11825(gabD)/KCX_24465  KCX_0980/KCX_11825(gabD)/KCX_24465  KCX_0980/KCX_11825(gabD)/KCX_24465  KCX_00505  KCX_00505  KCX_00575  KCX_00505  KCX_14645  KCX_14645  KCX_16115(pepN)  KCX_16115(pepN)  KCX_00505  K	suc - s glc + fru dchrocmo -> dchrooe tcmbo -> Zmac ntphp -> pnp + pi 7m366ccaa + coa -> Smh4ecoa + accoa 5m364hcaa + coa -> Smccoa + accoa nad + sucsal <> nadh + succ abaa + akg -> glu + succa abaa + akg -> glu + succal 2 atp + gln + hco3 -> 2 adp + cap + glu + pi dglu <-> glu atp + cys + glu -> adp + gcys + pi atp + gys + gly -> adp + rgt + pi akg + gln + nadph -> 2 glu + nadp akg + gln + nadph -> 2 glu + nadp algu + nad <-> akg + nadh + nh4 gln -> glu + nh4 sln -> glu + nh4 slg +> gly + succal glutma + gln + atp -> ghrtma + glu + pi + adp progly -> gly + pro cysly -> cys + gly cysly -> cys + gly sly + glu cysly -> cys + gly sla + nadq -> adp + gtspmd + pi rgt -> cysgly + glu cysly -> cys + gly hzo2 + 2 rgt <-> ogt cysl + nadh slp -> alp + nadh slp -> alp + rgt + sprmd atp + gl -> adp + glyc3p t3 + nad <-> gl + nadh gly -> slprop + nadh gl -> sllprop slprop + nadh -> 13pdo + nad gl -> sllprop + nadh gl -> slprop + nadh gl -> slprop + nadh gl -> sllprop + nadh gl -> sllprop + nadh -> slpropanol + nad
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABATI CABPS GLUR GGLUCYSS GTHRDS GLUS1 GLUS2 GLUS1 GLUS1 GLUS1 GLUS1 GLUS1 GLUS1 GLUS1 GLUS2 GLUS1 GLUS1 GLUS2 GLUS1 GLUS3 GLUS3 GLUS3 GLUS3 GLUS3 GLUS3 GLUS3 GLUS3 GLUS4 GLUS1 GLU	Chirocyclohexane and chlorobenzene degradation Chirocyclohexane and chlorobenzene degradation Gamma-Heazchlorocyclohexane degradation gamma-Heazchlorocyclohexane degradation Gamma-Heazchlorocyclohexane degradation Geraniol degradation Geraniol degradation Glutamate metabolism Glutamate destabolism Glutamate destabolism Glutamate Metabolism Glutathione Metabolism Glycerolipid Metabolism	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-CoA aryltransferase acetyl-CoA aryltransferase succinate-semialdehyde dehydrogenase (NAD) 4-aminobutyrate transaminase carbamoryl-phosphate synthase (glutamine-hydrolysing) glutamate racemase gamma-glutamylcysteine synthetase glutamate synthase glutamate synthase glutamate synthase glutamate dehydrogenase glutamate synthase glutamate dehydrogenase glutamate aryltranspitale glutamine synthetase synthetase glutamine glutamyteriase glutamine glutamyteriase glutamine peroxidase glutathione pero	32126 31145 31145 31145 31145 3132 3131 23116 23116 23116 12116 63.15 63.22 63.35 14.113 14.114 14.14 14.14 14.13 35.12 63.12 63.12 63.18 23.21 43.11 11.11 27.129	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_02815(aphA)/KCX_14030/KCX_18070  KCX_12385  KCX_07830(adA)/KCX_26660(fad)  KCX_07830(adA)/KCX_26660(fad)  KCX_07830(adA)/KCX_26660(fad)  KCX_0980/KCX_11825(gabD)/KCX_24465  KCX_04875  KCX_04875  KCX_00505  KCX_0675  KCX_00505  KCX_0675  KCX_00505  KCX_0675  KCX_03860(gaB)/KCX_03865(ghD)  KCX_03860(gaB)/KCX_03865(ghD)  KCX_03860(gaB)/KCX_03865(ghD)  KCX_14645  KCX_14645  KCX_14645  KCX_14645  KCX_146785  KCX_146785  KCX_146785  KCX_146785  KCX_146785  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_03160/KCX_03175  KCX_03160/KCX_031460(pduD)/KCX_01466  KCX_01515  KCX_01515  KCX_01515  KCX_01515  KCX_01515	suc -> g(s + fru dchrocmo -> dchrooe  tcmbo -> Zmac  ntphp -> pnp + pi  7m366ccaa + coa -> Smh4ecaa + accaa  5m364hcaa + coa -> Smcoa + accoa  5m364hcaa + coa -> Smcoa + accoa  nad + sucal <> nadh + succ  gaba + akg -> glu + sucsal  2 atp + gln + hca3 -> 2 adp + cap + glu + pi  dglu <>> glu  atp + (ys + glu -> adp + gcys + pi  atp + gys + glu -> adp + gys + pi  akg + gln + nadph -> 2 glu + nadp  akg + gln + nadph -> 2 glu + nadp  akg + gln + nadh -> 2 glu + nad  glu - nadq -> akg + nadh + nbd  glu - nadq -> akg + nadh + nbd  glu - nadq -> glu + suc + nadp  akg + gln + nadh -> 2 glu + nad  glu - ydu + nbd -> adp + gln + pi  akg + gln + nadh -> 2 glu + nad  glu -> glu + nbd -> adp + gln + pi  akg + gln + sadh -> 2 glu + nad  glu -> glu + nbd -> adp + gln + pi  atp + glu + nbd -> adp + gln + pi  atp + glu + nbd -> adp + gln + pi  atp + glu + nbd -> adp + gls + pi  atp + glu + pi +> adp + gls + pi  atp + gl +> gln + nadh -> adp + gtspmd + pi  rgt -> crysgly + glu  crysgly -> gly + pro  atp + gl + sprmd -> adp + gtspmd + pi  rgt -> crysgly + gly  5ts -> ds -> gl + nadh  gtspmd -> rgt + sprmd  atp + gl -> adp + glyc3p  st + nad -<> gl -> nadh  gl + nad -<> gl -> nadh  gl + nad -<> gl -> nadh  gl + nadh -> 13pdo + nadh  12ppd-R -> propanal  propanal + nadh -> 2 propanal
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS GLUR GGLUCYSS GTHRDS GLUSS GLUB1 GLUSS GLUDH2 GLUDH1 GLUDH1 GLUN1 GINST1 GABAT2 GTADT1 MAAMPT GTSPMDS GTHHR ALAAPT GTSPMDS GTHHR ALAAPT GTSPMDS GLUTHR GTSPMDDS GLUTHR GTSPMDAS G	Chlorocyclohexane and chlorobenzene degradation Chlorocyclohexane and chlorobenzene degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation Geraniol degradation Geraniol degradation Geraniol degradation Glutamate metabolism Glutathione Metabolism Glutathione Metabolism Glutathione Metabolism Glutathione Metabolism Glutathione Metabolism Glutathione Metabolism Glycerolipid Metabolism Glycerolip	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-CoA aryltransferase acetyl-CoA aryltransferase succinate-semialdehyde dehydrogenase (NAD) 4-aminobutyrate transaminase carbamoryl-phosphate synthase (glutamine-hydrolysing) glutamate racemase gamma-glutamylcysteine synthetase glutamate synthase glutamate synthase glutamate synthase glutamate dehydrogenase glutamate dehydrogenase glutamate aryltransferase glutamine synthetase glutaminopeptidase glutaminopeptidase glutathione peroxidase glutathione pe	32126 31145 31145 31145 31145 31145 3132 3131 123116 23116 121116 23116 121116 6355 5113 6322 6314113 14114 1413 14113 14114 1413 35112 6312 6318 2322 341112 6318 2322 341119 1817 35178 27130 1111 1817 35178 27130 11110 27129 1116 42130 111102 42128	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_02815(aphA)/KCX_14030/KCX_18070  KCX_02815(aphA)/KCX_14030/KCX_18070  KCX_07830(adA)/KCX_26660(fad1)  KCX_07830(adA)/KCX_26660(fad1)  KCX_07830(adA)/KCX_26660(fad1)  KCX_0980/KCX_11825(gabD)/KCX_24465  KCX_04875  KCX_06855/KCX_10660(car8)  KCX_07425  KCX_00505  KCX_0675  KCX_00505  KCX_0675  KCX_03860(gal8)/KCX_03865(ghD)  KCX_03860(gal8)/KCX_03865(ghD)  KCX_18085  KCX_14645  KCX_16895(ghA)/KCX_16795  KCX_16785  KCX_16785  KCX_16785  KCX_07835(ghC)/KCX_16795  KCX_0835(ghB)/KCX_16795  KCX_0835(ghC)/KCX_16795  KCX_0835(ghC)/KCX_16795  KCX_0835(ghC)/KCX_16795  KCX_0835(ghC)/KCX_16795  KCX_0835(ghC)/KCX_16795  KCX_0835(ghC)/KCX_16795  KCX_0835(ghC)/KCX_16795  KCX_0835(ghC)/KCX_16795  KCX_0835(ghC)/KCX_16795  KCX_0835(ghC)/KCX_13865  KCX_06675/KCX_13865  KCX_06975/KCX_03175  KCX_03160/KCX_03175  KCX_03160/KCX_03175  KCX_011615  KCX_011615  KCX_011615  KCX_011615  KCX_011615(gpdx)  KCX_05810(gpsA)	suc -> g(s + fru dchrocmo -> dchrooe tcmbo -> Zmac ntphp -> pnp + pi 7m366ccna + coa -> Smh4ecna + accna 5m364bcna + coa -> 3mccna + accna nad + sucal <> nadh + succ gaba + akg -> glu + succal gaba + akg -> glu + succal 2 atp + gin + hoa3 -> 2 adp + cap + glu + pi dglu <>> glu atp + yos + glu -> adp + gys + pi atp + gys + gly -> adp + grt + pi akg + gin + nadph -> 2 glu + nadp akg + gin + nadph -> 2 glu + nadp glu - nadp -> akg + nadph + nhd glu - nad <>> akg + nadph + nhd atp - glu + shd -> adp + gln + pi atp + yos + glu -> adp + gln + pi atp + gys + gly -> bag + gln + pi atp + gys + gly -> bag + gln + pi atp + gys + gly + bag + gln + pi glu -> glu + nhd -> adp + gln + pi atp + glu + nhd -> adp + gln + pi atp + gln + atp -> glntma + glu + pi + adp progly -> gly + pro atp + rgt + sprmd -> adp + gtspmd + pi rgt -> yosply + glu cygly -> cys + gly hoc2 + 2 rgt <>> opt gt + nadph -> 2 rgt + nadp gtspmd -> rgt + sprmd atp + gl -> adp + gylyap gl -> adp -> gln + nadh gl -> adp -> gln + padp gl -> adp -> gln + glyprag gl -> adp -> gln -> adp -> gln -> adp gl -> adp -> gln -> gln -> gln -> adp gl -> adp -> gln -> adp gl -> adp -> gln -> adp gl -> adp -> gln -> adp gl -> a
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS GLUR GGLUCYSS GTHRDS GLUSS GLUDH2 GLUDH1 GLUN1 GLNST1 GABAT2 GTADT1 MAAMPT GTSPMDS GTHHR ALAAPT GTSPMDS GLUTHR GTSPMDS GLUTHR GTSPMDS GTHHR ALAAPT GTSPMDS GTHHR ALAAPT GTSPMDS GLUTHR GTSPMDDS GLUTHR GTSPMDAS GLUTHR GTGTMAS GLU	Chloroyclohexane and chlorobenzene degradation Chloroyclohexane and chlorobenzene degradation gamma-Hexachloroyclohexane degradation gamma-Hexachloroyclohexane degradation gamma-Hexachloroyclohexane degradation Geraniol degradation Geraniol degradation Glutamate metabolism Glutamatione Metabolism Glutathione Metabolism Glutathione Metabolism Glutathione Metabolism Glutathione Metabolism Glutathione Metabolism Glycerolipid Met	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-Coa acytransferase acetyl-Coa acytransferase acetyl-Coa acytransferase succinate-semialdehyde dehydrogenase (NAD) 4-aminobutyrate transaminase carbamoyl-phosphate synthase (glutamine-hydrolysing) glutamate racemase gamma-glutamylcysteine synthetase glutamate dehydrogenase glutamate synthase glutamate dehydrogenase glutamate dehydrogenase glutamate dehydrogenase glutamine synthetase glutathionylupermidine synthetase glutathion peroxidase glutathionylupermidine amidase/synthetase glycerol dehydrogenase (glycerol dehydrogenase glycerol dehydrogenase glycerol dehydrogenase glycerol dehydrogenase glycerol dehydrogenase propanal:NAD- oxidoreductase propanal:NAD- oxidoreductase propanal:NAD- oxidoreductase propanal:NAD- oxidoreductase propanal:NAD- oxidoreductase phosphoglycerol transferase alpha-galactosidase glycerol-3-phosphate dehydrogenase (NAD)	32126 31145 31145 31145 3132 3131 3131 23116 23116 23116 23116 23117 6312 6312 6312 6312 6312 6311 14114 1413 1413 14114 1413 3512 6312 6318 2322 341112 6318 2322 341117 11119 1817 35178 27130 1111 1817 35178 27130 11110 1110 1110 111	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_02815(aphA)/KCX_14030/KCX_18070  KCX_12285  KCX_07830(adA)/KCX_26660(fad1)  KCX_07830(adA)/KCX_26660(fad1)  KCX_07830(adA)/KCX_26660(fad1)  KCX_07850(fadA)/KCX_26660(fad1)  KCX_07850(fadA)/KCX_26660(fad1)  KCX_07850(fadA)/KCX_078660(fad1)  KCX_07850(fadA)/KCX_078660(fad1)  KCX_07850(fadA)/KCX_03865(ght)  KCX_07850(fadB)/KCX_03865(ght)  KCX_07850(fadB)/KCX_03865(ght)  KCX_08895(ght)  KCX_08895(ght)  KCX_08895(ght)  KCX_16115(pepN)  KCX_08895(ght)  KCX_0780(fadB)/KCX_16795  KCX_0780(fadB)/KCX_16795  KCX_0780(fadB)/KCX_18895(fadB)  KCX_08895(ght)  KCX_07895(fadB)/KCX_16795  KCX_07895(fadB)/KCX_16795  KCX_08895(ght)  KCX_07895(fadB)/KCX_16795  KCX_08895(fadB)/KCX_16795  KCX_08895(fadB)/KCX_16795  KCX_08895(fadB)/KCX_16795  KCX_08895(fadB)/KCX_16795  KCX_08895(fadB)/KCX_16795  KCX_08895(fadB)/KCX_16795  KCX_08895(fadB)/KCX_16795  KCX_08895(fadB)/KCX_16795  KCX_08705(faCC)/KCX_07466(fadB)/KCX_27465(gldA)  KCX_011515  KCX_101575  KCX_101516(fadB)/KCX_16445  KCX_05810(gpsA)  KCX_05810(gpsA)	suc -> g(x - fru dchrocmo -> dchrooe tcmbo -> Zmac ntphp -> pnp + pi ntphp -> pnp + pi ntphp-> pnp + pi sucal-<-> nadh + succ gaba + akg -> glu + succal gaba + akg -> glu + sucal gaba + akg +> glu + sucal gaba + akg +> adp + radp + radp akg + gin + nadph -> 2 glu + nadp akg + gin + nadph -> 2 glu + nadp glu -> nadq -> akg + nadph + nhd glu -> nadq -> akg + nadph + nhd glu -> glu + nhd -> akg + nadph + nhd glu -> glu + nhd -> akg + nadph + nhd glu -> glu + nhd -> akg + nadph + nhd glu -> glu + nhd -> akg + nadph + nhd glu -> glu + rhd -> adp + gln + pi aba + akg -> glu + sucal glutma + gln + atp -> glntma + glu + pi + adp progly -> gly + pro atp + rgt +> prmd -> adp + gtspmd + pi rgt -> yosply + glu cysgly -> cys + gly hoc2 + 2 rgt -> osp gt +> adq -> gl + nadp gtspmd -> rgt + sprmd atp + gl -> adp + glycap 13 + nad -> gl + nadh gly -> alpr -> nadh gl +> adq -> gl + nadh gl +> adq -> gl +> adq -> gl + nadh gl +> adq -> gl +> adq -> gl +> adq
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS GLUR GGLUCYSS GTHRDS GLUSS GLUB1 GLUSS GLUDH2 GLUDH1 GLUDH1 GLUN1 GINST1 GABAT2 GTADT1 MAAMPT GTSPMDS GTHHR ALAAPT GTSPMDS GTHHR ALAAPT GTSPMDS GLUTHR GTSPMDDS GLUTHR GTSPMDAS G	Chlorocyclohexane and chlorobenzene degradation Chlorocyclohexane and chlorobenzene degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation Geraniol degradation Geraniol degradation Geraniol degradation Glutamate metabolism Glutathione Metabolism Glutathione Metabolism Glutathione Metabolism Glutathione Metabolism Glutathione Metabolism Glutathione Metabolism Glycerolipid Metabolism Glycerolip	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-CoA acyltransferase acetyl-CoA acyltransferase acetyl-CoA acyltransferase succinate-semialdehyde dehydrogenase (NAD) 4-aminobutyrate transaminase carbamoyl-phosphate synthase (glutamine-hydrolysing) glutamate racemase gamma-glutamylcysteine synthetase glutamate synthase glutamate synthase glutamate synthase glutamate synthase glutamate dehydrogenase glutamate dehydrogenase glutamine synthetase altoramate dehydrogenase glutamine synthetase 4-aminobutyrate transaminase aspartyl-tRNA/Asni/glutamyl-tRNA/Asni/glutamyl-tRNA/Asni/glutamyl-tRNA/Asni/glutamyl-tRNA/Asni/glutamyl-tRNA/Asni/glutamyl-transaminase apartyl-tRNA/Asni/glutamyl-transaminase apartyl-tRNA/Asni/glutamyl-transaminase altoramine peroxidase glutathione peroxida	32126 31145 31145 31145 31145 31145 3132 3131 123116 23116 121116 23116 121116 6355 5113 6322 6314113 14114 1413 14113 14114 1413 35112 6312 6318 2322 341112 6318 2322 341119 1817 35178 27130 1111 1817 35178 27130 11110 27129 1116 42130 111102 42128	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_028515(aphA)/KCX_14030/KCX_18070  KCX_07830(fadA)/KCX_14030/KCX_18070  KCX_07830(fadA)/KCX_26660(fad)  KCX_07830(fadA)/KCX_26660(fad)  KCX_0980/KCX_11825(gabD)/KCX_24465  KCX_0980/KCX_11825(gabD)/KCX_24465  KCX_00505  KCX_00505  KCX_00505  KCX_00505  KCX_00505  KCX_03860(gl8)/KCX_03865(gltD)  KCX_03860(gl8)/KCX_03865(gltD)  KCX_03860(gl8)/KCX_03865(gltD)  KCX_14645  KCX_14645  KCX_14645  KCX_14645  KCX_146785  KCX_146785  KCX_146785  KCX_146785  KCX_146785  KCX_02835  KCX_03160/KCX_021745  KCX_03160/KCX_03175  KCX_03160/KCX_03175  KCX_03150/KCX_03175  KCX_01515  KCX_01510  KCX_051510  KCX_05180(gps4)  KCX_05180(gps4)  KCX_051955/KCX_126955/KCX_26955/KCX_26965	suc-s gick - fru dchrocmo -> dchrooe tcmbo -> Zmac rttphp -> pnp + pi 7m366ccaa - coa -> SmMecoa + accoa 5m364kcaa + coa -> Smccaa + accoa sm364kcaa + coa -> Smccaa + accoa nad + sucal <> nadc + succa gaba + akg -> giu + succa gaba + akg +> gy -> adp + rgt + pi akg + gin + nadph -> 2 giu + nadp akg + gin + nadph -> 2 giu + nadp giu + nad -> akg + nadh + nh4 giu -> giu
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS GLUR GGLUCYSS GTHRDS GLUS1 GLUS2 GLUDH1 GLUS1 GABAT2 GTADT1 MAAMPT GTSPMDS GTHRM GTSPMDS GTHR GTSPMDAS GLYCK ALDCg DHACK GLYDH GLUTT 13PDODH PROPCOA PROPDD PROPCOA PROPDD PROPCOA PROPDD PGT AGALCTS9 GL3PD GL3PDD GL3PDD ETHAML	Chlorocyclohexane and chlorobenzene degradation Chlorocyclohexane and chlorobenzene degradation gamma-Heazchlorocyclohexane degradation gamma-Heazchlorocyclohexane degradation Gamma-Heazchlorocyclohexane degradation Geraniol degradation Geraniol degradation Glutamate metabolism Glutamate destabolism Glutamate metabolism Glutathione Metabolism Glycerolipid Metabolism	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acesl-CoA acyltransferase acesl-CoA acyltransferase acesl-CoA acyltransferase succinate-semialdehyde dehydrogenase (NAD) 4-aminobutyrate transaminase carbamoyl-phosphate synthase (glutamine-hydrolysing) glutamate racemase gamma-glutamylcysteine synthetase glutamate synthase glutamate synthase glutamate synthase glutamate synthase glutamate dehydrogenase glutamate dehydrogenase glutamine synthetase alanyl aminotransferase membrane alanyl aminopeptidase glutathione hydralase glutathione peroxidase glutathio	32126 31145 31145 31145 31145 3132 3131 23116 23116 23116 12116 63.15 63.22 63.35 14.113 14.114 14.14 14.14 14.14 14.14 14.14 14.14 14.14 14.14 14.15 15.12 63.12 26.119 63.57 34.112 26.119 11.110 27.129 11.110 11.110 27.129 11.110 11.110 27.129 11.110 11.1202 42.128	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_02815(aphA)/KCX_14030/KCX_18070  KCX_12385  KCX_07830(adA)/KCX_26660(fad)  KCX_07830(adA)/KCX_26660(fad)  KCX_07830(adA)/KCX_26660(fad)  KCX_0980/KCX_11825(gabD)/KCX_24465  KCX_0980/KCX_11825(gabD)/KCX_24465  KCX_00505  KCX_07425  KCX_00505  KCX_07425  KCX_00505  KCX_0866(gab)/KCX_03865(gitD)  KCX_03866(gib)/KCX_03865(gitD)  KCX_03866(gib)/KCX_03865(gitD)  KCX_14645  KCX_14645  KCX_14645  KCX_14645  KCX_146785  KCX_146785  KCX_146785  KCX_147886(ggl/KCX_16795  KCX_04875  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_03160/KCX_031456  KCX_13956/KCX_13865  KCX_14678C 33136/KCX_031460(pduD)/KCX_01466  KCX_01510  KCX_01510  KCX_01516  KCX_01510  KCX_05810(gpsA)  KCX_05810(gpsA)  KCX_05895(kcx_126955/KCX_26955/KCX_26960  KCX_05895(kcx)_16265	suc-sigle + fru dchrocmo > dchrooe  tcmbo > Zmac  ntphp > pnp + pi  7m366ccaa + coa > Smh4ecaa + accaa  5m364hcaa + coa > Smcaa + accaa  5m364hcaa + coa > Smcaa + accaa  and + sucal <> nadh + succ  gaba + akg -> glu + sucal  2 atp + gln + hca3 > 2 adp + cap + glu + pi  dglu <>> glu  atp + gys + glu -> adp + gys + pi  atp + gys + gly -> adp + rgt + pi  akg + gln + nadph -> 2 glu + nadp  akg + gln + nadph -> 2 glu + nadp  akg + gln + nadph -> 2 glu + nadp  akg + gln + nadph -> 2 glu + pi  akg + glu + nah -> adp + gln + pi  akg + glu + nah -> adp + gln + pi  akg + glu + nah -> adp + gln + pi  akg + glu + nah -> adp + gln + pi  akg + glu + nah -> adp + gln + pi  aba + akg -> glu + sucal  glurnar + gln + atp -> glntrna + glu + pi + adp  progly -> gly + pro  atp + rgt + sprmd -> adp + gtspmd + pi  rgt -> cysgly + glu  cysgly - glu  sty -> cysgly + glu  dgt -> adp -> gl - nadh  glyn -> glu + nadp  sty -> gly -> pi  sty -> gly -> pi  sty -> gly -> gly -> pi  atp + gl -> adp + glyc3p  sty -> dgt -> adp + glyc3p  sty -> dg -> adp + glyc3p  sty -> dg -> adp -> gl -> adp  sty -> gly -> pi  sty -> gly -> pi  sty -> gl -> adp  sty -> ad
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS GLUR GGLUCYSS GTHRDS GLUSS GLUP1 GLUDH1 GLUDH1 GLUNT GLUDH2 GLUDH1 GLUNT GHAPT GTSPMDS GTHHR ALAAPT GTSPMDS GTHHR GTSPMDS GLUTHR GTSPMDDS GLUTHR GTSPMDS GLUTHR GTSPMDS GLUTHR GTSPMDAS GLUT	Chlorocyclohexane and chlorobenzene degradation Chlorocyclohexane and chlorobenzene degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation Geraniol degradation Geraniol degradation Geraniol degradation Glutamate metabolism Glutathione Metabolism Glutathione Metabolism Glutathione Metabolism Glutathione Metabolism Glutathione Metabolism Glutathione Metabolism Glycerolipid Metabolism Glycerolip	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-Coa aryttransferase acetyl-Coa aryttransferase acetyl-Coa aryttransferase succinate-semialdehyde dehydrogenase (NAD) 4-aminobutyrate transaminase carbamoyl-phosphate synthase (glutamine-hydrolysing) glutamate races glutamate glutamyleysteine synthetase glutamate synthase glutamate synthase glutamate synthase glutamate synthase glutamate synthase glutamate synthase glutaminase	32126 31145 31145 31145 31145 3132 3131 23116 23116 23116 23116 12116 63.57 5113 63.22 63.18 14114 1413 14113 14114 1413 2312 6312 6318 232 34111/34112/34 1123/3413 11110 1817 35178 27130 11110 27129 11116 42130 111202 42128	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_028515(aphA)/KCX_14030/KCX_18070  KCX_07830(fadA)/KCX_14030/KCX_18070  KCX_07830(fadA)/KCX_26660(fad)  KCX_07830(fadA)/KCX_26660(fad)  KCX_0980/KCX_11825(gabD)/KCX_24465  KCX_0980/KCX_11825(gabD)/KCX_24465  KCX_00505  KCX_00505  KCX_00505  KCX_00505  KCX_00505  KCX_03860(gl8)/KCX_03865(gltD)  KCX_03860(gl8)/KCX_03865(gltD)  KCX_03860(gl8)/KCX_03865(gltD)  KCX_14645  KCX_14645  KCX_14645  KCX_14645  KCX_146785  KCX_146785  KCX_146785  KCX_146785  KCX_146785  KCX_02835  KCX_03160/KCX_021745  KCX_03160/KCX_03175  KCX_03160/KCX_03175  KCX_03150/KCX_03175  KCX_01515  KCX_01510  KCX_051510  KCX_05180(gps4)  KCX_05180(gps4)  KCX_051955/KCX_126955/KCX_26955/KCX_26965	suc-s gik + fru  dchrocmo -> dchrooe  tcmbo -> Zmac  ntphp -> pnp + pi  7m366ccaa + cca -> Smh4ecaa + accaa  5m34hcaa + cca -> Smcaa + accaa  sm34hcaa + cca -> Smcaa + accaa  nad + sucsal <> nadh + succa  abaa + akg -> giu + succal  2 atp + gin + hca3 -> 2 adp + cap + giu + pi  dgiu <-> giu  atp + cys + giu -> adp + gsys + pi  atp + gys + gy -> adp + rgt + pi  akg + gin + nadph -> 2 giu + nadp  akg + gin + nadph -> 2 giu + nad  giu + nad -> akg + nadh + nh4  gin -> giu + nh4  atp + giu + nh4 -> adp + gin + pi  gaba + akg <-> giu + succal  glutma+ gin + atp + sprmd -> adp + gstpmd + pi  rgt -> cysgly + giu  cysgly -> cys + gly  hzo + z cyt + sprmd  atp + rgt + sprmd -> adp + gstpmd + pi  rgt -> cysgly + giu  cysgly -> cys + gly  hzo + z cyt + sadp  atp + gl -> adp + gyd3p  13 + nad <-> gl + nadh  gly -> adp + gyd3p  13 + nad <-> gl + nadh  gly -> adp + gyd3p  13 + nad <-> gl + nadh  gl -> sliprop  haprop + nadh -> 13pdo + nad  gl -> sliprop  haprop + nadh -> 13pdo + nad  gl -> gly -> gr + propanal  propanal + nadh -> 2 propanal  propanal + nadh -> 2 propanal  propanal + nadh -> 2 propanal  propanal + nadh -> 3 propanol + nad  gl -> glycjp + nad <-> dhap + nadh  glycjp + nade -> dhap + nadh  glycjp + nade -> dhap + nadp  ctha <-> c> acal + nh4  glycjp + nade -> dhap + nadp
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS GLUR GGLUCYSS GTHRDS GLUS1 GLUS2 GLUDH1 GLUS1 GABAT2 GTADT1 MAAMPT GTSPMDS GTHRM GTSPMDS GTHR GTSPMDAS GLYCK ALDCg DHACK GLYDH GLUTT 13PDODH PROPCOA PROPDD PROPCOA PROPDD PROPCOA PROPDD PGT AGALCTS9 GL3PD GL3PDD GL3PDD ETHAML	Chlorocyclohexane and chlorobenzene degradation Chlorocyclohexane and chlorobenzene degradation gamma-Heazchlorocyclohexane degradation gamma-Heazchlorocyclohexane degradation Gamma-Heazchlorocyclohexane degradation Geraniol degradation Geraniol degradation Glutamate metabolism Glutamate destabolism Glutamate metabolism Glutathione Metabolism Glycerolipid Metabolism	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-Coa aryttransferase acetyl-Coa aryttransferase acetyl-Coa aryttransferase succinate-semialdehyde dehydrogenase (NAD) 4-aminobutyrate transaminase carbamoyl-phosphate synthase (glutamine-hydrolysing) glutamate transaminase agamma-glutamylcysteine synthetase glutamate synthase glutamate synthase glutamate synthase glutamate synthase glutamate synthase glutamate synthase glutaminase glutaminobutyrate transaminase apartyl-tRNA (slin) amidotransferase membrane alamy aminopeptidase glutathione peroxidase glutathione peroxidase glutathione peroxidase glutathione peroxidase glutathione peroxidase glutathione peroxidase glutathione reductase glutathionylspermidine amidase/synthetase glycerol dehydrogenase glycerol dehydrogenase glycerol dehydrogenase glycerol dehydrogenase glycerol dehydrogenase phosphoglycerol transferase alpha-galactosidase propanal-NAD- oxidoreductase (CoA-axylating) 1-propanol dehydrogenase phosphoglycerol transferase alpha-galactosidase glycerol-3-phosphate dehydrogenase (NAD) Ethanolamine ammonia-lyase	32126 31145 31145 31145 31145 3132 3131 23116 23116 23116 12116 63.15 63.22 63.35 14.113 14.114 14.14 14.14 14.14 14.14 14.14 14.14 14.14 14.14 14.15 15.12 63.12 26.119 63.57 34.112 26.119 11.110 27.129 11.110 11.110 27.129 11.110 11.110 27.129 11.110 11.1202 42.128	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_02815(aphA)/KCX_14030/KCX_18070  KCX_12385  KCX_07830(adA)/KCX_26660(fad)  KCX_07830(adA)/KCX_26660(fad)  KCX_07830(adA)/KCX_26660(fad)  KCX_0980/KCX_11825(gabD)/KCX_24465  KCX_0980/KCX_11825(gabD)/KCX_24465  KCX_00505  KCX_07425  KCX_00505  KCX_07425  KCX_00505  KCX_0866(gab)/KCX_03865(gitD)  KCX_03866(gib)/KCX_03865(gitD)  KCX_03866(gib)/KCX_03865(gitD)  KCX_14645  KCX_14645  KCX_14645  KCX_14645  KCX_146785  KCX_146785  KCX_146785  KCX_147886(ggl/KCX_16795  KCX_04875  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_03160/KCX_031456  KCX_13956/KCX_13865  KCX_14678C 33136/KCX_031460(pduD)/KCX_01466  KCX_01510  KCX_01510  KCX_01516  KCX_01510  KCX_05810(gpsA)  KCX_05810(gpsA)  KCX_05895(kcx_126955/KCX_26955/KCX_26960  KCX_05895(kcx)_16265	suc-sigle + fru dchrocmo > dchrooe tcmbo > Zmac  ntphp > pnp + pi  7m366ccaa + coa > Smh4ecaa + accaa 5m364kcaa + coa > 3mccaa + accaa sm364kcaa + coa > 3mccaa + accaa nad + sucal <> nadh + succ gabaa + akg > glu + sucal 2 atp + gln + hca3 > 2 adp + cap + glu + pi dglu <> glu + gln + hca3 > 2 adp + cap + glu + pi dglu <> glu + gln + andph > 2 glu + nadp akg + gln + nadph > 2 glu + nadp akg + gln + nadph > 2 glu + nadp algu + nadc > akg + nadh + nh4 gln > glu + hd <> adp + gln + pi aga + gln + nadph > 2 glu + pi aga + gln + nadph > 2 glu + pi aga + gln + nadph > 2 glu + pi aga + gln + nadph > 2 glu + pi aga + gln + nadph > 2 glu + pi aga + gln + nadph > 2 glu + pi aga + gln + nadph > 2 glu + pi aga + gln + nadph > 2 glu + pi aga + gln + pi aga + akg <>> glu + sucsal glurma + gln + atp > glntrna + glu + pi + adp progly > gly + pro atp + glu + pi atp +
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS GLUR GGLUCYSS GTHRDS GLUS1 GLUS2 GLUDH1 GLUS1 GABAT2 GTADT1 MAAMPT GTSPMDS GTHRM GTSPMDS GTHR GTSPMDAS GLYCK ALDCg DHACK GLYDH GLUTT 13PDODH PROPCOA PROPDD PROPCOA PROPDD PROPCOA PROPDD PGT AGALCTS9 GL3PD GL3PDD GL3PDD ETHAML	Chloroyclohexane and chlorobenzene degradation Chloroyclohexane and chlorobenzene degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation Geraniol degrdation Geraniol degrdation Glutamate metabolism Glutathione Metabolism Glutathione Metabolism Glutathione Metabolism Glutathione Metabolism Glutathione Metabolism Glycerolipid Metabolism	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-CoA acyltransferase acetyl-CoA acyltransferase acetyl-CoA acyltransferase succinate-semialdehyde dehydrogenase (NAD) 4-aminobutyrate transaminase carbamoyl-phosphate synthase (glutamine-hydrolysing) glutamate racemase gamma-glutamylcysteine synthetase glutamate synthase glutamate synthase glutamate synthase glutamate dehydrogenase glutamate dehydrogenase glutamate dehydrogenase glutamine synthetase 4-aminobutyrate transaminase asparty-tRNA/Asni/glutamyl-tRNA/Asni/glutamyl-tRNA/Asni/glutamyl-tRNA/Asni/glutamyl-tRNA/Asni/glutamyl-tRNA/Asni/glutamyl-tRNA/Asni/glutamyl-tRNA/Asni/glutamyl-transaminase aparty-tRNA/Asni/glutamyl-transaminase aparty-tRNA/Asni/glutamyl-transaminase aparty-tRNA/Asni/glutamyl-transaminase aparty-tRNA/Asni/glutamyl-transaminase alanyl aminopeptidase glutathione peroxidase glutathione peroxidase glutathione peroxidase glutathione reductase (Jutathione peroxidase glutathione peroxi	32126 31145 31145 31145 31145 3132 3131 23116 23116 23116 12116 63.15 63.22 63.35 14.113 14.114 14.14 14.14 14.14 14.14 14.14 14.14 14.14 14.14 14.15 15.12 63.12 26.119 63.57 34.112 26.119 11.110 27.129 11.110 11.110 27.129 11.110 11.110 27.129 11.110 11.1202 42.128	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_02815(aphA)/KCX_14030/KCX_18070  KCX_12385  KCX_07830(adA)/KCX_26660(fad)  KCX_07830(adA)/KCX_26660(fad)  KCX_07830(adA)/KCX_26660(fad)  KCX_0980/KCX_11825(gabD)/KCX_24465  KCX_0980/KCX_11825(gabD)/KCX_24465  KCX_00505  KCX_07425  KCX_00505  KCX_07425  KCX_00505  KCX_0866(gab)/KCX_03865(gitD)  KCX_03866(gib)/KCX_03865(gitD)  KCX_03866(gib)/KCX_03865(gitD)  KCX_14645  KCX_14645  KCX_14645  KCX_14645  KCX_146785  KCX_146785  KCX_146785  KCX_147886(ggl/KCX_16795  KCX_04875  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_02835  KCX_03160/KCX_031456  KCX_13956/KCX_13865  KCX_14678C 33136/KCX_031460(pduD)/KCX_01466  KCX_01510  KCX_01510  KCX_01516  KCX_01510  KCX_05810(gpsA)  KCX_05810(gpsA)  KCX_05895(kcx_126955/KCX_26955/KCX_26960  KCX_05895(kcx)_16265	suc -> gic + flu dchrocmo -> dchrooe tcmbo -> Zmac ntphp -> pnp + pi 7m366ccaa + coa -> Smh4ecaa + accaa 5m364bcaa + coa -> 3mccaa + accaa sm364bcaa + coa -> 3mccaa + accaa nad + sucal <>- nadh + succ gaba + akg -> giu + succal gaba + akg -> giu + succal gaba + akg -> giu + succal 2 atp + gin + hoa3 -> 2 adp + cap ++ giu + pi dgiu <>-> giu atp + yos + giu -> adp + gys + pi atp + yos + giu -> adp + gys + pi atp + gys + giy -> adp + rgt + pi akg + gin + nadph -> 2 giu + nadp akg + gin + nadph -> 2 giu + nadp akg + gin + nadph -> 2 giu + nadp giu -> giu + nhd -> 2 giu + nad giu -> giu + nhd -> 3 giu + succal glutma + gin + atp -> gintma + giu + pi + adp progly -> ygl y + pro atp + rgt + sprmd -> adp + gtspmd + pi rgt -> yosply + giu cysgly -> yos + gly hoc2 + 2 rgt <>-> ogt gt + nadph -> 2 rgt + nadp gtspmd -> rgt + sprmd atp + gi -> adp + gylxp gtspmd -> rgt + sprmd atp + gi -> adp + gylxp gtspmd -> rgt + sprmd atp + gi -> adp + gylxp gtspmd -> rgt + sprmd atp + gi -> adp + gylxp gtspmd -> rgt + sprmd atp + gi -> adp + gylxp gtspmd -> rgt + sprmd atp + gi -> adp + gylxp gtspmd -> rgt + sprmd atp + gi -> adp + gylxp gtspmd -> rgt + sprmd atp + gi -> adp + gylxp gtspmd -> rgt + sprmd atp + gi -> adp + gylxp gtspmd -> rgt + sprmd atp + gi -> adp + gylxp gtspmd -> rgt + sprmd atp + gi -> adp + gylxp gtspmd -> rgt + sprmd atp + gi -> adp + gylxp gtspmd -> rgt + sprmd atp + gi -> adp + gylxp gtspmd -> rgt + sprmd atp + gi -> adp + gylxp gtspmd -> rgt + sprmd atp + gi -> adp + gylxp gtspmd -> rgt + sprmd atp + gi -> adp -> gylxp gtspmd -> rgt + sprmd atp + gi -> spropanal propanal + nadh -> tpropanal + nadh gtygh - tpropanal + nadh -> tpropanal + nadh gtygh - tpropanal + radh -> tpropanal + radh etha -> acal + nh4 ctha -> acal + nh4 ctha -> acal + nh4
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP1 4NPHP2 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS GLUR GGLUCYSS GTHRDS GLUS1 GL	Chlorocyclohexane and chlorobenzene degradation Chlorocyclohexane and chlorobenzene degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation Geraniol degradation Geraniol degradation Geraniol degradation Glutamate metabolism Glutathione Metabolism Glutathione Metabolism Glutathione Metabolism Glutathione Metabolism Glutathione Metabolism Glycerolipid Metab	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-CoA aryltransferase acetyl-CoA aryltransferase acetyl-CoA aryltransferase succinate-semialdehyde dehydrogenase (NAD) 4-aminobutyrate transaminase carbamoyl-phosphate synthase (glutamine-hydrolysing) glutamate racemase gamma-glutamylcysteine synthetase glutamate dehydrogenase glutamate synthase glutamate dehydrogenase glutamate dehydrogenase glutamate and synthase glutamine synthetase glutathione peroxidase glutathion	32126 31145 31145 31145 31145 3132 3131 23116 23116 23116 23116 23116 6321 6355 5113 6322 6323 14113 14114 1414 1414 1413 3512 6312 26119 6357 34112 6318 2322 34111/3411/3411/341 1119 1817 35178 27130 1111 27129 11116 42130 111102 27128 111102 27128 111102 27128 111104 111102 27128 111102 27130 11111 27129 11110 27129 27820	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_02815(aphA)/KCX_14030/KCX_18070  KCX_12285  KCX_07830(adA)/KCX_26660(fad1)  KCX_07830(adA)/KCX_26660(fad1)  KCX_07830(adA)/KCX_26660(fad1)  KCX_07845  KCX_07845  KCX_07845  KCX_07845  KCX_07845  KCX_07855  KCX_16115(pepN)  KCX_0885(ghB)/KCX_16795  KCX_07855  KCX_07856  KCX_07856  KCX_07857  KCX_07856  KCX_07857  KCX_07856  KCX_07857  KCX_07856  KCX_07857  KCX_07856  KCX_07857  KCX_07856  KCX_07856  KCX_07857  KCX_07856  KCX_07857  KCX_07856  KCX	suc-sigle+ fruid chromon > dichromon > dic
GLUCSD2 CMBLD1 CMBLD2 4NPHP1 4NPHP1 ACCOAA2 ACCOAA3 SUCSD2 GABAT1 CABPS GLUR GGLUCYSS GTHRDS GLUS1 GLUS1 GLUS2 GLUDH2 GLUS1 GL	Chloroyclohexane and chlorobenzene degradation Chloroyclohexane and chlorobenzene degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation gamma-Hexachlorocyclohexane degradation Geraniol degrdation Geraniol degrdation Glutamate metabolism Glutathione Metabolism Glutathione Metabolism Glutathione Metabolism Glutathione Metabolism Glutathione Metabolism Glycerolipid Metabolism	carboxymethylenebutenolidase carboxymethylenebutenolidase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase 4-nitrophenyl phosphatase acetyl-CoA acyltransferase acetyl-CoA acyltransferase acetyl-CoA acyltransferase succinate-semialdehyde dehydrogenase (NAD) 4-aminobutyrate transaminase carbamoyl-phosphate synthase (glutamine-hydrolysing) glutamate racemase gamma-glutamylcysteine synthetase glutamate synthase glutamate synthase glutamate synthase glutamate dehydrogenase glutamate dehydrogenase glutamate dehydrogenase glutamine synthetase 4-aminobutyrate transaminase asparty-tRNA/Asni/glutamyl-tRNA/Asni/glutamyl-tRNA/Asni/glutamyl-tRNA/Asni/glutamyl-tRNA/Asni/glutamyl-tRNA/Asni/glutamyl-tRNA/Asni/glutamyl-tRNA/Asni/glutamyl-transaminase aparty-tRNA/Asni/glutamyl-transaminase aparty-tRNA/Asni/glutamyl-transaminase aparty-tRNA/Asni/glutamyl-transaminase aparty-tRNA/Asni/glutamyl-transaminase alanyl aminopeptidase glutathione peroxidase glutathione peroxidase glutathione peroxidase glutathione reductase (Jutathione peroxidase glutathione peroxi	32126 31145 31145 31145 31145 3132 3131 23116 23116 23116 23116 23116 6321 6322 6323 14113 14114 1414 1414 1414 1413 3512 6312 26119 6357 34112 6318 2322 34111/3411/3411/34 1111 27129 1111 27129 1111 27129 1111 27128 11110 211202 27820 32122 11194 11194 4317 23115	KCX_02855/KCX_07760  KCX_02855/KCX_07760  KCX_02815(aphA)/KCX_14030/KCX_18070  KCX_12285  KCX_07830(adA)/KCX_26660(fad1)  KCX_07830(adA)/KCX_26660(fad1)  KCX_07830(adA)/KCX_26660(fad1)  KCX_07845  KCX_07845  KCX_07845  KCX_07845  KCX_0785  KCX_0785  KCX_08560(jal8)/KCX_03865(ghD)  KCX_08560(jal8)/KCX_03865(ghD)  KCX_08560(jal8)/KCX_03865(ghD)  KCX_18085  KCX_14645  KCX_16785  KCX_0885(jal8)/KCX_16795  KCX_0885(jal8)/KCX_16795  KCX_0885(jal8)/KCX_16795  KCX_0885(jal8)/KCX_16795  KCX_0885(jal8)/KCX_16795  KCX_0885(jal8)/KCX_16795  KCX_0885(jal8)/KCX_16795  KCX_0885(jal8)/KCX_16795  KCX_0885(jal8)/KCX_16795  KCX_0885(jal8)/KCX_1865(jal8)/KCX_18958/KCX	suc-sigle + fru dehrecmo -> dehrooe  tembo -> Zmac  ntphp -> pnpp + pi  7m366ccap + coa -> Smh4ecap + accap 5m364bcap + coa -> Smcap + accap 5m364bcap + coa -> Smcap + accap 5m364bcap + coa -> 3mccap + accap 12 atp + gin + hoa3 -> 2 adp + cap + giu + pi 13 dgiu <-> giu 14 p + yos + giu -> adp + gys + pi 15 dgiu <-> giu 15 p + yos + giu -> adp + gys + pi 16 dgiu + nadp -> 2 giu + nadp 16 aig + gin + nadp -> 2 giu + nadp 16 aig + gin + nadp -> 2 giu + nadp 16 giu + nadp -> 3 akg + nadph + nhd 17 giu + nad +> 3 giu + nad 18 giu + nadp -> 3 giu + nad 19 giu + nadp -> 3 giu + nad 19 giu + nadp -> 3 giu + nad 19 giu + nadp -> 3 giu + nad 19 giu + nadp -> 3 giu + nad 19 giu + nadp -> 3 gin + nadp + gin + pi 17 giu +> yiu + hoh4 -> adp + gin + pi 18 pab + akg <-> giu + succal 19 lurna + gin + atp -> gintrna + giu + pi + adp 19 progly -> giy + pro 18 p + rgt + sprmd -> adp + gtspmd + pi 17 rgt -> yosply + giu 17 yosply -> yos + gly 18 hoz2 + 2 rgt -> osp 19 yi + aap -> dap + gylsp 19 horop + nadh -> 13pdo + nad 12ppd-R -> propanal 19 propanal + nad + coa -> ppcoa + nadh 19 propanal + nad + coa -> ppcoa + nadh 19 propanal + nad + coa -> ppcoa + nadh 19 propanal + nad + coa -> ppcoa + nadh 19 propanal + nad -> coa -> ppcoa + nadh 19 propanal + nad -> coa -> ppcoa + nadh 19 propanal + nad -> coa -> ppcoa + nadh 19 propanal + nad -> coa -> ppcoa + nadh 19 propanal + nad -> coa -> ppcoa + nadh 19 propanal -> dhap + nadh 19 yi-3p -> nadc -> dhap + nadh 10 yi-3p -> nadc -> dhap + nadh 11 yi-3p -> nadc -> dhap + nadh 12 ppd-A -> nadc -> dhap + nadh 13 pyd-A -> nadc -> dhap + nadh 14 pyd-Sp -> 0sc 12 naCP -> 0sc 12 naCP +> 0sc 12 naCP -> 0sc 12 naCP -

PPTCT	Glycerophospholipid Metabolism	phosphatidate	2.7.7.41	KOX_11475(cdsA)	pa + ctp -> cdpdg + ppi
PPGS		cyticiyiyitransterase	2.7.8.5	KOX 24100	cdpdg + glyc3p -> cmp + pgp
PPSERS	Glycerophospholipid Metabolism	Phosphatidylserine syntase	2.7.8.8	KOX_27630(pssA)	cdpdg + ser -> cmp + ps
PLIPASA1C	Glycerophospholipid Metabolism	Phospholipase A1 (phosphatidylcholine)	3.1.1.32	KOX_07705	pc -> 2ag3pc + 0.06 c120 + 0.003 c130 + 0.144 c140 + 0.005 c151 + 0.378 c160 + 0.061 c161 + 0.256 c170 + 0.001 c171 + 0.005 c180 + 0.053 c181 + 0.034 c190
PLIPASA1S		Phospholipase A1	3.1.1.32		ps -> 2ag3ps + 0.06 c120 + 0.003 c130 + 0.144 c140 + 0.005 c151 + 0.378 c160 + 0.061 c161 + 0.256 c170
		(Pnospnatidylserine)  Phospholipara A1			+ 0.001 c171 + 0.005 c180 + 0.053 c181 + 0.034 c190  pe -> 2aq3pe + 0.06 c120 + 0.003 c130 + 0.144 c140 + 0.005 c151 + 0.378 c160 + 0.061 c161 + 0.256 c170
PLIPASA1E	Glycerophospholipid Metabolism	(phosphatidylethanolamine)	3.1.1.32	KOX_07/05	+ 0.001 c171 + 0.005 c180 + 0.053 c181 + 0.034 c190
PLIPASA1g		Phospholipase A1 (phosphatidylglycerol)	3.1.1.32		pg -> 2ag3pg + 0.06 c120 + 0.003 c130 + 0.144 c140 + 0.005 c151 + 0.378 c160 + 0.061 c161 + 0.256 c170 + 0.001 c171 + 0.005 c180 + 0.053 c181 + 0.034 c190
		2-Acyl-sn-glycero-3-			+ 0.001 C1/1 + 0.005 C100 + 0.055 C101 + 0.054 C190
AGPEACT			2.3.1.40	KOX_01650	2ag3pe + aACP -> pe + ACP
		acyltransferase Lysophospholipase L (acyl-			2ag3pc -> g3pc + 0.06 c120 + 0.003 c130 + 0.144 c140 + 0.005 c151 + 0.378 c160 + 0.061 c161 + 0.256
LPLIPAc	Glycerophospholipid Metabolism	glycerophosphocholinel)	3.1.1.5	KOA_07750	c170 + 0.001 c171 + 0.005 c180 + 0.053 c181 + 0.034 c190
LPLIPAe	Glycerophospholipid Metabolism	Lysophospholipase L (acyl- glycerophosphoethanolamine)	3.1.1.5		2ag3pe -> g3pe + 0.06 c120 + 0.003 c130 + 0.144 c140 + 0.005 c151 + 0.378 c160 + 0.061 c161 + 0.256 c170 + 0.001 c171 + 0.005 c180 + 0.053 c181 + 0.034 c190
LPLIPAs	Glycerophospholipid Metabolism	Lysophospholipase L (acyl-	3.1.1.5	VOV 07720	2ag3ps -> g3ps + 0.06 c120 + 0.003 c130 + 0.144 c140 + 0.005 c151 + 0.378 c160 + 0.061 c161 + 0.256
		glycerophosphoserine) Lysophospholipase L (acyl-			c170 + 0.001 c171 + 0.005 c180 + 0.053 c181 + 0.034 c190 2ag3pg -> g3pg + 0.06 c120 + 0.003 c130 + 0.144 c140 + 0.005 c151 + 0.378 c160 + 0.061 c161 + 0.256
LPLIPAg	Glycerophospholipid Metabolism	glycerophosphoglycerol)	3.1.1.5		c170 + 0.001 c171 + 0.005 c180 + 0.053 c181 + 0.034 c190
PGRPP	Glycerophospholipid Metabolism	phosphatidylglycerol phosphate phosphatase	3.1.3.27	KOX_12595/KOX_18425	pgp -> pg + pi
		Glycerophosphodiester			
GPPDPD1			3.1.4.46	KOX_04790(udpQ)/KOX_26160(glpQ)	g3pc -> choline + glyc3p
		(Glycerophosphocholine) Glycerophosphodiester			
GPPDPD2	Glycerophospholipid Metabolism		3.1.4.46	KOX_04790(udpQ)/KOX_26160(glpQ)	g3pe -> etha + glyc3p
		(Glycerophosphoethanolamine) Glycerophosphodiester			
GPPDPD3			3.1.4.46	KOX_04790(udpQ)/KOX_26160(glpQ)	g3ps -> glyc3p + ser
		(Glycerophosphoserine) Glycerophosphodiester			
GPPDPD4	Glycerophospholipid Metabolism	phosphodiesterase	3.1.4.46	KOX_04790(udpQ)/KOX_26160(glpQ)	g3pg -> gl + glyc3p
		(Glycerophosphoglycerol) Glycerophosphodiester			
GPPDPD5	Glycerophospholipid Metabolism	phosphodiesterase	3.1.4.46	KOX_04790(udpQ)/KOX_26160(glpQ)	g3pi -> glyc3p + mi
		(Glycerophosphoinositol) CDP-diacylglycerol			
CDPDGP	diycerophospholipid Metabolism	pyrophosphatase	3.6.1.26	KOX_06055	cdpdg -> pa + cmp
PSERD		Phosphatidylserine decarboxylase	4.1.1.65	KOX_08795(psd)	ps -> pe + co2
CLPNS1	Glycerophospholipid Metabolism	cardiolipin synthase	2.7.8		2 pg <-> dpn + gl
CLPNS2	Glycerophospholipid Metabolism	cardiolipin synthase	2.7.8	KOX_15005/KOX_22980(cls)	pg + cdpdg -> clpn + cmp
ETNP	diyeeropriosprioripia metabolism	e	2.7.8.1		pe + cmp <-> cdpetn + dgr
GALGCER			3.2.1.23		bgalgcer -> glucer + glac
AGALCTS10	Glycerophospholipid metabolism	Hudrownsun water reductors	3.2.1.22		dgalcer -> galcer + glac
HPYRR	Glycine, Serine and threonine Metabolism	(NADH)	1.1.1.79	KOX_00275/KOX_17100(ghrA)	hpyr + nadh -> glyc-R + nad
HPYRRp	Glycine, Serine and threonine Metabolism	Hydroxypyruvate reductase (NADPH)	1.1.1.81	KOX_00275/KOX_17100(ghrA)	hpyr + nadph <-> glyc-R + nadp
THRDH	Glycine, Serine and threonine Metabolism		1.1.1.103	KOX 05850(tdh)	nad + thr -> 2aobut + nadh
		D 2 phorphophysorate			
PGLCED		dehydrogenase	1.1.1.95	KOX_02525/KOX_05145/KOX_14075/KOX_20995	3pg + nad <-> 3php + nadh
GLYHMT	Glycine, Serine and threonine Metabolism	glycine hydroxymethyltransferase	2.1.2.1	KOX_27430(glyA)	ser + thf -> gly + metthf
GLYCAT	Glycine, Serine and threonine Metabolism		2.3.1.29	KOX_05855	accoa + gly <-> 2aobut + coa
	diyene, serine and uncomine metabolish	giyeine e deciyindisierdae	2.3.223	KOX_03033	decour gly ( ) Idebut ( cou
PSERT	Glycine, Serine and threonine Metabolism	phosphoserine transaminase	2.6.1.52	KOX_15995	3php + glu <-> akg + pser
GLYCEK2	Glycine, Serine and threonine Metabolism	glycerate kinase	2.7.1.31	KOX_01170/KOX_03460	atp + glyc-R <-> 2pg + adp
PSERP	Glycine, Serine and threonine Metabolism	phosphoserine phosphatase (L-	3.1.3.3	KOX 10335(serB)	
PSERP	diyelle, serile and threonine Metabolishi	serine)	3.1.3.3	KOX_10333(Serb)	pser -> pi + ser
SERD	Glycine, Serine and threonine Metabolism	L-serine deaminase	4.3.1.17	KOX_01230/KOX_23635	and a substitution of the
					ser -> nh4 + pyr
DSERD	Glycine, Serine and threonine Metabolism	D-serine dehydratase	4.3.1.18		dser <-> nh4 + pyr
DSERD	Glycine, Serine and threonine Metabolism		4.3.1.18	KOX_06460	dser <-> nh4 + pyr
DSERD MNAO1	Glycine, Serine and threonine Metabolism	monoamine oxidase			
	Glycine, Serine and threonine Metabolism Glycine, Serine and Threonine	monoamine oxidase	4.3.1.18	KOX_06460	dser <-> nh4 + pyr
MNAO1 HSERD	Glycine, Serine and threonine Metabolism Glycine, Serine and Threonine Metabolism Glycine, Serine and Threonine	monoamine oxidase homoserine dehydrogenase (NADH) homoserine dehydrogenase	4.3.1.18 1.4.3.21 1.1.1.3	KOX_06460  KOX_19410(tynA)  KOX_07315(mett.)/KOX_10410(thrA)	dser <-> nh4 + pyr  aact + o2 -> h2o2 + mtg + nh4  hser + nad <-> aspsa + nadh
MNAO1 HSERD HSERDp	Glycine, Serine and threonine Metabolism Glycine, Serine and Threonine Metabolism Glycine, Serine and Threonine Metabolism	monoamine oxidase homoserine dehydrogenase (NADH) homoserine dehydrogenase (NADPH) aspartate.semialdehyda	4.3.1.18 1.4.3.2.1 1.1.1.3	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)	dser <-> nh4 + pyr  aact + o2 -> h2o2 + mtg + nh4  hser + nad <-> aspsa + nadh  hser + nad <-> aspsa + nadph
MNAO1 HSERD	Glycine, Serine and threonine Metabolism Glycine, Serine and Threonine Metabolism Glycine, Serine and Threonine Metabolism Glycine, Serine and Threonine Metabolism	monoamine oxidase homoserine dehydrogenase (NADH) homoserine dehydrogenase (NADPH) aspartate.semialdehyda	4.3.1.18 1.4.3.21 1.1.1.3	KOX_06460  KOX_19410(tynA)  KOX_07315(mett.)/KOX_10410(thrA)	dser <-> nh4 + pyr  aact + o2 -> h2o2 + mtg + nh4  hser + nad <-> aspsa + nadh
MNAO1 HSERD HSERDp	Glycine, Serine and threonine Metabolism Glycine. Serine and Threonine Metabolism Glycine, Serine and Threonine Metabolism Glycine, Serine and Threonine Metabolism Glycine, Serine and Threonine	monoamine oxidase homoserine dehydrogenase (NADH) homoserine dehydrogenase (NADPH) aspartate-semialdehyde dehydrogenase	4.3.1.18 1.4.3.2.1 1.1.1.3	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)	dser <-> nh4 + pyr  aact + o2 -> h2o2 + mtg + nh4  hser + nad <-> aspsa + nadh  hser + nad <-> aspsa + nadph
MNAO1 HSERD HSERDp ASPSAD HSERK	Glycine, Serine and threonine Metabolism Glycine, Serine and Threonine Metabolism Glycine, Serine and Threonine Metabolism Glycine, Serine and Threonine Metabolism	monoamine oxidase homoserine dehydrogenase (NADH) homoserine dehydrogenase (NADPH) aspartate-semialdehyde dehydrogenase homoserine kinase	4.3.118 1.4.3.21 1.1.13 1.1.13 1.2.111 2.7.1.39	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_04740  KOX_04740	dser <>> nh4 + pyr  aact + c2 -> h2c2 + mtg + nh4  hser + nad <>> stpsa + nadph  hser + nadp <>> stpsa + nadph  aspsa + nadp + pi <>> basp + nadph  atp + hser -> adp + phser
MNAO1 HSERD HSERDp ASPSAD HSERK ASPK	Glycine, Serine and threonine Metabolism Metabolism Glycine, Serine and Threonine	monoamine oxidase homoserine dehydrogenase (NADH) homoserine dehydrogenase (NADPH) aspartate semialdehyde dehydrogenase homoserine kinase aspartate kinase	4.3.118 1.4.3.21 1.1.1.3 1.1.1.3 1.2.1.11 2.7.1.39	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_04740  KOX_10415  KOX_07315(metL)/KOX_08160/KOX_10410(thrA)	dser <>> nh4 + pyr  aact + o2 <> h2o2 + mtg + nh4  hser + nad <>> aspsa + nadh  hser + nadp <>> aspsa + nadph  aspsa + nadp + pi <>> basp + nadph  atp + hser -> adp + phser  asp + atp <<> basp + adp
MNAO1 HSERD HSERDp ASPSAD HSERK	Glycine, Serine and threonine Metabolism Metabolism	monoamine oxidase homoserine dehydrogenase (NADH) homoserine dehydrogenase (NADPH) aspartate semialdehyde dehydrogenase homoserine kinase aspartate kinase	4.3.118 1.4.3.21 1.1.13 1.1.13 1.2.111 2.7.1.39	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_04740  KOX_04740	dser <>> nh4 + pyr  aact + c2 -> h2c2 + mtg + nh4  hser + nad <>> stpsa + nadph  hser + nadp <>> stpsa + nadph  aspsa + nadp + pi <>> basp + nadph  atp + hser -> adp + phser
MNAO1 HSERD HSERDp ASPSAD HSERK ASPK	Glycine, Serine and threonine Metabolism Glycine, Serine and Threonine Metabolism Glycine, Serine and Threonine	monoamine oxidase homoserine dehydrogenase (NADH) homoserine dehydrogenase (NADPH) aspartate-semialdehyde dehydrogenase homoserine kinase aspartate kinase	4.3.118 1.4.3.21 1.1.1.3 1.1.1.3 1.2.1.11 2.7.1.39	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_04740  KOX_10415  KOX_07315(metL)/KOX_08160/KOX_10410(thrA)	dser <>> nh4 + pyr  aact + o2 <> h2o2 + mtg + nh4  hser + nad <>> aspsa + nadh  hser + nadp <>> aspsa + nadph  aspsa + nadp + pi <>> basp + nadph  atp + hser -> adp + phser  asp + atp <<> basp + adp
MNAO1 HSERD HSERDP ASPSAD HSERK ASPK THRAD2 THRAD1	Glycine, Serine and threonine Metabolism	monoamine oxidase homoserine dehydrogenase (NADH) homoserine dehydrogenase (NADPH) asapartate-semialdehyde dehydrogenase homoserine kinase aspartate kinase L-allo-threonine aldolase threonine aldolase	4.3.118 1.4.3.21 1.1.1.3 1.1.1.3 1.2.1.11 2.7.1.39 2.7.2.4 4.1.2.5 4.1.2.5	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_04740  KOX_10415  KOX_07315(metL)/KCX_08160/KCX_10410(thrA)  KOX_15770  KOX_15770	dser <> nh4 + pyr  aact + o2 > h2o2 + mtg + nh4  hser + nad <> aspsa + nadh  hser + nadp <> aspsa + nadph  aspsa + natp + pi <> basp + nadph  atp + hser -> adp + phser  asp + atp <> basp + adp  athr <> acal + gly  thr <>> acal + gly
MNAO1 HSERD HSERD ASPSAD HSERK ASPK THRAD2 THRAD1 THRS	Glycine, Serine and threonine Metabolism	monoamine oxidase homoserine dehydrogenase (NADH) homoserine dehydrogenase (NADPH) sapartate-semialdehyde dehydrogenase homoserine kinase aspartate kinase L-allo-threonine aldolase threonine aldolase threonine synthase	4.3.118 14.3.21 1.1.13 1.1.13 1.2.1.11 2.7.1.39 2.7.2.4 4.1.2.5	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_04740  KOX_10415  KOX_07315(metL)/KOX_08160/KOX_10410(thrA)  KOX_15770	dser <>> nh4 + pyr  aact + o2 <> h2o2 + mtg + nh4  hser + nad <>> aspsa + nadh  hser + nadp <>> aspsa + nadph  aspsa + nadp + pi <>> basp + nadph  atp + hser >> adp + phser  asp + atp <>> basp + adp  athr <>> acal + gly
MNAO1 HSERD HSERDP ASPSAD HSERK ASPK THRAD2 THRAD1	Glycine, Serine and threonine Metabolism	monoamine oxidase homoserine dehydrogenase (NADH) homoserine dehydrogenase (NADH) sapartate semialdehyde dehydrogenase homoserine kinase aspartate kinase L-allo-threonine aldolase threonine aldolase threonine synthase L-2-amino-3-oxobutanoate decarboxylation (spontaneous)	4.3.118 1.4.3.21 1.1.1.3 1.1.1.3 1.2.1.11 2.7.1.39 2.7.2.4 4.1.2.5 4.1.2.5	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_04740  KOX_10415  KOX_07315(metL)/KCX_08160/KCX_10410(thrA)  KOX_15770  KOX_15770	dser <> nh4 + pyr  aact + o2 > h2o2 + mtg + nh4  hser + nad <> aspsa + nadh  hser + nadp <> aspsa + nadph  aspsa + natp + pi <> basp + nadph  atp + hser -> adp + phser  asp + atp <> basp + adp  athr <> acal + gly  thr <>> acal + gly
MNAO1 HSERD HSERD ASPSAD HSERK ASPK THRAD2 THRAD1 THRS	Glycine, Serine and threonine Metabolism Glycine, Serine and Threonine Metabolism Glycine, Serine and Threonine Metabolism Glycine, Serine and Threonine Metabolism Glycine, Serine and Threonine Metabolism Glycine, Serine and Threonine Metabolism M	monoamine oxidase homoserine dehydrogenase (NADH) homoserine dehydrogenase (NADPH) aspartate-semialdehyde dehydrogenase homoserine kinase aspartate kinase L-allo-threonine aldolase threonine aldolase threonine syntase L-2-amino-3-oxobutanoate decarboylation (spontaneous) betaine-aldehydra	4.3.118 1.4.3.21 1.1.1.3 1.1.1.3 1.2.1.11 2.7.1.39 2.7.2.4 4.1.2.5 4.1.2.5	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_04740  KOX_10415  KOX_07315(metL)/KCX_08160/KCX_10410(thrA)  KOX_15770  KOX_15770	dser <> nh4 + pyr  aact + o2 > h2o2 + mtg + nh4  hser + nad <> aspsa + nadh  hser + nadp <> aspsa + nadph  aspsa + natp + pi <> basp + nadph  atp + hser >> adp + phser  asp + atp <> basp + adp  athr <> acal + gly  thr <>> acal + gly  phser >> pi + thr
MNAO1 HSERD HSERD ASPSAD HSERK ASPK THRAD2 THRAD1 THRAD AGBUIDCS BETALDDH1	Glycine, Serine and threonine Metabolism	monoamine oxidase homoserine dehydrogenase (NADH) homoserine dehydrogenase (NADH) sapartate-semialdehyde dehydrogenase homoserine kinase aspartate kinase L-allo-threonine aldolase threonine aldolase threonine aldolase threonine synthase L-2-amino-3-oxobutanoate decarboxylation (spontaneous) betaine-aldelyde dehydrogenase horasos-ine kinase betaine-aldelyde dehydrogenase horasos-ine kinase betaine-aldelyde dehydrogenase horasos-ine kinase horasos-ine kinase betaine-aldelyde dehydrogenase horasos-ine kinase horasos-ine kin	43118 14321 1113 11113 12111 27139 2724 4125 4125 4231	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_04740  KOX_10415  KOX_07315(metL)/KCX_08160/KCX_10410(thrA)  KOX_15770  KOX_15770  KOX_10420	dser <> nh4 + pyr  aact + o2 > h2o2 + mtg + nh4  hser + nad <> aspsa + nadh  hser + nadp <> aspsa + nadph  aspsa + natp + pi <> basp + nadph  atp + hser >> adp + phser  asp + atp <> basp + adp  athr <> acal + gly  thr <> acal + gly  phser >> pi + thr  2aobut >> aact + co2  bal + nad >> glyb + nadh
MNAO1 HSERD HSERD ASPSAD HSERK ASPK THRAD2 THRAD1 THRAD1 THRAD3 AOBUIDCS	Glycine, Serine and threonine Metabolism	monoamine oxidase homoserine dehydrogenase (NADH) homoserine dehydrogenase (NADH) saspartate semialdehyde dehydrogenase homoserine kinase aspartate kinase L-allo-threonine aldolase threonine aldolase threonine synthase L-2-amino-3-oxobutanoate decarboylation (spontaneous) betaine-aldelyde dehydrogenase betaine-aldelyde dehydrogenase	43118 14321 1113 1113 12111 27139 2724 4125 4125 4231	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_04740  KOX_04740  KOX_07315(metL)/KOX_08160/KOX_10410(thrA)  KOX_15770  KOX_15770  KOX_10420	dser <> nh4 + pyr  aact + o2 > h2o2 + mtg + nh4  hser + nad <> aspsa + nadh  hser + nadp <> aspsa + nadph  aspsa + natp + pi <> basp + nadph  atp + hser >> adp + phser  asp + atp <> basp + adp  athr <> acal + gly  thr <> acal + gly  phser >> pi + thr  2aobut >> aact + co2
MNAO1 HSERD HSERD ASPSAD HSERK ASPK THRAD2 THRAD1 THRAD AGBUIDCS BETALDDH1	Glycine, Serine and threonine Metabolism	monoamine oxidase homoserine dehydrogenase (NADH) homoserine dehydrogenase (NADH) sapartate-semialdehyde dehydrogenase homoserine kinase aspartate kinase L-allo-threonine aldolase threonine aldolase threonine aldolase threonine synthase L-2-amino-3-oxobutanoate decarboylation (spontaneous) betaine-aldelyte dehydrogenase betaine-aldelhyd dehydrogenase	43118 14321 1113 11113 12111 27139 2724 4125 4125 4231	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_04740  KOX_10415  KOX_07315(metL)/KCX_08160/KCX_10410(thrA)  KOX_15770  KOX_15770  KOX_10420	dser <> nh4 + pyr  aact + o2 > h2o2 + mtg + nh4  hser + nad <> aspsa + nadh  hser + nadp <> aspsa + nadph  aspsa + natp + pi <> basp + nadph  atp + hser >> adp + phser  asp + atp <> basp + adp  athr <> acal + gly  thr <> acal + gly  phser >> pi + thr  2aobut >> aact + co2  bal + nad >> glyb + nadh
MNAO1 HSERD HSERD HSERD ASPSAD HSERK ASPK THRAD2 THRAD1 THRS AOBUIDCS BETALDDH1 BETALDDH2	Glycine, Serine and threonine Metabolism Glycine, Serine and Threonine Metabolism Glycine, Serine and Threonine	monoamine oxidase homoserine dehydrogenase (NADH) homoserine dehydrogenase (NADH) sapartate-semialdehyde dehydrogenase homoserine kinase aspartate kinase L-allo-threonine aldolase threonine aldolase threonine aldolase threonine synthase L-2-amino-3-oxobutanoate decarboxylation (spontaneous) betaine-aldehyde dehydrogenase betaine-aldehyde dehydrogenase L-serine dehydratase	43118 14321 1113 11113 12111 27139 2724 4125 4125 4231 1218	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_04740  KOX_10415  KOX_07315(metL)/KCX_08160/KCX_10410(thrA)  KOX_15770  KOX_15770  KOX_10420  KOX_13815  KOX_13815	dser <>> nh4 + pyr  aact + o2 > h2o2 + mtg + nh4  hser + nad <>> aspsa + nadh  hser + nadp <>> aspsa + nadph  aspsa + nadp + pi <>> basp + nadph  atp + hser >> adp + phser  asp + atp <>> basp + adp  athr <>> acal + gly  phser >> pi + thr  2aobut >> aact + co2  bal + nad >> glyb + nadph  bal + nadp >> glyb + nadph
MNAO1 HSERD HSERD HSERD HSERK ASPK THRAD2 THRAD1 THRS AOBUIDCS BETALDDH1 BETALDDH2 SERDHT1 THRD_L	Glycine, Serine and threonine Metabolism	monoamine oxidase homoserine dehydrogenase (NADH) homoserine dehydrogenase (NADH) sapartate-semialdehyde dehydrogenase homoserine kinase aspartate kinase aspartate kinase L-allo-threonine aldolase threonine aldolase threonine aldolase threonine synthase L-2-amino-3-oxobutanoate decarboxylation (spontaneous) betaine-aldehyde dehydrogenase betaine-aldehyde dehydrogenase L-serine dehydratase threonine dehydratase	43118 14321 1113 12111 27139 2724 4125 4125 4231 1218 1218 43119 43119	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_04740  KOX_10415  KOX_07315(metL)/KCX_08160/KCIX_10410(thrA)  KOX_15770  KOX_15770  KOX_10420  KOX_13815  KOX_13815  KOX_07465/KCX_24645  KOX_07465/KCX_24645	dser <>> nh4 + pyr  aact + o2 > h2o2 + mtg + nh4  hser + nad <>> aspsa + nadh  hser + nadp <>> aspsa + nadph  aspsa + nadp + pi <>> basp + nadph  atp + hser >> adp + phser  asp + atp <>> basp + adp  athr <>> acal + gly  thr <>> acal + gly  pheer -> pi + thr  2aobut >> act + co2  bal + nad >> glyb + nadh  bal + nadp >> glyb + nadph  ser >> nh4 + pyr  thr >> obut + nh4
MNAO1 HSERD HSERD HSERD HSERK ASPK THRAD2 THRAD1 THRS AOBUIDCS BETALDOH1 BETALDOH2 SERDHT1 THRD_L GLVD	Glycine, Serine and threonine Metabolism	monoamine oxidase homoserine dehydrogenase (NADH) homoserine dehydrogenase (NADH) sapartate-semialdehyde dehydrogenase homoserine kinase aspartate kinase aspartate kinase L-allo-threonine aldolase threonine aldolase threonine aldolase threonine synthase L-2-amino-3-oxobutanoate decarboxylation (spontaneous) betaine-aldehyde dehydrogenase betaine-aldehyde dehydrogenase L-serine dehydratase threonine dehydratase	43118 14321 1113 1113 12111 27139 2724 4125 4125 4231 1218 1218 43119 43119 1442	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_04740  KOX_10415  KOX_07315(metL)/KOX_08160/KCIX_10410(thrA)  KOX_15770  KOX_15770  KOX_10420  KOX_13815  KOX_13815  KOX_07465/KOX_24645  KOX_07465/KCX_24645  KOX_07465/KCX_24645	dser <>> nh4 + pyr  aact + o2 > h2o2 + mtg + nh4  hser + nad <>> aspsa + nadh  hser + nadp <>> aspsa + nadph  aspsa + nadp + pi <>> basp + nadph  atp + hser >> adp + phser  asp + atp <>> basp + adp  athr <>> acal + gly  phser >> pi + thr  2aobut >> aact + co2  bal + nad >> glyb + nadph  bal + nadp >> glyb + nadph  ser >> nh4 + pyr  thr >> obut + nh4  gly + lipop >> sap + co2
MNAO1 HSERD HSERD HSERD HSERK ASPK THRAD2 THRAD1 THRS AOBUIDCS BETALDDH1 BETALDDH2 SERDHT1 THRD_L	Glycine, Serine and threonine Metabolism Metabolism and Threonine Metabolism Glycine, Serine and Threonine	monoamine oxidase homoserine dehydrogenase (NADH) homoserine dehydrogenase (NADH) sapartate-semialdehyde dehydrogenase homoserine kinase aspartate kinase aspartate kinase L-allo-threonine aldolase threonine aldolase threonine aldolase threonine synthase L-2-amino-3-oxobutanoate decarboxylation (spontaneous) betaine-aldehyde dehydrogenase betaine-aldehyde dehydrogenase L-serine dehydratase threonine dehydratase	43118 14321 1113 12111 27139 2724 4125 4125 4231 1218 1218 43119 43119	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_04740  KOX_10415  KOX_07315(metL)/KCX_08160/KCIX_10410(thrA)  KOX_15770  KOX_15770  KOX_10420  KOX_13815  KOX_13815  KOX_07465/KCX_24645  KOX_07465/KCX_24645	dser <>> nh4 + pyr  aact + o2 > h2o2 + mtg + nh4  hser + nad <>> aspsa + nadh  hser + nadp <>> aspsa + nadph  aspsa + nadp + pi <>> basp + nadph  atp + hser >> adp + phser  asp + atp <>> basp + adp  athr <>> acal + gly  thr <>> acal + gly  pheer -> pi + thr  2aobut >> act + co2  bal + nad >> glyb + nadh  bal + nadp >> glyb + nadph  ser >> nh4 + pyr  thr >> obut + nh4
MNAO1 HSERD HSERD HSERD HSERK ASPK THRAD2 THRAD1 THRS AOBUIDCS BETALDOH1 BETALDOH2 SERDHT1 THRD_L GLVD	Glycine, Serine and Threonine Metabolism Glycine, Serine and Threonine Metabolism (Glycine, Serine and Threonine and Threonine and Threonine Metabolism (Glycine, Serine and Threonine and Threonine Americane)	monoamine oxidase homoserine dehydrogenase (NADH) homoserine dehydrogenase (NADH) sapartate-semialdehyde dehydrogenase homoserine kinase aspartate sinase L-allo-threonine aldolase threonine aldolase threonine aldolase threonine synthase L-2-amino-3-oxobutanoate decarboxylation (spontaneous) betaine-aldehyde dehydrogenase betaine-aldehyde dehydrogenase L-serine dehydratase threonine dehydratase glycine dehydrogenase aminomethyltransferase dihydrolipoamide	43118 14321 1113 1113 12111 27139 2724 4125 4125 4231 1218 1218 43119 43119 1442	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_04740  KOX_10415  KOX_07315(metL)/KOX_08160/KCIX_10410(thrA)  KOX_15770  KOX_15770  KOX_10420  KOX_13815  KOX_13815  KOX_07465/KOX_24645  KOX_07465/KCX_24645  KOX_07465/KCX_24645	dser <>> nh4 + pyr  aact + o2 > h2o2 + mtg + nh4  hser + nad <>> aspsa + nadh  hser + nadp <>> aspsa + nadph  aspsa + nadp + pi <>> basp + nadph  atp + hser >> adp + phser  asp + atp <>> basp + adp  athr <>> acal + gly  phser >> pi + thr  2aobut >> aact + co2  bal + nad >> glyb + nadph  bal + nadp >> glyb + nadph  ser >> nh4 + pyr  thr >> obut + nh4  gly + lipop >> sap + co2
MNAO1 HSERD HSERD HSERD HSERK ASPK THRAD2 THRAD1 THRS AOBUTDCs BETALDDH1 BETALDDH2 SERDHT1 THRD_L GLYD AMTF1 DLPD	Glycine, Serine and threonine Metabolism	monoamine oxidase homoserine dehydrogenase (NADH) nomoserine dehydrogenase (NADH) sapartate-semialdehyde dehydrogenase homoserine kinase aspartate simialdehyde dehydrogenase homoserine kinase aspartate kinase L-allo-threonine aldolase threonine aldolase threonine aldolase threonine aldolase threonine synthase L-2-amino-3-oxobutanoate decarboxylation (spontaneous) betaine-aldehyde dehydrogenase L-serine dehydratase threonine dehydratase threonine dehydratase glycine dehydrogenase aminomethyltransferase dihydrolipoamide dehydrogenase	43118 1.4321 1.113 1.1.13 1.2.111 2.7.139 2.7.24 4.1.25 4.1.25 4.2.31 1.2.18 1.2.18 4.3.119 4.3.119 1.4.4.2 2.1.2.10 1.8.1.4	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_04740  KOX_10415  KOX_07315(metL)/KOX_08160/KOX_10410(thrA)  KOX_15770  KOX_15770  KOX_15770  KOX_13815  KOX_13815  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_02480  KOX_02490(gxvT)  KOX_11055/KOX_20455	dser <>> nh4 + pyr  aact + o2 > h2o2 + mtg + nh4  hser + nad <>> aspsa + nadh  hser + nadp <>> aspsa + nadph  aspsa + nadp + pi <>> basp + nadph  aspsa + nadp + pi <>> basp + nadph  atp + hser >> adp + phser  asp + atp <>> basp + adp  athr <>> acal + gly  thr <>> acal + gly  pheer -> pi + thr  2aobut >> aact + co2  bal + nad >> glyb + nadh  bal + nadp >> glyb + nadph  ser >> nh4 + pyr  thr -> obut + nh4  gly + lipop >> sap + co2  sap + thf >> dlipop + methf + nh4  dlipop + nad -> lipop + nadh
MNAO1 HSERD HSERD HSERD HSERK ASPK THRAD2 THRAD1 THRS AOBUIDCs BETALDOH1 BETALDOH2 SERDHTI THRD, L GLVD AMIF1	Glycine, Serine and threonine Metabolism	monoamine oxidase homoserine dehydrogenase (NADH) homoserine dehydrogenase (NADH) sapartate-semialdehyde dehydrogenase homoserine kinase aspartate semialdehyde dehydrogenase homoserine kinase  L-allo-threonine aldolase threonine aldolase threonine aldolase threonine synthase L-2-amino-3-oxobutanoate decarboxylation (spontaneous) betaine-aldehyde dehydrogenase betaine-aldehyde dehydrogenase L-serine dehydratase threonine dehydratase threonine dehydratase glycine dehydrogenase aminomethyltransferase dihydrolipoamide dehydrogenase choline dehydrogenase choline dehydrogenase	43118 1.4321 1.113 1.113 1.2111 2.7139 2.724 4.125 4.125 4.125 4.231 1.218 1.218 4.3119 4.3119 1.442 2.1210	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_04740  KOX_10415  KOX_07315(metL)/KOX_08160/KCIX_10410(thrA)  KOX_15770  KOX_15770  KOX_10420  KOX_13815  KOX_13835  KOX_07465/KOX_24645  KOX_07465/KCX_24645  KOX_07465/KCX_24645  KOX_02480  KOX_02480(gcvT)	dser <>> nh4 + pyr  aact + o2 > h2o2 + mtg + nh4  hser + nad <>> aspsa + nadh  hser + nadp <>> aspsa + nadph  aspsa + nadp + pi <>> basp + nadph  atp + hser >> adp + phser  asp + atp <>> basp + adp  athr <>> acal + gly  thr <>> acal + gly  phser >> pi + thr  2aobut >> aact + co2  bal + nad >> glyb + nadph  bal + nad >> glyb + nadph  ser >> nh4 + pyr  thr >> obut + nh4  gly + lipop >> sap + co2  sap + thf >> dipop + methf + nh4
MNAO1 HSERD HSERD HSERD HSERK ASPK THRAD2 THRAD1 THRS AOBUTDCs BETALDDH1 BETALDDH2 SERDHT1 THRD_L GLYD AMTF1 DLPD	Glycine, Serine and threonine Metabolism Glycine, Serine and Threonine Metabol	monoamine oxidase homoserine dehydrogenase (NADH) nomoserine dehydrogenase (NADH) sapartate-semialdehyde dehydrogenase homoserine kinase aspartate simialdehyde dehydrogenase homoserine kinase L-allo-threonine aldolase threonine aldolase threonine aldolase threonine aldolase threonine synthase L-2-amino-3-oxobutanoate decarboxylation (spontaneous) betaine-aldehyde dehydrogenase L-serine dehydratase threonine dehydratase threonine dehydratase glycine dehydrogenase aminomethyltransferase dihydrolipoamide dehydrogenase choline dehydrogenase	43118 1.4321 1.113 1.1.13 1.2.111 2.7.139 2.7.24 4.1.25 4.1.25 4.2.31 1.2.18 1.2.18 4.3.119 4.3.119 1.4.4.2 2.1.2.10 1.8.1.4	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_04740  KOX_10415  KOX_07315(metL)/KOX_08160/KOX_10410(thrA)  KOX_15770  KOX_15770  KOX_15770  KOX_13815  KOX_13815  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_02480  KOX_02490(gxvT)  KOX_11055/KOX_20455	dser <>> nh4 + pyr  aact + o2 > h2o2 + mtg + nh4  hser + nad <>> aspsa + nadh  hser + nadp <>> aspsa + nadph  aspsa + nadp + pi <>> basp + nadph  aspsa + nadp + pi <>> basp + nadph  atp + hser >> adp + phser  asp + atp <>> basp + adp  athr <>> acal + gly  thr <>> acal + gly  pheer -> pi + thr  2aobut >> aact + co2  bal + nad >> glyb + nadh  bal + nadp >> glyb + nadph  ser >> nh4 + pyr  thr -> obut + nh4  gly + lipop >> sap + co2  sap + thf >> dlipop + methf + nh4  dlipop + nad -> lipop + nadh
MNAO1 HSERD HSERD HSERD HSERK ASPK THRAD2 THRAD1 THRS AOBUTDCs BETALDDH1 BETALDDH2 SERDH11 THRD, L GLYD AMTF1 DLPD CHOLD1	Glycine, Serine and threonine Metabolism Glycine, Serine and Threonine Metabolism (Glycine, Serine and Threonine and Threonine Americana a	monoamine oxidase homoserine dehydrogenase (NADH) nomoserine dehydrogenase (NADH) sapartate-semialdehyde dehydrogenase homoserine kinase aspartate sinase L-allo-threonine aldolase threonine aldolase threonine aldolase threonine synthase L-2-amino-3-oxobutanoate decarboxylation (spontaneous) betaine-aldehyde dehydrogenase betaine-aldehyde dehydrogenase L-serine dehydratase threonine dehydratase dilycine dehydrogenase aminomethyltransferase dihydrolipoamide dehydrogenase choline dehydrogenase dihydrolipoamide dehydrogenase choline dehydrogenase	43118 1.4321 1.113 1.113 1.2111 2.7139 2.724 4.125 4.125 4.125 4.231 1.218 1.218 4.3119 4.3119 1.442 2.1210 1.814 1.1991	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_04740  KOX_10415  KOX_07315(metL)/KOX_08160/KOX_10410(thrA)  KOX_15770  KOX_15770  KOX_10420  KOX_13815  KOX_07465/KOX_24645  KOX_07465/KOX_24655  KOX_11055/KOX_20455  KOX_13810/KOX_26150  KOX_13810/KOX_26150	dser <>> nh4 + pyr  aact + o2 >> h2o2 + mtg + nh4 hser + nad <>> aspsa + nadh hser + nadp <>> aspsa + nadph aspsa + nadp + pi <>> basp + nadph aspsa + nadp + pi <>> basp + nadph atp + hser >> adp + phser asp + atp <>> basp + adp athr <>> acal + gly thr <>> acal + gly phser >> pi + thr  2aobut >> aact + co2 bal + nad >> glyb + nadh bal + nadp >> glyb + nadph ser >> nh4 + pyr thr >> obut + nh4 gly + lipop >> sap + co2 sap + thf >> dlipop + metthf + nh4 dlipop + nad >> bilpop + metthf + nh4 dlipop + nad >> bilpop + madh choline + fad >> bal + fadh2 glu + aspsa >> skg + 24dab
MNAO1 HSERD HSERD HSERD HSERK ASPK THRAD2 THRAD1 THRS AOBUTDCs BETALDOH1 BETALDOH2 SEROH11 THRD_L GLVD AMTF1 DLPD CHOLD1 DABOT CYSTHS1	Glycine, Serine and threonine Metabolism	monoamine oxidase homoserine dehydrogenase (NADH) homoserine dehydrogenase (NADH) sapartate-semialdehyde dehydrogenase homoserine kinase aspartate semialdehyde dehydrogenase homoserine kinase  L-allo-threonine aldolase threonine aldolase threonine aldolase threonine aldolase threonine synthase L-2-amino-3-oxobutanoate decarboxylation (spontaneous) betaine-aldehyd dehydrogenase L-serine dehydratase threonine dehydratase dylpine dehydrogenase aminomethyltransferase dihydrolpoamide dehydrogenase choline dehydrogenase diminobutytansferase diminofuncytransferase diminofunc	43118 1.4321 1.113 1.113 1.2111 2.7139 2.724 4.125 4.125 4.125 4.121 1.218 4.3119 4.3119 1.442 2.1210 1.814 1.1991 2.61.76 4.2122	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_04740  KOX_10415  KOX_07315(metL)/KOX_08160/KOX_10410(thrA)  KOX_15770  KOX_15770  KOX_10420  KOX_13815  KOX_13815  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_24655  KOX_13810/KOX_26150  KOX_13810/KOX_26150  KOX_13810/KOX_26150  KOX_022795	dser <>> nh4 + pyr  aact + o2 >> h2o2 + mtg + nh4 hser + nad <>> aspsa + nadh hser + nadp <>> aspsa + nadph aspsa + nadp + pi <>> basp + nadph atp + hser >> adp + phser asp + atp <>> basp + adp ath <>> basp + adp ath <>> cal + gly thr <>> acal + gly thr <>> acal + gly bal + nad >> glyb + nadh bal + nad >> glyb + nadh bal + nadp >> glyb + nadph ser >> nh4 + pyr thr >> obut + nh4 gly + lipop >> sap + co2 sap + thf >> dlipop + methtf + nh4 dlipop + nad >> bilpop + methtf + nh4 dlipop + nad >> bilpop + madh choline + fad -> bal + fadh2 glu + aspsa -> akg + 24dab ser + hcys -> lict
MNAO1 HSERD HSERD HSERD HSERK ASPK THRAD2 THRAD1 THRS AOBUTDCS BETALDDH1 BETALDDH2 SERDHT1 THRD, L GLYD AMTF1 DLPD CHOLD1 DABOT	Glycine, Serine and threonine Metabolism Glycine, Serine and Threonine	monoamine oxidase homoserine dehydrogenase (NADH) homoserine dehydrogenase (NADH) sapartate semialdehyde dehydrogenase homoserine kinase aspartate kinase L-allo-threonine aldolase threonine aldolase threonine aldolase threonine synthase L-2-amino-3-oxobutanoate decarboylation (spontaneous) betaine-aldelhyde dehydrogenase betaine-aldelhyde dehydrogenase t-serine dehydratase threonine dehydratase glycine dehydrogenase aminomethyltransferase dihydrolipoamide dehydrogenase choline dehydrogenase aminomethyltransferase dilhydrolipoamide dehydrogenase choline dehydrogenase choline dehydrogenase choline dehydrogenase	43118 1.4321 1.113 1.113 1.2111 2.7139 2.724 4.125 4.125 4.125 4.231 1.218 1.218 4.3119 4.3119 1.442 2.1210 1.814 1.1991 2.61.76	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_04740  KOX_10415  KOX_07315(metL)/KOX_08160/KOX_10410(thrA)  KOX_15770  KOX_15770  KOX_10420  KOX_13815  KOX_07465/KOX_24645  KOX_07465/KOX_26455  KOX_07465/KOX_26455  KOX_13810/KOX_26150  KOX_02320  KOX_02795	dser <>> nh4 + pyr  aact + o2 >> h2o2 + mtg + nh4 hser + nad <>> aspsa + nadh hser + nadp <>> aspsa + nadph aspsa + nadp + pi <>> basp + nadph aspsa + nadp + pi <>> basp + nadph atp + hser >> adp + phser asp + atp <>> basp + adp athr <>> acal + gly thr <>> acal + gly phser >> pi + thr  2aobut >> aact + co2 bal + nad >> glyb + nadh bal + nadp >> glyb + nadph ser >> nh4 + pyr thr >> obut + nh4 gly + lipop >> sap + co2 sap + thf >> dlipop + metthf + nh4 dlipop + nad >> bilpop + metthf + nh4 dlipop + nad >> bilpop + madh choline + fad >> bal + fadh2 glu + aspsa >> skg + 24dab
MNAO1 HSERD HSERD HSERD HSERK ASPK THRAD2 THRAD1 THRS AOBUTDCs BETALDOH1 BETALDOH2 SEROH11 THRD_L GLVD AMTF1 DLPD CHOLD1 DABOT CYSTHS1	Glycine, Serine and threonine Metabolism Glycine, Serine and Threonine	monoamine oxidase homoserine dehydrogenase (NADH) homoserine dehydrogenase (NADH) sapartate-semialdehyde dehydrogenase homoserine kinase aspartate semialdehyde dehydrogenase homoserine kinase aspartate kinase L-allo-threonine aldolase threonine aldolase threonine aldolase threonine synthase L-2-amino-3-oxobutanoate decarboylation (spontaneous) betaine-aldehyde dehydrogenase L-serine dehydratase threonine dehydratase dehydrogenase dehydrogenase dehydrogenase dehydrogenase diminomethytransferase dimydrolipoamide dehydrogenase diminomethydrate-2-oxoglutarate transaminase cystathionine beta-synthase cystathionine beta-synthase cystathionine beta-synthase	43118 1.4321 1.113 1.113 1.2111 2.7139 2.724 4.125 4.125 4.125 4.121 1.218 4.3119 4.3119 1.442 2.1210 1.814 1.1991 2.61.76 4.2122	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_10415  KOX_10415  KOX_10415  KOX_15770  KOX_15770  KOX_10420  KOX_13815  KOX_07465/KCX_24645	dser <>> nh4 + pyr  aact + o2 >> h2o2 + mtg + nh4 hser + nad <>> aspsa + nadh hser + nadp <>> aspsa + nadph aspsa + nadp + pi <>> basp + nadph atp + hser >> adp + phser asp + atp <>> basp + adp ath <>> basp + adp ath <>> cal + gly thr <>> acal + gly thr <>> acal + gly bal + nad >> glyb + nadh bal + nad >> glyb + nadh bal + nadp >> glyb + nadph ser >> nh4 + pyr thr >> obut + nh4 gly + lipop >> sap + co2 sap + thf >> dlipop + methtf + nh4 dlipop + nad >> bilpop + methtf + nh4 dlipop + nad >> bilpop + madh choline + fad -> bal + fadh2 glu + aspsa -> akg + 24dab ser + hcys -> lict
MNAO1 HSERD HSERD HSERD HSERD HSERK ASPK THRAD2 THRAD1 THRS AOBUTDCS BETALDDH1 BETALDDH2 SERDHT1 THRD_L GLVD AMTF1 DUPD CHOLD1 DABOT CYSTHS1 CYSTHS2 240ABDC PGLCM	Glycine, Serine and Threonine Metabolism Glycine, Serine and Threonine Metabolism (Glycine, Serine and Threonine M	monoamine oxidase homoserine dehydrogenase (NADH) homoserine dehydrogenase (NADH) sapartate-semialdehyde dehydrogenase homoserine kinase aspartate-semialdehyde dehydrogenase homoserine kinase aspartate kinase L-allo-threonine aldolase threonine aldolase threonine aldolase threonine synthase L-2-amino-3-oxobutanoate decarboxylation (spontaneous) betaine-aldehyde dehydrogenase L-serine dehydratase threonine dehydratase dihydrolepoamide dehydrogenase aminomethyltransferase dihydrolepoamide dehydrogenase diminobutyrate-2-oxoglutarate transaminase cystathionine beta-synthase cystathionine beta-synthase L-2-d-diaminobutyrate plosophosphosphosphosphosphosphosphosphosp	43118 1.4321 1.113 1.113 1.2111 2.7139 2.724 4.125 4.125 4.231 1.218 4.3119 4.3119 1.442 2.11210 1.814 1.1991 2.61.76 4.2122 4.2122 4.1186 5.422	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_04740  KOX_10415  KOX_07315(metL)/KOX_08160/KOX_10410(thrA)  KOX_15770  KOX_15770  KOX_10420  KOX_13815  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_02480(gv/T)  KOX_105400  KOX_105700  KOX_13810/KOX_25150  KOX_105700  KOX_02795  KOX_02155  KOX_10430	doer <>> nh4 + pyr  aact + o2 >> h2o2 + mtg + nh4 hser + nad <>> aspsa + nadh hser + nadp <>> aspsa + nadph aspsa + nadp + pi <>> basp + nadph atp + hser >> adp + phser asp + atp <>> basp + adp athr <<>> acal + gly thr <>> acal + gly phser >> pi + thr 2aobut >> act + co2 bal + nad >> glyb + nadph ser -> nh4 + pyr thr <>> hoth + pyr thr >> old + nadph ser -> nh4 + pyr thr >> old + nadph ser -> nh4 + pyr thr >> old + nad >> glyb + nadph ser -> nh4 + pyr thr >> old + nad >> dlpop + methf + nh4 dlipop + nad >> blal + fadh2 glu + aspsa -> akg + 24dab ser + hcys -> lct ser + h2s -> cys 24dab -> 13dapro + co2 glp <> sp + fb <> sp -> cys 24dab -> 13dapro + co2 glp <> sp + fb <> sp -> co2 glp <> sp +> bg fb -> co2 glp <> sp -> bg fb -> co2 glp <> sp -> bg fb -> co2 glp <> sp -> gb fb -> co2 glp <
MNAO1 HSERD HSERD HSERD HSERK ASPK THRAD2 THRAD1 THRAD1 THRS AOBUTDCs BETALDDH1 BETALDDH2 SERDHT1 THRD_L GLVD AMTF1 DLPD CHOLD1 DABOT CYSTHS1 CYSTHS2 Z4DABDC PGLCM LACDH	Glycine, Serine and threonine Metabolism Glycine, Serine and Threonine Metabol	monoamine oxidase homoserine dehydrogenase (NADH) homoserine dehydrogenase (NADH) sapartate-semialdehyde dehydrogenase homoserine kinase aspartate-semialdehyde dehydrogenase homoserine kinase  L-allo-threonine aldolase threonine aldolase threonine aldolase threonine synthase L-2-amino-3-oxobutanoate decarboxylation (spontaneous) betaine-aldehyde dehydrogenase L-serine dehydratase threonine dehydratase dylpine dehydrogenase aminomethyltransferase dihydrolipoamide dehydrogenase choline dehydrogenase diaminobutytarse-2-oxoglutarate transaminase cystathionine beta-synthase cystathionine beta-synthase L-2-4-d-diaminobutyrate decaphydogenase l-alcate dehydrogenase	43118 14321 1113 11113 12111 27139 2724 4125 4125 4125 4231 1218 43119 43119 1442 21210 1814 11991 26176 42122 41186 55422 11127	KOX_104406)  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_10415  KOX_10415  KOX_10415  KOX_15770  KOX_15770  KOX_16420  KOX_13815  KOX_07465/KCX_24645  KOX_	doer <>> nh4 + pyr  aact + o2 > h2o2 + mtg + nh4 hser + nad <>> aspsa + nadh hser + nadp <>> aspsa + nadph aspsa + nadp + pi <>> basp + nadph atp + hser >> adp + phser asp + atp <>> basp + adp athr <>> acal + gly thr <>> acal + gly phser >> pi + thr  2aobut >> aact + co2 bal + nad >> glyb + nadh bal + nadp >> glyb + nadh bal + nadp >> glyb + nadph ser >> nh4 + pyr thr >> obut + nh4 gly + lipop >> sap + co2 sap + thf >> dlipop + methf + nh4 dlipop + nad >> bilpop + madh choline + fad -> bal + fadh2 glu + aspsa >> akg + 24dab ser + hys -> lict ser + h2s -> cys 24dab >> 13dapro + co2 glu + co2 glu + osp >> sep glu <>> co2 glu + osp >> ser h2s -> co2 glu + osp >> lict ser + h2s -> cys 24dab >> 13dapro + co2 glu + co >> glp glu <> psp glu + osp >> lict ser + h2s -> cys
MNAO1 HSERD HSERD HSERD HSERK ASPK THRAD2 THRAD1 THRAD1 THRS AOBUIDCS BETALDOH1 BETALDOH2 SERDHT1 THRD_L GLVD AMIF1 DLPD CHOLD1 DABOT CVSTHS1 CVSTHS2 Z4DABDC RGLCM HALCOH GASPD	Glycine, Serine and threonine Metabolism Glycine, Serine and Threonine Glycine, Serine and Threonine Glycine, Serine and Threonine Glycine, Serine and	monoamine oxidase homoserine dehydrogenase (NADH) homoserine dehydrogenase (NADH) sapartate-semialdehyde dehydrogenase homoserine kinase aspartate semialdehyde dehydrogenase homoserine kinase aspartate kinase L-allo-threonine aldolase threonine aldolase threonine aldolase threonine synthase L-2-amino-3-oxobutanoate decarboxylation (spontaneous) betaine-aldehyde dehydrogenase betaine-aldehyde dehydrogenase threonine dehydratase threonine dehydratase glycine dehydrogenase aminomethyltransferase dihydrolipoamide dehydrogenase choline dehydrogenase choline dehydrogenase choline dehydrogenase cystathionine beta-synthase cystathionine beta-synthase cystathionine beta-synthase L-2.4-diaminobutyrate decarboxylase phosphoglucomutase L-Icatate dehydrogenase glyceraldehyde-3-phosphate dehydrogenase	43118 14321 1113 12111 27139 2724 4125 4125 4231 1218 1218 43119 43119 1442 21210 1814 11991 26176 42122 42122 41186 5422 111127	KOX_10440(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_04740  KOX_10415  KOX_10415  KOX_15770  KOX_15770  KOX_10420  KOX_13815  KOX_10420  KOX_13815  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_10520  KOX_10520  KOX_10520  KOX_10520  KOX_20299  KOX_02795  KOX_20315  KOX_20315  KOX_20315  KOX_213985(gapA)/KOX_19365/KOX_19540  KOX_17985(gapA)/KOX_19365/KOX_19540	dser <>> nh4 + pyr  aact + o2 > h2o2 + mtg + nh4 hser + nad <>> aspsa + nadh hser + nadp <>> aspsa + nadph aspsa + nadp + pi <>> basp + nadph aspsa + nadp + pi <>> basp + nadph atp + hser >> adp + phser asp + atp <>> basp + adp athr <>> acal + gly thr <>> bash + nadp >> glyb + nadh bal + nadp >> glyb + nadh bal + nadp >> glyb + nadph ser >> nh4 + pyr thr >> obut + nh4 gly + lipop >> sap + co2 sap + thf >> dlipop + methf + nh4 dlipop + nad >> bal + fadh2 glu + aspsa >> akg + 24dab ser + hys >> lict ser + hys >> lict ser + hys >> lict ser + hys <> glp lic + nad >> pyr + nadh glp + nad + pi <>> 13dapro + co2 glp <>> gsp th >< 3dap + nad + pi <>> lict ser + hys >> lict ser + hys <> glp lic + nad >> pyr + nadh glp + nad + pi <>> 13dapro + co2 glp <>> gsp
MNAO1 HSERD HSERD HSERD HSERD HSERK ASPK THRAD2 THRAD1 THRS AOBUTDCS BETALDDH1 BETALDDH2 SERDHT1 LTHBQ_L GLVD AMTF1 DUPD CCHOLD1 DABOT CYSTHS1 CYSTHS2 240ABDC PRACM PRACM GGJPD GGJRD GGJPD GGJRD GGJ	Glycine, Serine and Threonine Metabolism Metab	monoamine oxidase homoserine dehydrogenase (NADH) homoserine dehydrogenase (NADH) sapartate-semialdehyde dehydrogenase homoserine kinase aspartate-semialdehyde dehydrogenase homoserine kinase aspartate kinase L-allo-threonine aldolase threonine aldolase threonine aldolase threonine synthase L-2-amino-3-oxobutanoate decarboylation (spontaneous) betaine-aldehyde dehydrogenase betaine-aldehyde dehydrogenase threonine dehydratase threonine dehydratase dehydrogenase choline dehydrogenase dehydrogenase dehydrogenase dehydrogenase choline dehydrogenase diaminobutytrate-2-oxoglutarate transaminase cystathionine beta-synthase L-24-diaminobutyate decarboylase phosphoglucomutase L-lactate dehydrogenase l-lactate dehydrogenase l-lactate dehydrogenase l-lactate dehydrogenase	43118 1.4321 1.113 1.113 1.2111 2.7139 2.724 4.125 4.125 4.231 1.218 4.3119 4.3119 1.442 2.1210 1.814 4.11.99.1 2.61.76 4.2122 4.2122 4.11.186 5.422 1.1.127 1.2.112	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_04740  KOX_10415  KOX_07315(metL)/KOX_08160/KOX_10410(thrA)  KOX_15770  KOX_15770  KOX_1420  KOX_13815  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_02490(gsvT)  KOX_105400  KOX_13810/KOX_26150  KOX_1055/KOX_26150  KOX_02795  KOX_02795  KOX_02795  KOX_02795  KOX_02195  KOX_17985(gspA)/KOX_19365/KOX_19540	dser <>> nh4 + pyr  aact + c2 >> h2c2 + mtg + nh4 hser + nad <>> aspsa + nadph hser + nadp <>> aspsa + nadph aspsa + nadp + pi <>> basp + nadph atp + hser >> adp + phser asp + atp <>> basp + adp athr <<>> acal + gly thr <>> acal + gly phser -> pi + thr 2aobut >> aact + co2 bal + nad >> glyb + nadph bal + nad >> glyb + nadph ser >> nh4 + pyr thr <>> bout + nh4 gly + lipop >> sap + co2 sap + thf >> dlipop + methf + nh4 dlipop + nad >> bal + fadh2 glu + aspsa >> akg + 24dab ser + hcys -> lict ser + hcys -> lict ser + hcys -> lict ser + hcys -> cys 24dab >> 13dapro + co2 glp + co g6p liac + nad >> pyr + nadh glp + nad >> pyr + nadh glp + nad -> pyr + nadh
MNAO1 HSERD HSERD HSERD HSERK ASPK THRAD2 THRAD1 THRAD1 THRS AOBUIDCS BETALDOH1 BETALDOH2 SERDHT1 THRD_L GLVD AMIF1 DLPD CHOLD1 DABOT CVSTHS1 CVSTHS2 Z4DABDC RGLCM HALCOH GASPD	Glycine, Serine and threonine Metabolism Glycine, Serine and Threonine Glycine, Serine and Threonine Glycine, Serine and Glycine, S	monoamine oxidase homoserine dehydrogenase (NADH) homoserine dehydrogenase (NADH) sapartate-semialdehyde dehydrogenase homoserine kinase aspartate semialdehyde dehydrogenase homoserine kinase  L-allo-threonine aldolase threonine aldolase threonine aldolase threonine aldolase threonine synthase L-2-amino-3-oxobutanoate decarboxylation (spontaneous) betaine-aldehyde dehydrogenase betaine-aldehyde dehydrogenase threonine dehydratase threonine dehydratase dihydrolipoamide dehydrogenase choline dehydrogenase dihydrolipoamide dehydrogenase choline dehydrogenase choline dehydrogenase choline dehydrogenase choline dehydrogenase L-24-diaminobutyrate-2-oxoglutarate transaminase cystathionine beta-synthase cystathionine beta-synthase L-24-diaminobutyrate decarboxylase phosphoglucomutase L-I-alcatate dehydrogenase glycraldehydrogenase glycraldehydrogenase glycraldehydrogenase glycraldehydrogenase	43118 14321 1113 12111 27139 2724 4125 4125 4231 1218 1218 43119 43119 1442 21210 1814 11991 26176 42122 42122 41186 5422 111127	KOX_10440(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_04740  KOX_10415  KOX_10415  KOX_15770  KOX_15770  KOX_10420  KOX_13815  KOX_10420  KOX_13815  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_10520  KOX_10520  KOX_10520  KOX_10520  KOX_20299  KOX_02795  KOX_20315  KOX_20315  KOX_20315  KOX_213985(gapA)/KOX_19365/KOX_19540  KOX_17985(gapA)/KOX_19365/KOX_19540	dser <>> nh4 + pyr  aact + o2 > h2o2 + mtg + nh4 hser + nad <>> aspsa + nadh hser + nadp <>> aspsa + nadph aspsa + nadp + pi <>> basp + nadph aspsa + nadp + pi <>> basp + nadph atp + hser >> adp + phser asp + atp <>> basp + adp athr <>> acal + gly thr <>> bash + nadp >> glyb + nadh bal + nadp >> glyb + nadh bal + nadp >> glyb + nadph ser >> nh4 + pyr thr >> obut + nh4 gly + lipop >> sap + co2 sap + thf >> dlipop + methf + nh4 dlipop + nad >> bal + fadh2 glu + aspsa >> akg + 24dab ser + hys >> lict ser + hys >> lict ser + hys >> lict ser + hys <> glp lic + nad >> pyr + nadh glp + nad + pi <>> 13dapro + co2 glp <>> gsp th >< 3dap + nad + pi <>> lict ser + hys >> lict ser + hys <> glp lic + nad >> pyr + nadh glp + nad + pi <>> 13dapro + co2 glp <>> gsp
MNAO1 HSERD HSERD HSERD HSERK ASPK THRAD2 THRAD1 THRAD1 THRS AOBUTDCs BETALDOH1 BETALDOH1 GLYD CHOLD1 DLPD CHOLD1 DABOT CYSTHS1 CYSTHS2 Z4DABDC PGLCM GA3PD GLK PVK PGK FBP	Glycine, Serine and threonine Metabolism Glycine, Serine and Threonine Metabol	monoamine oxidase homoserine dehydrogenase (NADH) nomoserine dehydrogenase (NADH) nomoserine dehydrogenase (NADH) sapartate-semialdehyde dehydrogenase homoserine kinase  L-allo-threonine aldolase threonine aldolase threonine aldolase threonine aldolase threonine aldolase threonine aldolase threonine synthase L-2-amino-3-oxobutanoate decarboxylation (spontaneous) betaine -aldehyde dehydrogenase betaine -aldehyde dehydrogenase threonine dehydratase glycine dehydrogenase aminomethyltransferase dihydrolipoamide dehydrogenase choline dehydrogenase choline dehydrogenase choline dehydrogenase choline dehydrogenase L-24-diaminobutyrate transaminase cystathionine beta-synthase L-24-diaminobutyrate clacate dehydrogenase glyceriadehyde-3-phosphate dehydrogenase glyceriadehyde-3-phosphate dehydrogenase glyceriadehyde-3-phosphate dehydrogenase glyceriadehyde-3-phosphate dehydrogenase glycokinase pyruvate kinase phosphoglycerate kinase	43118 1.4321 1.113 1.113 1.113 1.2111 2.7139 2.724 4.125 4.125 4.125 4.125 4.231 1.218 1.218 4.3119 4.3119 1.442 2.1210 1.81.4 1.1991 2.61.76 4.21.22 4.11.86 5.422 1.11.27 1.21.12 2.71.2 2.71.40 2.72.3 3.13.11	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07410  KOX_10415  KOX_07315(metL)/KOX_08160/KOX_10410(thrA)  KOX_15770  KOX_15770  KOX_15770  KOX_145770  KOX_145780  KOX_14815  KOX_07465/KOX_24645  KOX_07465/KOX_16445  KOX_07465/KOX	doer <>> nh4 + pyr  aact + o2 >> h2o2 + mtg + nh4 hser + nad <>> aspsa + nadh hser + nadp <>> aspsa + nadph aspsa + nadp + pi <>> basp + nadph aspsa + nadp + pi <>> basp + nadph atp + hser >> adp + phser asp + atp <>> basp + adp ath <>> acal + gly thr <>> acal + gly phser >> pi + thr  2aobut >> aact + co2 bal + nad >> glyb + nadh bal + nad >> glyb + nadph ser >> nh4 + pyr thr >> obut + nh4 gly + lipop >> sap + co2 sap + thf >> dlipop + metthf + nh4 dlipop + nad >> bal + fadh2 glu + aspsa >> akg + 24dab ser + ho2s >> ltt ser + h2s >> cys 24dab >> 13dapro + co2 glp <>> g6p lla + nad >> pyr + nadh glp + nad + pi <>> ltt ser + h2s >> cys 24dab >> 13dapro + co2 glp <>> g6p lla + nad > pyr + nadh glp + nad + pi <<> 13pdg + nadh atp + glc >> adp + g6p adp + pep >> atp + pyr 3gg + gat <>> 13pdg + adp tip >> Slp + sad + pi <>> 13pdg + adp tip >> Slp + sad + pi <>> 13pdg + adp tip >> Slp + sad + pi + pyr 3gg + gat <>> 13pdg + adp tip >> Slp + sad + pi tip >> Slp + pi ti
MNAO1 HSERD HSERD HSERD ASPSAD HSERK ASPK THRAD2 THRAD1 THRS AOBUIDGS BETALDDH1 BETALDDH2 SSERDHT1 THRD_L GLYD AMIF1 DLPD CHOLD1 DABOT CYSTHS1 CYSTHS2 Z4DABDC PGLCM LACDH GAGJPD GLK PPK PGK FBP APPS1	Glycine, Serine and threonine Metabolism Glycine, Serine and Threonine Glycine, Se	monoamine oxidase homoserine dehydrogenase (NADH) homoserine dehydrogenase (NADH) homoserine dehydrogenase homoserine dehydrogenase homoserine dehydrogenase homoserine kinase aspartate-semialdehyde dehydrogenase homoserine kinase aspartate kinase L-allot-threonine aldolase threonine aldolase threonine aldolase threonine synthase L-2-amino-3-oxobutanoate decarboylaton (sportaneous) betaine-aldehyde dehydrogenase betaine-aldehyde dehydrogenase threonine dehydratase glycine dehydrogenase diaminobutyrate-2-oxoglutarate trans-aminase cystathionine beta-synthase cystathionine beta-synthase L-2d-diaminobutyrate decarboylase phosphoglycomutase L-lactate dehydrogenase L-lactate dehydrogenase L-lactate dehydrogenase glyceraldehyde-3-phosphate dehydrogenase glycucokinase physosphoglycareate kinase physosphoglycareate kinase fructose-bisphosphatase acylphosphatase acylphosphatase	43118 14321 1113 12111 27139 2724 4125 4212 4212 4211 1218 43119 1442 21210 1814 11991 26176 42122 42122 41186 5422 11117 2712 2712 27140 2713 333111	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_04740  KOX_10415  KOX_07315(metL)/KOX_08160/KOX_10410(thrA)  KOX_15770  KOX_15770  KOX_1420  KOX_13815  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_02480  KOX_02795  KOX_02795  KOX_02155  KOX_14430  KOX_12795(gapA)/KOX_19365/KOX_19540  KOX_12755(gik)  KOX_17655(gik)  KOX_17655(gik)  KOX_17655(gik)  KOX_02755(gik)	dser <>> nh4 + pyr  aact + c2 >> h2c2 + mtg + nh4 hser + nadc <>> aspsa + nadh hser + nadp <>> aspsa + nadph aspsa + nadp + pi <>> basp + nadph atp + hser >> adp + phser asp + atp <>> basp + adp athr <>> acal + gly thr <>> acal + gly phser >> pi + thr 2aobut >> acal + co2 bal + nad >> glyb + nadph ser >> nh4 + pyr thr >> obut + nh4 gly + lipop >> sap + co2 sap + thf >> dlipop + methf + nh4 dlipop + nad >> blipop + nadh choline + fad >> bal + fadh2 glu + aspsa >> akg + 24dab ser + hc5 >> cys 24dab >> 13dapro + co2 glp <>> g6p llac + nad >> pyr + nadh glp + mad >> pyr + nadh dp >> g6p llac + nad >> pyr + nadh glp + methf + nb4 dlipop + methf + nb4 dlipop + nad >> blipop + nadh choline + fad -> bal + fadh2 glu - aspsa -> akg + 24dab ser + hc5 -> cys 24dab >> 13dapro + co2 glp <>> g6p llac + nad -> pyr + nadh glp + nad + pi <>> 13pdg + nadh atp + glc -> adp + g6p adp -> ppr >> atp -> pyr alpog -> atp e>> 13pdg + adp fop >> fop + pi lapdg -> 3pg + pti
MNAO1 HSERD HSERD HSERD HSERD HSERK ASPK THRAD2 THRAD1 THRS AOBUTDCS BETALDDH1 BETALDDH2 SERDHT1 THRD_L GGLVD AMNTF1 DUPD CCHOLD1 DABOT CYSTHS1 CYSTHS2 240ABDC PGLCM HACDH GGLK PPK PPK PBP PBC FBP GGRPD GGLK FBP FBA	Glycine, Serine and threonine Metabolism Metabol	monoamine oxidase homoserine dehydrogenase (NADH) nomoserine dehydrogenase (NADH) sapartate-semialdehyde dehydrogenase homoserine kinase aspartate-semialdehyde dehydrogenase homoserine kinase aspartate kinase L-allo-threonine aldolase threonine aldolase threonine aldolase threonine synthase L-2-amino-3-oxobutanoate decarboxylation (spontaneous) betaine-aldehyde dehydrogenase betaine-aldehyde dehydrogenase L-serine dehydratase threonine dehydratase dihydrolipoamide dehydrogenase diminobutyrate-2-oxoglutarate transaminase cystathionine beta-synthase L-24-diaminobutyrate-2-oxoglutarate transaminase cystathionine beta-synthase L-24-diaminobutyrate decarboxylase phosphoglucomutase L-lactate dehydrogenase glycerafdehydr-3-phosphata dehydrogenase glycerafdehydr-3-phosphata dehydrogenase glycucokinase pruvate kinase prosphosphatase acylphosphatase acylphosphatase fructose-bisphosphata aldolase	43118 1.4321 1.113 1.113 1.1113 1.2111 2.7139 2.72.4 4.12.5 4.12.5 4.2.31 1.2.18 1.2.18 4.3.1.19 4.3.1.19 1.4.42 2.1.2.10 1.8.1.4 1.1.9.1 2.6.1.76 4.2.1.2 4.2.1.2 4.2.1.2 4.2.1.2 2.7.1.4 2.7.2.3 3.3.3.11 3.6.1.7 4.1.2.13	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_10415  KOX_10415  KOX_10415  KOX_15770  KOX_15770  KOX_1420  KOX_13815  KOX_13815  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_02480  KOX_12570  KOX_11055/KOX_24645  KOX_02480  KOX_02490(gsvT)  KOX_11055/KOX_24645  KOX_02795  KOX_02795  KOX_02795  KOX_02795  KOX_13810  KOX_12795  KOX_14430  KOX_12795  KOX_1795(gspA)/KOX_19365/KOX_19540  KOX_12750/KOX_23870  KOX_1795S(gspA)/KOX_19365/KOX_19540  KOX_1675S(gsl)	doer <>> nh4 + pyr  aact + c2 >> h2c2 + mtg + nh4 heer + nad <>> aspsa + nadph hser + nadp <>> aspsa + nadph aspsa + nadp + pi <>> basp + nadph atp + hser >> adp + phser asp + atp <>> basp + adp athr <>> acal + gly thr <>> acal + gly phser >> pi + thr 2aobut >> aact + co2 bal + nad >> glyb + nadph bal + nadp >> glyb + nadph ser >> nh4 + pyr thr <>> bout + nh4 gly + lipop >> sap + co2 sap + thf >> dlipop + methf + nh4 dlipop + nad >> blipop + madh choline + fad >> bal + fadh2 glu + aspsa >> akg + 24dab ser + h0s >> lct ser + h2s >> cys 24dab >> 13dapro + co2 glp + >> g6p liac + nad >> pyr + nadh glp + nad >> plop + nadh dlipop + pad >> lipop + methf + nh4 dlipop + nad >> lipop + nadh choline + fad >> bal + fadh2 glu + aspsa >> akg + 24dab ser + h0s -> lct ser + h2s > cys 24dab >> 13dapro + co2 glp + >> g6p liac + nad >> pyr + nadh glp + nad + pi <>> 13pdg + nadh glp + pgc >> adp + psp +> adp + pfc  >> adp + pfc  >> adp + psp +> adp + pfc  >> adp + pf
MNAO1 HSERD HSERD HSERD ASPSAD HSERK ASPK THRAD2 THRAD1 THRS AOBUIDGS BETALDDH1 BETALDDH2 SSERDHT1 THRD_L GLYD AMIF1 DLPD CHOLD1 DABOT CYSTHS1 CYSTHS2 Z4DABDC PGLCM LACDH GAGJPD GLK PPK PGK FBP APPS1	Glycine, Serine and threonine Metabolism Glycine, Serine and Threonine Metabol	monoamine oxidase homoserine dehydrogenase (NADH) nomoserine dehydrogenase (NADH) sapartate-semialdehyde dehydrogenase homoserine kinase aspartate-semialdehyde dehydrogenase homoserine kinase  L-allo-threonine aldolase threonine aldolase threonine aldolase threonine aldolase threonine synthase L-2-amino-3-oxobutanoate decarboxylation (spontaneous) betaine-aldehyde dehydrogenase betaine-aldehyde dehydrogenase L-serine dehydratase glycine dehydrogenase aminomethyltransferase dihydrolipoamide dehydrogenase choline dehydrogenase dihydrolipoamide dehydrogenase choline dehydrogenase cystathionine beta-synthase cystathionine beta-synthase cystathionine beta-synthase cystathionine beta-synthase L-2-d-daminobutyrate L-2-d-daminobutyrate L-2-d-daminobutyrate devarboxylase glyceraldehyde-3-phosphate dehydrogenase glyceraldehyde-3-phosphate dehydrogenase phosphoglycerate kinase phosphoglycerate kinase phosphoglycerate kinase phosphoglycerate kinase phosphoglycerate kinase fructose-bisphosphatase enolase	43118 14321 1113 12111 27139 2724 4125 4212 4212 4211 1218 43119 1442 21210 1814 11991 26176 42122 42122 41186 5422 11117 2712 2712 27140 2713 333111	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_10415  KOX_07315(metL)/KOX_08160/KOX_10410(thrA)  KOX_15770  KOX_15770  KOX_145770  KOX_145770  KOX_145780  KOX_14815  KOX_07465/KOX_24645  KOX_07465/KOX_16450  KOX_07465/KOX_16450  KOX_07465/KOX_16450  KOX_1785/KOX_16450  KOX_1785/KOX_16450  KOX_17985(gapA)/KOX_19365/KOX_19540  KOX_17985(gapA)/KOX_19365/KOX_19540  KOX_17985(gapA)/KOX_19365/KOX_19540  KOX_17985(gapA)/KOX_19365/KOX_19540  KOX_17985(gapA)/KOX_19365/KOX_19540  KOX_17985(gapA)/KOX_19365/KOX_19540  KOX_161595  KOX_16159	deer <> nh4 + pyr  aact + o2 > h2o2 + mtg + nh4 hser + nad <> aspsa + nadh hser + nadp <> aspsa + nadph aspsa + nadp + pi <> basp + nadph aspsa + nadp + pi <> basp + nadph atp + hser >> adp + phser asp + atp <> basp + adp athr <> acal + gly thr <> acal + gly phser >> pi + thr  2aobut >> aact + co2 bal + nad >> glyb + nadh bal + nadp >> glyb + nadph ser >> nh4 + pyr thr >> obut + nh4 gly + lipop >> sap + co2 sap + thf >> dlipop + methtf + nh4 dlipop + nad >> bilpop + nadh choline + fad >> bal + fadh2 glu + aspsa >> akg + 24dab ser + hys >> ltt ser + h2s >> cys 24dab >> l3dapro + co2 glp <>> g6p like + nad >> pyr + nadh glp + nad + pi <>> 13pdg + nadh atp + gic >> adp + g6p adp + pap >> atp + pyr 3pg + st + os 13pdg + adp fifty >> Sgp + pi 13pdg >> Sgp + pi
MNAO1 HSERD HSERD HSERD HSERK ASPK THRAD2 THRAD1 THRAD1 THRS AOBUTDCs BETALDDH1 BETALDDH2 SERDHT1 THRD,L GLYD CHOLD1 DJPD CHOLD1 DJPD CHOLD1 DJPD CHOLD1 DABOT CYSTHS1 CYSTHS2 Z4DABDC PGLCM GA3PD GLK PCK PGK PGR PPR PPR PPR PPR PPR PPR PPR PPR PPR	Glycine, Serine and threonine Metabolism Glycine, Serine and Threonine Glyci	monoamine oxidase homoserine dehydrogenase (NADH) homoserine dehydrogenase (NADH) sapartate-semialdehyde dehydrogenase homoserine kinase aspartate-semialdehyde dehydrogenase homoserine kinase aspartate kinase L-allo-threonine aldolase threonine aldolase threonine aldolase threonine synthase L-2-amino-3-oxobutanoate decarboylation (spontaneous) betaine-aldehyde dehydrogenase betaine-aldehyde dehydrogenase threonine dehydratase glycine dehydrogenase dehydrogenase choline dehydrogenase diaminobutyrate-2-oxoglutarate transaminase cystathionine beta-synthase cystathionine beta-synthase L-24-diaminobutyrate decarboylase phosphoglucomitase L-lacitate dehydrogenase glyceraldehyde-3-phosphate dehydrogenase flactionine beta-synthase cystathionine beta-synthase cystathionine beta-synthase rystathionine beta-synthase transaminase cystathionine beta-synthase flactione-phosphate kinase fructose-bisphosphatase fructose-bisphosphatase fructose-bisphosphatase nolase troose-phosphate isomerase	43118 14321 1113 11113 12111 27.139 27.24 4.125 4.125 4.231 1218 12218 4.3119 1.442 2.1210 1.81.4 1.1991 1.442 2.1210 4.1186 5.422 1.1127 1.2112 2.712 2.712 2.712 2.712 3.33311 4.2111 5.3311	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_10415  KOX_10415  KOX_10415  KOX_10415  KOX_15770  KOX_15770  KOX_15770  KOX_1420  KOX_13815  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_2465  KOX_1055/KOX_2465  KOX_11055/KOX_2465  KOX_11055/KOX_2465  KOX_1295  KOX_12975  KOX_12975	dser <>> nh4 + pyr  aact + c2 >> h2c2 + mtg + nh4 hser + nadc <>> aspsa + nadh hser + nadp <>> aspsa + nadph aspsa + nadp + pi <>> basp + nadph atp + hser >> adp + phser asp + atp <>> basp + adp athr <>> acal + gly thr <>> acal + gly phser >> pi + thr 2aobut >> aact + co2 ball + nad >> glyb + nadph ser >> nh4 + pyr thr >> obut + nh4 gly + lipop >> sap + co2 sap + thf >> dlipop + methf + nh4 dlipop + nad >> lipop + nadh choline + fad >> bal + fadh2 glu + aspsa >> akg + 24dab ser + hoys >> llct ser + h2s >> cys 24dab >> 13dapro + co2 glp <>> g6p liae + nad >> pyr + nadh atp + gic >> adp + g6p adp >= pp >> atp + pic >> 13pdg + adp figo >= adp >= pp >= atp + pic glog >= adp >= pp >= pp figo >= pp >= dp == pic figo >= cod >= pp figo >= pp >= dp == pic figo >= cod >= pp figo >= pp figo >= pp >= dp == pp figo >= cod >= pp figo >= pp
MNAO1 HSERD HSERD HSERD ASPSAD HSERK ASPK THRAD2 THRAD1 THRS AOBUIDGS BETALDDH1 BETALDDH2 SERDHT1 THRD,L GLYD AMIF1 DUPD CHOLD1 DABOT CYSTHS1 CYSTHS2 Z4DABDC PGLCM GAGJPD GGLK PPK PGK FBR PRAPPS1 FBA ENO TIT	Glycine, Serine and threonine Metabolism Glycine, Serine and Threonine Metabolism (Glycine, Serine and Threonine Metabolism (Glycine, Serine and Threonine Metabolism) (Glycine, Serine and Threonine	monoamine oxidase homoserine dehydrogenase (NADH) homoserine dehydrogenase (NADH) sapartate-semialdehyde dehydrogenase homoserine kinase aspartate-semialdehyde dehydrogenase homoserine kinase aspartate kinase L-allo-threonine aldolase threonine aldolase threonine aldolase threonine synthase L-2-amino-3-oxobutanoate decarboxylation (spontaneous) betaine-aldehyde dehydrogenase betaine-aldehyde dehydrogenase threonine dehydratase dhydrogenase threonine dehydratase dhydrogenase choline dehydrogenase dhydrogenase choline dehydrogenase diaminobutyrate-2-oxoglutarate transaminase cystathionine beta-synthase L-24-diaminobutyrate decarboxylase phosphoglucomutase L-lactate dehydrogenase L-lactate dehydrogenase glycerafdehyd-3-phosphate dehydrogenase pruvate kinase prosphosphogleverate kinase fructose-bisphosphatase arylphosphatase arylphosphatase arylphosphatase arolphosphata isomerase glucose-6-phosphate isomerase	43118 14321 1113 11113 12111 27.139 27.24 4.125 4.125 4.231 1218 12218 4.3119 1.442 2.1210 1.81.4 1.1991 1.442 2.1210 4.1186 5.422 1.1127 1.2112 2.712 2.712 2.712 2.712 3.33311 4.2111 5.3311	KOX_06466)  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_04740  KOX_10415  KOX_07315(metL)/KOX_08160/KOX_10410(thrA)  KOX_15770  KOX_15770  KOX_140420  KOX_13815  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_02490(gv/T)  KOX_11055/KOX_24645  KOX_13810/KOX_25150  KOX_13810/KOX_16150  KOX_13810/KOX_16150  KOX_13810/KOX_16150  KOX_13810/KOX_16150  KOX_13810/KOX_16150  KOX_13810/KOX_19365/KOX_19365/KOX_19540  KOX_17955  KOX_17955(g)  KOX_17956(g)  K	doer <>> nh4 + pyr  aact + c2 >> h2c2 + mtg + nh4 heer + nad <>> aspsa + nadph heer + nadp <>> aspsa + nadph aspsa + nadp + pi <>> basp + nadph atp + hser >> adp + phser asp + atp <>> basp + adp athr <<>> acal + gly thr <>> bacl + gly thr <>> bacl + gly phser >> pi + thr 2aobut >> act + co2 ball + nad >> glyb + nadph ball + nadp >> glyb + nadph ser >> nh4 + pyr thr >> obut + nh4 gly + lipop >> sap + co2 sap + thf >> dlipop + metthf + nh4 dlipop + nad >> lipop + nadh choline + fad >> bal + fadh2 glu + aspsa >> alkg + 24dab ser + hogs >> lct ser + h2s >> cys 24dab >> 13dapro + co2 glp <>> glp + co glp liac + nad >> pyr + nadh glp + nad >> pyr + nadh glp + nad >> pyr + nadh glp + nad >> pyr + nadh choline + fad >> bal + fadh2 glu + aspsa >> akg + 24dab ser + hgs -> lct ser + h2s -> cys 24dab >> 13dapro + co2 glp <>> glp cos glp liac + nad >> pyr + nadh glp + nad + pi <>> 13pdg + nadh atp + glc >> adp + gls adp + pep >> atp + pyr 3pg + pap + ppr spg + pap + ppr sp
MNAO1 HSERD HSERD HSERD HSERD ASPSAD HSERK ASPK THRAD2 THRAD1 THRS AOBUTICS BETALDDH1 BETALDDH2 SERDHT1 THRD_L GLVD AAMTE1 DUPD CHOLD1 DABOT CYSTHS1 CYSTHS2 Z4DABDC PGLCM HACDH GGJRP GGJRP GGJR FBP PGK FBP FBR END TIT FBA	Glycine, Serine and Threonine Metabolism Glycine, Serine and Threonine Metabolism (Glycine, Serine and Threonine Metabolism (Gycine, Serine and Threonine Metabo	monoamine oxidase homoserine dehydrogenase (NADH) homoserine dehydrogenase (NADH) sapartate-semialdehyde dehydrogenase homoserine kinase aspartate-semialdehyde dehydrogenase homoserine kinase aspartate kinase L-allo-threonine aldolase threonine aldolase threonine aldolase threonine synthase L-2-amino-3-oxobutanoate decarboxylation (spontaneous) betaine-aldehyde dehydrogenase betaine-aldehyde dehydrogenase threonine dehydratase dehydrogenase dehydrogenase dehydrogenase dehydrogenase dehydrogenase dehydrogenase choline dehydrogenase diaminobutyrate-2-oxoglutarate transaminase cystathionine beta-synthase L-24-diaminobutyrate decarboxylase phosphoglycenate kinase pruvate dehydrogenase diydrofipogenase l-lactate dehydrogenase pytuvate kinase pyruvate kinase pyruvate kinase pruvate kinase fructose-bisphosphata aldolase enolase glucose-5-phosphate isomerase glucose-5-phosphate isomerase phosphoglycerate mutase provate dehydrogenase glucose-5-phosphate isomerase	43118 1.4321 1.113 1.113 1.113 1.2111 2.7139 2.724 4.125 4.125 4.231 1.218 1.218 4.3119 4.3111 5.3119 5.3119	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_10415  KOX_10415  KOX_10415  KOX_15770  KOX_15770  KOX_15770  KOX_15770  KOX_15770  KOX_15770  KOX_16420  KOX_16480  KOX_16480  KOX_16480  KOX_16480  KOX_16480  KOX_10480  KOX_10480  KOX_10480  KOX_10480  KOX_10480  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_26150  KOX_0795  KOX	doer <>> nh4 + pyr  aact + o2 >> h2o2 + mtg + nh4 hser + nad <>> aspsa + nadh hser + nadp <>> aspsa + nadph aspsa + nadp + pi <>> basp + nadph atp + hser >> adp + phser asp + atp <>> basp + adp athr <>> acal + gly thr <>> acal + gly phser >> pi + thr  2aobut >> aact + co2 bal + nad >> glyb + nadh bal + nadp >> glyb + nadph ser >> nh4 + pyr thr >> obut + nh4 gly + lipop >> sap + co2 sap + thf >> dlipop + methf + nh4 dlipop + nad >> blipop + methf + nh4 dlipop + nad >> blipop + nadh choline + fad >> bal + fadh2 glu + aspsa >> akg + 24dab ser + hcys >> lict ser + h2s >> cys 24dab >> 13dapro + co2 glp <>> g6p lisc + nad >> pyr + nadh glp + pro >> sap + pyr + nadh glp + pro >> sap + pyr + nadh glp + pro >> sap + pyr + nadh glp + pro >> sap + pyr + nadh glp + pro >> gp glp +>> g6p lisc + nad >> pyr + nadh glp + pro >> gp + pyr + nadh glp + pro >> gp + pyr + nadh glp + pro >> gp + pyr + nadh glp + pro >> gp + pyr + nadh glp + pro >> gp + pyr + nadh glp + pro >> gp + pyr + nadh glp + pro >> gp + pyr + nadh glp + pro >> gp + pyr + nadh glp + pro >> gp + pyr + gp + g
MNAO1 HSERD HSERD HSERD HSERK ASPK THRAD2 THRAD1 THRS AOBUTDCS BETALDDH1 BETALDDH2 SERDHT1 THRD,L GLYD AMTF1 DLPD CHOLD1 DABOT CYSTHS1 CYSTHS1 CYSTHS2 240ABDC PGLCM GA3PD GLK PPK PPK PPK PPK PPK PRP PRAPS1 FBA ENO TPI PGM	Glycine, Serine and threonine Metabolism Glycine, Serine and Threonine Metabol	monoamine oxidase homoserine dehydrogenase (NADH) nomoserine dehydrogenase (NADH) sapartate-semialdehyde dehydrogenase homoserine kinase aspartate-semialdehyde dehydrogenase homoserine kinase  L-allo-threonine aldolase threonine aldolase threonine aldolase threonine synthase L-2-amino-3-oxobutanoate decarboxylation (spontaneous) betaine-aldehyde dehydrogenase betaine-aldehyde dehydrogenase L-serine dehydratase glycine dehydrogenase aminomethyltransferase dihydrolpoamide dehydrogenase choline dehydrogenase diminobutytate-2-oxoglutarate transaminase cystathionine beta-synthase cystathionine beta-synthase cystathionine beta-synthase cystathionine beta-synthase phosphoglucomutase L-lactate dehydrogenase glyceraldehyde-3-phosphate dehydrogenase glyceralderhyde-3-phosphate dehydrogenase glycoshiphatase phosphoglycerate kinase fructose-bisphosphatase acyghosphatase ricutose-bisphosphatase fructose-bisphosphatase enolase triose-phosphate isomerase glyucose-6-phosphate isomerase phosphoglycerate mutase pyruvate dehydrogenase se 1 component	43118 14321 1113 1113 11113 12111 27.139 27.24 4.125 4.125 4.125 4.1218 1218 1218 1218 4.3119 1442 21210 1814 11.991 261.76 4.2122 4.1186 5.422 11.127 12.112 27.124 27.124 27.124 27.124 27.124 27.125 31.311 33.61.7 4.1213 4.2111 5.3119 5.421	KOX_06466)  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_04740  KOX_10415  KOX_07315(metL)/KOX_08160/KOX_10410(thrA)  KOX_15770  KOX_15770  KOX_140420  KOX_13815  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_02490(gv/T)  KOX_11055/KOX_24645  KOX_13810/KOX_25150  KOX_13810/KOX_16150  KOX_13810/KOX_16150  KOX_13810/KOX_16150  KOX_13810/KOX_16150  KOX_13810/KOX_16150  KOX_13810/KOX_19365/KOX_19365/KOX_19540  KOX_17955  KOX_17955(g)  KOX_17956(g)  K	doer <>> nh4 + pyr  aact + c2 >> h2c2 + mtg + nh4 heer + nad <>> aspsa + nadph heer + nadp <>> aspsa + nadph aspsa + nadp + pi <>> basp + nadph atp + hser >> adp + phser asp + atp <>> basp + adp athr <<>> acal + gly thr <>> bacl + gly thr <>> bacl + gly phser >> pi + thr 2aobut >> act + co2 ball + nad >> glyb + nadph ball + nadp >> glyb + nadph ser >> nh4 + pyr thr >> obut + nh4 gly + lipop >> sap + co2 sap + thf >> dlipop + metthf + nh4 dlipop + nad >> lipop + nadh choline + fad >> bal + fadh2 glu + aspsa >> alkg + 24dab ser + hogs >> lct ser + h2s >> cys 24dab >> 13dapro + co2 glp <>> glp + co glp liac + nad >> pyr + nadh glp + nad >> pyr + nadh glp + nad >> pyr + nadh glp + nad >> pyr + nadh choline + fad >> bal + fadh2 glu + aspsa >> akg + 24dab ser + hgs -> lct ser + h2s -> cys 24dab >> 13dapro + co2 glp <>> glp cos glp liac + nad >> pyr + nadh glp + nad + pi <>> 13pdg + nadh atp + glc >> adp + gls adp + pep >> atp + pyr 3pg + pap + ppr spg + pap + ppr sp
MNAO1 HSERD HSERD HSERD HSERK ASPK THRAD2 THRAD1 THRS AOBUTDCS BETALDDH1 BETALDDH2 SERDHT1 THRD,L GLYD AMTF1 DLPD CHOLD1 DABOT CYSTHS1 CYSTHS1 CYSTHS2 240ABDC PGLCM GA3PD GLK PPK PPK PPK PPK PPK PRP PRAPS1 FBA ENO TPI PGM	Glycine, Serine and threonine Metabolism Glycine, Serine and Threonine Metabol	monoamine oxidase homoserine dehydrogenase (NADH) nomoserine dehydrogenase (NADH) sapartate-semialdehyde dehydrogenase homoserine kinase aspartate-semialdehyde dehydrogenase homoserine kinase  L-allo-threonine aldolase threonine aldolase threonine aldolase threonine synthase L-2-amino-3-oxobutanoate decarboxylation (spontaneous) betaine-aldehyde dehydrogenase betaine-aldehyde dehydrogenase L-serine dehydratase glycine dehydrogenase aminomethyltransferase dihydrolipoamide dehydrogenase choline dehydrogenase diminobutyrate-2-oxoglutarate transaminase cystathionine beta-synthase cystathionine beta-synthase cystathionine beta-synthase cystathionine beta-synthase l-2-4-diaminobutyrate decarboxylase phosphoglucomutase L-lactate dehydrogenase glyceraldehyde-3-phosphate dehydrogenase phosphoglycerate kinase fructose-bisphosphatase acyghosphatase ricutose-bisphosphatae lomerase glyucose-6-phosphate isomerase phosphoglycerate mutase prowate dehydrogenase E1 component	43118 1.4321 1.113 1.113 1.113 1.1211 1.27139 2.7724 4.125 4.125 4.125 4.231 1.128 1.218 4.31.19 4.31.31 4.31.31 4.31.31 4.31.31 5.31.31 5.31.31 5.31.31 5.31.31 5.31.31 5.31.31 5.31.31 5.31.31	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_10415  KOX_10415  KOX_10415  KOX_15770  KOX_15770  KOX_15770  KOX_15770  KOX_15770  KOX_15770  KOX_16420  KOX_16480  KOX_16480  KOX_16480  KOX_16480  KOX_16480  KOX_10480  KOX_10480  KOX_10480  KOX_10480  KOX_10480  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_26150  KOX_0795  KOX	doer <>> nh4 + pyr  aact + o2 >> h2o2 + mtg + nh4 hser + nad <>> aspsa + nadh hser + nadp <>> aspsa + nadph aspsa + nadp + pi <>> basp + nadph atp + hser >> adp + phser asp + atp <>> basp + adp athr <>> acal + gly thr <>> acal + gly phser >> pi + thr  2aobut >> aact + co2 bal + nad >> glyb + nadh bal + nadp >> glyb + nadph ser >> nh4 + pyr thr >> obut + nh4 gly + lipop >> sap + co2 sap + thf >> dlipop + methf + nh4 dlipop + nad >> blipop + methf + nh4 dlipop + nad >> blipop + nadh choline + fad >> bal + fadh2 glu + aspsa >> akg + 24dab ser + hcys >> lict ser + h2s >> cys 24dab >> 13dapro + co2 glp <>> g6p lisc + nad >> pyr + nadh glp + pro >> sap + pyr + nadh glp + pro >> sap + pyr + nadh glp + pro >> sap + pyr + nadh glp + pro >> sap + pyr + nadh glp + pro >> gp glp +>> g6p lisc + nad >> pyr + nadh glp + pro >> gp + pyr + nadh glp + pro >> gp + pyr + nadh glp + pro >> gp + pyr + nadh glp + pro >> gp + pyr + nadh glp + pro >> gp + pyr + nadh glp + pro >> gp + pyr + nadh glp + pro >> gp + pyr + nadh glp + pro >> gp + pyr + nadh glp + pro >> gp + pyr + gp + g
MNAO1 HSERD HSERD HSERD ASPSAD HSERK ASPK THRAD2 THRAD1 THRS AOBUIDGS BETALDDH1 BETALDDH2 SSERDHT1 THRD,L GLYD AMIF1 DUPD CHOLD1 DABOT CYSTHS1 CYSTHS2 24DABDC PGLKM LACDH GAGPID GLK PPK PGK FBP PRI FBA ENO TIP PGI PGI PPGM PPOH1	Glycine, Serine and threonine Metabolism Metabolism Glycolysis Gluconeogenesis Glycolysis Gluconeogene	monoamine oxidase homoserine dehydrogenase (NADH) homoserine dehydrogenase (NADH) homoserine dehydrogenase homoserine dehydrogenase homoserine dehydrogenase homoserine kinase aspartate-semialdehyde dehydrogenase homoserine kinase aspartate kinase L-allot-threonine aldolase threonine aldolase threonine aldolase threonine synthase L-2-amino-3-oxobutanoate decarboylation (spontaneous) betaine aldehyde dehydrogenase betaine aldehyde dehydrogenase testime aldehyde dehydrogenase charine dehydratase glycine dehydrogenase diminobutyrate-2-oxoglutarate transaminase cystathionine beta-synthase cystathionine beta-synthase cystathionine beta-synthase L-2-d-diaminobutyrate decarboxylase phosphoglucomutase L-actate dehydrogenase glycotine dehydrogenase phosphoglycerate kinase phosphoglycerate kinase fructose-bisphosphates fructose-bisphosphates irfoxes-phosphate isomerase plucosin-sphosphate isomerase phosphoglycerate mutaze pyruvate dehydrogenase E1 component pyruvate dehydrogenase E2 component glydrogenase E2 component glydrogenase E2 component glydrogenase E2 component glydrogenase E2 component	43118 14321 1113 11113 12111 27139 2724 4125 4212 4212 4212 43119 1442 21210 1814 11991 26176 42122 42122 41186 5422 11127 12112 2712 2712 2714 2712 2712	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_04740  KOX_10415  KOX_10415  KOX_15770  KOX_15770  KOX_15770  KOX_15770  KOX_10420  KOX_13815  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_2465  KOX_10450  KOX_11055/KOX_26150  KOX_11055/KOX_26150  KOX_2795  KOX_13810/KOX_26150  KOX_2795  KOX_12810/KOX_19365/KOX_19540  KOX_27575(KOX_19540)  KOX_17858(gapA)/KOX_19365/KOX_19540  KOX_27575(KOX_25480)  KOX_07575/KOX_25480  KOX_07575/KOX_25480  KOX_06845(pa)/KOX_06125/KOX_06980/  KOX_06845(pa)/KOX_17440(pa)  KOX_06830(po)/KOX_2615/KOX_19325  KOX_011045 (aceel/KOX_20465)  KOX_11045 (aceel/KOX_20465)  KOX_11050(aceel/KOX_20465)  KOX_11050(aceel/KOX_20465)  KOX_11050(aceel/KOX_20460)	deer <>> nh4 + pyr  aact + c2 >> h2c2 + mtg + nh4 heer + nadc <>> aspsa + nadh heer + nadp <>> aspsa + nadph aspsa + nadp + pi <>> basp + nadph atp + hser >> adp + phser asp + atp <>> basp + adp athr <>> acal + gly thr <>> acal + gly phser >> pi + thr 2aobut >> acal + co2 ball + nad >> glyb + nadph ser >> nh4 + pyr thr >> obut + nh4 gly + lipop >> sap + co2 sap + thf >> dlipop + methf + nh4 dlipop + nad >> lipop + nadh choline + fad >> bal + fadh2 glu + aspsa >> akg + 24dab ser + hoys >> llet ser + h2s >> cys 24dab >> 13dapro + co2 glp <>> g6p liae + nad >> pyr + nadh atp + gic >> adp + g6p adp + pse >> atp + pyr + lipo >> adlipo + co2 coa + adlipo >> accoa + dlipo
MNAO1 HSERD HSERD HSERD HSERD ASPSAD HSERK ASPK THRAD2 THRAD1 THRS AOBUIDGS BETALDDH1 BETALDDH2 SERDHT1 THRD_L GGLVD AAMTF1 DUPD CCHOLD1 DABOT CYSTHS1 CYSTHS2 240ABDC PRACM P	Glycine, Serine and Threonine Metabolism Glycine, Serine and Threonine Metabolism (Glycine, Serine and Threonine Metabolism (Glycine, Serine and Threonine Metabolism) (Glycine, Serine and Threonine	monoamine oxidase homoserine dehydrogenase (NADH) nomoserine dehydrogenase (NADH) sapartate-semialdehyde dehydrogenase homoserine kinase aspartate-semialdehyde dehydrogenase homoserine kinase aspartate kinase L-allo-threonine aldolase threonine aldolase threonine aldolase threonine synthase L-2-amino-3-oxobutanoate decarboylation (spontaneous) betaine-aldehyde dehydrogenase betaine-aldehyde dehydrogenase chesine dehydratase threonine dehydratase dehydrogenase dehydrogenase dehydrogenase choline dehydrogenase dehydrogenase dehydrogenase dehydrogenase choline dehydrogenase diaminobutyrate-2-oxoglutarate transaminase cystathionine beta-synthase cystathionine beta-synthase L-24-diaminobutyrate-2-oxoglutarate transaminase cystathionine beta-synthase L-24-diaminobutyrate decarboylase phosphoglucomutase L-lactate dehydrogenase glycorafdehydra-3-phosphate dehydrogenase glycorafdehydra-3-phosphate dehydrogenase glycorafer kinase fructose-bisphosphatase anolpse pruvate dehydrogenase glucose-6-phosphate isomerase glucose-6-phosphate-isomerase glucose-	43118 1.4321 1.113 1.113 1.113 1.1211 2.7139 2.724 4.125 4.125 4.125 4.231 1.128 1.218 4.3119 1.442 2.1210 1.814 1.1991 2.61.76 4.2122 4.2122 4.1127 1.1217 1.2112 2.71.40 2.72.73 3.33111 3.61.7 4.1213 4.2111 5.311 5.319 5.421 1.241 2.3112	KOX_06466  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_04740  KOX_10415  KOX_10415  KOX_10415  KOX_10415  KOX_15770  KOX_15770  KOX_14020  KOX_14040  KOX_1	doer <>> nh4 + pyr  aact + c2 >> h2c2 + mtg + nh4 heer + nad <>> aspsa + nadph hser + nadp <>> aspsa + nadph aspsa + nadp + pi <>> basp + nadph atp + hser >> adp + phser asp + atp <>> basp + adp athr <>> acal + gly thr <>> acal + gly phser >> pi + thr 2aobut >> acca + co2 bal + nad >> glyb + nadph bal + nadp >> glyb + nadph ser >> nh4 + pyr thr >> obut + nh4 gly + lipop >> sap + co2 sap + thf >> dlipop + methf + nh4 dlipop + nad >> lipop + nadh choline + fad >> bal + fadh2 glu + aspsa >> akg + 24dab ser + h0s >> lct ser + h2s >> cys 24dab >> 13dapro + co2 glp >> 3gp + co 3gp + pi figh >> 3gp + pi + radh gly + lipop >> adp + psp + adph gly + lipop >> lct ser + h2s >> cys 24dab >> 13dapro + co2 glp >> 3gp + co 3gp + pi figh >> 3gp + pi + radh gly + lipop >> adp + psp >> adp >> ad
MNAO1 HSERD HSERD HSERD ASPSAD HSERK ASPK THRAD2 THRAD1 THRS AOBUIDGS BETALDDH1 BETALDDH2 SSERDHT1 THRD,L GLYD AMIF1 DUPD CHOLD1 DABOT CYSTHS1 CYSTHS2 24DABDC PGLKM LACDH GAGPID GLK PPK PGK FBP PRI FBA ENO TIP PGI PGI PPGM PPOH1	Glycine, Serine and threonine Metabolism Metabolism Glycolysis Gluconeogenesis Glycolysis Gluconeogene	monoamine oxidase homoserine dehydrogenase (NADH) nomoserine dehydrogenase (NADH) sapartate-semialdehyde dehydrogenase homoserine kinase aspartate-semialdehyde dehydrogenase homoserine kinase aspartate kinase L-allo-threonine aldolase threonine aldolase threonine aldolase threonine synthase L-2-amino-3-oxobutanoate decarboylation (spontaneous) betaine-aldehyde dehydrogenase betaine-aldehyde dehydrogenase chesine dehydratase threonine dehydratase dehydrogenase dehydrogenase dehydrogenase choline dehydrogenase dehydrogenase dehydrogenase dehydrogenase choline dehydrogenase diaminobutyrate-2-oxoglutarate transaminase cystathionine beta-synthase cystathionine beta-synthase L-24-diaminobutyrate-2-oxoglutarate transaminase cystathionine beta-synthase L-24-diaminobutyrate decarboylase phosphoglucomutase L-lactate dehydrogenase glycorafdehydra-3-phosphate dehydrogenase glycorafdehydra-3-phosphate dehydrogenase glycorafer kinase fructose-bisphosphatase anolpse pruvate dehydrogenase glucose-6-phosphate isomerase glucose-6-phosphate-isomerase glucose-	43118 14321 1113 11113 12111 27139 2724 4125 4212 4212 4212 43119 1442 21210 1814 11991 26176 42122 42122 41186 5422 11127 12112 2712 2712 2714 2712 2712	KOX_06460  KOX_19410(tynA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_07315(metL)/KOX_10410(thrA)  KOX_04740  KOX_10415  KOX_10415  KOX_15770  KOX_15770  KOX_15770  KOX_15770  KOX_10420  KOX_13815  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_24645  KOX_07465/KOX_2465  KOX_10450  KOX_11055/KOX_26150  KOX_11055/KOX_26150  KOX_2795  KOX_13810/KOX_26150  KOX_2795  KOX_12810/KOX_19365/KOX_19540  KOX_27575(KOX_19540)  KOX_17858(gapA)/KOX_19365/KOX_19540  KOX_27575(KOX_25480)  KOX_07575/KOX_25480  KOX_07575/KOX_25480  KOX_06845(pa)/KOX_06125/KOX_06980/  KOX_06845(pa)/KOX_17440(pa)  KOX_06830(po)/KOX_2615/KOX_19325  KOX_011045 (aceel/KOX_20465)  KOX_11045 (aceel/KOX_20465)  KOX_11050(aceel/KOX_20465)  KOX_11050(aceel/KOX_20465)  KOX_11050(aceel/KOX_20460)	deer <>> nh4 + pyr  aact + c2 >> h2c2 + mtg + nh4 heer + nadc <>> aspsa + nadh heer + nadp <>> aspsa + nadph aspsa + nadp + pi <>> basp + nadph atp + hser >> adp + phser asp + atp <>> basp + adp athr <>> acal + gly thr <>> acal + gly phser >> pi + thr 2aobut >> acal + co2 ball + nad >> glyb + nadph ser >> nh4 + pyr thr >> obut + nh4 gly + lipop >> sap + co2 sap + thf >> dlipop + methf + nh4 dlipop + nad >> lipop + nadh choline + fad >> bal + fadh2 glu + aspsa >> akg + 24dab ser + hoys >> llet ser + h2s >> cys 24dab >> 13dapro + co2 glp <>> g6p liae + nad >> pyr + nadh atp + gic >> adp + g6p adp + pse >> atp + pyr + lipo >> adlipo + co2 coa + adlipo >> accoa + dlipo

GLC1P	Glycolysis/Gluconeogenesis	Glucose-1-phosphatase	3.1.3.10	KOX_16950	glp -> glc + pi
ABT6PGH	Glycolysis/Gluconeogenesis	Arbutin 6-phosphate glucohydrolase	3.2.1.86	KOX_00650/KOX_02465/KOX_06100/KOX_09245 KOX_15175/KOX_18215/KOX_25655/KOX_27145	abtep -> nqn + gep
SALC6PGH	Glycolysis/Gluconeogenesis	Salicin 6-phosphate glucohydrolase	3.2.1.86	KOX_00650/KOX_02465/KOX_06100/KOX_09245 KOX_15175/KOX_18215/KOX_25655/KOX_27145	/salc6p -> salchol + g6p
ABTpts	Glycolysis/Gluconeogenesis	Arbutin transport via PEP:Pyr PTS	2.7.1.69	KOX_00645/KOX_06485/KOX_26855	abt_e + pep -> abt6p + pyr
SALCpts	Glycolysis/Gluconeogenesis	Salicin transport via PEP:Pyr PTS	2.7.1.69	KOX_00645/KOX_26855	salc_e + pep -> salc6p + pyr
TARSAR	Glyoxylate and Dicarboxylate metabolism	tartronate semialdehyde	1.1.1.60	KOX_03465(garR)	h3op + nadh <-> glyc-R + nad
LCTAD1	Glyoxylate and Dicarboxylate metabolism	reductase	1.2.1.22	KOX_19535	llald + nad -> llac + nadh
LCTAD3 PGLYCP	Glyoxylate and Dicarboxylate metabolism Glyoxylate and Dicarboxylate metabolism		1.2.1.22	KOX_19535 KOX_04585	llald + nad <-> llac + nadh 2ppg -> glycolate + pi
GLCALDD	Glyoxylate and Dicarboxylate metabolism	Glycolaldehyde dehydrogenase	1.2.1.21	KOX_19535	glal + nad -> glycolate + nadh
LALDR2 GLYCEK1	Glyoxylate and Dicarboxylate metabolism Glyoxylate and Dicarboxylate metabolism	glycerate kinase	1.1.1.77 2.7.1.31	KOX_00865 KOX_01170/KOX_03460	glal + nadh <-> eglycol + nad atp + glyc-R -> 3pg + adp
GLYCDHp	Glyoxylate and Dicarboxylate metabolism	Glycolate dehydrogenase (NADP)	1.1.1.79	KOX_00275/KOX_17100(ghrA)	glx + nadph <-> glycolate + nadp
GLYCDH	Glyoxylate and Dicarboxylate metabolism	Glycolate dehydrogenase (NADP)	1.1.1.79	KOX_00275/KOX_17100(ghrA)	glx + nadh <-> glycolate + nad
FHL	Glyoxylate and Dicarboxylate metabolism	Formate-hydrogen lyase			formate -> co2 + h2
TARTRD TARTRDH	Glyoxylate and Dicarboxylate metabolism Glyoxylate and Dicarboxylate metabolism		4.2.1.32 1.1.1.93	KOX_03975/KOX_03980 KOX_16905	tartr <-> oaa tartr + nad <-> oxglycolate + nadh
MTARTRDH	Glyoxylate and Dicarboxylate metabolism	tartrate dehydrogenase	1.1.1.93	KOX_16905	mtartr + nad <-> oxglycolate + nadh
HAKGA	Glyoxylate and Dicarboxylate metabolism	aldolase	4.1.3.16	KOX_23850	hydroxyakg <-> pyr + glx
HISTDH ATPPRT	Histidine Metabolism Histidine Metabolism	histidinol dehydrogenase ATP phosphoribosyltransferase	1.1.1.23 2.4.2.17	KOX_25035(hisD) KOX_25030(hisG)	hisol + 2 nad -> his + 2 nadh atp + prpp <-> ppi + prbatp
HISTPT	Histidine Metabolism	histidinol-phosphate transaminase	2.6.1.9	KOX_25040	glu + imACP -> akg + hisolp
HISTP	Histidine Metabolism	histidinol-phosphatase	3.1.3.15	KOX_25045	hisolp -> hisol + pi
PRAMPCH	Histidine Metabolism	phosphoribosyl-AMP cyclohydrolase	3.5.4.19	KOX_25065	prbamp -> prfp
PRATPPP	Histidine Metabolism	phosphoribosyl-ATP pyrophosphatase	3.6.1.31	KOX_25065	prbatp -> ppi + prbamp
IMGPDH	Histidine Metabolism	imidazoleglycerol-phosphate	4.2.1.19	KOX_25045	dimgp -> imACP
		dehydratase 1-(5-phosphoribosyl)-5-[(5-			
PRMIIZCI	Histidine Metabolism	phosphoribosylamino)methylide neamino)imidazole-4-	5.3.1.16	KOX_25055	prfp -> prlp
		carboxamide isomerase			
IMG3PS	Histidine Metabolism	Imidazole-glycerol-3-phosphate synthase		KOX_25060/KOX_25050(hisH)	gln + prlp -> aicar + dimgp + glu
HISAL UROCH	Histidine metabolism Histidine metabolism	histidine ammonia-lyase urocanate hydratase	4.3.1.3 4.2.1.49	KOX_11930/KOX_14895 KOX_11955/KOX_14890	his -> urocan + nh4 urocan -> 4i5p
IMZPP	Histidine metabolism	imidazolonepropionase	3.5.2.7	KOX_11965/KOX_14880	4i5p -> nfglu
NFGLUAH	Histidine metabolism	N-formylglutamate amidohydrolase	3.5.3.8	KOX_11970	nfglu -> glu + fa
ALHD7	Histidine metabolism	aldehyde dehydrogenase (NAD+)	1.2.1.3	KOX_00375	i4aa + nad -> i4ac + nadh
MSDHA	Inositol metabolism	malonate-semialdehyde	1.2.1.18/1.2.1.27	KOX 09140/KOX 09360	3opp + coa + nad -> accoa + co2 + nadh
MI1P	Inositol Phosphate Metabolism	dehydrogenase (acetylating) myo-inositol 1-phosphatase	3.1.3.25	KOX_14040/KOX_27375	dmilp -> mi + pi
MI3P MI4P	Inositol Phosphate Metabolism	myo-inositol 3-phosphatase	3.1.3.25	KOX_14040/KOX_27375	dmi3p -> mi + pi
MI2DH	Inositol Phosphate Metabolism Inositol Phosphate Metabolism		3.1.3.25 1.1.1.18	KOX_14040/KOX_27375 KOX_09385/KOX_13300	dmi4p -> mi + pi mi + nad <-> scinos + nadh
MIS2D	Inositol Phosphate Metabolism	myo-inosose-2 dehydratase 3D-(3,5/4)-	4.2.1.44	KOX_09395/KOX_20350	scinos <-> thcych12d
THCYCH12DH	Inositol Phosphate Metabolism	trihydroxycyclohexane-1,2-	3.7.1	KOX_09380	thcych12d -> 5dglucn
5DGLUCNI	Inositol Phosphate Metabolism	dione hydrolase 5-deoxy-glucuronate isomerase	5.3.1	KOX_09365	5dglucn -> 2d5kglcn
5DH2DGK	Inositol Phosphate Metabolism	5-dehydro-2- deoxygluconokinase	2.7.1.92	KOX_09375	2d5kglcn + atp -> 2d5kglcn6p + adp
MIHKP4P	Inositol Phosphate Metabolism	myo-inositol-hexakisphosphate	3.1.3.26	KOX_14030	phytate -> in12356pkp + pi
UDPAGAT	Lipopolysaccharide Biosynthesis	4-phosphohydrolase UDP-N-acetylglucosamine	2.3.1.129	KOX_11505	3hmrsACP + udpnag <-> ACP + udpg2aa
LIPADSS	Lipopolysaccharide Biosynthesis	acyltransferase Lipid A disaccaride synthase	2.4.1.182	KOX_11510(lpxB)	lipidX + udpq23a -> lipidAds + udp
TADSK	Lipopolysaccharide Biosynthesis	Tetraacyldisaccharide 4'kinase 3-deoxy-manno-octulosonate	2.7.1.130	KOX_16030(lpxK)	atp + lipidAds -> adp + lipidA
KDOCTT	Lipopolysaccharide Biosynthesis	cytidylyltransferase	2.7.7.38	KOX_16045	ctp + kdo -> ckdo + ppi
KDO8PP	Lipopolysaccharide Biosynthesis	3-deoxy-manno-octulosonate- 8-phosphatase	3.1.3.45	KOX_03795	kdo8p -> kdo + pi
		2-dehydro-3- deoxyphosphooctonate			
KDO8PS	Lipopolysaccharide Biosynthesis	aldolase (3-deoxy -D-manno-	2.5.1.55	KOX_23165	a5p + pep -> kdo8p + pi
		octulosonic -acid 8-phosphate synthase)			
AGMHEP	Lipopolysaccharide Biosynthesis	ADP-D-glycero-D-manno- heptose epimerase	5.1.3.20	KOX_05860(rfaD)	adpdgdmhep -> adphep
EDOTXS1	Lipopolysaccharide Biosynthesis	Endotoxin Synthesis (lauroyl	2.3.1	KOX 17165	c120ACP + k2lipiv -> ACP + lk2lipiv
EDOTXS2	Lipopolysaccharide Biosynthesis	transferase) Endotoxin Synthesis (myristoyl	2.3.1	KOX_23895	lk2lipiv + c140ACP -> ACP + lipa
		transferase) D-glycero-D-manno-hepose 1-			
GMHEPADT	Lipopolysaccharide Biosynthesis	phosphate adenyltransferase	2.7.7.70	KOX_03040	atp + dgdmh1p -> adpdgdmhep + ppi
GMHEPK	Lipopolysaccharide Biosynthesis	D-glycero-D-manno-heptose 7- phosphate kinase	2.7.1.167	KOX_03040	atp + dgdmh7p -> adp + dgdmh17bp
GMHEPBP	Lipopolysaccharide Biosynthesis	D-glycero-D-manno-heptose 1,7-bisphosphate phosphatase	3.1.3.82	KOX_11610	dgdmh17bp -> dgdmh1p + pi
GMHEPBPa	Lipopolysaccharide Biosynthesis	D-glycero-D-manno-heptose	3.1.3.83	KOX_11610	dgadmh17bp -> dgadmh1p + pi
		1,7-bisphosphate phosphatase			
DMOAT	Lipopolysaccharide Biosynthesis	acid transferase	2.4.99.12	KOX_05915	ckdo + lipidA -> cmp + kdolipid4
DMOAT2	Lipopolysaccharide Biosynthesis	acid transferase	2.4.99.13	KOX_05915	ckdo + kdolipid4 -> cmp + k2lipiv
S7PISM	Lipopolysaccharide Biosynthesis	sedoheptulose 7-phosphate isomerase	5.3.1.28	KOX_11680(gmhA)	s7p -> dgdmh7p
S7PISMa	Lipopolysaccharide Biosynthesis	sedoheptulose 7-phosphate isomerase	5.3.1.28	KOX_11680(gmhA)	s7p -> dgadmh7p
U3HGAAT	Constitution of the control of the c	UDP-3-O-(3-	2.3.1.191	VOV 11405/1D'	2h1CD2h
U3HGAAT	Lipopolysaccharide Biosynthesis	hydroxymyristoyl)glucosamine acyltransferase	2.3.1.191	KOX_11495(lpxD)	3hmrsACP + u3hga -> ACP + udpg23a
U3AGDA	Lipopolysaccharide Biosynthesis	UDP-3-O-acetylglucosamine deacetylase	3.5.1.108	KOX_10955(lpxC)	udpg2aa -> ac + u3hga
UDPSH	Lipopolysaccharide Biosynthesis	UDP-sugar hydrolase	3.6.1.54	KOX_13205	udpg23a -> lipidX + ump
HCITS DHDCR	Lysine Biosynthesis  Lysine Biosynthesis	homocitrate synthase dihydrodipicolinate reductase	2.3.3.14 1.3.1.26	KOX_24970 KOX_10650	accoa + akg -> hcit + coa dhdp + nadph -> nadp + tdhdp
		(NADPH) tetrahydrodipicolinate			
THDPSUC	Lysine Biosynthesis	succinylase	2.3.1.117	KOX_11425(dapD)/KOX_1199	succoa + tdhdp -> coa + sl2a6o
SUCDPT	Lysine Biosynthesis	succinyldiaminopimelate transaminase	2.6.1.17	KOX_04525(argD)	akg + sl26da <-> glu + sl2a6o
SUCDPDS	Lysine Biosynthesis	succinyl-diaminopimelate desuccinylase	3.5.1.18	KOX_20740/KOX_27065	sl26da -> 26dap-LL + succ
DAPMDC	Lysine Biosynthesis	diaminopimelate decarboxylase		KOX_01685	26dap-M -> co2 + lys
DHDPCS DAPME	Lysine Biosynthesis Lysine Biosynthesis	dihydrodipicolinate synthase diaminopimelate epimerase	4.2.1.52 5.1.1.7	KOX_04820/KOX_11900/KOX_24090/KOX_27100 KOX_07665(dapF)	aspsa + pyr -> dhdp 26dap-LL <-> 26dap-M
		2-oxoglutarate dehydrogenase E2 component			
OGDH2	Lysine degradation	(dihydrolipoamide	2.3.1.61	KOX_14595	coa + sgdhl <-> glutcoa + dlipoe
OGDH1	Lysine degradation	succinyltransferase) 2-oxoglutarate dehydrogenase	1.2.4.2	KOX 14590(sucA)	2oad + lipoe -> sqdhl + co2
		E1 component aldehyde dehydrogenase			
ALHD17	Lysine degradation	(NAD+)	1.2.1.3	KOX_00375	4tmab + nad -> 4tmabn + nadh
LYSDC ENCOAH3	Lysine degradation Membrane Lipid Metabolism	lysine decarboxylase enoyl-CoA hydratase	4.1.1.18 4.2.1.17	KOX_11535/KOX_13270 KOX_07835(fadB)/KOX_19445/KOX_26655(fadJ)	lys -> 15dap + co2 3mccoa <-> 3hivcoa
ENCOAH4 ENCOAH5	Membrane Lipid Metabolism Membrane Lipid Metabolism	enoyl-CoA hydratase enoyl-CoA hydratase	4.2.1.17 4.2.1.17	KOX_07835(fadB)/KOX_19445/KOX_26655(fadJ) KOX_07835(fadB)/KOX_19445/KOX_26655(fadJ)	2mp2ecoa -> 3hibcoa 2m2ecoa -> s3h2mbcoa
		3-hydroxyacyl-CoA			
HACOAD2	Membrane Lipid Metabolism	dehydrogenase (3- oxohexanoyl-CoA)	1.1.1.35	KOX_07835(fadB)/KOX_26655(fadJ)	s3h2mbcoa + nad <-> 2maaccoa + nadh
HACOAD3	Membrane Lipid Metabolism	3-hydroxyacyl-CoA dehydrogenase (3-oxooctanoyl-	1.1.1.35	KOX_07835(fadB)/KOX_26655(fadJ)	hibut + nad <-> mmsa + nadh
ENCOAH6	Membrane Lipid Metabolism	CoA) enoyl-CoA hydratase	42.1.17	KOX_07835(fadB)/KOX_19445/KOX_26655(fadJ)	
		y ryuruuse			

HACOAD4		3-hydroxyacyl-CoA		NON GEORGE IN MON DESCRIPTION	
ENCOAH7	Membrane Lipid Metabolism  Membrane Lipid Metabolism	dehydrogenase (3- oxodecanoyl-CoA) enoyl-CoA hydratase	1.1.1.35 4.2.1.17	KOX_07835(fadB)/KOX_26655(fadJ)  KOX_07835(fadB)/KOX_19445/KOX_26655(fadJ)	hadpcoa + nad -> ooadpcoa + nadh 2e5mhdcoa -> 3h5m4ecoa
HACOAD5	Membrane Lipid Metabolism	3-hydroxyacyl-CoA dehydrogenase (3-	1.1.1.35	KOX_07835(fadB)/ KOX_26655(fadJ)	3h5m4ecoa + nad -> 5m3o4hcoa + nadh
		oxododecanoyl-CoA) 3-hydroxy-myristoyl-ACP	1.1.1.55	KOX_U/655(Idub)/ KOX_20055(Idu)	
3HMYSAS FALDHD	Membrane Lipid Metabolism  Methane Metabolism	synthesis	1.1.1.284	KOX 19595	c120ACP + malACP + nadph -> 3hmrsACP + ACP + co2 + nadp
FGMTH	Methane Metabolism	S-formylglutathione hydrolase	3.1.2.12	KOX_25755	hmgth + nad <-> fmgt + nadh fmgt -> formate + rgt
CATL2	Methane Metabolism	catalase 2-keto-4-methylthiobutyrate	1.11.1.6/1.11.1.21		methanol + h2o2 -> formald
2KMBT METS	Methionine Metabolism	transamination	2.6.1.57	KOX_08310	2kmb + glu -> akg + met
METADT	Methionine Metabolism  Methionine Metabolism	methionine synthase methionine adenosyltransferase	2.1.1.13	KOX_08065(metH) KOX_02650	mthf + hcys <-> met + thf atp + met -> sam + pi + ppi
		S-adenosylhomocysteine			
ADHCYSNS	Methionine Metabolism	nucleosidase	3.2.2.9	KOX_11395	sah -> ad + srlh
CYTTS1 CYSTBL1	Methionine Metabolism Methionine Metabolism	cystathionine gamma-synthase cystathionine b-lyase	2.5.1.48 4.4.1.8	KOX_07310 KOX_02875/KOX_21920	cys + oslhser -> llct + succ llct -> hcys + nh4 + pyr
ADHC1 CYTTS2	Methionine metabolism Methionine metabolism	adenosylhomocysteinase cystathionine gamma-synthase	3.3.1.1	KOX_24860 KOX_07310	sah <-> adn + hcys oslhser <-> obut + succ + nh4
CYTTS3	Methionine metabolism	cystathionine gamma-synthase	2.5.1.48	KOX_07310	oahser + cys <-> llct + ac
CYTTS4	Methionine metabolism	cystathionine gamma-synthase O-acetylhomoserine (thiol)-		KOX_07310	oahser + h2s -> hcys + ac
OAHSL1	Methionine metabolism	lyase	2.5.1.48	KOX_07310	oahser + tsul + rthio -> hcys + so3 + othio + ac
CYTTSS	Methionine metabolism	cystathionine gamma-synthase 5-	2.5.1.48	KOX_07310	oslhser + h2s <-> hcys + succ
MTTGH	Methionine metabolism	methyltetrahydropteroyltrigluta matehomocysteine methyltransferase	2.1.1.14	KOX_07750/KOX_21350/KOX_21375	Smtglu + hcys -> tglu + met
HCYSMT	Methionine metabolism	homocysteine S- methyltransferase	2.1.1.10	KOX_12250(mmuM)	hcys + sam -> met + sah
DNACYSM	Methionine metabolism	DNA (cytosine-5-)- methyltransferase	2.1.1.37	KOX_15390/KOX_24195/KOX_24335	sam + dnacys -> sah + dna5mcys
SAMDC	Methionine metabolism	S-adenosylmethionine	4.1.1.50	KOX 11105	sam -> sama + co2
	Marie Company	decarboxylase 5'-methylthioadenosine	2220	KON 44205	Smta -> arl + Smtrib
5MTAN 5MTRIBK	Methionine metabolism  Methionine metabolism	nucleosidase	3.2.2.9		5mta -> ad + 5mtrib 5mtrib + atp -> 5mtribp + adp
5MTRIBPI	Methionine metabolism	5-methylthioribose kinase methylthioribose-1-phosphate	5.3.1.23		Smtribo -> Smtribuo
		isomerase methylthioribulose-1-phosphate		_	
MTRIBUPD	Methionine metabolism	denydratase	4.2.1.109	KOX_14065	5mtribup -> dikmtpenp
DIKMTPENPP	Methionine metabolism	2,3-diketo-5-methylthio-1- phosphopentane phosphatase	3.1.3.77	KOX_14115	dikmtpenp -> 12dhmetpeno + pi
12DHMETPEND1	Methionine metabolism	1,2-dihydroxy-3-keto-5- methylthiopentene dioxygenase	1.13.11.54	KOX_14110	12dhmetpeno + o2 -> 2kmb + formate
12DHMETPEND2	Methionine metabolism	1,2-dihydroxy-3-keto-5-	1.13.11.53	KOX_14110	12dhmetpeno + o2 -> 3metpro + formate + co
		methylthiopentene dioxygenase			
SALCH1	Naphthalene and Anthracene degradation		1.14.13.1	KOX_25675	hnaptho + nadh + o2 -> napth12d + co2 + nad
SALCH2 NACMNP	Dioxin degradation  Nicotinate and Nicotinamide metabolism	salicylate hydroxylase nicotinic acid mononucleotide	1.14.13.1 2.4.2.11	KOX_25675 KOX_16110	salcyl + o2 + nadh -> catech + co2 + nad nac + prpp <-> nacn + ppi
IVACIVING	reconnate and reconnaming metabolism	pyrophosphorylase	2.4.2.11	KOX_10110	пас т ргрр с-> паст т ррг
NACNDP	Nicotinate and Nicotinamide metabolism	nicotinate-nucleotide diphosphorylase (carboxylating)	2.4.2.19	KOX_11010	prpp + qa -> co2 + nacn + ppi
NADK	Nicotinate and Nicotinamide metabolism		2.7.1.23	KOX_00110(ppnK)	atp + nad -> adp + nadp
NAMNAT	Nicotinate and Nicotinamide metabolism	nicotinamide-nucleotide adenylyltransferase	2.7.7.18	KOX_14250(nadD)	atp + namn <-> nad + ppi
NACM	Nicotinate and Nicotinamide metabolism	nicotinamidase	3.5.1.19	KOX_18050	nam -> nac + nh4
NADDP1 NADDP1e	Nicotinate and Nicotinamide metabolism Nicotinate and Nicotinamide metabolism		3.6.1.22 3.6.1.22	KOX_07975(nudC) KOX_07975(nudC)	nad -> amp + namn nad -> amp + namn_e
ASPOX2	Nicotinate and Nicotinamide metabolism	L-aspartate oxidase	1.4.3.16	KOX_27585	asp + o2 <-> h2o2 + iasp
ASPOX3 ASPOX4	Nicotinate and Nicotinamide metabolism Nicotinate and Nicotinamide metabolism	L-aspartate oxidase	1.4.3.16 1.4.3.16	KOX_27585	asp + uq -> iasp + uqh2 asp + mk -> iasp + mqn
ASPOX5 QULS	Nicotinate and Nicotinamide metabolism Nicotinate and Nicotinamide metabolism		1.4.3.16 2.5.1.72		asp + fum -> iasp + succ dhap + iasp <-> pi + qa
NTNAT	Nicotinate and Nicotinamide metabolism	nicotinate-nucleotide	2.7.7.18	KOX_14250(nadD)	atp + nacn <-> dnad + ppi
NTD13	Nicotinate and Nicotinamide metabolism	adenylyltransferase	3.1.3.5	VOV 01045/2-25/VOV 00535/VOV 00680/VOV 1	namn -> namd + pi
				0270/KOX_13075(ushA)/KOX_26410 KOX_01045(surE)KOX_09525/KOX_09680/KOX_1	
NTD14	Nicotinate and Nicotinamide metabolism		3.1.3.5	0270/KOX_13075(ushA)/KOX_26410	nacn -> nacd + pi
NADDP2 NADSYN	Nicotinate and Nicotinamide metabolism Nicotinate and Nicotinamide metabolism		3.6.1.22 6.3.1.5	KOX_07975(nudC) KOX_18185(nadE)	dnad -> amp + nacn atp + dnad + nh4 -> amp + ppi + nad
PUNPP9	Nicotinate and Nicotinamide metabolism	purine-nucleoside	2.4.2.1		namd + pi <-> nam + r1p
PLINIPP10	Nicotinate and Nicotinamide metabolism	phosphorylase purine-nucleoside	2.4.2.1		nacd + pi <-> nac + r1p
NODOX1	Nitrogen Metabolism	phosphorylase nitric oxide dioxygenase	1.14.12.17	KOX_27435	nadh + 2 no + 2 o2 -> nad + 2 no3
	Nitrogen Metabolism	nitric oxide dioxygenase	1 14 12 17	KOX_27435	
NODOX2		mare oxide dioxygenase			nadph + 2 no + 2 o2 -> nadp + 2 no3
NODOX2 NO3RUq1	Nitrogen Metabolism	Nitrate reductase (Ubiquinol-8)	1.7.99.4	KOX_19980/KOX_19985/KOX_19990/KOX_19995/ KOX_23065/KOX_23070/KOX_23075/KOX_23080/	
			1.7.99.4 1.13.12.16	KOX_23065/KOX_23070/KOX_23075/KOX_23080/ KOX_23105	
NO3RUq1 NITNMOX NITRT1	Nitrogen Metabolism Nitrogen Metabolism Nitrogen metabolism	Nitrate reductase (Ubiquinol-8) nitronate monooxygenase nitrite reductase	1.13.12.16 1.7.1.4	KOX_23065/KOX_23070/KOX_23075/KOX_23080/ KOX_23105 KOX_21140 KOX_04560/KOX_04565(nirD)/KOX_23110	no3 + uqh2 -> no2 + uq + 2 hext ethnit + o2 + fmnh2 -> acal + no2 + fmn no2 + 3 nadh -> 3 nad + nh4
NO3RUq1 NITNMOX NITRT1 NITRT2	Nitrogen Metabolism Nitrogen Metabolism Nitrogen metabolism Nitrogen metabolism	Nitrate reductase (Ubiquinol-8) nitronate monooxygenase nitrite reductase nitrite reductase	1.13.12.16 1.7.1.4 1.7.1.4	KOX_23065/KOX_23070/KOX_23075/KOX_23080/ KOX_23105 KOX_21140 KOX_04560/KOX_04565(nirD)/KOX_23110 KOX_04560/KOX_04565(nirD)/KOX_23110 KOX_24920/KOX_24925/KOX_24930/KOX_24975/	no3 + ugh2 -> no2 + ug + 2 hext tethnit + o2 + fmnh2 -> acal + no2 + fmn no2 + 3 nadh -> 3 nad + nb4 no3 + 3 nadh -> 3 nadh -> 3 nadh -> 10
NO3RUq1 NITNMOX NITRT1	Nitrogen Metabolism Nitrogen Metabolism Nitrogen metabolism Nitrogen metabolism Nitrogen metabolism	Nitrate reductase (Ubiquinol-8) nitronate monooxygenase nitrite reductase nitrite reductase nitrogenase	1.13.12.16 1.7.1.4	KOX, 23065/KOX, 23070/KOX, 23075/KOX, 23080/ KOX, 23105 KOX, 21140 KOX, 04560/KOX, 04565(nirD)/KOX, 23110 KOX, 04560/KOX, 04565(nirD)/KOX, 23110 KOX, 04500/KOX, 24925/KOX, 24930/KOX, 24975/ KOX, 14410/KOX, 249990/	no3 + uqh2 -> no2 + uq + 2 hext ethnit + o2 + fmnh2 -> acal + no2 + fmn no2 + 3 nadh -> 3 nad + nh4 no2 + 3 nadph -> 3 nadp + nh4 16 atp + n2 + 8 rdferdx -> 16 pi + 16 adp + 8 oxferdx + 2 nh4 + h2
NO3RUq1 NITNIMOX NITRT1 NITRT2 NITGEN CAPK2 CARBONAH	Nitrogen Metabolism	Nitrate reductase (Ubiquinol-8) nitronate monooxygenase nitrite reductase nitrote reductase nitrogenase carbamate kinase carbamate kinase	1.13.12.16 1.7.14 1.7.14 1.18.6.1 2.7.22 4.2.11	KOX, 23056,/KOX, 23076/KOX, 23075,/KOX, 23080/ KOX, 23105 KOX, 21140 KOX, 04560/KOX, 04565(nicD)/KOX, 23110 KOX, 04560/KOX, 04565(nicD)/KOX, 23110 KOX, 24020/KOX, 24925/KOX, 24930/KOX, 24975/ KOX, 24375/ KOX, 24375/ KOX, 24375/ KOX, 04315/KOX, 21145/KOX, 22245	no3 + uqh2 -> no2 + uq + 2 hext ethnit + o2 + fmnh2 -> acal + no2 + fmn no2 + 3 nadh -> 3 nad + nh4 no2 + 3 nadph -> 3 nadp + nh4 16 atp + n2 + 8 rdferdx -> 16 pi + 16 adp + 8 oxferdx + 2 nh4 + h2 cabm + atp -> cap + adp h2co3 <-> co2
NO3RUq1 NITNMOX NITRT1 NITRT2 NITGEN CAPK2	Nitrogen Metabolism Nitrogen Metabolism Nitrogen metabolism Nitrogen metabolism Nitrogen metabolism Nitrogen metabolism	Nitrate reductase (Ubiquinol-8) nitronate monooxygenase nitrite reductase nitrite reductase nitrite reductase nitrite reductase nitrogenase carbamate kinase carbonic anhydrase adentylate kinase (GTP) adentylate kinase (GTP)	1.13.12.16 1.7.14 1.7.14 1.18.6.1 2.7.22	KOX, 23065/KOX, 23070/KOX, 23075/KOX, 23080/ KOX, 231105 KOX, 21140 KOX, 04560/KOX, 04565(nirD)/KOX, 23110 KOX, 04560/KOX, 04565(nirD)/KOX, 23110 KOX, 24920/KOX, 24925/KOX, 24930/KOX, 24975/ KOX, 14410/KOX, 24990/ KOX, 23275	no3 + uqh2 -> no2 + uq + 2 hext ethnit + o2 - fmm2 -> scal + no2 + fmn no2 + 3 nadh -> 3 nad + nh4 no2 + 3 nadph -> 3 nadp - mh4 16 atp + n2 + 8 rdferdx -> 16 pi + 16 adp + 8 oxferdx + 2 nh4 + h2 cabm + atp -> cap + adp
NO3RUq1 NITNIMOX NITRT1 NITRT2 NITGEN CAPK2 CARBONAH ADNK3	Nitrogen Metabolism	Nitrate reductase (Ubiquinol-8) nitronate moncoxygenase nitrite reductase nitrite reductase nitrogenase carbamate kinase carbonic anhydrase adentylate kinase (GTP) adentylate kinase (GTP) defnylate (GTP	1.13.12.16 1.7.14 1.7.14 1.18.6.1 2.7.2.2 4.2.1.1 2.7.4.3 2.7.4.3 1.1.1.133	KOX, 23056,/KOX, 23070/KOX, 23075,/KOX, 23080/ KOX, 23105 KOX, 21140 KOX, Q4560,/KOX, Q4565(nirD)/KOX, 23110 KOX, Q4500/KOX, Q4556(nirD)/KOX, 23110 KOX, 24920/KOX, 24925/KOX, 24930/KOX, 24975/ KOX, 24125/KOX, 24925/KOX, 24930/KOX, 22245 KOX, Q4135/KOX, 11145/KOX, 22245 KOX, Q4135/KOX, 11145/KOX, 22245 KOX, Q4135/KOX, 11145/KOX, 22245	no3 + uqh2 -> no2 + uq + 2 hext ethnit + o2 + fmnh2 -> acal + no2 + fm no2 - 3 nadh -> 3 nad + nh4 no2 + 3 nadph -> 3 nadp + nh4 16 atp n - 2 * 8 ffedtex -> 16 pi + 16 adp + 8 oxferdx + 2 nh4 + h2 cabm + atp -> cap + adp h2co3 <> co2 amp + gtp <> adp + gdp
NO3RUq1 NITNMOX NITR11 NITR12 NITGEN CAPK2 CARBONAH ADNK3 ADNK4	Nitrogen Metabolism  Nucleotide Salvage Pathway	Nitrate reductase (Ubiquinol-8) nitronate monoxygenase nitrite reductase nitrite reductase nitrogenase carbamate kinase carbamate kinase (GP) adentylate kinase (GP) adentylate kinase (GP) adentylate kinase (GP) adentylate kinase (GP) UDP-4-dely/dromlamnose reductase UDPglucose 6-delyydrogenase	1.13.12.16 1.7.14 1.7.14 1.18.6.1 2.7.2.2 4.2.1.1 2.7.4.3 2.7.4.3 1.1.1.133	KOX ,23056,/KOX ,23070/KOX ,23075,/KOX ,23080/ KOX ,23106 KOX ,21140 KOX ,04560/KOX ,04565/nirDI/KOX ,23110 KOX ,04560/KOX ,04565/nirDI/KOX ,23110 KOX ,24920/KOX ,24925/KOX ,24930/KOX ,24975/ KOX ,2475/ KOX ,4410/KOX ,2490/ KOX ,2475/ KOX ,41050/Galki KOX ,04155/KOX ,11145/KOX ,22245 KOX ,13050/arki KOX ,23510 KOX ,25130	no3 + uqh2 -> no2 + uq + 2 hext  ethnit + o2 + fmnh2 -> acal + no2 + fmn no2 + 3 nadh -> 3 nad + nh4 no2 + 3 nadph -> 3 nadph -> 10 nadph
NO3RUq1 NITNMOX NITRT1 NITRT2 NITGEN CAPK2 CARBONAH ADNK3 ADNK4 TDPDRHR	Nitrogen Metabolism Nutceotide Salvage Pathway Nucleotide Salvage Pathway Nucleotide Salvage Pathway Nucleotide sugars metabolism	Nitrate reductase (Ubiquinol-8) nitronate monoxygenase nitrite reductase nitrite reductase nitrogenase carbamate kinase carbonic anhydrase adenylate kinase (GTP) adenylate kinase (GTP) adenylate kinase (GTP) adenylate kinase (GTP) UDP-4-dehydromannose reductase UDPglucose 6-dehydrogenase glucose 1-phosphate thymidylytransferase	1.13.12.16 1.7.14 1.7.14 1.18.6.1 2.7.2.2 4.2.1.1 2.7.4.3 2.7.4.3 1.1.1.133	KOX_2365,/KOX_23070/KOX_23075,/KOX_23080/ KOX_23105 KOX_21140 KOX_04560/KOX_04565(nirD)/KOX_233110 KOX_04560/KOX_04565(nirD)/KOX_233110 KOX_24620/KOX_24925/KOX_24930/KOX_24975/ KOX_24207 KOX_24207 KOX_24207 KOX_04135/KOX_11145/KOX_22245 KOX_13050(adk) KOX_1235/KOX_11145/KOX_22245 KOX_13050(adk) KOX_25130	no3 + uqh2 -> no2 + uq + 2 hext  ethnit + o2 + fmnh2 -> acal + no2 + fmn no2 + 3 nadh -> 3 nad + nh4 no2 + 3 nadph -> 3 nadp + nh4 16 atp + n2 + 8 rdferdx -> 16 pi + 16 adp + 8 oxferdx + 2 nh4 + h2 cathm + atp -> cap + adp h2co3 -< co2 amp + gtp <> adp + gdp amp + gtp <> adp + idp dtdp4d6dm + nadph -> dtdprmn + nadp
NO3RUq1 NITNMOX NITRT1 NITRT2 NITGEN CAPK2 CARBONAH ADNIK3 ADNIK4 TDPDRHR UDPG6D	Nitrogen Metabolism  Nucleotide Salvage Pathway	Nitrate reductase (Ubiquinol-8) nitronate monooxygenase nitrire reductase nitrire reductase nitrire reductase nitrire reductase nitrogenase carbamate kinase carbonic anhydrase adentylate kinase (GTP) (GTP) adentylate kinase (GTP) (GTP) adentylate kinase (GTP) (GTP) adentylate kinase (GTP) adentylate kinase (GTP) (GTP) adentylate kinase (GTP) adentylate kinase (GTP) adentylate (GT	1.13.12.16 1.7.14 1.7.14 1.18.6.1 2.7.22 4.2.11 2.7.43 2.7.43 1.1.1133 1.1.122	KOX ,23056,/KOX ,23070/KOX ,23075,/KOX ,23080/ KOX ,23106 KOX ,21140 KOX ,04560/KOX ,04565/nirDI/KOX ,23110 KOX ,04560/KOX ,04565/nirDI/KOX ,23110 KOX ,24920/KOX ,24925/KOX ,24930/KOX ,24975/ KOX ,2475/ KOX ,4410/KOX ,2490/ KOX ,2475/ KOX ,41050/Galki KOX ,04155/KOX ,11145/KOX ,22245 KOX ,13050/arki KOX ,23510 KOX ,25130	no3 + uqh2 -> no2 + uq + 2 hext  ethnit + o2 + fmnh2 -> acal + no2 + fmn no2 + 3 nadh -> 3 nad + nh4 no2 + 3 nadph -> 3 nadp + nh4 16 atp + n2 + 8 rdferdx -> 16 pi * 16 adp + 8 oxferdx + 2 nh4 + h2  caltm + stp -> cap + adp  h2c3 -< > co2 amp + pp <-> adp + gdp amp + ipp <-> adp + idp  didphiddim + nadph -> drdprmn + nadp 2 nad + udpg -> 2 nadh + udpglcur
NO3RUq1 NITMMOX NITRI1 NITRI2 NITGEN CAPK2 CARBONAH ADNK3 ADNK4 TDPORHR UDPG6D G1PTT1	Nitrogen Metabolism Nucleotide Salvage Pathway Nucleotide Salvage Pathway Nucleotide Salvage Pathway Nucleotide Salvage Pathway Nucleotide salvages metabolism Nucleotide salvages metabolism Nucleotide salvages metabolism Nucleotide salvages metabolism	Nitrate reductase (Ubiquinol-8) nitronate monooxygenase nitrire reductase nitrire reductase nitrire reductase nitrire reductase nitrire reductase nitrogenase carbamate kinase carbonic anhydrase adenhylate kinase (GTP) adenhylate kinase (GTP) adenylate kinase (GTP) adenylate kinase (GTP) ubiplate kinase (GTP	113.12.16 1.7.14 1.7.14 1.18.6.1 2.7.22 4.21.1 2.7.43 2.7.43 1.11.133 1.11.122 2.7.7.24	KOX_2365-K/COX_23070/KOX_23075-K/COX_23080/ KOX_23105 KOX_21140 KOX_04560/KOX_04565(niiD)/KOX_23110 KOX_04560/KOX_04565(niiD)/KOX_23110 KOX_04560/KOX_04565(niiD)/KOX_23110 KOX_4400/KOX_24959/ KOX_42157 KOX_4100/KOX_24950/ KOX_24157 KOX_1315/KOX_11145/KOX_22245 KOX_13050(adik) KOX_25130 KOX_25130 KOX_25130	no3 + uqh2 -> no2 + uq + 2 hext  ethnit + o2 + fmnh2 -> acal + no2 + fmn no2 + 3 nadh -> 3 nad + nh4 no2 + 3 nadph -> 3 nadp + nh4 16 atp + n2 + 8 rdferdx -> 16 pi * 16 adp + 8 oxferdx + 2 nh4 + h2  cathm + stp -> cap + adp h2co3 -< >co2 amp + ptp -<> adp + gdp amp + tpt -<> adp + idp  dtdp46dcm + nadph -> dtdprmn + nadp 2 nad + udpg -> 2 nadh + udpglcur  dttp + g1p -> dtdpplu + ppi
NO3RUq1 NITMMOX NITRT1 NITRT2 NITGEN CAPK2 CARBONAH ADNK3 ADNK4 TDPORHR UDPGGD G1PTT1 UG1PUT	Nitrogen Metabolism  Nucleoticé salvage Pathway  Nucleoticé salvage Pathway  Nucleoticé salvage Pathway  Nucleoticé salvage retabolism  Nucleotide sugars metabolism  Nucleotide sugars metabolism  Nucleotide sugars metabolism	Nitrate reductase (Ubiquinol-8) nitronate monoxygenase nitrite reductase nitrite reductase nitrite reductase nitrogenase carbamate kinase carbonic anhydrase adenylate kinase (GTP) adenylate kinase (GTP) adenylate kinase (GTP) adenylate kinase (GTP) upproprinte kinase (GTP) adenylate kinase (GTP) a	113.12.16 1.77.4 1.71.4 1.18.6.1 2.7.22 4.21.1 2.7.43 2.7.43 1.11.133 1.11.122 2.7.7.24 2.7.7.9	KOX_23056,/KOX_23070/KOX_23075/KCX_23080/ KOX_21140 KOX_04560/KOX_04565(nirt)/KOX_23110 KOX_045660/KOX_04565(nirt)/KOX_23110 KOX_04560/KOX_04565(nirt)/KOX_23110 KOX_44010/KOX_24959/KOX_24930/KOX_24975/ KOX_1410/KOX_24959/ KOX_13256(nirt)/KOX_22245 KOX_04135/KOX_11145/KOX_22245 KOX_13505(nirt) KOX_13505(nirt) KOX_13505(nirt) KOX_25130 KOX_25130 KOX_25135 KOX_25135	no3 + uqh2 -> no2 + uq + 2 hext  ethnit + o2 + fmnh2 -> scal + no2 + fmn no2 + 3 nadh -> 3 nad + nh4  no2 + 3 nadph -> 3 nadp + nh4  16 atp + n2 + 8 rdferdx -> 16 pi + 16 adp + 8 oxferdx + 2 nh4 + h2  cabm + atp -> cap + adp n2ca3 -< co2  amp + tgh c-> adp + gdp amp + tgh c-> adp + gdp amp + tgh c-> adp + bdp  dtdpddddm + nadph> - dtdpmn + nadp  2 nad + udpg -> 2 nadh + udpglcur  dttp + g1p -> dtdpglu + ppi  g1p + utp -> ppi + udpg
NO3RUq1  NITMMOX NITET1  NITGET  CAPEC CARBONAH ADNES ADNER  LOPPGED  GIPTT1  UGIPUT  TDPGLUD  TDPGLUD  TDPGLUD  TDPGLEL  UPPGEE1	Nitrogen Metabolism  Nutceden metabolism  Nucleotide Salvage Pathway  Nucleotide Salvage Pathway  Nucleotide Salvage Pathway  Nucleotide Salvage Pathway  Nucleotide sugars metabolism	Nitrate reductase (Ubiquinol-8) nitronate monoxygenase nitrite reductase nitrite reductase nitrite reductase nitrogenase carbamate kinase carbonic anhydrase adentyfate kinase (GTP) adentyfate (GTP) adentyfate (GTP) adentyfate (GTP) adentyfatase (GTP) adenty	113.12.16 1.71.4 1.71.4 1.71.4 1.86.1 2.72.2 42.11 2.74.3 1.11.133 1.11.122 2.77.24 2.77.24 2.77.9 4.21.46 5.13.13 5.13.2	KOX_23056,/KOX_23070/KOX_23075/KOX_23080/ KOX_21140 KOX_04560/KOX_04565(nirt)/KOX_23110 KOX_045660/KOX_04565(nirt)/KOX_23110 KOX_04560/KOX_04565(nirt)/KOX_23110 KOX_44060/KOX_24959/KOX_24930/KOX_24975/ KOX_41410/KOX_24959/ KOX_13550(nirt) KOX_13505(nirt) KOX_13505(nirt) KOX_13505(nirt) KOX_25130 KOX_25130 KOX_25135 KOX_25135 KOX_23140 KOX_25140 KOX_251440 KOX_25155 KOX_21785	no3 + uqh2 -> no2 + uq + 2 hext  ethnit + o2 + fmnh2 -> acal + no2 + fmn no2 + 3 nadh -> 3 nad+ nh4 no2 + 3 nadph -> 3 nadp + nh4 16 atp + n2 + 8 rdferdx -> 16 pi + 16 adp + 8 oxferdx + 2 nh4 + h2 caltm + stp -> cap + adp h2co3 -< r co2 amp + stp -> cap + adp h2co3 -< r co2 amp + stp -> adp + stp ddpddded nadph -> dtdprmn + nadp 2 nad + udpg -> 2 nadh + udpglcur dttp + g1p -> dtdpglu + ppi g1p + utp -> ppi + udpg dtdpglu -> dtdp4d6dg dtdp4d6dg -> dtdp4d6dg dtdp4d6dg -> dtdp4d6dg dtdp4d6dg -> dtdp4d6dg dtdpglu -> dtdp4d6dg dtdpglu -> dtdp4d6dg dtdpglu -> dtdp4d6dd dtdpglu -> dtdp4d6dd
NO3RUq1 NITNMOX NITRI1 NITRI2 NITRI2 NITGEN CAPK2 CARBONAH ADNK3 ADNK4 TDPDRHR UDPG6D G1PTT1 UGIPUT TDPGLUD TDPDRHE	Nitrogen Metabolism Nucleotide Salvage Pathway Nucleotide Salvage Pathway Nucleotide sugars metabolism	Nitrate reductase (Ubiquinol-8) nitronate monooxygenase nitrite reductase nitrite reductase nitrite reductase nitrogenase carbonic anhydrase carbonic anhydrase carbonic anhydrase adentylate kinase (GTP) adentylate	1131216 1.7.14 1.7.14 1.7.14 1.8.6.1 2.7.22 4.2.11 2.7.4.3 2.7.4.3 1.11.133 1.11.132 2.7.7.24 2.7.7.9 4.2.1.46 5.1.3.13	KOX_23065,/KOX_23070/KOX_23075,/KOX_23080/ KOX_23105 KOX_21140 KOX_04560/KOX_04565/initD/KOX_233110 KOX_04560/KOX_04565/initD/KOX_233110 KOX_04560/KOX_04555/KOX_23110 KOX_2420/KOX_24075/KOX_24930/KOX_24975/ KOX_1410/KOX_24990/ KOX_23275 KOX_13050(adk) KOX_25130 KOX_25130 KOX_25120 KOX_25130 KOX_25130 KOX_25130 KOX_25130 KOX_25130 KOX_25130 KOX_25130 KOX_25130 KOX_25130 KOX_25130 KOX_25130 KOX_25130 KOX_25130 KOX_25130 KOX_25130 KOX_25130 KOX_25130 KOX_25130	no3 + uqh2 -> no2 + uq + 2 hext  ethnit + o2 + fmnh2 -> acal + no2 + fmn no2 + 3 nadh -> 3 nad + nh4 no2 + 3 nadh -> 3 nad + nh4 16 atp + n2 + 8 rdferdx -> 16 pi + 16 adp + 8 oxferdx + 2 nh4 + h2  cathm + atp -> cap + adp  cathm + atp -> cap + adp  cathm + atp -> cap + adp  dtdp-4d6dm + nadph -> dtdprmn + nadp  2 nad + udpg -> 2 nadh + udpglour  dttp + g1p -> dtdpful + ppi  g1p + utp -> ppi + udpg  dtdpdplu> dtdpdd6ddg  dtdp-4d6ddg  dtdp-4d6ddg
NO3RUq1  NITNMOX NITRI1 NITRI2 NITRI2 NITRI2 CARBONAH ADNK3 ADNK4 TDPDRHR UDPG6D G1PTT1  UG1PUT TDPGLUD TDPDRHE UDPG4E1 UDPG4E1 UDPG4E2	Nitrogen Metabolism Nucleotide Salvage Pathway Nucleotide Salvage Pathway Nucleotide Salvage Pathway Nucleotide sugars metabolism	Nitrate reductase (Ubiquinol-8) nitronate monooxygenase nitrite reductase nitrite reductase nitrite reductase nitrogenase carbonic and programme carbonic anhydrase adentylate kinase (GTP) adentylate (	1131216 1.7.14 1.7.14 1.7.14 1.8.6.1 2.7.22 4.2.11 2.7.43 2.7.43 1.11.133 1.11.122 2.7.7.24 2.7.7.9 4.2.1.46 5.1.3.13 5.1.3.2 5.1.3.2	KOX, 23656,/KOX, 23070/KOX, 23075,/KOX, 23080/ KOX, 23105 KOX, 21140 KOX, Q4560/KOX, Q4565/initD)/KOX, 23310 KOX, Q4566/KOX, Q4565/initD)/KOX, 23310 KOX, Q450/KOX, Q4555/KOX, 24935/KOX, 24975/ KOX, 14410/KOX, 24990/ KOX, 24375 KOX, Q4305/KOX, 11145/KOX, 22245 KOX, Q4305/KOX, 11145/KOX, 22245 KOX, 13050/adk) KOX, 25130 KOX, 25120 KOX, 25130 KOX, 25120 KOX, 25140 KOX, 25155 KOX, 23040/KOX, 25220 KOX, 25125 KOX, 25125 KOX, 25125 KOX, 25125 KOX, 25125 KOX, 25125 KOX, 25125 KOX, 24785 KOX, 14785 KOX, 14785	no3 + uqh2 -> no2 + uq + 2 hext  ethnit + o2 + fmnh2 -> acal + no2 + fmn no2 + 3 nadh -> 3 nad + nh4 no2 + 3 nadh -> 3 nad + nh4 16 atp + n2 + 8 rdferdx -> 16 pi + 16 adp + 8 oxferdx + 2 nh4 + h2  cabm + atp -> cap + adp  brood -> co2 amp + gtp -<> adp + gdp amp + tp (-> adp + idp  dtdp-4d6dm + nadph -> dtdprmn + nadp  2 nad + udpg -> 2 nadh + udpglour  dttp + g1p -> dtdpful + ppi  g1p + utp -> ppi + udpg  dtdpdplu> - dtdpdd6dg  dtdp4d6dg -> dtdp4d6dm  dtdpglu -> dtdp4d6dg  dtdp4d6dg -> dtdp4d6dm  dtdpglu -> dtdp4d1  dtdp3ul -> dtdp4d6dm  dtdpdplu -> dtdp4d1  dtdp3ul -> dtdp4d6dm  dtdp4d6dg -> dtdp4d6dm  dtdp4dgu -> dtdp4d1  dtdp4ul -> dtdp4d1  dtdp4ul -> dtdp4d1  dtdp4ul -> dtdp4d6dp  dtdp4d6dg -> dtdp4d6dm  dtdp4dpul -> dtdp4d1
NO3RUq1 NITMMOX NITR11 NITR12 NITGEN CAPK2 CARBONAH ADNK3 ADNK4 TDPDRHR UDPG6D GIPTT1 UG1PUT TDPGLUD TDPDRHE UDPG4E1 UDPG4E2 AMTF2 METHEH FORTF	Nitrogen Metabolism  Nucleotide Salvage Pathway  Nucleotide Salvages metabolism  Nucleotide sugars metabolism  One carbon pool by Folate	Nitrate reductase (Ubiquinol-8) nitronate monooxygenase nitrite reductase nitrite reductase nitrite reductase nitrogenase carbamate kinase carbamate kinase carbonic anhydrase adentylate kinase (ITP)	1131216 17.14 17.14 118.6.1 27.22 42.11 27.43 27.43 11.1133 11.122 27.7.24 27.7.9 5.13.13 5.13.2 5.13.2 5.13.2 5.13.2 6.3.3.2	KOX_23056,/KOX_23070/KOX_23075/KOX_23080/ KOX_23105 KOX_23110 KOX_Q4506/KOX_Q4565/iniD)/KOX_23110 KOX_Q4566/KOX_Q4555/KOX_Q4555/KOX_23110 KOX_Q4566/KOX_Q4555/KOX_Q4555/KOX_Q4575/KOX_Q44576/KOX_Q45576/KOX_Q45576/KOX_Q45576/KOX_Q45576/KOX_Q45576/KOX_Q45576/KOX_Q45576/KOX_Q45576/KOX_Q45576/KOX_Q45576/KOX_Q45576/KOX_Q45576/KOX_Q45576/KOX_Q45576/KOX_Q45576/KOX_Q45576/KOX_Q45576/KOX_Q45576/KOX_Q4567	no3 + uqh2 -> no2 + uq + 2 hext  ethnit + o2 + fmnh2 -> acal + no2 + fmn no2 + 3 nadh -> 3 nad + nh4 no2 + 3 nadh -> 3 nad + nh4 16 atp + n2 + 8 rdferdx -> 16 pi + 16 adp + 8 oxferdx + 2 nh4 + h2  calhm + stp -> cap + adp h2c3 -< > co2 amp + stp -> cap + adp h2c3 -< > co2 amp + stp -> adp + sdp amp + itp -> adp + idp dtdp4d6dm + nadph -> dtdprmn + nadp 2 nad + udpg -> 2 nadh + udpglcur dttp + stp -> stdp + idp dtdp4d6ddgdd -> dtdp4d6dd dtddglu -> dtdp9d6dd dtdp4d6dd -> dtdp4d6dd dtdp4lu -> dtdp4d6dd dtdp4lu -> dtdp4d6dd dtdp4ddd -> dtdp9al udp9 -> udpgal
NO3RUq1 NITMMOX NITRI1 NITRI2 NITGEN CAPK2 CARBONAH ADNK3 ADNK4 TDPORHR UDPG6D GJPTT1 UG1PUT TDPGLUD TDPORHE UDPG6E1 UDPG6E2 MMTF2 METHFH	Nitrogen Metabolism  Nucleotide Salvage Pathway  Nucleotide Salvage Pathway  Nucleotide Salvage Pathway  Nucleotide Salvage Pathway  Nucleotide sugars metabolism  One carbon pool by Folate  One carbon pool by Folate	Nitrate reductase (Ubiquinol-8) nitronate monooxygenase nitrite reductase nitrite reductase nitrite reductase nitrogenase carbamate kinase carbamate kinase carbonia anhydrase ademylate kinase (GTP) addrykate (GTP) add	1131216 17.14 17.14 118.6.1 27.22 42.11 27.43 27.73 11.1133 11.122 27.7.24 27.79 42.1.46 51.313 51.32 21.210 35.49	KOX_2365,KOX_23070/KOX_23075/KOX_23080/ KOX_23105 KOX_21140 KOX_04560/KOX_04565/iniD/KOX_23110 KOX_04560/KOX_04565/iniD/KOX_23110 KOX_04560/KOX_04555/kinD/KOX_23110 KOX_2420/KOX_24455/KOX_24930/KOX_24975/ KOX_1410/KOX_24990/ KOX_23275 KOX_143050(adk) KOX_25130 KOX_25130 KOX_25120 KOX_25120 KOX_25120 KOX_25120 KOX_25120 KOX_25125 KOX_25125 KOX_25125 KOX_25125 KOX_25125 KOX_25125 KOX_25125 KOX_25125 KOX_25125 KOX_25125 KOX_25125 KOX_14785	no3 + uqh2 -> no2 + uq + 2 hext  ethnit + o2 + fmnh2 -> acal + no2 + fmn no2 + 3 nadh -> 3 nad + nh4 no2 + 3 nadh -> 3 nad + nh4 16 atp + n2 + 8 rdferdx -> 16 pi + 16 adp + 8 oxferdx + 2 nh4 + h2  calhm + stp -> cap + adp h2co3 -< > co2 amp + ptp -<> adp + gdp amp + itp -<> adp + idp  dtdp4d6dm + nadph -> dtdprmn + nadp 2 nad + udpg -> 2 nadh + udpglcur  dttp + g1p -> tdtp4d6dg dtdp4d6dg -> dtdp4d6dg dtdp4d6dg -> dtdp4d6dg
NO3RUq1 NITMMOX NITR11 NITR12 NITGEN CAPK2 CARBONAH ADNK3 ADNK4 TDPDRHR UDPG6D GIPTT1 UG1PUT TDPGLUD TDPDRHE UDPG4E1 UDPG4E2 AMTF2 METHEH FORTF	Nitrogen Metabolism  Nucleotide Salvage Pathway  Nucleotide Salvages metabolism  Nucleotide sugars metabolism  One carbon pool by Folate	Nitrate reductase (Ubiquinol-8) nitronate monoxygenase nitrite reductase nitrite reductase nitrite reductase nitrogenase carbamate kinase carbamate kinase carbonic anhydrase adenylate kinase (ITP) admylate kinase (ITP) dTDP-4-dehydrorhamnose reductase UDP-glucose 6-dehydrogenase glucose-1-phosphate UTP-glucose-1-phosphate UTP-glucose-1-phosphate UTP-glucose-4-phosphate utnylkytransferase UTP-glucose 4-dehydratase dTDP-4-dehydrorhamnose 3,5-epimerase UDP-glucose 4-epimerase uDP-glucose 4-pimerase aminomethyltransferase 5,10-Methenyltetranyldrofolate 5-hydrolase (decyclizing) 5-formyltetrahydrofolate cycloligase L-lactate dehydrogenase (ubiquinone) L-lactate dehydrogenase (menaquinone) L-lactate dehydrogenase (menaquinone)	1131216 17.14 17.14 118.6.1 27.22 42.11 27.43 27.43 11.1133 11.122 27.7.24 27.7.9 5.13.13 5.13.2 5.13.2 5.13.2 5.13.2 6.3.3.2	KOX_23056,/KOX_23070/KOX_23075/KOX_23080/ KOX_23105 KOX_23110 KOX_Q4506/KOX_Q4565/iniD)/KOX_23110 KOX_Q4566/KOX_Q4555/KOX_Q4555/KOX_23110 KOX_Q4566/KOX_Q4555/KOX_Q4555/KOX_Q4575/KOX_Q44576/KOX_Q45576/KOX_Q45576/KOX_Q45576/KOX_Q45576/KOX_Q45576/KOX_Q45576/KOX_Q45576/KOX_Q45576/KOX_Q45576/KOX_Q45576/KOX_Q45576/KOX_Q45576/KOX_Q45576/KOX_Q45576/KOX_Q45576/KOX_Q45576/KOX_Q45576/KOX_Q45576/KOX_Q4567	no3 + uqh2 -> no2 + uq + 2 hext  ethnit + o2 + fmnh2 -> acal + no2 + fmn no2 + 3 nadh -> 3 nad + nh4 no2 + 3 nadh -> 3 nad + nh4 16 atp + n2 + 8 rdferdx -> 16 pi + 16 adp + 8 oxferdx + 2 nh4 + h2  calbm + stp -> cap + adp h2c3 -< > o2 amp + stp -> cap + adp h2c3 -< > o2 amp + stp -> adp + sdp dtop4d6dm + nadph -> dtdprmn + nadp  2 nad + udpg -> 2 nadh + udpglcur dttp + stp -> stp + udp dtdp4d6dd +> stdpplm + stdpplm + sdtdpslu -> stdp + sdp dtdp4d6dd +> dtdpdslu -> stdpdsld + spi stdp -> tdp -> dtdp4d6dd dtdp1u -> stdp4d6dd dtdp1u -> stdp4d6dd dtdp1u -> stdp4d6dd dtdp1u -> stdp3dd stdp4d6dd -> stdp3d stdp4dd -> stdp3d stdp4dd -> stdp4dd -> stdp4d stdp4d -> stdp4dd -> stdp4d stdp4d -> stdp4dd -> stdp4dd -> stdp4d stdp4d -> stdp4dd -> stdp
NO3RUq1 NITMMOX NITR11 NITR12 NITGEN CAPK2 CARBONAH ADNK3 ADNK4 TDPDRHR UDPG6D GIPTT1 UG1PUT TDPGLUD TDPDRHE UDPG4E1 UDPG4E2 AMTF2 METHEH FORTF LACDHq	Nitrogen Metabolism  Nucleotide Salvage Pathway  Nucleotide sugars metabolism  One carbon pool by Folate	Nitrate reductase (Ubiquinol-8) nitronate monoxygenase nitrite reductase nitrite reductase nitrite reductase nitrogenase carbamate kinase carbamate kinase carbonic anhydrase adenylate kinase (GTP) adenylate (GTP) ade	1131216 1714 1714 11861 2722 4211 2743 111133 11112 277.724 277.79 51313 5132 51312 5132 5132 6332	KOX_23065,/KOX_23070/KOX_23075,/KOX_23080/ KOX_23105 KOX_23110 KOX_241140 KOX_Q4506/KOX_Q4565/initD)/KOX_23110 KOX_Q4506/KOX_Q4555/KinD)/KOX_23110 KOX_Q4566/KOX_Q4555/KinD)/KOX_23110 KOX_Q4506/KOX_Q4555/KIND, 24935/KOX_24935/KOX_Q4935/KOX_Q4935/KOX_Q4936/KOX_24975/ KOX_Q431401/KOX_24990/ KOX_23275 KOX_Q4135,/KOX_11145/KOX_22245 KOX_1309(jadk) KOX_25130 KOX_25130 KOX_25135 KOX_25135 KOX_25145 KOX_25145 KOX_25145 KOX_25145 KOX_2514785 KOX_Q490(jav7) KOX_13225 KOX_Q490(jav7) KOX_13225 KOX_Q5795(lidD) KOX_05795(lidD)	no3 + uqh2 -> no2 + uq + 2 hext  ethnit + o2 + fmnh2 -> acal + no2 + fmn no2 + 3 nadh -> 3 nad + nh4 no2 + 3 nadh -> 3 nad + nh4 16 atp + n2 + 8 rdferdx -> 16 pi + 16 adp + 8 oxferdx + 2 nh4 + h2  calbm + stp -> cap + adp h2c3 -< > o2 amp + stp -> cap + adp h2c3 -< > o2 amp + stp -> adp + idp  dtop4d6dm + nadph -> dtdprmn + nadp 2 nad + udpg -> 2 nadh + udpglcur dttp + stp -> stp + udp glp -> dtdp4d6ddg dtdp4d6dg -> dtdp4d6dd dtdp9lu -> dtdp4d6dg dtdp4d6dg -> dtdp3d6dd dtdp4d6dg -> dtdp3dl methf -> 5fthf methf -> 5fthf methf -> fthf  Sfthf + atp -> adp + pi + methf  llac + uq -> pyr + uqh2
NO3RUq1 NITMMOX NITRT1 NITRT2 NITRT2 NITRT2 CAPK2 CARRONAH ADNK3 ADNK4 TUPDGED G1PTT1 UG1PUT TDPGLUD TUPDGE1 UDPGGE1 UDPGGE2 AMTF2 METHEH FORTF LACDHq LACDHm PRGNFT2 GL3PDq	Nitrogen Metabolism  Nucleotide Sugars metabolism  Oncardon pool by Folate  One carbon pool by Folate  One carbon pool by Folate  Oxidative Phosphorylation  Oxidative Phosphorylation	Nitrate reductase (Ubiquinol-8) nitronate monoxygenase nitrite reductase nitrite reductase nitrite reductase nitrite reductase nitrogenase carbamate kinase carbonic anhydrase adenylate kinase (GTP) adenylate (	1131216 1714 1714 11861 2722 4211 2743 111133 11112 27.724 27.724 27.79 42146 51313 5132 51312 51312 5132 11123 11123 11123 121210 35.49 6332 1123 1123 1123 1123 1123	KOX_23065,/KOX_23070/KOX_23075,/KCX_23080/ KOX_23105 KOX_231140 KOX_Q4506/KOX_Q4565/iniD)/KOX_23110 KOX_Q4506/KOX_Q4555/KinD)/KOX_23110 KOX_Q4566/KOX_Q4055/KIND)/KOX_23110 KOX_Q456/KOX_Q4055/KOX_Q4055/KOX_Q4057/KOX_Q	no3 + uqh2 -> no2 + uq + 2 hext  ethnit + o2 + fmnh2 -> acal + no2 + fmn no2 + 3 nadh -> 3 nad + nh4 no2 + 3 nadh -> 3 nad + nh4 16 atp + n2 + 8 rdferdx -> 16 pi + 16 adp + 8 oxferdx + 2 nh4 + h2  cabm + atp -> cap + adp  brood -> o20  amp + gtp -<> adp + gdp  amp + gtp -<> adp + gdp  dtdp-dd6dm + nadph -> dtdprmn + nadp  2 nad + udpg -> 2 nadh + udpglour  dttp + g1p -> dtdpflglu + ppi  g1p + utp -> ppi + udpg  dtdpdplu> -> dtdpdd6dm  dtdpdplu> -> dtdpdd6dm  dtdpdplu> -> dtdpdd6dm  ftdpglu -> btdpglu + ppi  g1p + utp -> ppi + udpg  dtdpdplu> -> dtdpddddm  ftdpglu -> btdpddddg  ftdpddddg -> dtdpddddm  ftdpglu -> ftdpddidm  ftdpglu -> fthf  Sfthf + atp -> adp + pi + methf  llac + uq -> pyr + uqh2  llac + mk -> pyr + mqn  methf + gar -> thf + fgam  gly<3p + uq -> dhap + uqh2
NO3RUq1 NITMMOX NITR11 NITR12 NITGEN CAPK2 CARBONAH ADNK3 ADNK4 TDPDRHR UDPG6D GIPTT1 UG1PUT TDPGLUD TDPDRHE UDPG4E1 UDPG4E2 AMTF2 METHEH FORTF LACDHq LACDHm PRGNFT2	Nitrogen Metabolism Nucleotide Salvage Pathway Nucleotide Salvage Pathway Nucleotide Salvage Pathway Nucleotide Salvage Pathway Nucleotide Salvages metabolism Nucleotide sugars metabolism Once acrbon pool by Folate One carbon pool by Folate Oxidative Phosphonylation Oxidative Phosphonylation One carbon pool by Folate	Nitrate reductase (Ubiquinol-8) nitronate monoxygenase nitrite reductase nitrite reductase nitrite reductase nitrogenase carbamate kinase carbonic anhydrase adenyfate kinase (GTP) adenyfate kinase (GTP) adenyfate kinase (TP) dTDP-4-dehydrorhamnose reductase UDPglucose 6-dehydrorhamnose reductase UTP-glucose 6-dehydrorhamnose troughyftransferase (TP-glucose 1-phosphate utrighyftransferase (TP-glucose 4-dehydratase dTDP-4-dehydrorhamnose 3,5-epimerase UDP-glucose 4-epimerase aminomethyftransferase S,10-Methenyttetrahydrofolate 5-hydrolase (dekyclizing) 5-formyftetrahydrofolate cycloligase L-lactate dehydrogenase (ubiquinone) phosphorbosylghcinamide formyftransferase glycerol-3-phosphate dehydrogenase (ubiquinone-8)	1131216 1714 1714 11861 2722 4211 2743 111133 11112 27,724 27,724 27,729 421,46 51313 5132 5132 21210 35,49 63,32 1123 1123 1123	KOX_23065,/KOX_23070/KOX_23075,/KCX_23080/ KOX_23105 KOX_231140 KOX_Q4506/KOX_Q4565/iniD)/KOX_23110 KOX_Q4506/KOX_Q4555/KinD)/KOX_23110 KOX_Q4566/KOX_Q4055/KIND)/KOX_23110 KOX_Q456/KOX_Q4055/KOX_Q4055/KOX_Q4057/KOX_Q	no3 + uqh2 -> no2 + uq + 2 hext  ethnit + o2 + fmnh2 -> acal + no2 + fmn no2 + 3 nadh -> 3 nad + nh4 no2 + 3 nadh -> 3 nad + nh4 16 atp + n2 + 8 rdferdx -> 16 pi + 16 adp + 8 oxferdx + 2 nh4 + h2  cathm + stp -> cap + adp h2c3 -< > o2 amp + gtp -> adp + gdp amp + tg +> adp + idp  dtdp-ld6dm + nadph -> dtdprmn + nadp 2 nad + udpg -> 2 nadh + udpglcur  dttp + gtp -> dtdp-ld6dg ld6dg ld7dg ld
NO3RUq1 NITMMOX NITRT1 NITRT2 NITRT2 NITRT2 CAPK2 CARRONAH ADNK3 ADNK4 TUPDGED G1PTT1 UG1PUT TDPGLUD TUPDGE1 UDPGGE1 UDPGGE2 AMTF2 METHEH FORTF LACDHq LACDHm PRGNFT2 GL3PDq	Nitrogen Metabolism  Nucleotide Sugars metabolism  Oncardon pool by Folate  One carbon pool by Folate  One carbon pool by Folate  Oxidative Phosphorylation  Oxidative Phosphorylation	Nitrate reductase (Ubiquinol-8) nitronate monoxygenase nitrite reductase nitrite reductase nitrite reductase nitrogenase carbamate kinase carbamate kinase carbonic anhydrase adentylate kinase (ITP) adentylate (ITP) adentylate kinase (ITP) adentylate (ITP) ade	1131216 1714 1714 1714 11861 2722 4211 2743 27743 111133 11122 27724 22779 42146 51313 5132 5132 5132 5132 5132 1123 1123	KOX_23065,/KOX_23070/KOX_23075,/KCX_23080/ KOX_23105 KOX_231140 KOX_Q4506/KOX_Q4565/iniD)/KOX_23110 KOX_Q4506/KOX_Q4555/KinD)/KOX_23110 KOX_Q4566/KOX_Q4055/KIND)/KOX_23110 KOX_Q456/KOX_Q4055/KOX_Q4055/KOX_Q4057/KOX_Q	no3 + uqh2 -> no2 + uq + 2 hext  ethnit + o2 + fmnh2 -> acal + no2 + fmn no2 + 3 nadh -> 3 nad + nh4 no2 + 3 nadh -> 3 nad + nh4 16 atp + n2 + 8 rdferdx -> 16 pi + 16 adp + 8 oxferdx + 2 nh4 + h2  cabm + atp -> cap + adp  brood -> o20  amp + gtp -<> adp + gdp  amp + gtp -<> adp + gdp  dtdp-dd6dm + nadph -> dtdprmn + nadp  2 nad + udpg -> 2 nadh + udpglour  dttp + g1p -> dtdpflglu + ppi  g1p + utp -> ppi + udpg  dtdpdplu> -> dtdpdd6dm  dtdpdplu> -> dtdpdd6dm  dtdpdplu> -> dtdpdd6dm  ftdpglu -> btdpglu + ppi  g1p + utp -> ppi + udpg  dtdpdplu> -> dtdpddddm  ftdpglu -> btdpddddg  ftdpddddg -> dtdpddddm  ftdpglu -> ftdpddidm  ftdpglu -> fthf  Sfthf + atp -> adp + pi + methf  llac + uq -> pyr + uqh2  llac + mk -> pyr + mqn  methf + gar -> thf + fgam  gly<3p + uq -> dhap + uqh2
NO3RUq1  NITMMOX NITET1 NITRT2  NITGEN CAPK2 CARBONAH ADNK3 ADNK4 TDPORHR UDPG6D GIPTT1 UG1PUT TDPGLUD TDPORHE UDPG4E1 UDPG4E1 UDPG4E2 METHFH FORTF LACDHq LACDHm PRGNFT2 GL3PDq GL3PDd	Nitrogen Metabolism  Nucleatide Salvage Pathway  Nucleatide Salvage Pathway  Nucleatide Salvage Pathway  Nucleatide sugars metabolism  Nuc	Nitrate reductase (Ubiquinol-8) nitronate monooxygenase nitrite reductase nitrite reductase nitrite reductase nitrite reductase nitrogenase carbamate kinase carbonic anhydrase adentylate kinase (GTP) adentylate (GTP) adent	1131216 1714 1714 1714 11861 2722 4211 2743 27743 111133 11122 27724 22779 42146 51313 5132 5132 5132 5132 5132 1123 1123	KOX_23056,/KOX_23070/KOX_23075/KOX_23080/ KOX_23105 KOX_23110 KOX_Q4506/KOX_04565(nitD)/KOX_23110 KOX_04506/KOX_04565(nitD)/KOX_23110 KOX_04566/KOX_04565(nitD)/KOX_23110 KOX_04506/KOX_04565(nitD)/KOX_23110 KOX_14401/KOX_24959/KOX_04930/KOX_24975/ KOX_04138/KOX_11145/KOX_22245 KOX_13050(nitd) KOX_25130 KOX_13050(nitd) KOX_25130 KOX_25130 KOX_25140 KOX_25140 KOX_25145 KOX_14785 KOX_14785 KOX_14785 KOX_14785 KOX_14785 KOX_14785 KOX_14785 KOX_14785 KOX_05795(lidD) KOX_05795(lidD) KOX_05795(lidD) KOX_05795(lidD) KOX_05795(lidD)	no3 + uqh2 -> no2 + uq + 2 hext  ethnit + o2 + fmnh2 -> acal + no2 + fmn no2 + 3 nadh -> 3 nad + nh4 no2 + 3 nadh -> 3 nad + nh4 16 atp + n2 + 8 rdferdx -> 16 pi + 16 adp + 8 oxferdx + 2 nh4 + h2  cathm + atp -> cap + adp  brood -> o2  amp + gtp -> adp + gdp  amp + tp (-> adp + gdp  amp + tp (-> adp + idp  dtdp4d6dm + nadph -> dtdprmn + nadp  2 nad + udpg -> 2 nadh + udpglcur  dttp + g1p -> dtdpfulp + ppi  g1p + utp -> ppi + udpg  dtdp4d6dg -> dtdp4d6dm  dtdpqlu -> dtdp4d6dm  dtdpqlu -> dtdp4d6dm  ftdpqlu -> tdtppall  udpg -> udpg -> bdgpall  methf -> 5thtf  methf -> fhf  5fhf + atp -> adp + pi + methf  llac + uq -> pyr + uqh2  llac + mk -> pyr + mqh  methf + gar -> thf + fgam  gly-3p + ud-> dhap + uqh2  gly-3p + mk -> dhap + mqn
NO3RUq1  NITMMOX NITRI1 NITRI2  NITGEN CAPK2 CARBONAH ADNK3 ADNK4 TDPORHR UDPG6D GIPTT1 UG1PUT TDPGLUD TDPORHE UDPG6E1 UDPG6E2 AMTF2 METHEH FORTF LACDHq LACDHm PRGNFTZ GL3PDq GL3PDd	Nitrogen Metabolism  Nucleotide Salvage Pathway  Nucleotide Salvage Pathway  Nucleotide Salvage Pathway  Nucleotide sugars metabolism  Once carbon pool by Folate  One carbon pool by Folate  One carbon pool by Folate  Oxidative Phosphonylation  Oxidative Phosphonylation  Oxidative Phosphonylation  Oxidative Phosphonylation	Nitrate reductase (Ubiquinol-8) nitronate monooxygenase nitrite reductase nitrite reductase nitrite reductase nitrite reductase nitrogenase carbamate kinase carbonic anhydrase adentylate kinase (GTP) adentylate (	1131216 1714 1714 11861 2722 4211 2743 111133 11112 27724 27724 27729 42146 51313 5132 5132 21210 3549 6332 1123 1123 1123 1123 1123 11295 11995	KOX_23056,/KOX_23070/KOX_23075/KOX_23080/ KOX_23105 KOX_23110 KOX_Q4506/KOX_04565(nitD)/KOX_23110 KOX_04506/KOX_04565(nitD)/KOX_23110 KOX_04566/KOX_04565(nitD)/KOX_23110 KOX_04506/KOX_04565(nitD)/KOX_23110 KOX_14401/KOX_24959/KOX_04930/KOX_24975/ KOX_04138/KOX_11145/KOX_22245 KOX_13050(nitd) KOX_25130 KOX_13050(nitd) KOX_25130 KOX_25130 KOX_25140 KOX_25140 KOX_25145 KOX_14785 KOX_14785 KOX_14785 KOX_14785 KOX_14785 KOX_14785 KOX_14785 KOX_14785 KOX_05795(lidD) KOX_05795(lidD) KOX_05795(lidD) KOX_05795(lidD) KOX_05795(lidD)	no3 + uqh2 -> no2 + uq + 2 hext  ethnit + o2 + fmnh2 -> acal + no2 + fmn no2 +3 nadh -> 3 nad + nh4 no2 +3 nadh -> 3 nad + nh4 16 atp + n2 +8 rdferdx -> 16 pi + 16 adp +8 oxferdx +2 nh4 + h2  cathm + stp -> cap + adp h2c3 -< > o2 mp + gtp -> adp + gdp amp + tp c-> adp + jdp  dtdp-4d6dm + nadph -> dtdprmn + nadp 2 nad + udpg -> 2 nadh + udpglcur  dttp + gtp -> dtdp-3d6dg dtdp-4d6dg dtdp-4d6dg dtdp-4d6dg dtdp-4d6dg dtdp-4d6dg dtdp-3de dtdp-3d
NO3RUq1  NITMMOX NITRT1 NITRT2 NITRT2 NITGEN CAPK2 CARBONAH ADNK3 ADNK4 TDPORHR UDPGGD G1PTT1 UG1PUT TDPGLUD TDPDRHE UDPGGE1 UDPGGE2 AMTF2 METHEH FORTF LACDHq LACDHm PRGNFT2 GL3PDd GL3PDd GL3PDd GL3PDm	Nitrogen Metabolism  Nucleotide sugars metabolism  One carbon pool by Folate  One carbon pool by Folate  One carbon pool by Folate  Oxidative Phosphonylation  Oxidative Phosphonylation  Oxidative Phosphonylation  Oxidative Phosphonylation	Nitrate reductase (Ubiquinol-8) nitronate monooxygenase nitrite reductase nitrite reductase nitrite reductase nitrite reductase nitrogenase carbamate kinase carbonic anhydrase adentylate kinase (GTP) adentylate (	1131216 1714 1714 11861 2722 4211 2743 111133 11112 27.724 27.724 27.79 42146 51313 5132 51312 5132 21210 35.49 6332 11123 11123 1123 11123 1129 11995 11995	KOX_2365_KOX_23070/KOX_23075/KOX_23080/ KOX_23105 KOX_23110 KOX_24140 KOX_04560/KOX_04565(nirb)/KOX_23110 KOX_04560/KOX_04565(nirb)/KOX_23110 KOX_04560/KOX_04565(nirb)/KOX_23110 KOX_04560/KOX_04565(nirb)/KOX_23110 KOX_14560/KOX_14565(nirb)/KOX_23110 KOX_1450/KOX_1456(nirb)/KOX_24930/KOX_24975/ KOX_04135/KOX_11145/KOX_22245 KOX_23275 KOX_125130 KOX_25130 KOX_25130 KOX_25135 KOX_25140 KOX_25135 KOX_23040/KOX_25220 KOX_25140 KOX_14785 KOX_14785 KOX_14785 KOX_14785 KOX_14785 KOX_14785 KOX_14785 KOX_14785 KOX_15795(lidb) KOX_05795(lidb) KOX_05795(lidb) KOX_05795(lidb) KOX_05795(lidb) KOX_05795(lidb) KOX_05795(lidb)	no3 + uqh2 -> no2 + uq + 2 hext  ethnit + o2 + fmnh2 -> acal + no2 + fmn no2 + 3 nadqh -> 3 nadq + nh4 no2 + 3 nadqh -> 3 nadq + nh4 16 atp + n2 + 8 rdferdx -> 16 pi + 16 adp + 8 oxferdx + 2 nh4 + h2 caltm + stp -> cap + adp hzca3 -< > ca2 amp + gtp -<> adp + gdp amp + itp -<> adp + idp didp4dddm + nadqh -> drdpmm + nadp 2 nad + udpg -> 2 nadh + udpglcur dttp + g1p -> drdpplu + ppi g1p + utp -> ppi + udpg drddpdddd -> drdpdddddddddddddddddddddddddddddddddd
NO3RUq1  NITMMOX NITET1 NITRT2  NITGEN CAPK2 CARBONAH ADNK3 ADNK4 TDPDRHR UDPG6D G1PTT1  UG1PUT TDPGUD TDPDRHE UDPG6E1 UDPG6E2 AMT62 METHFH FORTF LACDHq LACDHm PRGNFT2 GL3PDd GL3PDd GL3PDd GL3PDd HYDGq HYDGd	Nitrogen Metabolism  Nucleotide Salvage Pathway  Nucleotide Salvage Pathway  Nucleotide Salvage Pathway  Nucleotide Salvage Pathway  Nucleotide sugars metabolism  One carbon pool by Folate  One carbon pool by Folate  Oxidative Phosphorylation  Oxidative Phosphorylation  Oxidative Phosphorylation  Oxidative Phosphorylation  Oxidative Phosphorylation	Nitrate reductase (Ubiquinol-8) nitronate monooxygenase nitrite reductase nitrite reductase nitrite reductase nitrite reductase nitrogenase carbamate kinase carbonic anhydrase adentylate kinase (GTP) adentylate (GTP)	1131216 1714 1714 171861 1727 2722 4211 2743 111133 11122 27724 2779 42146 51313 5132 5132 7121 3549 6332 1123 1123 1123 1123 1129 11995 11995 11995 118991	KOX_2365_KOX_23070/KOX_23075/KOX_23080/ KOX_23105 KOX_23110 KOX_24140 KOX_04560/KOX_04565(nirb)/KOX_23110 KOX_04560/KOX_04565(nirb)/KOX_23110 KOX_04560/KOX_04565(nirb)/KOX_23110 KOX_04560/KOX_04565(nirb)/KOX_23110 KOX_14560/KOX_14565(nirb)/KOX_23110 KOX_1450/KOX_1456(nirb)/KOX_24930/KOX_24975/ KOX_04135/KOX_11145/KOX_22245 KOX_23275 KOX_125130 KOX_25130 KOX_25130 KOX_25135 KOX_25140 KOX_25135 KOX_23040/KOX_25220 KOX_25140 KOX_14785 KOX_14785 KOX_14785 KOX_14785 KOX_14785 KOX_14785 KOX_14785 KOX_14785 KOX_15795(lidb) KOX_05795(lidb) KOX_05795(lidb) KOX_05795(lidb) KOX_05795(lidb) KOX_05795(lidb) KOX_05795(lidb)	no3 + uqh2 -> no2 + uq + 2 hext  ethnit + o2 + fmnh2 -> acal + no2 + fmn no2 + 3 nadqh -> 3 nadq + nh4 no2 + 3 nadqh -> 3 nadq + nh4 16 atp + n2 + 8 rdferdx -> 16 pi + 16 adp + 8 oxferdx + 2 nh4 + h2 caltm + stp -> cap + adp hzca3 -< > o22 amp + gtp -> adp + gdp amp + itp -> adp + idp didp4dddm + nadqh -> drdpmn + nadp 2 nad + udpg -> 2 nadh + udpglcur dttp + g1p -> drdpplu + ppi g1p + utp -> ppi + udpg drddpddddm + ox drdpfmd drdpglu -> drdp4dddg drddpddddg -> drdpddddg drddpdddg -> drdpddddg drdpglu -> brdp4dddg drdpglu -> brdp4dddg drdpglu -> brdp5ddfdm drdpglu -> brdp4ddfdm drdpglu -> brdp5ddfdm drdpglu -> brdp4ddfdm drdpglu -> brdp4ddfdm methf -> 5thrf sethf -> xpr + uqh2 llac + wc -> pyr + uqh2 llac + mk -> pyr + mqn methf + gar -> thf + fgam glyc3p + uq -> dhap + uqh2 glyc3p + 2dmmq8 -> dhap + mqn uq + h2 -> udh2 + 2 hext 2dmmq8 + h2 -> 2dmmql8 + 2 hext
NO3RUq1  NITMMOX NITET1 NITRT2  NITGEN CAPK2 CARBONAH AONK3 AONK4 TDPDRHR UDPG6D G1PTT1  UG1PUT TDPGLUD TDPDRHE UDPG6E1 UDPG6E2 AMT62 METHFH FORTF LACDHq LACDHm PRGNFT2 GL3PDd GL3PDd GL3PDd HYDGq HYDGd HYDGd HYDGd	Nitrogen Metabolism  Nucleotide Salvage Pathway  Nucleotide Salvage Pathway  Nucleotide Salvage Pathway  Nucleotide sugars metabolism  One carbon pool by Folate  One carbon pool by Folate  Oxidative Phosphorylation  Oxidative Phosphorylation  Oxidative Phosphorylation  Oxidative Phosphorylation  Oxidative Phosphorylation  Oxidative Phosphorylation	Nitrate reductase (Ubiquinol-8) nitronate monooxygenase nitrite reductase nitrite reductase nitrite reductase nitrogenase carbamate kinase carbamate kinase carbonic anhydrase adentylate kinase (GTP) adentylate kinase (GTP) adentylate kinase (GTP) adentylate kinase (TIP) adentylate (TIP) adentylate kinase (TIP) adentylate (TIP) adenty	1131216 1714 1714 1714 1186.1 27.22 4211 27.43 27.43 111122 27.724 22.779 421.46 51313 51.12 51.32 51.	KOX_2365_KOX_23070/KOX_23075/KOX_23080/ KOX_23105 KOX_23110 KOX_24140 KOX_04560/KOX_04565(nirb)/KOX_23110 KOX_04560/KOX_04565(nirb)/KOX_23110 KOX_04560/KOX_04565(nirb)/KOX_23110 KOX_04560/KOX_04565(nirb)/KOX_23110 KOX_14560/KOX_14565(nirb)/KOX_23110 KOX_1450/KOX_1456(nirb)/KOX_24930/KOX_24975/ KOX_04135/KOX_11145/KOX_22245 KOX_23275 KOX_04135/KOX_11145/KOX_22245 KOX_25130 KOX_25130 KOX_25130 KOX_25135 KOX_25140 KOX_25135 KOX_14785 KOX_15795(lidb) KOX_05795(lidb) KOX_05795(lidb) KOX_05795(lidb) KOX_05795(lidb) KOX_23845(purT)/KOX_27160(purN)	no3 + uqh2 -> no2 + uq + 2 hext  ethnit + o2 + fmnh2 -> acal + no2 + fmn no2 + 3 nadqh -> 3 nadq + nh4 no2 + 3 nadqh -> 3 nadq + nh4 16 atp + n2 + 8 rdferdx -> 16 pi + 16 adp + 8 oxferdx + 2 nh4 + h2 caltm + stp -> cap + adp hzca3 -< > ca2 amp + gtp -<> adp + gdp amp + itp -<> adp + idp didp4dddm + nadqh -> drdpmm + nadp 2 nad + udpg -> 2 nadh + udpglcur dttp + g1p -> drdpplu + ppi g1p + utp -> ppi + udpg drddpdddd -> drdpdddddddddddddddddddddddddddddddddd

POX	Oxidative Phosphorylation	pyruvate oxidase	1.2.5.1	KOX_15775 KOX_08760/KOX_08765/KOX_08770/KOX_08775	
SUCCDq	Oxidative Phosphorylation	succinate dehydrogenase	1.3.99.1	KOX_14570(sdhC)/KOX_14575(sdhD)/KOX_1458 (sdhA)/KOX_14585(sdhB)/KOX_21720	0 uq + succ -> fum + uqh2
NADPTH	Oxidative Phosphorylation	NAD(P) transhydrogenase	1.6.1.1/1.6.1.2	KOX_07395/KOX_21820(pntB)/KOX_21825(pntA KOX_26335/KOX_26340/KOX_26345/KOX_26350	
NADHHq1	Oxidative Phosphorylation	NADH dehydrogenase (ubiquinone-8 & 3 protons)	1.6.5.3/1.6.99.3	KOX_26355/KOX_26360/KOX_26365/KOX_26370 KOX_26375/KOX_26380/KOX_26385/KOX_26390 KOX_26395/KOX_17375	)/naun + uq -> nau + uqnz + 3 next
NADHHd1	Oxidative Phosphorylation	NADH dehydrogenase (demethylmenaquinone-8 & 3 protons)	1.6.5.3/1.6.99.3	KOX_26395/KOX_1/3/5	0/ nadh + 2dmmq8 -> nad + 2dmmql8 + 3 hext
NADHHm1	Oxidative Phosphorylation	NADH dehydrogenase (menaquinone-8 & 3 protons)	1.6.5.3/1.6.99.3	KOX_26335/KOX_26340/KOX_26345/KOX_26350 KOX_26355/KOX_26360/KOX_26365/KOX_26370 KOX_26375/KOX_26380/KOX_26385/KOX_26390 KOX_26395/KOX_17375	0/ nadh + mk -> nad + mqn + 3 hext
NADHHq2	Oxidative Phosphorylation	NADH dehydrogenase (ubiquinone-8)	1.6.5.3/1.6.99.3	KOX_26335/KOX_26340/KOX_26345/KOX_26350 KOX_26355/KOX_26360/KOX_26365/KOX_26370 KOX_26375/KOX_26380/KOX_26385/KOX_26390 KOX_26395/KOX_17375	0/ nadh + uq -> nad + uqh2
NADHHd2	Oxidative Phosphorylation	NADH dehydrogenase (demethylmenaquinone-8)	1.6.5.3/1.6.99.3	KOX_26335/KOX_26340/KOX_26345/KOX_26350 KOX_26355/KOX_26360/KOX_26365/KOX_26370 KOX_26375/KOX_26380/KOX_26385/KOX_26390 KOX_26395/KOX_17375	0/ nadh + 2dmmq8 -> nad + 2dmmql8
NADHHm2	Oxidative Phosphorylation	NADH dehydrogenase (menaquinone-8 )	1.6.5.3/1.6.99.3	KOX_26335/KOX_26340/KOX_26345/KOX_26350 KOX_26355/KOX_26360/KOX_26365/KOX_26370 KOX_26375/KOX_26380/KOX_26385/KOX_26390 KOX_26395/KOX_17375	0/ nadh + mk -> nad + mqn
NO3RUq2	Oxidative Phosphorylation	Nitrate reductase (ubiquinol-8)	1.7.99.4	KOX_19980/KOX_19985/KOX_19990/KOX_19995 KOX_23065/KOX_23070/KOX_23075/KOX_23086 KOX_23105 KOX_19980/KOX_19985/KOX_19990/KOX_19995	0/no3 + uqh2 -> no2 + uq + 2 hext
NO3RUm	Oxidative Phosphorylation	Nitrate reductase (menaquinol- 8)	1.7.99.4	KOX_19980/KOX_19985/KOX_19990/KOX_19999 KOX_23065/KOX_23070/KOX_23075/KOX_23080 KOX_23105	
THIORp	Oxidative Phosphorylation	thioredoxin reductase (NADPH)		KOX_15885	nadph + othio -> nadp + rthio
ATPSYN	Oxidative Phosphorylation	ATP synthase (four protons for one ATP)	3.6.3.14	KOX_06705(atpC)/KOX_06710/KOX_06715/KOX_ 06720/KOX_06725/KOX_06730/KOX_06735/KOX_	
BTCRNCT	Oxidative Phosphorylation	gamma-butyrobetainyl-CoA:		06740	bbtcoa + crn <-> crncoa + gbbtn
CTBTCRNCT	Oxidative Phosphorylation	carnitine CoA transferase crotonobetainyl-CoA: carnitine			crn + ctbtcoa <-> crncoa + ctbt
CRNCDH	Oxidative Phosphorylation	CoA transferase Carnityl-CoA dehydratse	4.2.1.89		crncoa <-> ctbtcoa
CRNCOAL	Oxidative phosphorylation	Carnitine-CoA Ligase cytochrome oxidase bd			atp + coa + crn -> adp + crncoa + pi
CYTCOBDq	Oxidative Phosphorylation	(ubiquinol-8: 2 protons) cytochrome oxidase bo3			0.5 o2 + uqh2 -> uq + 2 hext
CYTCOBOq3	Oxidative Phosphorylation	(ubiquinol-8: 4 protons)			0.5 o2 + uqh2 -> uq + 4 hext
NADTRHG NITRR	Oxidative Phosphorylation Oxidative Phosphorylation	NAD transhydrogenase nitrite Reductase (NADH)			nad + nadph -> nadh + nadp 3 nadh + no2 -> 3 nad + nh4
SUCCD2 DMSORDm	Oxidative phosphorylation Oxidative phosphorylation	succinate dehydrogenase Dimethyl sulfoxide reductase	1.8.5.3	KOX_15920	fadh2 + uq -> fad + uqh2 dmso + mqn -> dms + mk
		(Menaquinol 8) Dimethyl sulfoxide reductase			
DMSORDd	Oxidative phosphorylation	(Demethylmenaquinol 8) Dimethyl sulfoxide reductase	1.8.5.3	KOX_15920	dmso + 2dmmql8 -> dms + 2dmmq8
DMSORDme	Oxidative phosphorylation	(Menaquinol 8) Dimethyl sulfoxide reductase	1.8.5.3	KOX_15920	dmso_e + mqn -> dms_e + mk
DMSORDde	Oxidative phosphorylation	(Demethylmenaquinol 8)	1.8.5.3	KOX_15920	dmso_e + 2dmmql8 -> dms_e + 2dmmq8
TMAORm	Oxidative phosphorylation	Trimethylamine N-oxide reductase (menaquinol 8)			tmao + mqn -> tma + mk
TMAORd	Oxidative phosphorylation	Trimethylamine N-oxide reductase (demethylmenaquinol 8)			tmao + 2dmmql8 -> tma + 2dmmq8
TMAORme	Oxidative phosphorylation	Trimethylamine N-oxide reductase (menaquinol 8) Trimethylamine N-oxide			hext + tmao_e + mqn -> tma_e + mk
TMAORde	Oxidative phosphorylation	reductase (demethylmenaquinol 8) Glucose dehydrogenase			hext + tmao_e + 2dmmql8 -> tma_e + 2dmmq8
GLCDHe	Oxidative phosphorylation	(ubiquinone-8 as acceptor) NADPH Quinone Reductase			glc_e + uq -> gluc_e + hext + uqh2
NADPHQRq	Oxidative phosphorylation	(Ubiquinone-8)			nadph + uq -> nadp + uqh2
NADPHQRd	Oxidative phosphorylation	NADPH Quinone Reductase (Demethylmenaquinone-8)			nadph + 2dmmq8 -> nadp + 2dmmql8
NADPHQRm	Oxidative phosphorylation	NADPH Quinone Reductase (Menaquinone-8)			nadph + mk -> nadp + mqn
PPK2 PPK1	Oxidative phosphorylation Oxidative phosphorylation	polyphosphate kinase polyphosphate kinase	2.7.4.1 2.7.4.1	KOX_27185 KOX_27185	atp + ppi <-> adp + ppi atp + pi <-> adp + ppi
QUIMOXq	Oxidative phosphorylation	quinol monooxygenase (Ubiquinol-8)			2 o2 + uqh2 -> 2 o2s + uq
QUIMOXm	Oxidative phosphorylation	quinol monooxygenase			mqn + 2 o2 -> mk + 2 o2s
CYTCOBDm	Oxidative phosphorylation	(Menaquinol-8) cytochrome oxidase bd			mqn + 0.5 o2 -> 2 hext + mk
DP2R	Pantothenate and CoA biosynthesis	(menaquinol-8: 2 protons) 2-dehydropantoate 2-reductase	1.1.1.169	KOX_12630/KOX_20880	dhpant + nadph -> nadp + pant
MOBHMT	Pantothenate and CoA biosynthesis	3-methyl-2-oxobutanoate hydroxymethyltransferase	2.1.2.11	KOX_11215(panB)	3mob + metthf -> dhpant + thf
DPCOAK PNTOK1	Pantothenate and CoA biosynthesis Pantothenate and CoA biosynthesis	dephospho-CoA kinase pantothenate kinase	2.7.1.24 2.7.1.33	KOX_10985(coaE) KOX_07870	atp + dpcoa -> adp + coa
PTHPAT	Pantothenate and CoA biosynthesis	pantetheine-phosphate	2.7.7.3	KOX_07870 KOX_05925(coaD)	atp + pnto -> 4ppnto + adp atp + 4ppnte <-> dpcoa + ppi
ACPS	Pantothenate and CoA biosynthesis	adenylyltransferase acyl-carrier protein synthase	2.7.8.7	KOX_27530(acpS)/KOX_05045	apoACP + coa -> ACP + pap
PPTCDC	Pantothenate and CoA biosynthesis	phosphopantothenoylcysteine decarboxylase	4.1.1.36	KOX_05950	4ppcys -> co2 + 4ppnte
PANTOS	Pantothenate and CoA biosynthesis	pantothenate synthase	6.3.2.1	KOX_11210(panC)	bala + atp + pant -> amp + pnto + ppi
PPNTCL1	Pantothenate and CoA biosynthesis	phosphopantothenate-cysteine ligase	0.3.2.3	KOX_05950	4ppnto + atp + cys -> 4ppcys + amp + ppi
PPNTCL2	Pantothenate and CoA biosynthesis	phosphopantothenate-cysteine ligase	0.3.2.3	KOX_05950	4ppnto + ctp + cys -> 4ppcys + cmp + ppi
PNTOK2 PNTOK3	Pantothenate and Coa Biosynthesis Pantothenate and Coa Biosynthesis	pantothenate kinase pantothenate kinase	2.7.1.33 2.7.1.33	KOX_07870 KOX_07870	atp + pantcys -> adp + 4ppcys atp + ptt -> adp + 4ppnte
ACPPDE	Pantothenate and CoA biosynthesis	acyl carrier protein phosphodiesterase	3.1.4.14	KOX_12515	ACP -> 4ppnte + apoACP
ALTRNH	Pentose and glucuronate interconversion	altronate hydrolase	4.2.1.7	KOX_03375/KOX_04830	dalt -> kdg
TAGATNR MANND	Pentose and glucuronate interconversion Pentose and glucuronate interconversion		1.1.1.58 4.2.1.8	KOX_10130/KOX_21230 KOX_11855	tagatn + nadh -> dalt + nad kdg <-> mann
MANNOX GLUCIS1	Pentose and glucuronate interconversion Pentose and glucuronate interconversion		1.1.1.57 5.3.1.12	KOX_11850/KOX_21505 KOX_03380	mann + nad <-> frutn + nadh frutn <-> dgluc
GLUCIS2	Pentose and glucuronate interconversion	glucuronate isomerase	5.3.1.12	KOX_03380	dgalac -> tagatn
ARAIS LRIBK	Pentose and glucuronate interconversion Pentose and glucuronate interconversion	L-ribulokinase	5.3.1.4 2.7.1.16	KOX_10760 KOX_10765	larabinose <-> Irib Irib + atp <-> IrI5p + adp
LRIB5P4E	Pentose and glucuronate interconversion	L-ribulose-5-phosphate 4- epimerase	5.1.3.4	KOX_10755(araD)	lrl5p <-> xu5p
XYLK XYLIS1	Pentose and glucuronate interconversion Pentose and glucuronate interconversion	xylulokinase	2.7.1.17 5.3.1.5	KOX_05620/KOX_14070/KOX_25450 KOX_05625	xu5p + adp <-> xylu + atp xylu <-> xyl
XYLIS2	Pentose and glucuronate interconversion	xylose isomerase	5.3.1.5	KOX_05625	fru -> glc
DRIBK XYL5P3E	Pentose and glucuronate interconversion  Pentose and glucuronate interconversion	L-xylulose 5-phosphate 3-	2.7.1.16 5/5.1.3.22	KOX_10765 KOX_05705	drib + atp <-> rl5p + adp lxu5p <-> lrl5p
3DHG6PD	Pentose and glucuronate interconversion	epimerase 3-dehydro-L-gulonate-6-	4.1.1.85	KOX_05700(sgbH)	3dhg6p -> lxu5p + co2
SDHG6PD LXYLK	Pentose and glucuronate interconversion  Pentose and glucuronate interconversion	phosphate decarboxylase	4.1.1.85 2.7.1.53	KOX_05/00(sgbH) KOX_05695/KOX_14470/KOX_20985	3dhgbp -> lxu5p + co2 lxylu + atp <-> lxu5p + adp
RMKx	Pentose and glucuronate interconversion		2.7.1.5	KOX_07210(rhaB)	lxylu + atp <-> lxu1p + adp
RM1PAx	Pentose and glucuronate interconversion	aldolase	4.1.2.19	KOX_07200	lxu1p <-> dhap + glal
ARBTD 3DHGXYLK	Pentose and glucuronate interconversion Pentose and glucuronate interconversion		1.1.1.11 2.7.1.53	KOX_25455 KOX_05695/KOX_14470/KOX_20985	xylu + nadh <-> darbt + nad 3dhg + atp -> 3dhg6p + adp
DKGULNR	Pentose and glucuronate interconversion		e 1.1.1.130	KOX_05675	3dhg + nad <-> 23dkgul + nadh
GLCNK	Pentose Phosphate Pathway	gluconokinase	2.7.1.12	KOX_04750(gntK)	atp + gluc -> d6pgc + adp
DDGLCNK	Pentose Phosphate Pathway	2-dehydro-3- deoxygluconokinase	2.7.1.45	KOX_05360/KOX_05550	kdg + atp -> kdpg + adp
ABSPI	Pentose Phosphate Pathway	arabinose-5-phosphate isomerase	5.3.1.13	KOX_03790	rl5p <-> a5p
R15BPK	Pentose Phosphate Pathway	ribose-1,5-bisphosphokinase phosphoribosylpyrophosphate	2.7.4.23	KOX_08535	atp + r15bp -> adp + prpp
PRPPS	Pentose Phosphate Pathway	synthetase	2.7.6.1	KOX_04485/KOX_23205	atp + r5p <-> amp + prpp

G6PDH	Dankers Discoulants Dathwess	glucose 6-phosphate	1.1.149	KOX 33860	and a surday of Surday and also
	Pentose Phosphate Pathway	dehydrogenase		KOX_23860 KOX_02620/KOX_13875/KOX_13880/KOX_15060/	
TRKT1	Pentose Phosphate Pathway	transketolase	2.2.1.1	KOX_15065/KOX_15945/KOX_15950/KOX_17475/ KOX_26445/KOX_26450/KOX_27035 KOX_02620/KOX_13875/KOX_13880/KOX_15060/	
TRKT2	Pentose Phosphate Pathway	transketolase	2.2.1.1	KOX_15065/KOX_15945/KOX_15950/KOX_17475/ KOX_26445/KOX_26450/KOX_27035	
TRADL PGL	Pentose Phosphate Pathway Pentose Phosphate Pathway	transaldolase 6-phosphogluconolactonase	2.2.1.2 3.1.1.31	KOX_10435/KOX_17470 KOX_14825	g3p + s7p <-> e4p + f6p 6pgl -> d6pgc
EDA	Pentose Phosphate Pathway	2-dehydro-3-deoxy- phosphogluconate aldolase	4.1.2.14	KOX_23850	kdpg -> g3p + pyr
EDD	Pentose Phosphate Pathway	6-phosphogluconate dehydratase	4.2.1.12	KOX_23855	d6pgc -> kdpg
RPE	Pentose Phosphate Pathway	ribulose 5-phosphate 3- epimerase	5.1.3.1	KOX_04590	rl5p <-> xu5p
RPI	Pentose Phosphate Pathway	ribose-5-phosphate isomerase 6-phosphogluconate		KOX_02530/KOX_08520/KOX_17465	r5p <-> rl5p
GND	Pentose Phosphate Pathway	dehydrogenase	1.1.1.44	KOX_25145	d6pgc + nadp -> rl5p + nadph + co2
QUIGDH	Pentose Phosphate Pathway	quinoprotein glucose dehydrogenase	1.1.5.2	KOX_11135	glc + uq -> g15l + uqh2
DOXPAD RIBK1	Pentose Phosphate Pathway	deoxyribose-phosphate aldolase	4.1.2.4		g3p + acal <-> 2dr5p
RIBK1 RIBK2	Pentose Phosphate Pathway Pentose Phosphate Pathway	ribokinase ribokinase	2.7.1.15 2.7.1.15		2dr5p + adp <-> doxrib + atp rib + atp <-> r5p + adp
GLUCDHp GLUCDH	Pentose Phosphate Pathway Pentose Phosphate Pathway	gluconate 2-dehydrogenase gluconate 2-dehydrogenase	1.1.1.215 1.1.1.215		2kgluc + nadph <-> gluc + nadp 2kgluc + nadh <-> gluc + nad
PAMPPT	Peptidoglycan Biosynthesis	phospho-N-acetylmuramoyl- pentapeptide-transferase	2.7.8.13	KOX_10910(mraY)	udcpp + ugmda -> uagmda + ump
UDCPDP	Peptidoglycan Biosynthesis	(meso-2,6-diaminopimelate)	3.6.1.27	KOX_03065	
UAMAGDS	Peptidoglycan Biosynthesis	UDP-N-acetylmuramoyl-L-	6.3.2.13	KOX_03003	udcpdp -> pi + udcpp  26dap-M + atp + uamag -> adp + pi + ugmd
UAMAGDS	replicoglycan biosynthesis	alanyl-D-glutamyl-meso-2,6- diaminopimelate synthetase	0.3.2.13	KOX_10400	Zodap-m + atp + damag -> aup + pi + ugmu
UAMAGDAS	Peptidoglycan Biosynthesis	UDP-N-acetylmuramoyl-L- alanyl-D-glutamyl-meso-2,6-	6.3.2.10	KOX_10905(murF)	alaala + atp + ugmd -> adp + pi + ugmda
		diaminopimeloyl-D-alanyl-D- alanine synthetase			
UACMAS	Peptidoglycan Biosynthesis	UDP-N-acetylmuramoyl-L- alanine synthetase	6.3.2.8	KOX_10930(murC)	ala + atp + udpnam -> adp + pi + uama
UACMAGS	Peptidoglycan Biosynthesis	UDP-N-acetylmuramoyl-L- alanyl-D-glutamate synthetase	6.3.2.9	KOX_10915(murD)	atp + dglu + uama -> adp + pi + uamag
UAGMPUT	Peptidoglycan Biosynthesis	UDP-N-acetylglucosamine-N- acetylmuramyl-	241227	KOX 10925(murG)	udenza a uzamda a ude
UNGWIEUT	r epiloogiytatii biosyiithesis	(pentapeptide)pyrophosphoryl- undecaprenol N- acetylolucosamine transferase	L.M.L.C./	1032J(IIIIIO)	udpnag + uagmda -> uaagmda + udp
GLNST2	Peptidoglycan Biosynthesis	acetylglucosamine transferase glutamine synthetase	6.3.1.2		uaagmda + atp + nh4 -> uaagmmda + adp + pi
NACMAA	Peptidoglycan Biosynthesis	N-acetylmuramoyl-L-alanine amidase UDP-N-	3.5.1.28	KOX_01555/KOX_08830/KOX_15755/KOX_26930	acala -> acmur + ala
UNAMPLA	Peptidoglycan Biosynthesis	acetylmuramoylpentapeptide-	2.3.2.10		5 gly + uaagmmda -> uaagmm5da
PGPS	Peptidoglycan Biosynthesis	lysine N6-alanyltransferase peptidoglycan precursor			uaagmm5da -> udcpdp + ppeptido
DALAT	Peptidoglycan Biosynthesis	synthesis D-alanine transaminase	2.6.1.21		ppeptido + dala -> PEPTIDO + dala_e
ALHD3	Phenylalanine metabolism	aldehyde dehydrogenase (phenylacetaldehyde, NAD)	1.2.1.39		nad + pacald -> nadh + pac
OXP4EH	Toluene and Xylene degradation	4-hydroxy-2-oxopentanoate	4.2.1.80	KOX_22680(mhpD)	op4en -> hopt
4H2OPPL	Toluene and Xylene degradation	forming)	4.1.3.39		hopt -> acal + pyr
PHEACL 3HCINNMH	Phenylalanine metabolism Phenylalanine metabolism	phenylacetate-CoA ligase 3-hydroxycinnamate	6.2.1.30 1.14.13.127	KOX_07020 KOX_22695(mhpA)	atp + coa + pac -> amp + phaccoa + ppi 3hcinnm + nadh + o2 -> dhcinnm + nad
3HPPPNH	Phenylalanine metabolism	hydroxylase 3-(3-hydroxy-phenyl)propionate		KOX_22695(mhpA)	3hpppn + nadh + o2 -> dhpppn + nad
4H2OPNTA	ŕ	hydroxylase 4-hydroxy-2-oxopentanoate	4.1.3.39	KOX_22693(IIIII)A)	
HPPH	Phenylalanine metabolism Phenylalanine metabolism	aldolase hippurate hydrolase	3.5.1.32	KOX_22670 KOX_13405/KOX_18515/KOX_22550	hopt -> acal + pyr benzot + gly -> hppr
CNTOB	Phenylalanine metabolism	unclear reaction 4-hydroxyphenylpyruvate			cinnm + nad -> benzot + ac + nadh
4HPHED2	Phenylalanine metabolism	4-hydroxyphenylpyruvate dioxygenase	1.13.11.27 1.43.21	KOX_22735 KOX_19410(tynA)	phpyr + o2 -> 2hpa + co2
4HPHED2 MNAO9 DAAD2	Phenylalanine metabolism Phenylalanine metabolism Phenylalanine metabolism	4-hydroxyphenylpyruvate dioxygenase monoamine oxidase D-Amino acid dehydrogenase	1.4.3.21 1.4.99.1	KOX_19410(tynA) KOX_23495	phpyr + o2 -> 2hpa + co2 pamn + o2 -> pacald + nh4 + h2o2 dphe + fad -> phpyr + nh4 + fadh2
4HPHED2 MNAO9	Phenylalanine metabolism Phenylalanine metabolism	4-hydroxyphenylpyruvate dioxygenase monoamine oxidase	1.4.3.21 1.4.99.1 1.11.1.21	CX_19410(tynA) KOX_23495 KOX_20220 KOX_19420(paaA)/KOX_19425(paaB)/KOX_19430	phpyr + o2 -> 2hpa + co2 peamn + o2 -> pacald + nh4 + h2o2
4HPHED2 MNAO9 DAAD2 CATPRX PHACCOAO	Phenylalanine metabolism Phenylalanine metabolism Phenylalanine metabolism Phenylalanine metabolism Phenylalanine metabolism Phenylalanine metabolism	4-hydroxyphenylpyruvate dioxygenase monoamine oxidase D-Amino acid dehydrogenase catalase-peroxidase phenylacetate-CoA oxygenase 2-(1,2-epoxy-1,2-	1.4.3.21 1.4.99.1 1.11.1.21 1.14.13.149	KOX_19410(tynA) KOX_23495 KOX_2020 KOX_19420(paaA)/KOX_19425(paaB)/KOX_19430 /KOX_19435/KOX_19440	phpyr + o2 -> 2hpa + co2  peamn + o2 -> pacald + nh4 + h2o2  dphe + fad -> phpyr + nh4 + fadh2  phe + o2 -> pheact + co2  phaccoa + o2 + nadph -> Zepoxaccoa + nadp
4HPHED2 MNAO9 DAAD2 CATPRX PHACCOAO	Phenylalanine metabolism	4-hydroxyphenylpyruvate dioxygenase monoamine oxidase D-Amino acid dehydrogenase catalase-peroxidase phenylacetate-CoA oxygenase 2-(1,2-epoxy-1,2- dihydrophenyllacetyl-CoA isomerase	1.4.3.21 1.4.99.1 1.11.1.21 1.14.13.149 5.3.3.18	KOX_19410(tynA) KOX_23495 KOX_2020 KOX_19420(pasaAyKOX_19425(pasB)/KOX_19430 KOX_19430(pasaAyKOX_19440 KOX_19450	phpyr + o2 -> 2hpa + co2  peamn + o2 -> pacald + nh4 + h2o2 dphe + fad -> phpyr + nh4 + fadh2 phe + o2 -> pheact + co2  phaccoa + o2 + nadph -> 2epoxaccoa + nadp  2epoxaccoa <-> 2oxypaccoa
4HPHED2 MNAO9 DAAD2 CATPRX PHACCOAO	Phenylalanine metabolism Phenylalanine metabolism Phenylalanine metabolism Phenylalanine metabolism Phenylalanine metabolism Phenylalanine metabolism	4-hydroxyphenylpyruvate dioxygenase D-Amino acid dehydrogenase catalase-peroxidase phenylacetate-CoA oxygenase 2-(1,2-epoxy-1,2- dihydrophenyl)acetyl-CoA isomerase oxepin-CoA hydrolase 3-oxo-5,6-dehydrosubenyl-CoA	1.4.3.21 1.4.99.1 1.11.1.21 1.14.13.149	KOX_19410(tynA) KOX_23495 KOX_2020 KOX_19420(pasA),VKOX_19425(pasB),VKOX_19430 KOX_19430(pasA),VKOX_19440 KOX_19450 KOX_19415	phpyr + o2 -> 2hpa + co2  peamn + o2 -> pacald + nh4 + h2o2  dphe + fad -> phpyr + nh4 + fadh2  phe + o2 -> pheact + co2  phaccoa + o2 + nadph -> Zepoxaccoa + nadp
4HPHED2 MNAO9 DAAD2 CATPRX PHACCOAO ZEPOXACCOAIL OXPINCOAH 3OXDSCOASAD	Phenylalanine metabolism	4-hydroxyphenylpyruvate dioxygenase monoamine oxidase D-Amino acid dehydrogenase catalase-peroxidase phenylacetate-CoA oxygenase 2-(1,2-epoxy-1,2- dihydrophenyl)acetyl-CoA isomerase oxepin-CoA hydrolase 3-oxo-5,6-dehydrosubenyl-CoA semialdehyde dehydrogenase 2-(1,2-epoxy-1,2-	14.321 14.99.1 111.1.21 114.13.149 5.3.3.18 3.7.1.16 1.17.1.7	KOX_19410(tynA) KOX_2498 KOX_2020 KOX_19420(pasA)/KOX_19425(pasB)/KOX_19430 /KOX_19435/KOX_19440 KOX_19450 KOX_19415 KOX_19415	phpyr + o2 -> 2hpa + co2 peann + o2 -> pacald + nh4 + h2o2 dphe + fad -> phpyr + nh4 + fadh2 phe + o2 -> pheact + co2 phaccoa + o2 + nadph -> 2epoxaccoa + nadp  Zepoxaccoa <-> Zoxpyaccoa Zoxpyaccoa -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoa + nadph
4HPHED2 MNAO9 DAAD2 CATPRX PHACCOAO 2EPOXACCOAI1 OXPINCOAH 3OXDSCOASAD 2EPOXACCOAI2	Phenylalanine metabolism	4-hydroxyphenylpyruvate dioxygenase monoamine oxidase D-Amino acid deltydrogenase catalase-percoxidase phenylacetate-CoA oxygenase 2-(1,2-epoxy-1,2- dhydrophenylacetyl-CoA isomerase oxepin-CoA hydrolase 3-oxo-5,6-dehydrosuberyl-CoA semialdehyde dehydrogenase 2-(1,2-epoxy-1,2-) clidydrophenylacetyl-CoA isomerase	14.321 14.99.1 1111.121 114.13149 5.3.318 3.7.116 117.1.7 5.3.318	KOX_19410(tynA) KOX_2498 KOX_2020 KOX_19420(pasA)/KOX_19425(pas8)/KOX_19430 KOX_19435/KOX_19440 KOX_19450 KOX_19415 KOX_19450 KOX_19450 KOX_19450	phpyr + o2 -> 2hpa + co2 peann + o2 -> pacald + nh4 + h2o2 dphe + fad -> phpyr + nh4 + fadh2 phe + o2 -> pheact + co2 phaccoa + o2 + nadph -> 2epoxaccoa + nadp  Zepoxaccoa <-> 2oxpyaccoa  Zoxpyaccoa -> 3oxdscoasa  3oxdscoas + nadp -> 3oxdscoa + nadph  3oxdscoas + coa -> carpcoa + accoa
4HPHED2 MNAO9 DAAD2 CATPRX PHACCOAO ZEPOXACCOAIL OXPINCOAH 3OXDSCOASAD	Phenylalanine metabolism	4-hydroxyphenylpyruvate dioxygenase monoamine oxidase D-Amino acid dehydrogenase catalase-peroxidase phenylacetate-CoA oxygenase 2-(1,2-epoxy-1,2- dhydrophenylacetyl-CoA isomerase oxepin-CoA hydrolase 3-oxo-56-dehydrosuberyl-CoA semialdehyde dehydrogenase 2-(1,2-epoxy-1,2- dhydrophenylacetyl-CoA isomerase enoyl-CoA hydratase 3-hydroxyaoyl-CoA	14.321 14.99.1 111.1.21 114.13.149 5.3.3.18 3.7.1.16 1.17.1.7	KOX_19410(tynA) KOX_2049 KOX_2020 KOX_19420(pasA)/KOX_19425(pas8)/KOX_19430 KOX_19435/KOX_19440 KOX_19435 KOX_19415 KOX_19415 KOX_19450 KOX_19445	phpyr + o2 -> 2hpa + co2 peann + o2 -> pacald + nh4 + h2o2 dphe + fad -> phpyr + nh4 + fadh2 phe + o2 -> pheact + co2 phaccoa + o2 + nadph -> 2epoxaccoa + nadp  Zepoxaccoa <-> Zoxpyaccoa Zoxpyaccoa -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoa + nadph
4HPHED2 MNAO9 DAAD2 CATPRX PHACCOAO ZEPOXACCOAI1 OXPINCOAH 3OXDSCOASAD ZEPOXACCOAI2 ENCOAH8	Phenylalanine metabolism	4-hydroxyphenylpyruvate dioxygenase monoamine oxidase po-Amino acid dehydrogenase catalase-peroxidase phenylacetyl-CoA oxygenase 2-(1,2-epoxy-1,2-dihydrophenylacetyl-CoA isomerase oxepin-CoA hydrolase 3-oxo-56-dehydrosuberyl-CoA semiadehyde dehydrogenase 2-(1,2-epoxy-1,2-dihydrophenylacetyl-CoA isomerase oxepin-CoA hydratase 3-hydroxyacyl-CoA dehydrogenase 2-3-hydroxyacyl-CoA dehydrogenase 2-3-dihydrophenylacetyl-CoA dehydrogenase 2-3-dihydroxyacyl-CoA dehydrogenase 2-3-dihydroxyacyl-CoA dehydrogenase 2-3-dihydroxyacyl-CoA	14.321 14.991 1111.121 1.14.13.149 5.3.3.18 3.7.1.16 1.17.1.7 5.3.3.18 4.2.1.17	KOX_19410(tynA) KOX_2049 KOX_2020 KOX_19420(pasA)/KOX_19425(pasB)/KOX_19430 KOX_19435/KOX_19440 KOX_19450 KOX_19415 KOX_19415 KOX_19445 KOX_19445 KOX_19445 KOX_19445	phypr + o2 -> 2hpa + co2 peann + o2 -> pacald + nh4 + h2o2 dphe + fad -> phpyr + nh4 + fadh2 phe + o2 -> pheact + co2 phaccoa + o2 + nadph -> 2epoxaccoa + nadp  2epoxaccoa -> 2oxpyaccoa 2oxpyaccoa -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoas + nadph  3oxdscoas - coa -> carpcoa + accoa carpcoa -> hadpcoa
4HPHED2 MNAO9 DAAD2 CATPRX PHACCOAO  ZEPOXACCOAIL  OXPINCOAH 3OXDSCOASAD  ZEPOXACCOAIL  ENCOAH8 3HACOADH	Phenylalanine metabolism	4-hydroxyphenylpyruvate dioxygenase monoamine oxidase po-Amino acid dehydrogenase catalase-peroxidase phenylacetate-CoA oxygenase 2-(1.2-epoxy-1.2-dihydrophenyllacetyl-CoA isomerase oxepin-CoA hydrolase 3-oxo-56-dehydrosuberyl-CoA-smildehyde dehydrogenase 2-(1.2-epoxy-1.2-dihydrophenylacetyl-CoA isomerase encyl-CoA hydratase 3-hydroxyacyl-CoA dehydrogenase 2-3-dihydroxyphenylpropionate 1.2-dioxygenase 1.2-dioxygenase 1.2-dioxygenase 2.3-dihydroxyphenylpropionate 1.2-dioxygenase 2-3-dihydroxyphenylpropionate 1.2-dioxygenase	14.321 14.991 1111.121 114.13.149 5.3.3.18 3.7.116 117.1.7 5.3.3.18 4.2.1.17 11.1.157	KOX_19410(tynA) KOX_2495 KOX_20295 KOX_19420(pasA)/KOX_19425(pasB)/KOX_19430 KOX_19435/KOX_19440 KOX_19435 KOX_19415 KOX_19415 KOX_19450 KOX_19455 KOX_19455 KOX_19455 KOX_19455	phypr + o2 -> 2hpa + co2 peann + o2 -> pacald + nh4 + h2o2 dphe + fad -> phpyr + nh4 + fadh2 phe + o2 -> pheact + co2 phaccoa + o2 + nadph -> 2epoxaccoa + nadp  2epoxaccoa -> 2oxpyaccoa 2oxpyaccoa -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoas + nadph  3oxdscoas + coa -> carpcoa + accoa carpcoa -> hadpcoa hadpcoa + nad -> coadpcoa + nadh
4HPHED2 MNAO9 DAAD2 CATPRX PHACCOAO  2EPOXACCOAI1 OXPINCOAH 30XDSCOASAD 2EPOXACCOAI2 ENCOAH8 3HACOADH DHPHEPDO1	Phenylalanine metabolism	4-hydroxyphenylpyruvate dioxygenase monoamine oxidase po-amine oxidase po-Amino acid dehydrogenase catalase-peroxidase phenylacetate-CoA oxygenase 2-(1.2-epoxy-1.2-dhydrophenylacetyl-CoA isomerase oxepin-CoA hydrolase 3-oxo-56-dehydrosuberyl-CoA-smialdehyde dehydrogenase 2-(1.2-epoxy-1.2-dhydrophenylacetyl-CoA isomerase encoyl-CoA hydratase 3-hydroxyacyl-CoA dehydrogenase 1.2-dioxygenase 1.2-dio	14.321 14.991 1111.121 114.13.149 5.3.318 3.7.116 117.1.7 5.3.318 42.117 11.1157	KOX_19410(tynA) KOX_2049 KOX_2020 KOX_19420(pasA)/KOX_19425(pasB)/KOX_19430 KOX_19435/KOX_19440 KOX_19415 KOX_19415 KOX_19450 KOX_19455 KOX_19455 KOX_19450 KOX_26900	phypr + o2 -> 2hpa + co2 peann + o2 -> pacald + nh4 + h2o2 dphe + fad -> phpyr + nh4 + fadh2 phe + o2 -> pheact + co2 phaccoa + o2 + nadph -> 2epoxaccoa + nadp  2epoxaccoa -> 2oxpyaccoa 2oxpyaccoa -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoas + nadph  3oxdscoa + coa -> carpcoa + accoa carpcoa -> hadpcoa hadpcoa + nad -> coadpcoa + nadh dhcinnm + o2 -> 2h6kated
4HPHED2 MNAO9 DAAD2 CATPRX PHACCOAO  ZEPOXACCOAIL OXPINCOAH 30XDSCOASAD  ZEPOXACCOAIZ ENCOAH8 3HACOADH DHPHEPDO1 DHPHEPDO2	Phenylalanine metabolism	4-hydroxyphenylpyruvate dioxygenase monoamine oxidase monoamine oxidase po-4mine acid dehydrogenase catalase-peroxidase phenylacetate-CoA oxygenase 2-(1.2-epoxy-1.2-dhydrophenylacetyl-CoA isomerase oxepin-CoA hydrolase 3-tox-56-dehydrospubryl-CoA semiladehyde dehydrogenase 2-(1.2-epoxy-1.2-dhydrophenylacetyl-CoA isomerase enoyl-CoA hydratase 3-hydroxyacyl-CoA dehydrogenase 2.3-dhydroxyphenylpropionate 1.2-dioxygenase 2.3-dhydroxyphenylpropionate 1.2-dioxygenase 2.3-dhydroxyphenylpropionate 1.2-dioxygenase -2-hydroxy-k-ketonona-2,4-dienedioic acid hydrolase 2-hydroxy-k-ketonona-2,4-dienedioic acid hydrolase 2-hy	14.321 14.991 1111.121 11413.149 5.3.318 3.7.1.16 117.1.7 5.3.318 42.117 111.157 113.11.16	KOX_19410(tynA) KOX_24365 KOX_2020 KOX_19420(pasA)/KOX_19425(pas8)/KOX_19430 KOX_19436/KOX_19440 KOX_19450 KOX_19415 KOX_19415 KOX_19415 KOX_19455 KOX_19455 KOX_19455 KOX_26690 KOX_226690 KOX_22665	phypr + o2 -> 2hpa + co2 peann + o2 -> pacald + nh4 + h2o2 dphe + fad -> phpyr + nh4 + fadh2 phe + o2 -> pheact + co2 phaccoa + o2 + nadph -> 2epoxaccoa + nadp  2epoxaccoa <-> 2oxpyaccoa 2oxpyaccoa -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoasa acarpcoa -> hadpcoa hadpcoa + nad -> coadpcoa + nadh dhcinnm + o2 -> 2h6xded dhpppn + o2 -> 2h6xdend
4HPHED2 MNAO9 DAAD2 CATPRX PHACCOAO  ZEPOXACCOAIL OXPINCOAH 30XDSCOASAD  ZEPOXACCOAIZ ENCOAH8 3HACOADH DHPHEPDO1 DHPHEPDO2 2H6KDH1	Phenylalanine metabolism	4-hydroxyphenylpyruvate dioxygensse monoamine oxidase D-Amina acid dehydrogenase catalase-peroxidase phenylacetate-CoA oxygenase 2-(12-epoxy-12- dihydrophenyljacetyl-CoA isomerase 3-oxo-56-dehydrouberyl-CoA semialdehyde dehydrogenase dihydrophenylacetyl-CoA isomerase enoyl-CoA hydratase 3-hydroxysyl-CoA dehydrogense 2.3-dihydroxyphenylpropionate 1.2-dioxygenase 2.3-dihydroxyphenylpropionate 2.3-dihydroxyphenylpropionate 2.3-dihydroxyphenylpropionate 2.3-dihydroxyphenylpropionate 2.3-dihydroxyphenylpropionate 2.3-dihydroxyphenylpropionate 2.3-dihydroxyphenylpropionate 2.3-dihydroxyphenylpropionate 2.3-dihydroxyphenylpropionate 2.3-dihydroxyphenylpropionate 2.4-dixoxygenase 2.5-dixoxy-6-ketonona-2,4-dienedioia cald hydrolase	14321 14391 111121 11413149 53318 37.116 117.17 53318 42.117 111157 1131116 1131116 37.1-	KOX_19410(tynA) KOX_2495 KOX_2495 KOX_19420psabl/KOX_19425(paa8)/KOX_19430 KOX_19420psabl/KOX_19440 KOX_19450 KOX_19455 KOX_19415 KOX_19455 KOX_19455 KOX_19455 KOX_2660 KOX_22660 KOX_22665 KOX_22665 KOX_22665 KOX_24685	phypr + o2 -> 2hpa + co2 peann + o2 -> pacald + nh4 + h2o2 dphe + fad -> phpyr + nh4 + fadh2 phe + o2 -> pheact + co2 phaccoa + o2 + nadph -> 2epoxaccoa + nadp  2epoxaccoa -> 2oxpyaccoa 2oxpyaccoa -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoasa arpcoa -> hadpcoa hadpcoa + nad -> coadpcoa + nadh dhcinnm + o2 -> 2h6xdted dhpppn + o2 -> 2h6xdted  2h6kated -> op4en + fum
4HPHED2 MNAO9 DAAD2 CATPRX PHACCOAO  ZEPOXACCOAIL OXPINCOAH 30XDSCOASAD  ZEPOXACCOAIZ ENCOAH8 3HACOADH DHPHEPDO1 DHPHEPDO2 ZH6KDH1 2H6KDH2	Phenylalanine metabolism Phenylalanine, Tyrosine and Tryptophan biosynthesis Phenylalanine, Tyrosine and Tryptophan biosynthesis	4-hydroxyphenylpyruvate dioxygenase monoamine oxidase po-Amino addi dehydrogenase catalase-peroxidase phenylacetate-CoA oxygenase 2-(1,2-epoxy-1,2-didydropenylacetyl-CoA isomerase oxepin-CoA hydrolase 3-tox-56-dehydrosuberyl-CoA semiladehyde dehydrogenase 2-(1,2-epoxy-1,2-didydropenylacetyl-CoA isomerase enoyl-CoA hydratase 3-hydroxyacyl-CoA dehydropenase 2,3-dihydropenylpropionate 1,2-dioxygenase 2,3-dihydroxyphenylpropionate 1,2-dioxygenase 2,3-dihydroxyb-ketonona-2,4-dieneticiic acid hydrolase 2,4-dideneticiic acid hydrolase shikimate dehydrogenase quinate dehydrogenase	14321 14391 111121 11413149 53318 37.116 117.17 53318 42.117 111157 1131116 1131116 37.1- 37.1-	KOX_19410(tynA) KOX_2409 KOX_24020 KOX_19420 KOX_19435*KOX_19440 KOX_19450 KOX_19455 KOX_19450 KOX_19455 KOX_19455 KOX_19455 KOX_19455 KOX_19455 KOX_19455 KOX_19455 KOX_26600 KOX_226600 KOX_226600 KOX_226655 KOX_226655	phypr + o2 -> 2hpa + co2 peann + o2 -> pacald + nh4 + h2o2 dphe + fad -> phpyr + nh4 + fadh2 phe + o2 -> pheact + co2 phaccoa + o2 + nadph -> 2epoxaccoa + nadp  2epoxaccoa -> 2oxpyaccoa 2oxpyaccoa -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoasa acarpcoa -> hadpcoa hadpcoa + nad -> coadpcoa + nadh dhcinnm + o2 -> 2hf6xdted dhpppn + o2 -> 2hf6xdted 2hf6kated -> op4en + fum 2h6xxdiend -> op4en + succ
4HPHED2 MNAO9 DAAD2 CATPRX PHACCOAO  ZEPOXACCOAIL OXPINCOAH 30XDSCOASAD  ZEPOXACCOAIZ ENCOAH8 3HACOADH DHPHEPDO1 DHPHEPDO2 ZH6KDH1 ZH6KDH2 SHKDH	Phenylalanine metabolism Phenylalanine, sprosine and Tryptophan biosynthesis Phenylalanine, Tyrosine and Tryptophan biosynthesis Phenylalanine, Tyrosine and Tryptophan biosynthesis Phenylalanine, Tyrosine and Tryptophan biosynthesis	4-hydroxyphenylpyruvate dioxygenses monoamine oxidase D-Amino acid dehydrogenase catalase-peroxidase phenylacetate-CoA oxygenase 2-(12-epoxy-12-2 dihydrophenylacetyl-CoA somerase oxepin-CoA hydrolase 2-(12-epoxy-12- dihydrophenylacetyl-CoA somerase dihydrophenylacetyl-CoA somerase 2-(12-epoxy-12- dihydrophenylacetyl-CoA somerase 2-10-10-10-10-10-10-10-10-10-10-10-10-10-	14321 14391 111121 11413149 53318 37.116 117.17 53318 42.117 111157 1131116 1131116 37.1- 37.1-	KOX, 19410(tynA) KOX, 2496 KOX, 2020 KOX, 19420(pasA)/KOX, 19425(pasB)/KOX, 19430 KOX, 19430 KOX, 19450 KOX, 19455 KOX, 19415 KOX, 19455 KOX, 19455 KOX, 19455 KOX, 19465 KOX, 26690 KOX, 22660 KOX, 22665 KOX, 22665 KOX, 22685 KOX, 22685 KOX, 22685 KOX, 2188(ancE)/KOX, 08990/KOX, 10830(aroc)/KOX, 12885/KOX, 22725	phypr + o2 -> 2hpa + co2 peann + o2 -> pacald + nh4 + h2o2 dphe + fad -> phpyr + nh4 + fadh2 phe + o2 -> pheact + co2 phaccoa + o2 + nadph -> 2epoxaccoa + nadp  2epoxaccoa <-> 2oxpyaccoa  2oxpyaccoa -> 3oxdscoasa  3oxdscoasa + nadp -> 3oxdscoas + nadph  3oxdscoa + coa -> carpcoa + accoa  carpcoa -> hadpcoa hadpcoa + nad -> oxadpcoa + nadh  dhcinnm + o2 -> 2h6oxdlend  2h6kated -> op4en + fum  2h6oxdlend -> op4en + succ  dhsk + nadph <-> nadp + sme
4HPHED2 MNAO9 DAAD2 CATPRX PHACCOAO  ZEPOXACCOAIL OXPINCOAH 30XDSCOASAD  ZEPOXACCOAIZ ENCOAH8 3HACOADH DHPHEPDO1 DHPHEPDO2 ZH6KDH1 ZH6KDH2 SHKDH QTDH2 PPNDHG	Phenylalanine metabolism Phenylalanine, Tyrosine and Tryptophan biosynthesis	4-hydroxyphenylpyruvate dioxygenase monoamine oxidase po-amine add dehydrogenase catalase-peroxidase phenylacetate-CoA oxygenase 2-(1,2-epoxy-1,2-dihydropenylacetyl-CoA isomerase oxepin-CoA hydrolase 3-oxo-56-dehydrosuberyl-CoA semiladehyde dehydrogenase 2-(1,2-epoxy-1,2-dihydropenylacetyl-CoA isomerase enoyl-CoA hydratase 3-hydroxyacyl-CoA dehydropenase 2,3-dihydropyhenylpropionate 1,2-dioxygenase 2,3-dihydropyhenylpropionate 1,2-dioxygenase 2,3-dihydroysyhenylpropionate 1,2-dioxygenase 2,3-dihydroysyhenylpropionate 1,2-dioxygenase 2,1-dioxygenase 2,1	14321 14391 111121 11413149 53318 37.116 117.17 53318 42.117 111157 1131116 37.1- 37.1- 11125 1158 13112	KOX, 19410(tynA) KOX, 24940 KOX, 2020 KOX, 19440(tynA), KOX, 19445 KOX, 19450 KOX, 19450 KOX, 19450 KOX, 19455 KOX, 19455 KOX, 19455 KOX, 19455 KOX, 22690 KOX, 22685 KOX, 22685 KOX, 24805, KOX, 22275 KOX, 19605, KOX, 22275 KOX, 19605, KOX, 22295 KOX, 00040(tyrA)	phypr + o2 -> 2hpa + co2 peann + o2 -> pacald + ch4 + h2o2 dphe + fad -> phypr + nh4 + fadh2 phe + o2 -> pheact + co2 phaccoa + o2 + nadph -> 2epoxaccoa + nadp  2epoxaccoa -> 2oxpyaccoa  2oxpyaccoa -> 3oxdscoasa  3oxdscoas + nadp -> 3oxdscoas + nadph  3oxdscoa + coa -> carpcoa + accoa carpcoa -> hadpcoa hadpcoa + nad -> oxadpcoa + nadh  dhcinnm + o2 -> 2h6kated dhpppn + o2 -> 2h6xoxdlend  2h6kated -> opten + fum  2h6oxdlend -> opten + succ dhsk + nadph -> nadp + sme dhsk + paqh2 <-> paq + sme nad + phen -> 4hpp + co2 + nadh
4HPHED2 MNAO9 DAAD2 CATPRX PHACCOAO  ZEPOXACCOAIL OXPINCOAH 30XDSCOASAD  ZEPOXACCOAIZ ENCOAH8 3HACOADH DHPHEPDO1 DHPHEPDO2 ZH6KDH1 ZH6KDH2 SHKDH QTDH2 PPNDHG ANTPRT	Phenylalanine metabolism Phenylalanine, sprosine and Tryptophan biosynthesis Phenylalanine, Tyrosine and Tryptophan biosynthesis	4-hydroxyphenylpyruvate dioxygenase monoamine oxidase D-Amino addi dehydrogenase catalase-peroxidase phenylacetate-CoA oxygenase 2-(1,2-epoxy-1,2-dhydrosyense-1,2-epoxy-1,2-dhydrosyense-1,2-epoxy-1,2-dhydrosyense-1,2-epoxy-1,2-dhydrosyense-1,2-epoxy-1,2-dhydrosyense-2,1,2-epoxy-1,2-dhydrosyense-2,1,2-epoxy-1,2-dhydrosyense-2,1,2-dhydrosyense-2,3-dhydrosyense-2,	14321 14391 111121 11413149 53318 37.116 117.17 53318 42.117 111157 1131116 37.1- 37.1- 11125 115.8 13.112 24.218	KOX_19410(tynA) KOX_2409 KOX_2020 KOX_19420(pasA)/KOX_19425(pasB)/KOX_19430 KOX_19450 KOX_19455 KOX_19415 KOX_19455 KOX_19455 KOX_19455 KOX_22690 KOX_22685 KOX_22685 KOX_22685 KOX_22685 KOX_22685 KOX_21845 KOX_22685 KOX_2285 KOX_2285 KOX_2285 KOX_19484 KOX_2285	phypr + o2 -> 2hpa + co2 peann + o2 -> pacald + ch4 + h2o2 dphe + fad -> phypr + nh4 + fadh2 phe + o2 -> pheact + co2 phaccoa + o2 + nadph -> 2epoxaccoa + nadp  2epoxaccoa -> 2oxpyaccoa  2oxpyaccoa -> 3oxdscoasa  3oxdscoas + nadp -> 3oxdscoas + nadph  3oxdscoa + coa -> carpcoa + accoa carpcoa -> hadpcoa hadpcoa + nad -> coadpcoa + nadh  dhcinnm + o2 -> 2h6kated  dhpppn + o2 -> 2h6oxdlend  2h6kated -> opten + fum  2h6oxdlend -> opten + succ  dhsk + nadph -> nadp + sme dhsk + pqph2 -> pqq + sme nad + phen -> 4hpp + co2 + nadh an + prpp -> ppi + npran
4HPHED2 MNAO9 DAAD2 CATPRX PHACCOAO  ZEPOXACCOAIL OXPINCOAH 30XDSCOASAD  ZEPOXACCOAIZ ENCOAH8 3HACOADH DHPHEPDO1 DHPHEPDO2 ZH6KDH1 ZH6KDH2 SHKDH QTDH2 PPNDHG ANTPRT PSHKCVT	Phenylalanine metabolism Phenylalanine, Tyrosine and Tryptophan biosynthesis	4-hydroxyphenylpyruvate dioxygenase monoamine oxidase D-Amino add dehydrogenase catalase-peroxidase phenylacetate-CoA oxygenase 2-(1,2-epoxy-12-2 dihydrophenylacetyl-CoA isomerase oxepin-CoA hydrolase oxepin-CoA hydrolase 3-oxo-5-6-dehydrosubenyl-CoA semialdehyde dehydropenase 2-(1,2-epoxy-1-2-2 dihydrophenylacetyl-CoA isomerase enoyl-CoA hydratase 3-hydroxyacyl-CoA dehydropenase 2-3-dihydropenase 12-dioxygenase 12-dioxygenase 12-dioxygenase 12-dioxygenase 12-dioxygenase 2-hydroxys-festonona-2,4-dienedioic acid hydrolase shikimate dehydrogenase (pyrroloquinoline-quinone) prephenate dehydrogenase (pyrroloquinoline-quinone) prephenate dehydrogenase anthraniate phosphoriboxyltransferase 3-phosphorbixyltransferase 3-phosphorbixyltransferase	14321 14391 111121 11413149 53318 37.116 117.17 53318 42.117 111157 1131116 37.1- 37.1- 11125 115.8 131112 24.218 25.119	KOX_19410(tynA) KOX_24095 KOX_2020 KOX_19420(pasA)/KOX_19425(pasB)/KOX_19430 KOX_19450 KOX_19455 KOX_19455 KOX_19455 KOX_19455 KOX_26690 KOX_22669 KOX_22665 KOX_22685 KOX_22685 KOX_22685 KOX_22685 KOX_21845 KOX_22685	phypr + o2 -> 2hpa + co2 peann + o2 -> pacald + co2 peann + o2 -> pacald + hh4 + h2o2 dphe + fad -> phpyr + nh4 + fadh2 phe + o2 -> pheact + co2 phaccoa + o2 + nadph -> 2epoxaccoa + nadp  2epoxaccoa -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoasa acarpcoa -> hadpcoa hadpcoa + hadpooa hadpcoa + nad -> oxadpcoa + nadh dhcinnm + o2 -> 2h6kated dhpppn + o2 -> 2h6xodiend 2h6kated -> op4en + fum 2h6oxdiend -> op4en + succ dhsk + nadph -> nadp + sme dhsk + paqh2 -> paq + sme nad + phen -> 4hpp + co2 + nadh an + prop ->> pi+ npran pep + skm5p ->> 3psme + pi
4HPHED2 MNAO9 DAAD2 CATPRX PHACCOAO  ZEPOXACCOAIL OXPINCOAH 30XDSCOASAD  ZEPOXACCOAIZ ENCOAH8 3HACOADH DHPHEPDO1 DHPHEPDO2 ZH6KDH1 ZH6KDH2 SHKDH QTDH2 PPNDHG ANTPRT	Phenylalanine metabolism Phenylalanine, Tyrosine and Tryptophan biosynthesis	4-hydroxyphenylpyruvate dioxygenase monoamine oxidase D-Amino add dehydrogenase catalase-peroxidase phenylacetate-CoA oxygenase 2-(12-epoxy-12-dihydrophenylacetyl-CoA isomerase oxepin-CoA hydrolase oxepin-CoA hydrolase oxepin-CoA hydrolase oxepin-CoA hydrolase 3-oxo-5-G-dehydrosubenyl-CoA semiadehyde dehydropenase 2-(12-epoxyl-CoA) catalogo oxygenase oxepin-CoA hydratase enoyl-CoA hydratase 3-hydroxygh-CoA dehydrogenase 12-dioxygenase 12-dioxygenase 12-dioxygenase 12-dioxygenase 23-dihydroxyphenylpropionate 12-dioxygenase 2-dihydroxyphenylpropionate 12-dioxygenase 2-hydroxyn-6-ketonona-2,4-dienedioic acid hydrolase shikimate dehydrogenase (pyrroloquinoline-quinone) prephenate dehydrogenase (pyrroloquinoline-quinone) prephenate dehydrogenase anthranialae phosphoriboxyltransferase yyrosine transaminase	14321 14391 111121 11413149 53318 37.116 117.17 53318 42.117 111157 1131116 37.1- 37.1- 11125 115.8 13.112 24.218	KOX_19410(tynA) KOX_24095 KOX_19420(pasA)/KOX_19425(pasB)/KOX_19430 KOX_19420(pasA)/KOX_194425(pasB)/KOX_19430 KOX_19450 KOX_19455 KOX_19455 KOX_26690 KOX_226690 KOX_22665 KOX_22665 KOX_22685	phypr + o2 -> 2hpa + co2 peann + o2 -> pacald + co2 peann + o2 -> pacald + hh4 + h2o2 dphe + fad -> phpyr + nh4 + fadh2 phe + o2 -> pheact + co2 phaccoa + o2 + nadph -> 2epoxaccoa + nadp  2epoxaccoa -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoasa 3oxdscoas + coa -> carpcoa + accoa carpcoa -> hadpcoa hadpcoa + hadp -> 2h6kated dhcinnm + o2 -> 2h6kated dhpppn + o2 -> 2h6xoxdiend 2h6kated -> op4en + fum 2h6oxdiend -> op4en + succ dhsk + nadph -> nadp + sme dhsk + paqh2 -> paq + sme nad + phen -> 4hpp + co2 + nadh an + prep -> ppi + npran pep + skm5p -> 3psme + pi akg + tyr -> 4hpp + glu
4HPHED2 MNAO9 DAAD2 CATPRX PHACCOAO  ZEPOXACCOAIL OXPINCOAH 30XDSCOASAD  ZEPOXACCOAIZ ENCOAH8 3HACOADH DHPHEPDO1 DHPHEPDO2 ZH6KDH1 ZH6KDH2 SHKDH QTDH2 PPNDHG ANTPRT PSHKCVT TYRTA1 TYRTA2	Phenylalanine metabolism Phenylalanine, Tyrosine and Tryptophan biosynthesis	4-hydroxyphenylpyruvate dioxygenase monoamine oxidase D-Amino add dehydrogenase catalase-peroxidase phenylacetate-CoA oxygenase 2-(12-epoxy-12-dihydrophenylacetyl-CoA isomerase oxepin-CoA hydrolase oxepin-CoA hydrolase oxepin-CoA hydrolase 3-oxo-5-6-dehydrosubenyl-CoA semiadehyde dehydropenase 2-(12-epoxy-12-dihydrophenylacetyl-CoA isomerase enoyl-CoA hydratase 3-hydroxygol-CoA dehydrogenase 2-3-dihydroxyphenylpropionate 12-dioxygenase 2-3-dihydroxyphenylpropionate 12-dioxygenase 2-3-dihydroxyphenylpropionate 12-dioxygenase 2-2-hydroxy-6-ketonona-2,4-dienedioic acid hydrolase shikimate dehydrogenase (pyrroloquinoline-quinone) prephenate dehydrogenase (pyrroloquinoline-quinone) prephenate dehydrogenase (pyrroloquinoline-quinone) prephenate dehydrogenase anthraniate phosphoriboxyltransferase tyrosine transaminase tyrosine transaminase	14321 14391 1111.21 11413149 53.318 37.116 1171.7 53.318 42.117 111157 113.1116 37.1- 37.1- 11125 11.58 13.112 24.218 25.119 26.19 26.157	KOX_19410(tynA) KOX_2020 KOX_19420(toX,19425(pas8)/KOX_19430 KOX_19420(pasA)/KOX_19440 KOX_19450 KOX_19455 KOX_19455 KOX_19455 KOX_22690 KOX_226950 KOX_22685 KOX_22685 KOX_22685 KOX_22685 KOX_04188(araEpi/KOX_08090/KOX_10830(araEpi/KOX_19450) KOX_19450 KOX_19450 KOX_19450 KOX_19450 KOX_22690 KOX_22690 KOX_22695 KOX_22685 KOX_22685 KOX_22685 KOX_24186 KOX_04180(araEpi/KOX_08090/KOX_10830(araEpi/KOX_19605/KOX_22225) KOX_19605/KOX_22225 KOX_19605/KOX_22225 KOX_19605/KOX_22255 KOX_10040(bytA) KOX_18340 KOX_16000 KOX_25040 KOX_268310	phypr + o2 -> 2hpa + co2 peann + o2 -> pacald + ro4 phe + fad -> phypr + nh4 + fadh2 phe + o2 -> pheact + o22 phaccoa + o2 + nadph -> 2epoxaccoa + nadp  2epoxaccoa -> 2oxpyaccoa  2oxpyaccoa -> 3oxdscoasa  3oxdscoas + nadp -> 3oxdscoas + nadph  3oxdscoas + coa -> carpcoa + accoa  carpcoa -> hadpcoa hadpcoa + nad -> oxdpcoa + nadh  dhcinnm + o2 -> 2h6kated  dhpppn + o2 -> 2h6xodend  2h6kated -> op4en + fum  2h6oxdiend -> op4en + succ  dhsk + nadph -> nadp + sme  dhsk + pqqh2 -> pqq + sme  nad + phen -> 4hpp + co2 + nadh  an + prpp -> ppi + npran  pep + skm5p -> 3psme + pi  akg + tyr -> 4hpp + glu  akg + tyr -> 4hpp + glu  akg + tyr -> 4hpp + glu
4HPHED2 MNAO9 DAAD2 CATPRX PHACCOAO  ZEPOXACCOAIL OXPINCOAH 30XDSCOASAD  ZEPOXACCOAIZ ENCOAH8 3HACOADH DHPHEPDO1 DHPHEPDO2 ZH6KDH1 ZH6KDH2 SHKDH QTDH2 PPNDHG ANTPRT PSHKCVT TYRTA1 TYRTA2 PHETA	Phenylalanine metabolism Phenylalanine, Tyrosine and Tryptophan biosynthesis	4-hydroxyphenylpyruvate dioxygenase monoamine oxidase D-Amino add dehydrogenase catalase-peroxidase phenylacetate-CoA oxygenase 2-(1,2-epoxy-12-dihydrophenylacetyl-CoA isomerase oxepin-CoA hydrolase oxepin-CoA hydrolase 3-oxo-5,6-dehydrosubenyl-CoA semiadehyde dehydropenase 2-(1,2-epoxy-1-2-dihydrophenylacetyl-CoA isomerase enoyl-CoA fydratase 3-hydroxygol-CoA dehydropenase 2-1,2-dioxygenase 2-3-dihydroxyphenylpropionate 1,2-dioxygenase 2,3-dihydroxyphenylpropionate 1,2-dioxygenase 2,3-dihydroxyphenylpropionate 1,2-dioxygenase 2,2-didienedioic acid hydrolase shikimate dehydrogenase (pyrroloquinoline-quinone) prephenate dehydrogenase (pyrroloquinoline-quinone) prephenate dehydrogenase (pyrroloquinoline-quinone) prephenate dehydrogenase anthranialte phosphoriboxyltransferase tyrosine transaminase tyrosine transaminase	14321 14391 111121 11413149 53318 37.116 117.17 53318 42.117 111157 1131116 1131116 37.1- 37.1- 11125 115.8 13112 24.218 25.119 26.157 26.11726.	KOX_19410(tynA) KOX_2409 KOX_2020 KOX_19420(pash)/KOX_19425(pash)/KOX_19430 KOX_19450 KOX_19450 KOX_19455 KOX_19455 KOX_2690 KOX_22690 KOX_22695 K	phypr + o2 -> 2hpa + co2 peann + o2 -> pacald + ro4 phe + fad -> phypr + nh4 + fadh2 phe + o2 -> pheact + o22 phaccoa + o2 + nadph -> 2epoxaccoa + nadp  2epoxaccoa -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoasa arpcoa -> hadpcoa hadpcoa + hadpcoa hadpcoa + nad -> coadpcoa + nadh dhcinnm + o2 -> 2h6kated dhpppn + o2 -> 2h6xodiend 2h6kated -> op4en + fum 2h6oxdiend -> op4en + succ dhsk + nadph -> nadp + sme dhsk + paqh2 -> pqq + sme nad + phen -> 4hpp + co2 + nadh an + prep -> ppi + npran pep + skm5p -> 3psme + pi akg + tyr -> 4hpp + glu akg + tyr -> dhp + glu akg + phe -> glu + phpyr
4HPHED2 MNAO9 DAAD2 CATPRX PHACCOAO  ZEPOXACCOAIL OXPINCOAH 30XDSCOASAD  ZEPOXACCOAIL ENCOAHB 3HACOADH DHPHEPD01 DHPHEPD02 ZH6KDH1 ZH6KDH2 SHKDH QTDH2 PPNDHG ANTPRT PSHKCVT TYRTA1 TYRTA2 PHETA SHKK	Phenylalanine metabolism Phenylalanine, Tyrosine and Tryptophan biosynthesis	4-hydroxyphenylpyruvate dioxygenase monoamine oxidase D-Amino acid dehydrogenase catalase-peroxidase phenylacetate-CoA oxygenase 2-fl.2-epoxy-1,2-dihydrophenylacetyl-CoA isomerase oxygenic CoA hydrolase 3-oxo-56-dehydrosuberyl-CoA esmiadehyde dehydrogenase dihydrophenylacetyl-CoA isomerase enoyl-CoA hydralase 3-bydroxya-1,2-dihydroxya-1,2-dihydroxya-1,2-dioxygenase 2,3-dihydroxya-phenylpropionate 1,2-dioxygenase 2,3-dihydroxy-6-ketonona-2,4-dienedicia cald hydrolase shikimate dehydrogenase quinate dehydrogenase quinate dehydrogenase anthranilate phosphoriboxyltransferase 3-phosphoshikimate 1-carboxylinylinylinylinylinylinylinylinylinylin	14321 14391 111121 11413149 53318 37.116 117.17 53318 42.117 111157 1131116 1131116 37.1- 37.1- 11125 115.8 13112 24.218 25.119 26.157 26.1172619/26.1	KOX_19410(tynA) KOX_2409 KOX_2020 KOX_19420(pash)/KOX_19425(pash)/KOX_19430 KOX_19450 KOX_19455 KOX_19455 KOX_19455 KOX_26690 KOX_226690 KOX_22685 KOX_26685 KOX_2685 KOX_04180(are6y/KOX_08090/KOX_10830(are6y/KOX_1945) KOX_19450 KOX_26600 KOX_26600 KOX_26600 KOX_26600 KOX_26600 KOX_26600 KOX_19400 KOX_1940	phypr + o2 -> 2hpa + co2 peann + o2 -> pacald + ro4 phe + fad -> phypr + nh4 + fadh2 phe + o2 -> pheact + o22 phaccoa + o2 + nadph -> 2epoxaccoa + nadp  2epoxaccoa -> 3oxdscoasa  3oxdscoas + nadp -> 3oxdscoasa  3oxdscoas + nadp -> 3oxdscoas + nadph  3oxdscoa + oa -> carpcoa + accoa carpcoa -> hadpcoa hadpcoa + nad -> oaodpcoa + nadh  dhcinnm + o2 -> 2h6kated  dhpppn + o2 -> 2h6xodiend  2h6kated -> op4en + fum  2h6oxdiend -> op4en + succ  dhsk + nadph -> nadp + sme  dhsk + paqh2 -> pqq + sme  nad + phen -> 4hpp + co2 + nadh  an + prpr -> ppi + npran  pep + skm5p -> 3psme + pi  akg + tyr -> 4hpp + glu  akg + tyr -> 4hpp + glu  akg + phe -> glu + phpyr  atp + sme -> adp + skm5p
4HPHED2 MNAO9 DAAD2 CATPRX PHACCOAO  ZEPOXACCOAIL OXPINCOAH 30XDSCOASAD  ZEPOXACCOAIZ ENCOAH8 3HACOADH DHPHEPDO1 DHPHEPDO2 ZH6KDH1 ZH6KDH2 SHKDH QTDH2 PPNDHG ANTPRT PSHKCVT TYRTA1 TYRTA2 PHETA SHKK IG3PS	Phenylalanine metabolism Phenylalanine, Tyrosine and Tryptophan biosynthesis	4-hydroxyphenylpyruvate dioxygenase monoamine oxidase po-amine oxidase phenylacetate-CoA oxygenase catalase-peroxidase phenylacetate-CoA oxygenase 2-(12-epoxy-12-dihydrophenylacetyl-CoA isomerase oxepin-CoA hydrolase oxepin-CoA hydrolase oxepin-CoA hydrolase oxepin-CoA hydrolase 3-oxo-5-6-delydrosuberyl-CoA semialdehyde deltydropenase 2-(12-epoxy)-2-dihydrophenylacetyl-CoA isomerase enoyl-CoA hydratase 3-hydroxyacyl-CoA deltydropenase 12-dioxygenase 12-dioxygenase 12-dioxygenase 12-dioxygenase 12-dioxygenase 12-dioxygenase 2-hydroxy-6-tentona-2-dieneticiic acid hydrolase shikimate dehydrogenase (pyrroloquinoline-quinone) prephenate dehydrogenase (pyrroloquinoline-quinone) prephenate dehydrogenase tyroxine transaminase tyroxine transaminase tyroxine transaminase hydrolalanine transaminase indical-3-glycerol-phosphate synthase 3-d-ecoxy-7-phosphoheptulonate synthase	14321 14391 111121 11413149 53318 37.116 117.17 53318 42.117 111157 1131116 1131116 37.1- 37.1- 11125 115.8 13112 24.218 25.119 26.157 26.117 27.171 41.148	KOX_19410(tynA) KOX_2020 KOX_19420(pash)/KOX_19425(pash)/KOX_19430 KOX_19420(pash)/KOX_19440 KOX_19450 KOX_19455 KOX_19455 KOX_20690 KOX_22660 KOX_22665 KOX_22665 KOX_22685 KOX_04180(aroEy/KOX_08090/KOX_10830(aroE)/KOX_19450) KOX_19450 KOX_22685 KOX_19450 KOX_22685 KOX_19450 KOX_22685 KOX_19450	phypr + o2 -> 2hpa + co2 paann + o2 -> pacald + ro4 phe + fad -> phypr + nh4 + fadh2 phe + o2 -> pheact + o22 phaccoa + o2 + nadph -> 2epoxaccoa + nadp  2epoxaccoa -> 2oxpyaccoa  2oxpyaccoa -> 3oxdscoasa  3oxdscoasa + nadp -> 3oxdscoasa  3oxdscoasa + nadp -> 3oxdscoasa  3oxdscoasa + nadp -> 3oxdscoasa  darpcoa -> hadpcoa hadpcoa + nad -> oxapcoa + nadh  dhcinnm + o2 -> 2h6kated  dhpppn + o2 -> 2h6xoteind  2h6kated -> op4en + fum  2h6oxdiend -> op4en + succ  dhsk + nadph -> nadp + sme  dhsk + pqh2 -> pqq + sme  nad + phen -> 4hpp + co2 + nadh  an + prpp -> ppi + npran  pep + skm5p -> 3psme + pi  akg + tyr -> 4hpp + glu  akg + tyr -> 4hpp + glu  akg + phe -> glu + phypr  atp + sme -> adp + skm5p  2cpr5p -> 3ig3p + co2
4HPHED2 MNAO9 DAAD2 CATPRX PHACCOAO  ZEPOXACCOAIL OXPINCOAH 30XDSCOASAD  ZEPOXACCOAIZ ENCOAH8 3HACOADH DHPHEPDO1 DHPHEPDO2 ZH6KDH1 ZH6KDH2 SHKDH QTDH2 PPNDHG ANTPRT PSHKCVT TYRTA1 TYRTA2 PHETA SHKK IG3PS DOXPHS	Phenylalanine metabolism Phenylalanine, Tyrosine and Tryptophan biosynthesis	4-hydroxyphenylpyruvate dioxygenase monoamine oxidase D-Amino add dehydrogenase catalase-peroxidase phenylacetate-CoA oxygenase 2-(12-epoxy-12-dihydrophenylacetyt-CoA isomerase oxepin-CoA hydrolase oxepin-CoA hydrolase 3-oxo-5-6-dehydrosuberyt-CoA semiadehyde dehydropenase 2-(12-epoxy-12-dihydrophenylacetyt-CoA isomerase enoyt-CoA hydrolase 3-hydroxyacyt-CoA dehydropenase 2-12-dioxygenase 2-3-dihydroxyphenylpropionate 12-dioxygenase 2-3-dihydroxyphenylpropionate 12-dioxygenase 2-3-dihydroxyphenylpropionate 12-dioxygenase 2-1-hydroxys-ketonona-2-4-dienedioic acid hydrolase shikimate dehydrogenase (pyrroloquinoline-quinone) prephenate d	14321 14391 111121 11413149 53318 37.116 117.17 53318 42.117 111157 1131116 1131116 37.1- 37.1- 11125 115.8 13112 24.218 25.119 26.157 26.117 27.171 41.148 25.119	KOX_19410(tynA) KOX_2020 KOX_19420(panal)/KOX_19425(panal)/KOX_19430 KOX_19420(panal)/KOX_194425(panal)/KOX_19430 KOX_19445 KOX_19445 KOX_19445 KOX_19445 KOX_219455 KOX_26690 KOX_226690 KOX_22665 KOX_26685 KOX_26685 KOX_2685 KOX_27040(tynA) KOX_194840 KOX_194840 KOX_194850 KOX_26685 KOX_26685 KOX_26685 KOX_26685 KOX_19480(arcE)/KOX_08090/KOX_10830(arcE)/KOX_10830(	phypr + o2 -> 2hpa + co2 paann + o2 -> pacald + ro4 phe + fad -> phypr + nh4 + fadh2 phe + o2 -> pheact + o22 phaccoa + o2 + nadph -> 2epoxaccoa + nadp  2epoxaccoa -> 3oxdscoasa  3oxdscoasa + nadp -> 3oxdscoasa  3oxdscoasa + nadp -> 3oxdscoasa  3oxdscoasa + nadp -> 3oxdscoasa  arpcoa -> hadpcoa hadpcoa + coa -> carpcoa + accoa carpcoa -> hadpcoa hadpcoa + nad -> oxadpcoa + nadh  dhcinnm + o2 -> 2h6kxted  dhpppn + o2 -> 2h6xxted  dhpppn + o2 -> 2h6xotelend  2h6kated -> op4en + fum  2h6xxted -> op4en + succ  dhsk + nadph -> nadp + sme  dhsk + paqh2 -> paq + sme  nad + phen -> 4hpp + co2 + nadh  an + prpp -> ppi + npran  pep + skm5p ->> 3psme + pi  akg + tyr ->> 4hpp + glu  akg + tyr ->> 4hpp + glu  akg + phe ->> glu + phpyr  atp + sme -> adp + skm5p  2cpr5p -> 3ig3p + co2  e4p + pep -> 3ddah7p + pi
4HPHED2 MNAO9 DAAD2 CATPRX PHACCOAO  ZEPOXACCOAIL OXPINCOAH 30XDSCOASAD  ZEPOXACCOAIZ ENCOAH8 3HACOADH DHPHEPDO1 DHPHEPDO2 ZH6KDH1 ZH6KDH2 SHKDH QTDH2 PPNDHG ANTPRT PSHKCVT TYRTA1 TYRTA2 PHETA SHKK IG3PS DOXPHS ANTHS	Phenylalanine metabolism Phenylalanine, Tyrosine and Tryptophan biosynthesis	4-hydroxyphenylpyruvate dioxygenase monoamine oxidase D-Amino add dehydrogenase catalase-peroxidase phenylacetate-CoA oxygenase 2-(12-epoxy-12-2 dihydrophenylacetyl-CoA isomerase oxepin-CoA hydrolase oxepin-CoA hydrolase 3-oxo-5-6-dehydrosubenyl-CoA semiadethyde dehydropenase 2-(12-epoxy-12-2 dihydrophenylacetyl-CoA isomerase enoyl-CoA hydratase 3-hydroxygol-CoA dehydropenase 12-dioxygenase 2-diphydroxybe-tenona-2,4-dienedioic acid hydrolase shikimate dehydrogenase (pyrroloquinoline-quinone) prephenate dehydrogenase (pyrroloquinoline-quinone) prephenate dehydrogenase (pyrroloquinoline-quinone) prephenate dehydrogenase anthranialae phosphoriboxyltransferase tyrosine transaminase tyrosine transaminase phenylalanine transaminase shikimate kinase	14321 14391 111121 11413149 53318 37.116 117.17 53318 42.117 111157 1131116 1131116 37.1- 37.1- 37.1- 11125 11.58 13.112 24.218 25.119 26.157 26.11/26.19/26.1 57 27.171 41.148 25.154	KOX_19410(tynA) KOX_2020 KOX_19420(toX,19425(pas8)/KOX_19430 KOX_19420(pasA)/KOX_19440 KOX_19450 KOX_19455 KOX_19455 KOX_19455 KOX_22690 KOX_226960 KOX_22685 KOX_22685 KOX_22685 KOX_20685 KOX_241840(pasA)/KOX_10830(paroE)/KOX_19450 KOX_19450 KOX_19450 KOX_19450 KOX_21840 KOX_19450 KOX_21850 KOX_22680 KOX_22680 KOX_22680 KOX_22680 KOX_22680 KOX_24180(paroE)/KOX_08990/KOX_10830(paroE)/KOX_19450 KOX_19450 KOX_19450 KOX_19450 KOX_19450 KOX_19450 KOX_19450 KOX_19450 KOX_19450 KOX_18340 KOX_18340 KOX_18340 KOX_18340 KOX_18340 KOX_18340 KOX_18340 KOX_18340 KOX_18340 KOX_18345 KOX_18345 KOX_18345 KOX_18345	phypr + o2 -> 2hpa + co2 paann + o2 -> pacald + co2 phaenn + o2 -> pacald + nh4 + h2o2 dphe + fad -> phpyr + nh4 + fadh2 phe + o2 -> pheact + co2 phaccoa + o2 + nadph -> 2epoxaccoa + nadp  2epoxaccoa -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoasa 3oxdscoas + nadp -> 3oxdscoasa darpcoa -> hadpcoa hadpcoa + coa -> carpcoa + accoa carpcoa -> hadpcoa hadpcoa + nad -> oxadpcoa + nadh dhcimm + o2 -> 2h6kated dhpppn + o2 -> 2h6kated dhpppn + o2 -> 2h6xotlend 2h6kated -> op4en + fum 2h6oxdlend -> op4en + succ dhsk + nadph -> nadp + sme dhsk + paqh2 -> paq + sme nad + phen -> 4hpp + co2 + nadh an + prep -> ppi + npran pep + skm5p ->> 3psme + pi akg + tyr ->> 4hpp + glu akg + tyr ->> 4hpp + glu akg + tyr ->> 4hpp + glu akg + phe ->> glu + phpyr atp + sme -> adp + skm5p 2cpr5p -> 3lg3p + co2 e4p + pep -> 3ddah7p + pi chor + gln -> an + glu + pyr
4HPHED2 MNAO9 DAAD2 CATPRX PHACCOAO  ZEPOXACCOAIL OXPINCOAH 30XDSCOASAD  ZEPOXACCOAIL ENCOAH8 3HACOADH DHPHEPDO1 DHPHEPDO2 ZH6KDH1 ZH6KDH2 SHKDH QTDH2 PPNDHG ANTPRT PSHKCVT TYRTA1 TYRTA2 PHETA SHKK IG3PS DOXPHS ANTHS DHQND	Phenylalanine metabolism Phenylalanine, Tyrosine and Tryptophan biosynthesis	4-hydroxyphenylpyruvate dioxygenase monoamine oxidase D-Amino add dehydrogenase catalase-peroxidase phenylacetate-CoA oxygenase 2-(12-epoxy-12-dihydrophenylacetyt-CoA isomerase oxepin-CoA hydrolase oxepin-CoA hydrolase 3-oxo-5-6-dehydrosuberyt-CoA semialdehyde dehydropenase 2-(12-epoxy-12-dihydrophenylacetyt-CoA semialdehyde dehydropenase 2-(12-epoxy-12-dihydrophenylacetyt-CoA isomerase enoyt-CoA hydratase 3-hydroxyacyt-CoA dehydropenase 12-dioxygenase (pyrroloquinoline-quinone) prephenate dehydrogenase quinate dehydrogenase (pyrroloquinoline-quinone) prephenate dehydrogenase shikimate 1-carboxyvinyltransferase tyrosine transaminase phenylalanine transaminase shikimate kinase anthranilate synthase anthranilate synthase anthranilate synthase anthranilate synthase anthranilate synthase anthranilate synthase	14321 14391 111121 11413149 53318 37.116 117.17 53318 42.117 111157 1131116 1131116 37.1- 37.1- 11125 11.58 13.112 24.218 25.119 26.157 26.11/26.19/26.1 57 27.171 41.148 25.154 41.327 42.110	KOX_19410(tynA) KOX_22496 KOX_2020 KOX_19420(pasa)K/KOX_19425(pas8)K/KOX_19430 KOX_19450 KOX_19455 KOX_19455 KOX_19455 KOX_22690 KOX_226960 KOX_22685 KOX_22685 KOX_22685 KOX_22685 KOX_24810 KOX_194810(areE)KOX_08990/KOX_10830(areE)/KOX_19450 KOX_19450 KOX_19450 KOX_19450 KOX_21850 KOX_22680 KOX_22680 KOX_22680 KOX_22685 KOX_24080 KOX_24080 KOX_19460 KOX_	phypr + o2 -> 2hpa + co2 peann + o2 -> pacald + ro4 + h2o2 dphe + fad -> phypr + nh4 + fadh2 phe + o2 -> pheact + co2 phaccoa + o2 + nadph -> 2epoxaccoa + nadp  Zepoxaccoa -> 3oxdscoasa  3oxdscoasa + nadp -> 3oxdscoasa  3oxdscoasa + nadp -> 3oxdscoasa  3oxdscoas + nadp -> 3oxdscoasa  dostscoas + nadp -> 3oxdscoasa  dostscoas + nadp -> 3oxdscoasa  dostscoas + nadp -> 3oxdscoasa  arpcoa -> hadpcoa hadpcoa + nad -> ocapcoa + radh  dhcimm + o2 -> 2h6kxted  dhpppn + o2 -> 2h6kxted  dhpppn + o2 -> 2h6xotlend  Zh6kxted -> op4en + fum  Zh6oxdlend -> op4en + succ  dhsk + nadph -> nadp + sme  dhsk + pqh2 -> pqq + sme  nad + phen -> 4hpp + co2 + nadh  an + prpp -> ppi + npran pep + skm5p -> 3psme + pi  akg + tyr -> 4hpp + glu  akg + tyr -> 4hpp + glu  akg + phe -> glu + phpyr  att + sme -> adp + skm5p  2cpr5p -> 3lg3p + co2  e4p + pep -> 3ddah7p + pi  chor + gln -> up + pyr  dqt -> dqt -> dqt -> pyr  dqt -> dqt -> dqt -> pyr  dqt -> dqt -> qqr  dqt -> dqt -> pyr  dqt -> dqt -> qqr  dqt -> dqt -> qqr
4HPHED2 MNAO9 DAAD2 CATPRX PHACCOAO  ZEPOXACCOAIL OXFINCOAH 30XDSCOASAD  ZEPOXACCOAIZ ENCOAH8 3HACOADH DHPHEPDO1 DHPHEPDO2 ZH6KDH1 ZH6KDH2 SHKDH QTDH2 PPNDHG ANTPRT PSHKCVT TYRTA1 TYRTA2 PHETA SHKK IG3PS DOXPHS ANTHS DHQND TRPS1	Phenylalanine metabolism Phenylalanine, Tyrosine and Tryptophan biosynthesis	4-hydroxyphenylpyruvate dioxygenase monoamine oxidase D-Amino add dehydrogenase catalase-peroxidase phenylacetate-CoA oxygenase 2-(12-epoxy-12-dihydrophenylacetyt-CoA isomerase oxepin-CoA hydrolase oxepin-CoA hydrolase 3-oxo-5-6-dehydrosuberyt-CoA semialdehyde dehydropenase 2-(12-epoxy-12-dihydrophenylacetyt-CoA semialdehyde dehydropenase 2-(12-epoxy-12-dihydrophenylacetyt-CoA isomerase enoyt-CoA hydratase 3-hydroxygot-CoA dehydropenase 12-dioxygenase (pyrroloxymythydropenase quinate dehydrogenase quinate dehydrogenase (pyrroloxymythydropenase (pyrroloxymythydropenase (pyrroloxymythydropenase (pyrroloxymythydropenase (pyrroloxymythydropenase yhydroysine transaminase tyrosine transaminase tyrosine transaminase hydrolasine transaminase shikimate tinase indicale-3-glycerol-phosphate synthase 3-debydroquinate dehydratase tryptophan synthase	14321 14391 111121 11413149 53318 37.116 117.17 53318 42.117 111157 1131116 1131116 37.1- 37.1- 11125 11.58 13.112 24.218 25.119 26.157 26.11/26.19/26.1 57 27.171 41.148 25.154 41.327 42.110 42.120	KOX_19410(tynA) KOX_22490 KOX_19420(pasa)K/KOX_19425(pas8)K/KOX_19430 KOX_19420(pasa)K/KOX_19440 KOX_19415 KOX_19415 KOX_19415 KOX_19450 KOX_19455 KOX_22690 KOX_22690 KOX_22685 KOX_22685 KOX_22685 KOX_24685 KOX_24184 KOX_19450 KOX_19450 KOX_19450 KOX_19455 KOX_22680 KOX_22680 KOX_22680 KOX_22680 KOX_22680 KOX_22680 KOX_22680 KOX_24180(aracb_KOX_08990/KOX_10830(aracb_KOX_1940)KOX_1940 KOX_19400 KOX_18400	phypr + o2 -> 2hpa + co2 peann + o2 -> pacald + ro4 + h2o2 dphe + fad -> hphyr + nh4 + fadh2 phe + o2 -> pheact + co2 phaccoa + o2 + nadph -> 2epoxaccoa + nadp  Zepoxaccoa -> 3oxdscoasa  3oxdscoasa + nadp -> 3oxdscoasa  3oxdscoasa + nadp -> 3oxdscoasa  3oxdscoas + nadp -> 3oxdscoasa  3oxdscoas + nadp -> 3oxdscoasa  dostacoa + coa -> carpcoa + accoa carpcoa -> hadpcoa hadpcoa + nad -> oxadpcoa + nadh  dhcimm + o2 -> Zh6oxdend  Zh6kated -> op4en + fum  Zh6oxdlend -> op4en + succ dhsk + nadph -> nadp + sme dhsk + paqh2 -> pqq + sme nad + phen -> 4hpp + co2 + nadh an + prop -> ppi + npran pep + skm5p -> 3psme + pi akg + tyr -> 4hpp + glu akg + tyr -> 4hpp + glu akg + tyr -> 4hpp + glu akg + phe -> glu + phpyr att + sme -> adp + skm5p 2cpr5p -> 3ig3p + co2  e4p + pep -> 3ddah7p + pi chor + gln -> an + glu + pyr ddt -> dhsk 3ig3p + ser -> g3p + trp
4HPHED2 MNAO9 DAAD2 CATPRX PHACCOAO  ZEPOXACCOAIL OXFINCOAH 30XDSCOASAD  ZEPOXACCOAIZ ENCOAH8 3HACOADH DHPHEPDO1 DHPHEPDO2 ZH6KDH1 ZH6KDH2 SHKCH QTDH2 PPNDHG ANTPRT PSHKCVT TYRTA1 TYRTA2 PHETA SHKK IG3P5 DOXPHS ANTHS DHQND TRPS1 TRPS1	Phenylalanine metabolism Phenylalanine, Tyrosine and Tryptophan biosynthesis	4-hydroxyphenylpyruvate dioxygenase monoamine oxidase D-Amino add dehydrogenase catalase-peroxidase phenylacetate-CoA oxygenase 2-(12-epoxy-12-dihydrophenylacetyt-CoA isomerase oxepin-CoA hydrolase oxepin-CoA hydrolase 3-oxo-5-6-dehydrosuberyt-CoA semialdehyde dehydropenase 2-(12-epoxy-12-dihydrophenylacetyt-CoA semialdehyde dehydropenase 2-(12-epoxy-12-dihydrophenylacetyt-CoA isomerase enoyt-CoA hydratase 3-hydroxygot-CoA dehydropenase 12-dioxygenase 2-hydroxys-festonona-24-dieneticiic acid hydrolase shikimate dehydrogenase (pyrroloquinoline-quinone) prephenate dehydrogenase (pyrroloquinoline-quinone) prephenate dehydrogenase hydroxygenase transaminase hydroxygenase transaminase hydroxygenasianine transaminase hydroxygenasianine transaminase shikimate tinase in shikimate tinase in shikimate tinase anthranialite synthase anthranialite synthase anthranialite synthase arthranialite synthase typtophan synthase typtophan synthase	14321 14391 111121 11413149 53318 37.116 117.17 53318 42.117 111157 1131116 1131116 37.1- 37.1- 11125 11.58 13.112 24.218 25.119 26.157 26.11/26.19/26.1 57 27.171 41.148 25.154 41.327 42.110 42.120	KOX_19410(tynA) KOX_22496 KOX_20220 KOX_19420(pasalx)/KOX_19425(pas8)/KOX_19430 KOX_19450 KOX_19455 KOX_19455 KOX_19455 KOX_22690 KOX_22665 KOX_22665 KOX_22665 KOX_22665 KOX_22665 KOX_24685 KOX_04180(areEy/KOX_08090/KOX_10830(areEy/KOX_19450) KOX_19450 KOX_19450 KOX_19455 KOX_19455 KOX_22690 KOX_22690 KOX_22690 KOX_22690 KOX_22690 KOX_22695 KOX_20681 KOX_24685 KOX_24685 KOX_04180(areEy/KOX_08090/KOX_10830(areEy/KOX_19400) KOX_19450 KOX_19450 KOX_19450 KOX_19450 KOX_18400 KOX_18450	phypr + o2 -> 2hpa + co2 peann + o2 -> pacald + ro4 + h2o2 dphe + fad -> phypr + nh4 + fadh2 phe + o2 -> pheact + co2 phaccoa + o2 + nadph -> 2epoxaccoa + nadp  2epoxaccoa -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoasa doxdscoa + coa -> carpcoa + accoa carpcoa -> hadpcoa hadpcoa + nad -> ocadpcoa + nadh dhcimm + o2 -> 2h6bxited dhpppn + o2 -> 2h6bxitend 2h6kated -> op4en + furn 2h6oxdlend -> op4en + succ dhsk + nadph -> nadp + sme dhsk + pqh2 -> pqq + sme nad + phen -> 4hpp + co2 + nadh an + prpp -> ppi + npran pep + skm5p -> 3psme + pi akg + tyr -> 4hpp + glu akg + tyr -> 4hpp + glu akg + tyr -> 4hpp + glu akg + phe -> glu + phypr att + sme -> adp + skm5p 2cpr5p -> 3ig3p + co2 e4p + pep -> 3ddah7p + pi chor + gln -> an + glu + pyr ddt -> dnsk 3ig3p + ser -> g3p + trp indole + ser -> trp
AHPHED2 MNAO9 DAAD2 CATPRX PHACCOAO  ZEPOXACCOAIL OXPINCOAH 30XDSCOASAD  ZEPOXACCOAIL ENCOAH8 3HACOADH DHPHEPDO1 DHPHEPDO2 ZH6KDH1 ZH6KDH2 SHKDH QTDH2 PPNDHG ANTPRT PSHKCVT TYRTA1 TYRTA2 PHETA SHKK IG3PS DOXPHS ANTHS DHQND TRPS1 TRPS1 TRPS2 TRPS3	Phenylalanine metabolism Phenylalanine, Tyrosine and Tryptophan biosynthesis	4-hydroxyphenylpyruvate dioxygenase monoamine oxidase D-Amino add dehydrogenase catalase-peroxidase phenylacetate-CoA oxygenase 2-(12-epoxy-12-dihydrophenylacetyt-CoA isomerase oxepin-CoA hydrolase oxepin-CoA hydrolase 3-oxo-5-6-dehydrosuberyt-CoA semialdehyde dehydropenase 2-(12-epoxy-12-dihydrophenylacetyt-CoA semialdehyde dehydropenase 2-(12-epoxy-12-dihydrophenylacetyt-CoA isomerase enoyt-CoA hydratase 3-hydroxygot-CoA dehydrogenase 12-dioxygenase 2-hydroxys-festonona-24-dieneticiic acid hydrolase shikimate dehydrogenase (pyrroloquinoline-quinone) prephenate dehydrogenase (pyrroloquinoline-quinone) prephenate dehydrogenase (pyrroloquinoline-quinone) prephenate dehydrogenase hydrogenase hydrogenase hydrogenase shikimate thrasaminase hydrogenase hydrogenase anthranialte shase shikimate kinase ahdranialte synthase anthranialte synthase anthranialte synthase arthranialte synthase typtophan synthase typtophan synthase typtophan synthase typtophan synthase	14321 14391 111121 11413149 53.318 37.116 117.17 53.318 42.117 111.157 1131116 1131116 37.1- 37.1- 11125 11.58 13.112 24.218 25.119 26.157 26.11/26.19/26.1 57 27.171 41.148 25.154 41.327 42.110 42.120 42.120 42.120	KOX_19410(tynA) KOX_2209 KOX_19420(pasA),KOX_19425(pasB),KOX_19430 KOX_19450 KOX_19455 KOX_19455 KOX_19455 KOX_19455 KOX_22690 KOX_22665 KOX_22665 KOX_22665 KOX_22665 KOX_24685 KOX_241840(pasA),KOX_10830(paroE)/ KOX_19450 KOX_19455 KOX_19455 KOX_22690 KOX_22690 KOX_22690 KOX_22690 KOX_22690 KOX_22685 KOX_24085 KOX_24085 KOX_24085 KOX_24085 KOX_241830(paroE),KOX_10830(paroE)/ KOX_19450 KOX_19450(paroE),KOX_22295 KOX_19450(paroE),KOX_22295 KOX_19450(paroE),KOX_22410(paroE)/ KOX_18340 KOX_18335 KOX_04616(paroE),KOX_12410(paroE)/ KOX_18335 KOX_00045 KOX_18325(trpA),KOX_18330 KOX_18330 KOX_18330 KOX_18330 KOX_18335(trpA)	phypr + o2 -> 2hpa + co2 peann + o2 -> pacald + ro4 + h2o2 dphe + fad -> phypr + nh4 + fadh2 phe + o2 -> pheact + co2 phaccoa + o2 + nadph -> 2epoxaccoa + nadp  2epoxaccoa -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoasa 4oxdscoa + coa -> carpcoa + accoa carpcoa -> hadpcoa hadpcoa + nad -> ocadpcoa + nadh dhcimm + o2 -> 2h6bxted dhpppn + o2 -> 2h6bxted dhpppn + o2 -> 2h6bxted 2h6kxted -> op4en + fur 2h6bxted -> op4en + succ dhsk + nadph -> nadp + sme dhsk + pqh2 -> pqq + sme nad + phen -> 4hpp + co2 + nadh an + prpp -> ppi + npran pep + skm5p -> 3psme + pi akg + tyr -> 4hpp + glu akg + tyr -> 4hpp + glu akg + tyr -> 4hpp + glu akg + phe -> glu + phypr att + sme -> adp + skm5p 2cpr5p -> 3ig3p + co2 e4p + pep -> 3ddah7p + pi chor + gln -> an + glu + pyr ddt -> dnsk 3ig3p + ser -> g3p + trp indole + ser -> trp 3ig3p -> g3p + indole
AHPHED2 MNAO9 DAAD2 CATPRX PHACCOAO  ZEPOXACCOAIL OXFINCOAH 3OXDSCOASAD  ZEPOXACCOAIL ENCOAH8 3HACOADH DHPHEPDO1 DHPHEPDO2 ZH6KDH1 ZH6KDH2 SHKCH QTDH2 PPNDHG ANTPRT PSHKCVT TYRTA1 TYRTA2 PHETA SHKK IG3PS DOXPHS ANTHS DHQND TRPS1 TRPS2 TRPS3 PPNDHT	Phenylalanine metabolism Phenylalanine, Tyrosine and Tryptophan biosynthesis	4-hydroxyphenylpyruvate dioxygenase monoamine oxidase D-Amino add dehydrogenase catalase-peroxidase phenylacetate-CoA oxygenase 2-(12-epoxy-12-dihydrophenylacetyl-CoA isomerase oxepin-CoA hydrolase oxepin-CoA hydrolase 3-oxo-5-6-dehydrosuberyl-CoA semialdehyde dehydropenase 2-(12-epoxy-12-dihydrophenylacetyl-CoA semialdehyde dehydropenase 2-(12-epoxy-12-dihydrophenylacetyl-CoA dehydropenase 3-hydroxygol-CoA dehydrogenase 12-dioxygenase 2-hydroxy-6-teonon-2-d-dieneticiic acid hydrolase shikimate dehydrogenase (pyrroloquinoline-quinone) prephenate dehydrogenase (pyrroloquinoline-quinone) prephenate dehydrogenase hydroxygenase transaminase hydroxygenase transaminase hydroxygenase transaminase hydroxygenase transaminase hydroxygenase transaminase hydroxygenase anthranialte synthase 3-dehydroquinate dehydratase tryptophan synthase tryptophan synthase prephenate dehydratase byptophan synthase	14321 14391 143149 53318 37.116 117.17 53318 42.117 11.1157 1131116 1131116 37.1- 37.1- 11.125 11.58 13.112 24.218 25.119 26.157 26.11/26.19/26.1 57 27.171 41.148 25.154 41.327 42.110 42.120 42.120 42.120 42.120 42.151	KOX_19410(tynA) KOX_2209 KOX_19420(pasA)/KOX_19425(pasB)/KOX_19430 KOX_19450 KOX_19455 KOX_19455 KOX_19455 KOX_19455 KOX_22690 KOX_226960 KOX_22685 KOX_22665 KOX_22665 KOX_22665 KOX_24104 KOX_19450 KOX_19450 KOX_19455 KOX_19455 KOX_22690 KOX_22690 KOX_22690 KOX_22690 KOX_22690 KOX_22690 KOX_22685 KOX_24085 KOX_24180(araCb/KOX_08990/KOX_10830(araCb/KOX_19450) KOX_19450 KOX_19450(araCb/KOX_2225) KOX_19450(araCb/KOX_2225) KOX_19450(araCb/KOX_2225) KOX_19450(araCb/KOX_2225) KOX_19505/KOX_22255 KOX_19505/KOX_22255 KOX_19505/KOX_22255 KOX_19505/KOX_22255 KOX_19505/KOX_22255 KOX_19505/KOX_22255 KOX_19505/KOX_22255 KOX_10000 KOX_18340 KOX_18340 KOX_18335 KOX_18325(typA)/KOX_18330 KOX_18325(typA) KOX_18325(typA) KOX_18325(typA) KOX_100030(pheA)/KOX_00340	phypr + o2 -> 2hpa + co2 peann + o2 -> pacald + ro4 + h2o2 dphe + fad -> phypr + nh4 + fadh2 phe + o2 -> pheact + co2 phaccoa + o2 + nadph -> 2epoxaccoa + nadp  2epoxaccoa -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoa + nadph  3oxdscoa + coa -> carpcoa + accoa carpcoa -> hadpcoa hadpcoa + nad -> coadpcoa + nadh  dhcimm + o2 -> 2h6bxted  dhpppn + o2 -> 2h6bxted  dhpppn + o2 -> 2h6bxted  dhsk + nadph -> nadp + sme dhsk + paqh2 -> pqq + sme nad + phen -> 4hpp + co2 + nadh an + prpp -> ppi + npran pep + skm5p -> 3psme + pi akg + tyr -> 4hpp + glu akg + phe -> glu + phypr atp + sme -> adp + skm5p 2cpr5p -> 3ig3p + co2 e4p + pep -> 3ddah7p + pi chor + gln -> an + glu + pyr ddt -> dnsk 3ig3p -> g3p + indole phen -> co2 + phypr
AHPHED2 MNAO9 DAAD2 CATPRX PHACCOAO  ZEPOXACCOAIL OXFINCOAH 30XDSCOASAD  ZEPOXACCOAIZ ENCOAH8 3HACOADH DHPHEPDO1 DHPHEPDO2 ZH6KDH1 ZH6KDH2 SHKCH QTDH2 PPNDHG ANTPRT PSHKCVT TVRTA1 TVRTA2 PHETA SHKK IG3PS DOXPHS ANTHS DHQND TRPS1 TRPS2 TRPS3 PPNDHT CHORS	Phenylalanine metabolism Phenylalanine jurosine and Tryptophan biosynthesis Phenylalanine, Tyrosine and Tryptophan biosynthesis	4-hydroxyphenylpyruvate dioxygenase monoamine oxidase D-Amino add dehydrogenase catalase- peroxidase phenylacetate-CoA oxygenase 2-(12-epoxy-12-dihydrophenylacetyl-CoA isomerase oxepin-CoA hydrolase oxepin-CoA hydrolase oxepin-CoA hydrolase oxepin-CoA hydrolase 2-(12-epoxy-12-dihydrophenylacetyl-CoA semialdehyde dehydropenase 2-(12-epoxy-12-dihydrophenylacetyl-CoA isomerase enoyl-CoA hydratase 3-hydroxyphenylpropionate 12-dioxygenase 22-dihydroxyphenylpropionate 12-dioxygenase 22-dihydroxyphenylpropionate 12-dioxygenase 22-dihydroxyphenylpropionate 12-dioxygenase 22-dihydroxyphenylpropionate 12-dioxygenase (pyrdoxyphenylpropionate 12-dioxygenase 24-dydroxyphenylpropionate 12-dioxygenase oxygenase acid hydrolase shikimate dehydrogenase (pyroloquinoilme-quinone) prephenate dehydrogenase (pyroloquinoilme-quinone) prephenate dehydrogenase anthranilate phosphorbioxyltransferase 3-phosphorhikimate 1-carboxyvinytransferase syrosine transaminase phenylalanine transaminase phenylalanine transaminase shikimate kinase indole-3-glycerol-phosphate synthase 3-deoxy-7-phosphoheptulonate synthase anthranilate synthase tryptophan synthase tryptophan synthase chorismate synthase	14321 14391 143149 53318 37.116 117.17 53318 42.117 11.1157 1131116 1131116 37.1- 37.1- 11.125 11.58 13.112 24.218 25.119 26.157 26.11/26.19/26.1 57 27.171 41.148 25.154 41.327 42.110 42.120 42.120 42.120 42.120 42.151	KOX_19410(tynA) KOX_2209 KOX_19420(pasA)/KOX_19425(pasB)/KOX_19430 KOX_19450 KOX_19455 KOX_19455 KOX_19455 KOX_19455 KOX_22690 KOX_22665 KOX_22665 KOX_22665 KOX_22665 KOX_24685 KOX_241840(pasA)/KOX_10830(paroE)/KOX_19450 KOX_19455 KOX_19455 KOX_22690 KOX_22690 KOX_22690 KOX_22690 KOX_22690 KOX_22695 KOX_24085 KOX_24185 KOX_24180(paroE)/KOX_08990/KOX_10830(paroE)/KOX_12685/KOX_22255 KOX_19445 K	phypr + o2 -> 2hpa + co2 peann + o2 -> pacald + ro4 + h2o2 dphe + fad -> phypr + nh4 + fadh2 phe + c2 -> pheact + co2 phaccoa + o2 + nadph -> 2epoxaccoa + nadp  2epoxaccoa -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoasa 4oxdscoa + coa -> carpcoa + accoa carpcoa -> hadpcoa hadpcoa + nad -> ocadpcoa + nadh dhcimm + o2 -> 2h6bxted dhpppn + o2 -> 2h6bxted dhpppn + o2 -> 2h6bxted dhsk + nadph -> nadp + sme dhsk + paqh2 -> pqq + sme nad + phen -> 4hpp + co2 + nadh an + prpp -> ppi + npran pep + skm5p -> 3psme + pi akg + tyr -> 4hpp + glu akg + phe -> glu + phypr atp + sme -> adp + skm5p 2cpr5p -> 3ig3p + co2 e4p + pep -> 3ddah7p + pi chor + gln -> an + glu + pyr ddt -> dnsk 3ig3p -> g3p + indole phen -> co2 + phypr 3psme -> chor + pi
AHPHED2 MNAO9 DAAD2 CATPRX PHACCOAO  ZEPOXACCOAIL OXPINCOAH 30XDSCOASAD  ZEPOXACCOAIL ENCOAH8 3HACOADH DHPHEPDO1 DHPHEPDO2 ZH6KDH1 ZH6KDH2 SHKDH QTDH2 PPNDHG ANTPRT PSHKCVT TVRTA1 TVRTA2 PHETA SHKK IG3PS DOXPHS ANTHS DHQND TRPS1 TRPS2 TRPS3 PPNDHT CHORS PRANTI	Phenylalanine metabolism Phenylalanine, Tyrosine and Tryptophan biosynthesis	4-hydroxyphenylpyruvate dioxygenase monoamine oxidase D-Amino add dehydrogenase catalase-peroxidase phenylacetate-CoA oxygenase 2-(12-epoxy-12-dihydrophenylacetyt-CoA isomerase oxepin-CoA hydrolase oxepin-CoA hydrolase 3-oxo-5-6-dehydrosuberyt-CoA semialdehyde dehydropenase 2-(12-epoxy-12-dihydrophenylacetyt-CoA semialdehyde dehydropenase 2-(12-epoxy-12-dihydrophenylacetyt-CoA dehydropenase 13-ydroxygot-CoA dehydrogenase 12-dioxygenase 12-dioxygenase 12-dioxygenase 12-dioxygenase 12-dioxygenase 12-dioxygenase (2-dioxygenase 12-dioxygenase 12-dioxygenase 12-dioxygenase 12-dioxygenase (2-yhdroxy-6-ketonona-2-d-dienedioic acid hydrolase shikimate dehydrogenase (pyrroloquinoline-quinone) prephenate dehydrogenase (pyrroloquinoline-quinone) prephenate dehydrogenase hydroxygenase (pyrroloquinoline-quinone) prephenate dehydrogenase (pyrroloquinoline-quinone) prephenate dehydrogenase hydroxygenase shikimate 1-carboxyvinyltransferase hydroxygenase anthranialate shase phenylalanine transaminase hydroxydroquinate dehydrotase tyrytophan synthase tryptophan synthase tryptophan synthase tryptophan synthase prephenate dehydratase chorismate synthase phosphoriboxylanthranilate somerase	14321 14391 14314 111121 11413149 53318 37.16 117.17 53318 42.117 111157 113116 1131116 13311- 37.1- 37.1- 11125 11.58 13.112 24.218 25.119 26.157 26.11/26.19/26.1 57 27.171 41.148 25.154 41.327 42.110 42.120 42.120 42.120 42.151 42.35 53.124	KOX_19410(tynA) KOX_2020 KOX_19420(pasA)/KOX_19425(pasB)/KOX_19430 KOX_19450 KOX_19455 KOX_19455 KOX_19455 KOX_22690 KOX_22690 KOX_22695 KOX_22655 KOX_20655 KOX_20655 KOX_20610 KOX_19450 KOX_19455 KOX_19455 KOX_21845	phypr + o2 -> 2hpa + co2 paann + o2 -> pacald + rhd + h2o2 dphe+ fad -> phypr + nh4 + fadh2 phe + o2 -> pheact + co2 phaccoa + o2 + nadph -> 2epoxaccoa + nadp  2epoxaccoa -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoasa arpcoa -> hadpcoa hadpcoa + coa -> carpcoa + accoa carpcoa -> hadpcoa hadpcoa + nad -> oxadpcoa + nadh dhcinnm + o2 -> 2h6kated dhpppn + o2 -> 2h6xdtend 2h6kated -> op4en + fum 2h6oxdiend -> op4en + succ dhsk + nadph -> nadp + sme dhsk + paqh2 -> pqq + sme nad + phen -> 4hpp + co2 + nadh an + prpp -> ppi + npran pep + skm5p ->> 3psme + pi akg + tyr ->> 4hpp + glu akg + tyr ->> 4hpp + glu akg + tyr ->> 4hpp + glu akg + tyr ->> 3dphp + sm5p 2cpr5p -> 3ig3p + co2 e4p + pep -> 3ddah7p + pi chor + gln -> na + glu + pyr ddt -> dnsk 3ig3p ->> g3p + indole phen ->> co2 + phpyr 3psme ->> chor + pi npran ->>> chor + pi npran ->>> chor + pi npran ->>> chor + pi npran ->>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
AHPHED2 MNAO9 DAAD2 CATPRX PHACCOAO  ZEPOXACCOAIL OXFINCOAH 30XDSCOASAD  ZEPOXACCOAIZ ENCOAH8 3HACOADH DHPHEPDO1 DHPHEPDO2 ZH6KDH1 ZH6KDH2 SHKCH QTDH2 PPNDHG ANTPRT PSHKCVT TVRTA1 TVRTA2 PHETA SHKK IG3PS DOXPHS ANTHS DHQND TRPS1 TRPS2 TRPS3 PPNDHT CHORS	Phenylalanine metabolism Phenylalanine, Tyrosine and Tryptophan biosynthesis	4-hydroxyphenylpyruvate dioxygenase monoamine oxidase D-Amino acid dehydrogenase catalase-peroxidase phenylacetate-CoA oxygenase 2-(12-epoxy-12-dihydrophenylacetyl-CoA isomerase oxepin-CoA hydrolase 3-oxo 5-6-dehydrosubenyl-CoA isomerase oxepin-CoA hydrolase 3-hydrolase 3-hydroyacyl-CoA disomerase enoyl-CoA hydratase 3-hydroxysoyl-CoA dehydropensyl-cyl-CoA isomerase 2-3-dihydroxyphenylpropionate 12-dioxygenase 2-3-dihydroxysoyl-CoA dehydrogenase 2-3-dihydroxysoyl-CoA dehydrogenase 2-3-dihydroxysoyl-coA dehydrogenase 2-3-dihydroxysoyl-coA dehydrogenase 2-4-dixoxy-6-ketonona-2-4-dienedioic acid hydrolase shikimate dehydrogenase quinate dehydrogenase quinate dehydrogenase anthranilate phosphoribosyltransferase 3-phosphoshikimate 1-carboxyvinyltransferase tyrosine transaminase tyrosine transaminase tyrosine transaminase shikimate kinase indole-3-glycerol-phosphotase shikimate synthase 3-deoxy-7-phosphoheptulonate synthase tryptophan synthase tryptophan synthase tryptophan synthase tryptophan synthase phosphoribosylanthranilate phosphoribosylanthranilate phosphoribosylanthranilate phosphoribosylanthranilate phosphoribosylanthranilate phosphoribosylanthranilate	14321 14391 143149 53318 37.116 117.17 53318 42.117 11.1157 1131116 1131116 37.1- 37.1- 11.125 11.58 13.112 24.218 25.119 26.157 26.11/26.19/26.1 57 27.171 41.148 25.154 41.327 42.110 42.120 42.120 42.120 42.120 42.151	KOX_19410(tynA) KOX_2209 KOX_19420(pasA)/KOX_19425(pasB)/KOX_19430 KOX_19450 KOX_19455 KOX_19455 KOX_19455 KOX_19455 KOX_22690 KOX_22665 KOX_22665 KOX_22665 KOX_22665 KOX_24685 KOX_241840(pasA)/KOX_10830(paroE)/KOX_19450 KOX_19455 KOX_19455 KOX_22690 KOX_22690 KOX_22690 KOX_22690 KOX_22690 KOX_22695 KOX_24085 KOX_24185 KOX_24180(paroE)/KOX_08990/KOX_10830(paroE)/KOX_12685/KOX_22255 KOX_19445 K	phypr + o2 -> 2hpa + co2 paann + o2 -> pacald + rhd + h2o2 dphe+ fad -> phypr + nh4 + fadh2 phe + o2 -> pheact + co2 phaccoa + o2 + nadph -> 2epoxaccoa + nadp  2epoxaccoa -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoasa 3oxdscoasa + nadp -> 3oxdscoasa arpcoa -> hadpcoa hadpcoa + coa -> carpcoa + accoa carpcoa -> hadpcoa hadpcoa + nad -> oxadpcoa + nadh dhcinnm + o2 -> 2h6kated dhpppn + o2 -> 2h6xdtend 2h6kated -> op4en + fum 2h6oxdiend -> op4en + succ dhsk + nadph -> nadp + sme dhsk + paqh2 -> pqq + sme nad + phen -> 4hpp + co2 + nadh an + prpp -> ppi + npran pep + skm5p ->> 3psme + pi akg + tyr ->> 4hpp + glu akg + tyr ->> 4hpp + glu akg + tyr ->> 4hpp + glu akg + tyr ->> 3dphp + sm5p 2cpr5p -> 3ig3p + co2 e4p + pep -> 3ddah7p + pi chor + gln -> na + glu + pyr ddt -> dnsk 3ig3p ->> g3p + indole phen ->> co2 + phpyr 3psme ->> chor + pi npran ->>> chor + pi npran ->>> chor + pi npran ->>> chor + pi npran ->>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>

	DUOTE	Phenylalanine, Tyrosine and Tryptophan	2111	4224	VOV DATOE ( P)	2002
Series of the content	DHQTS	biosynthesis	3-dehydroquinate synthase	4.2.3.4	KOX_04605(aroB)	3ddah7p -> dqt + pi
NomeNomeAccount of the part of	QTDH1	biosynthesis	(pyrroloquinoline-quinone)	1.1.5.8	KOX_19605/KOX_22295	qt + pqq <-> dqt + pqqh2
	TYRTM			2.6.1.57	KOX_08310	phen + asp -> oaa + ag
Appeal of the company of the compan	AGDH1			4.2.1.51	KOX_00030(pheA)/KOX_00340	ag -> phe + co2
Appeal of the control of the contro	AGDH2	Phenylalanine, Tyrosine and Tryptophan	arogenate/prephenate	42191	KOX 00340	an -> phe + co2
Nome 1988	AGDH3	biosynthesis	dehydratase	4.2.1.91	KOX_00340	phen -> phpyr + co2
Modern Comment Comment Comment Marchannel Modern <td>PPACALDH</td> <td></td> <td></td> <td>3.11.1.1</td> <td>KOX_06380</td> <td>ppacald -&gt; acal + pi</td>	PPACALDH			3.11.1.1	KOX_06380	ppacald -> acal + pi
Appeal of the control of the contro	PPACH			3.11.1.2	KOX_08585	ppac -> ac + pi
	DAMEDDE			26127	NON USTAIL	Zeenen van van eenende vale
Manuface					_	
Professor   Prof	PPTCACT		acetyltransferase	2.3.1.183	KOX_19805/KOX_25625	dmppth + accoa -> nadpt + coa
Pages   Page	CPPPGO	Porphyrin and Chlorophyll metabolism		1.3.3.3	KOX_26935	cpp + o2 -> 2 co2 + pphg
ModernSymbolSeptiment of Dennish (miner)Septiment of Dennish (miner)URL COImplies of Colonglin (miner)Colonglin (miner)1,111 (miner)Dennish (miner)Septiment of Dennish (miner)URL COSeptiment of Colonglin (miner)Colonglin (miner)Colonglin (miner)Colonglin (miner)Septiment of Dennish (miner)URL COSeptiment of Colonglin (miner)Colonglin (miner)Colonglin (miner)Colonglin (miner)Septiment of Dennish (miner)URL COSeptiment of Colonglin (miner)Colonglin (miner)Colonglin (miner)Septiment of Dennish (miner)Septiment of Dennish (miner)URL COSeptiment of Colonglin (miner)Colonglin (miner)Septiment of Dennish (miner)Septiment of Dennish (miner)URL COSeptiment of Colonglin (miner)Colonglin (miner)Septiment of Dennish (miner)Septiment of Dennish (miner)URL COSeptiment of Colonglin (miner)Colonglin (miner)Septiment of Dennish (miner)Septiment of Dennish (miner)URL COSeptiment of Colonglin (miner)Colonglin (miner)Septiment of Dennish (miner)Septiment of Dennish (miner)URL COSeptiment of Colonglin (miner)Colonglin (miner)Septiment of Dennish (miner)Septiment of Dennish (miner)URL COSeptiment of Colonglin (miner)Septiment of Dennish (miner)Septiment of Dennish (miner)Septiment of Dennish (miner)URL COSeptiment of	CPPPGOO	Porphyrin and Chlorophyll metabolism		1.3.99.22	KOX_02720/KOX_06875	cpp + 2 sam -> pphg + 2 co2 + 2 met + 2 da-5
Professor   Company of Control Professor   C	PRICO					
Page	PPRIGO	Porphyrin and Chlorophyri metabolishi	(40.00.0)	1.3.3.4		3 02 + 2 ppng -> 2 ppnx
Mary   May and Orough remained   May and May and Mary   Part   M	PPHGOx	Porphyrin and Chlorophyll metabolism	(anaerobic)	1.3.3.4		3 fum + pphg -> ppix + 3 succ
Mary	PPHGOmq	Porphyrin and Chlorophyll metabolism		1.3.5.3	KOX_07855(hemG)	pphg + 3 mk -> ppix + 3 mqn
Mary	UPPMT	Porphyrin and Chlorophyll metabolism	uroporphyrinogen	2.1.1.107	KOX 01090/KOX 04575(cvsG)/KOX 07615	2 sam + uppg3 -> 2 sah + dsd
Perspect of Services   Perspect of Services   1985   198	CBIAT1			2.5.1.17		
	LIBROC1		uroporphyrinogen	41127	VOV 07090(homE)	
Mathem   March   Mar	OPPDCI			4.1.1.37	KOX_0/960(rieffic)	
Minimum						
Minimum	UPPG3S	Porphyrin and Chlorophyll metabolism	uroporphyrinogen-III synthase	4.2.1.75		hmb -> uppg3
Miles   Mile					KOX 13055(hemH)	
Minimum			glutamate-1-semialdehyde		= : :	
ACCISION         Persphyran and Contemply materials         ACCISIAN (Including and Contemply materials)         ACCISIAN (Including and Contemply and Contem					-	atp + qlu + trnaqlu -> amp + qlutrna + ppi
ACCOURS         Polythym and Collegation floatication of processing and proces			Adenosyl cobinamide		- •	
ACM			Adenosyl cobinamide kinase			
1.11	ADCOBPS		Adenosylcobalamin 5'-	2.7.8.26		
Marchine		Porphyrin and Chlorophyll metabolism	glutamyl-tRNA reductase			glutrna + nadph -> glu1sa + nadp + trnaglu
Second   Purple of Colors   Pu					=	
	UPPDC2	Porphyrin and Chlorophyll metabolism	decarboxylase	4.1.1.37	KOX_07980(hemE)	uppg1 -> cppi + 4 co2
March   Purplem of Colorophy methods   March   Marc	SRHCC	Porphyrin and Chlorophyll metabolism		4.99.1.3	KOX_01380	shcl + cobalt2 -> cobtpc
College			Cobinamide adenyltransferase			
Content					=	
Content	COBBP1	Porphyrin and Chlorophyll metabolism	CobC	0.3.1.10	KOX_01425(codD)	atp + acha + amppo -> adp + pi + adcba
Modern   Prophysm and Colongolyll methodols   Colongoly   Colon	COBBP2	Porphyrin and Chlorophyll metabolism		6.3.1.10	KOX_01425(codD)	acha + dlap2oop + atp -> adcbap + adp + pi
Content						
International Confect						
CORTICNED   Populyman and Chlorophy metablosine   Populyman and Chlo	COFACMI	Porpnyrin and Chiorophyli metabolism		2.1.1.151	KOX_01375	cootpc + sam -> cotac3 + san
COBITCAMT   Purplyin and Chicarphyll metabloim   Purplyin and Chicarphyll metabloim   COBITCAM   Purplyin and Chicarphyll metabloim   COBITCAM   Purplyin and Chicarphyll metabloim   Cobit   Purplyin and Chicarphyll metabloim   Cobit   C	COFACTOPC	Porphyrin and Chlorophyll metabolism	incomplete reaction			cofac3 <-> cobtpc3
CORTICOM   Poptlymin and Chrosophyl metabolism   Collab processor A CIU   CORTICOM   Poptlymin and Chrosophyl metabolism   Collab processor A cylindae	COBTPC3MT	Porphyrin and Chlorophyll metabolism	cobalt-precorrin-3B C(17)-	2.1.1.131	KOX_01390(cbiH)	cobtpc3 + sam -> cobtpc4 + sah
CORTICION   Popsylym and Changegyly metabolism   Colling Control Age						
COBTICATION   Pophysis and Charepylal metabolam (COBTICATION   Pophysis and Charepyl			methyltransferase			
COBTICION   Popphysis and Chinosphyll metabolism   Cobtine   Popphysis and Chinosphyll metabolism   Cobtine   Popphysis and Chinosphyll metabolism   Popphysis and Chinosphy						·
COURTON			cohalt processin 6v reductare			·
COBTYCEM   Prophysis and Chicrophyll metabolism   Prop			cobalt-precorrin-6Y C(5)-			
Coorange	COBTPC6YM	Porphyrin and Chlorophyll metabolism	methyltransferase	2.1.1.132	KOX_01410	cobtpc6b + sam -> cobtpc7 + sah
COBTROM         Porphyrin and Chlorophyll metabolism         cobab precent a Kernifymutate objective and Chlorophyll metabolism         5.41.2         KOX_01830         cobpute and Chlorophyll metabolism         cobput and Chlorophyll metabolism         Common and Chlorophyll metabolism         cobput and Chlorophyll	COBTPC7M	Porphyrin and Chlorophyll metabolism		2.1.1.196	KOX_01405	cobtpc7 + sam -> cobtpc8 + sah
	CORTRONA	Danielia and Chlassical matchalian	,	5412	KOX 01420/-E/C)	
Pool						•
PCM	COBRINDIS	Porphyrin and Chlorophyll metabolism	synthase	6.3.5.11	KOX_01430	cobrin + 2 gln + 2 atp -> cobrindi + 2 glu + 2 adp + 2 pi
PCMM         Pophlysin and Chlorophyll metabolism (methyltraneferase proconial of CLT) (CLT)	PC2M	Porphyrin and Chlorophyll metabolism		2.1.1.130	KOX_01375	dscl + sam -> pc3a + sah
Pop-	PC3M	Porphyrin and Chlorophyll metabolism	precorrin-3B C17-	211131	KOX 01390(chiH)	nr3h + sam -> nr4 + sah
PCROBE   Perphysim and Chicrophyll metabolism   PCROMAM   Perphysin and Chicrophyll metabolism   PCROMAM   Perphysin and Chicrophyll metabolism   PCROMAM   Perphysim and Chicrophyll metabolism   PCROMAM   PCR						
Possible			methyltransferase			
HotRNBDS   Porphyrin and Chlorophyll metabolism   Fazzangsen undoeredutate synthates   Fazzangsen undoeredutate synthates   Fazzangsen undoeredutate   Fa						
FCOXIX			Hydrogenobyrinate a,c diamide			
Final Collaboration   Perphyrim and Chlorophylim metabolism   APL-theroine O-phosphotransferase ethonoclimania denosystransferase aquacobalismi reductase aquacobalismi reductase aquacobalismi reductase ethonoclimania denosystransferase ethonoclimania denosystransferase aquacobalismi reductase (2.72.1 KOX_07820(fee) aqctl 3 nadn -> cb2 + nad apps -> stp + ppa (2.75) ppa (2.7	FEO2OX	Porphyrin and Chlorophyll metabolism		1.16.3.1		o2 + 4 fe2 -> 4 fe3
Propagate metabolism   Propanote metabolism   Undear reaction   Propanote metabolism   Undear reaction   Propanote metabolism   Undear reaction   Propanote metabolism   Undear reaction   Propanote metabolism   Propanote metabolism   Propanote metabolism   Propanote metabolism   Undear reaction   Propanote metabolism			threonine-phosphate			
Porphyrin and Chlorophyll metabolism   Proparative metabolism   Prop	THRAOT		ATP:L-threonine O-	2.7.1		thr + atp -> thro3p + ado
ELCOBALID         Prophymin and Chlorophyll metabolism         cobalamin adenosytransferase         25.117         KOX_7/DID         coll + sip > adoctor + ado           ACCESIRD         Prophymin and Chlorophyll metabolism         Propionate in an adoctor in an adoctor in a path of the pape (~> adpt.8 a hadh > cbt.2 + and adp + ppap (~> adpt.8 a hadh > cbt.2 + and adp + adpt.8 a			F		VOV 27010	The state of the s
PRACK Propanoate metabolism Propinate kinase 2-2xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx			cobalamin adenosyltransferase			
OBUTE         Propanoate metabolism         2-Oxobutanoate formate lyase         2 3.15.4 ptp.         SOX 7770/KOX 15275/KOX 15975/KOX					KOX_01540/KOX_26435	adp + ppap <-> atp + ppa
PACTF Propanoate metabolism Propanoate metabolism Propanoate metabolism Propanoate metabolism ACCSYN12 Propanoate metabolism acetyl-CoA synthatase 42.117 KOX,0846S Propanoate metabolism acetyl-CoA synthatase 62.11 KOX,0846S Propanoate metabolism acetyl-CoA synthatase 62.11 KOX,0846S Propanoate metabolism ACCSYN12 Propanoate metabolism ACCSYN12 Propanoate metabolism ACCSYN12 Propanoate metabolism ACCSYN12 Propanoate metabolism L-Latce dehydrogenase Active Propanoate metabolism L-Latce dehydrogenase ACCSYN12 Propanoate metabolism Unclear reaction Unclor Propanoate metabolism Unclear reaction UND Unclor Propanoate metabolism Unclear reaction UND Unclor Unclor Propanoate metabolism Unclear reaction UND Unclor Uncl	OBUTFL		2-Oxobutanoate formate lyase	2.3.1.54	KOX_09770/KOX_15225/KOX_15975/KOX_16885	(
ENCOAH2 Propanoate metabolism acetyl-CoA synthetase 6.21.1 KOX,0865 ppace amp <> ppace amp <> ppald + coa			Phosphate acetyltransferase	2.3.1.8	KOX_26440/KOX_01490(pduL)	pi + ppcoa <-> coa + ppap
ACCSYN2 Propanoate metabolism acetyl-CoA synthesise 62.11 KOX_08465 ppald + ppi → ppa + atp methylmidonate-semialdehyde dehydrogensise 1.12.17 KOX_08467 mmsa + coa + nad → ppcoa + co2 + nadh   Propanoate metabolism chiestory propinate (oA-transferse unclear reaction propinate (oA-transferse unclear reaction unclear reaction with propinate metabolism unclear reaction unclear re			enoyl-CoA hydratase			3hpcoa <-> ppecoa
L-LACCH Propanoate metabolism   L-lacte dehydrogenase   11.127   KOX_21270   2hba + nad > obut + nadh   PCT2 Propanoate metabolism propionate CoA-transferase   28.31   KOX_02010   lactcoa + ppa <> > llac + ppcoa   RCT2P Propanoate metabolism unclear reaction   maloca + nadp <> 3 appcoa + oa + nadph   PCT2P Propanoate metabolism unclear reaction   maloca + nadp <> 3 appcoa + oa + nadph   PCT2P Propanoate metabolism unclear reaction   maloca + nadp <> 3 appcoa + oa + nadph   PCT2P Propanoate metabolism   nuclear reaction   maloca + nadp <> 3 appcoa + oa + nadph   PCT2P Propanoate metabolism   nuclear reaction   nucl			acetyl-CoA synthetase			
L-IACTACM	MMSDH	Propanoate metabolism		1.2.1.27	KOX_09140/KOX_09360	mmsa + coa + nad -> ppcoa + co2 + nadh
MCTOP OPTHP         Propanoate metabolism Propanoate metabolism         unclear reaction undear reaction         Image: 10 cm and proper to a proposal and proper to a pagin cos 3 approas a nadph cos 2 approas 2 ap			L-lactate dehydrogenase			
OPTHP         Propanate metabolism         unclear reaction         3 oppcoa + nadgh <> 3 fpcoa + nadgh           ALHD16         Propanate metabolism         (NAD-1)         12.13         KOX_00375         2p1a + nad > ppn + nadh           2MCIDIT         Propanate metabolism         2-methylisocitrate dehydratase         42.199         KOX_11075         maco <> micit           MMCOADC         Propanate metabolism         methylimalonsi-case met				2.8.3.1	KUX_02010	
ALTION Propanoate metabolism (NAD-)  MMCOADC Propanoate metabolism 2-methylinositrate dehydratase 421.99 KOX_11075 maco <-> micit methylination to decarbosylase methylination tessemialdehyde dehydrogenase methylination at e-semialdehyde dehydrogenase methylination tessemialdehyde dehydrogenase d			unclear reaction			
MMCOADC   Propanoate metabolism   2-methylisocirtate dehydratase   24.19.9   KOX, 11075   maco <-> micit   maco (-> micit		Propanoate metabolism		1.2.1.3		2p1a + nad -> ppn + nadh
MMALSADH1 Propanoate metabolism decarboxylase metabolism delydrogenase metabolism methylmiaontate-semialdehyde delydrogenase metabolism methylmiaontate-semialdehyde delydrogenase metabolism methylmiaontate-semialdehyde delydrogenase metabolism methylmiaontate-semialdehyd delydrogenase semialdehydrogenase phosphorboxylminoinidazole carboxylase delydrogenase phosphorboxylminoinidazole carboxylase delydrogenase phosphorboxylminoinidazole carboxylase delydrogenase delydrogenase phosphorboxylminoinidazole carboxylase delydrogenase delydroge	2MCITDT	Propanoate metabolism	2-methylisocitrate dehydratase	4.2.1.99	KOX_11075	maco <-> micit
MMALSADH2 Propanoate metabolism embeding methylmiolante-semialdehyde delydrogenase metabolism embeding delydrogenase semialdehyde delydrogenase semialdehyde delydrogenase semialdehyde delydrogenase semialdehyde delydrogenase semialdehyde delydrogenase semialdehyde	MMCOADC	Propanoate metabolism	decarboxylase	4.1.1.41	KOX_02550	mmcoa-S -> ppcoa + co2
MMALSADH2         Propanoate metabolism         methylmalonate-semialdehyd edhydrogenase phosphoepatromutase phospho	MMALSADH1	Propanoate metabolism		1.2.1.18	KOX_09140/KOX_09360	3opp + coa + nad -> accoa + co2 + nadh
MMALSADH3	MMALSADH2	Propanoate metaholism	methylmalonate-semialdehyde	1.2.1.18	KOX 09140/KOX 09360	3opp + coa + nadp <-> malcoa + nadph
PENTIM   Purine metabolism   Properties   Pentime   Pentime   Properties   Properties   Pentime   Properties   P		•	dehydrogenase			
IMPCH         Purine metabolism         IMP cyclohydrolase phosphoribasylaminomidazole archrolysus archrolys		·	dehydrogenase			
PRAZCZ Purine and Pyrimidine Biosynthesis carboxylsam carboxylsam inoimidazole carboxylsam (arboxylsam carboxylsam						
GARTET         Purine and Pyrimidine Biosynthesis         GAR transformylase-T         21.2-         21.2-         atp + formate + gar → adp + fgam + pi           GTPDPK         Purine metabolism         GIP diphospholisnase         27.65         KOX 01155(relA)         atp + tgp → amp + pppgpp           GSTDPDP         Purine metabolism         guanorian-9-triphosphates diphosphates diphosphates ulreidoglycolate hydrolase         3.6.111/2.6.1.40         KOX 07535/KOX 27190         pppgpp → pi + ppgpp           URGLYCH         Purine metabolism         broundeciside-diphosphate reductase (ADP) reductase (ADP)         KOX 20440/KCXX 00445(rndF)/KOX 26135/KOX 2044 pt + 2 mb +			phosphoribosylaminoimidazole			
GTPDPK         Purine metabolism         GTP diphosphoficinase         2.7.6.5         KOX_01155(relA)         atp + gtp → amp + pppgpp           GSTDPDP         Purine metabolism         guanosine-5-triphosphate diphosphates diphosphate diphosphates of unded objects and produces discolated diphosphate reductase (ADP)         35.319         KOX_07353(xCX_27190         pppgpp → pi + ppppp           URGLYCH         Purine metabolism         thonucleoside-diphosphate reductase (ADP)         35.319         KOX_0745(xCX_27190         undglyc → cc2 + gix + 2 rh4           RNDPR1         Purine metabolism         thonucleoside-diphosphate reductase (ADP)         117.41         KOX_07044(XCX_00445(rndF)/KCX_26135/KCX_adp+ rhio → dadp +				2.1.2		
URGLYCH   Purine metabolism   diphosphates   diphosphate   di	GTPDPK		GTP diphosphokinase	2.7.6.5		
URGLYCH         Purine metabolism         Ureidoglycolate hydrolase         3.5.3.19         KOX_27445         urdglyc >> co2 + glx + 2 nh4           RNDPR1         Purine metabolism         ribonucleoside-diphosphate reductase (ADP)         117.4.1         KOX_00440/KOX_00445(nrdF)/KOX_26135/KOX_ adp + rthio -> dadp + othio           RNDP92         Purine metabolism         ribonucleoside-diphosphate reductase (ADP)         117.4.1         KOX_00440/KOX_00445(nrdF)/KOX_26135/KOX_ adp + rthio -> dadp + othio           RNDP92         Purine metabolism         RNDP92         NOX_00440/KOX_00445(nrdF)/KOX_26135/KOX_ adp + rthio -> dadp + othio		Purine metabolism				pppgpp -> pi + ppgpp
reductase (ADP)   26140(rrdB)   26140(rrdB			Ureidoglycolate hydrolase			
	RNDPR1	Purino motabolism		1.17.4.1		adp + rthio -> dadp + othio
		runie metabolism				
	RNDPR2		ribonucleoside-diphosphate	1.17.4.1		gdp + rthio -> dgdp + othio

RNDPR3	Purine metabolism	ribonucleoside-diphosphate reductase (CDP)	1.17.4.1	KOX_00440/KOX_00445(nrdF)/KOX_26135/KOX_ 26140(nrdB)	cdp + rthio -> dcdp + othio
RNDPR4	Purine metabolism	ribonucleoside-diphosphate	1.17.4.1	KOX_00440/KOX_00445(nrdF)/KOX_26135/KOX_	rthio + udp -> dudp + othio
PUNPP1	Purine metabolism	reductase (UDP) purine-nucleoside	2.4.2.1	26140(nrdB)	adn + pi <-> ad + rlp
PUNPPI	Purine metabolism	phosphorylase (Adenosine) purine-nucleoside	2.4.2.1	KOX_10320(deoD)	adn + pi <-> ad + rip
PUNPP2	Purine metabolism	phosphorylase	2.4.2.1	KOX_10320(deoD)	da + pi <-> dr1p + ad
DI INIDOS	D :	(Deoxyadenosine) purine-nucleoside	2424	VOV 10220 L D	
PUNPP3	Purine metabolism	phosphorylase (Guanosine)	2.4.2.1	KOX_10320(deoD)	gsn + pi <-> gn + r1p
PUNPP4	Purine metabolism	purine-nucleoside phosphorylase	2.4.2.1	KOX_10320(deoD)	dg + pi <-> dr1p + gn
		(Deoxyguanosine) purine-nucleoside			
PUNPP5	Purine metabolism	phosphorylase (Inosine)	2.4.2.1	KOX_10320(deoD)	ins + pi <-> hyxn + r1p
PUNPP6	Purine metabolism	purine-nucleoside phosphorylase (Deoxyinosine)	2.4.2.1	KOX_10320(deoD)	din + pi <-> dr1p + hyxn
PUNPP7	Purine metabolism	purine-nucleoside	2.4.2.1/2.4.2	KOX_10320(deoD)/KOX_26800	pi + xtsine <-> r1p + xan
XANPRT	Purine metabolism	phosphorylase (Xanthosine) xanthine	2.4.2.8/2.4.2.22	KOX_11140/KOX_11750	prpp + xan -> ppi + xmp
		phosphoribosyltransferase adenine			
ADPRT1	Purine metabolism	phosphoribosyltransferase	2.4.2.7	KOX_13025	ad + prpp -> amp + ppi
GNPRT	Purine metabolism	guanine phosphoribosyltransferase	2.4.2.8/2.4.2.22	KOX_11140/KOX_11750	gn + prpp -> gmp + ppi
HYXNPRT	Purine metabolism	hypoxanthine phosphoribosyltransferase	2.4.2.8	KOX_11140	hyxn + prpp -> imp + ppi
		(Hypoxanthine)		_	
DADNK ADNK1	Purine metabolism Purine metabolism	deoxyadenylate kinase adenylate kinase	2.7.4.3	KOX_13050(adk) KOX_13050(adk)	atp + damp <-> adp + dadp amp + atp <-> 2 adp
NUDPK1	Purine metabolism	nucleoside-diphosphate kinase	2.7.4.6	KOX_27290(ndk)	atp + gdp <-> adp + gtp
		(ATP:GDP) nucleoside-diphosphate kinase	2.7.4.6		
NUDPK5	Purine metabolism	(ATP:dGDP)	2.7.4.6	KOX_27290(ndk)	atp + dgdp <-> adp + dgtp
NUDPK8	Purine metabolism	nucleoside-diphosphate kinase (ATP:dADP)	2.7.4.6	KOX_27290(ndk)	atp + dadp <-> adp + datp
DGNK	Purine metabolism	deoxyguanylate kinase (dGMP:ATP)	2.7.4.8	KOX_06000(gmk)	atp + dgmp <-> adp + dgdp
GKN	Purine metabolism	guanylate kinase (GMP:ATP)	2.7.4.8	KOX_06000(gmk)	atp + gmp <-> adp + gdp
NUTD10	Purine metabolism	5'-nucleotidase (XMP)	3.1.3.5	KOX_01045(surE)/KOX_10270/KOX_13075(ushA)/ KOX_26410	xmp -> pi + xtsine
NUTD11	Purine metabolism	5'-nucleotidase (IMP)	3.1.3.5	KOX_01045(surE)/KOX_10270/KOX_13075(ushA)/	imp -> ins + pi
NUTD6	Purine metabolism	5'-nucleotidase (dAMP)	3.1.3.5	KOX_26410 KOX_01045(surE)/KOX_10270/KOX_13075(ushA)/	
NOTES	runne metabolism	,	3.1.3.3	KOX_26410	damp -> da + pi
NUTD7	Purine metabolism	5'-nucleotidase (AMP)	3.1.3.5	KOX_01045(surE)/KOX_10270/KOX_13075(ushA)/ KOX_26410	amp -> adn + pi
NUTD8	Purine metabolism	5'-nucleotidase (dGMP)	3.1.3.5	KOX_01045(surE)/KOX_10270/KOX_13075(ushA)/ KOX_26410	dgmp -> dg + pi
NUTD9	Purine metabolism	5'-nucleotidase (GMP)	3.1.3.5	KOX_01045(surE)/KOX_10270/KOX_13075(ushA)/	qmp -> qsn + pi
		ribonucleoside-triphosphate		KOX_26410	
RNTPR1	Purine metabolism	reductase	1.17.4.2	KOX_09230	gtp + rthio -> dgtp + othio
RNTPR2	Purine metabolism	ribonucleoside-triphosphate reductase	1.17.4.2	KOX_09230	atp + rthio -> datp + othio
NUTPTP1	Purine metabolism	Nucleoside triphosphate tripolyhydrolase	3.1.5.1	KOX_11400(dgt)	dgtp -> dg + pppi
NUTPTP2	Purine metabolism	Nucleoside triphosphate	3.1.5.1	KOX_11400(dgt)	gtp -> gsn + pppi
AMPNS	Purine metabolism	tripolyhydrolase AMP nucleosidase	3.2.2.4	KOX_24315	amp -> ad + r5p
GNDA ADNA	Purine metabolism	guanine deaminase	3.5.4.3 3.5.4.4	KOX_16755 KOX 21945	gn -> nh4 + xan
ADPRDP	Purine metabolism Purine metabolism	Adenosine deaminase ADPribose diphosphatase	3.6.1.13/3.6.1	KOX_21945 KOX_02975 (nudF)/KOX_04645(nudE)	adn -> ins + nh4 adprib -> amp + r5p
NUTP1	Purine metabolism	nucleoside-triphosphatase (ATP)	3.6.1.8	KOX_01150(mazG)	atp -> adp + pi
NUTP2	Purine metabolism	nucleoside-triphosphatase	3.6.1.8/3.6.1.19	KOX_01150(mazG)/KOX_02715	gtp -> gmp + ppi
		(GTP) nucleoside-triphosphatase			
NUTP3	Purine metabolism	(dITP)	3.6.1.19	KOX_02715	ditp -> dimp + ppi
NUTP4	Purine metabolism	nucleoside-triphosphatase (ITP)	3.6.1.8/3.6.1.19	KOX_01150(mazG)/KOX_02715	itp -> imp + ppi
NUTP5	Purine metabolism	nucleoside-triphosphatase (XTP)	20110	KOX_02715	
NUIPS	Pullie metabolism	nucleoside triphosphilatase (XIII)	3.6.1.19	KUX_02/15	xtp -> xmp + ppi
		nucleoside-triphosphatase			
NUTP6	Purine metabolism		3.6.1.8	KOX_01150(mazG)	atp -> amp + ppi
		nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP)			
NUTP6	Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase	3.6.1.8	KOX_01150(mazG)	atp -> amp + ppi
NUTP6 NUTP8 NUTP7 ADNCYC	Purine metabolism Purine metabolism Purine metabolism Purine metabolism Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (dGTP) adenylate cyclase	3.6.1.8 3.6.1.19 4.6.1.1	KOX_01150(mazG)  KOX_02150(mazG)  KOX_02715  KOX_07630(cyaA)	atp -> amp + ppi datp -> damp + ppi dgtp -> dgmp + ppi atp -> camp + ppi
NUTP6 NUTP8 NUTP7	Purine metabolism  Purine metabolism  Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (dGTP) adenylate cyclase Deoxyadenosine deaminase IMP dehydrogenase	3.6.1.8 3.6.1.8 3.6.1.19	KOX_01150(mazG)  KOX_01150(mazG)  KOX_02715	atp -> amp + ppi datp -> damp + ppi dgtp -> dgmp + ppi
NUTP6  NUTP8  NUTP7  ADNCYC  DANDA	Purine metabolism Purine metabolism Purine metabolism Purine metabolism Purine metabolism Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (dGTP) adenylate cyclase Deoxyadenosine deaminase IMP dehydrogenase phosphoribosylglycinamide	3.6.1.8 3.6.1.19 4.6.1.1 3.5.4.4	KOX_01150(max5)  KOX_01150(max5)  KOX_02715  KOX_07630(cyaA)  KOX_21945	atp -> amp + ppi datp -> damp + ppi datp -> dgmp + ppi atp -> camp + ppi da -> din + thM
NUTP6 NUTP8 NUTP7 ADNCYC DANDA IMPDH	Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (GGTP) adenylate cydase Deoxyadenosine deaminase IMP dehydrogenase phosphoribosylghycinamide formyt	3.6.1.8 3.6.1.19 4.6.1.1 3.5.4.4 1.1.1.2.05	KOX_01150(mazG)  KOX_01150(mazG)  KOX_02715  KOX_07630(cyaA)  KOX_21945  KOX_27220	atp -> amp + ppi datp -> damp + ppi dgtp -> dgmp + ppi atp -> camp + ppi da -> din + inb4 imp + nad -> nadh + xmp
NUTP6 NUTP7 ADNCYC DANDA IMPDH PRGNFT GARTFM	Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (dGTP) adenylate cyclase Deoxyadenosine deaminase IMP dehydrogenase phosphoribosylghrinamide formyttransferside	3.6.18 3.6.18 3.6.119 4.6.11 3.5.44 1.1.1205 2.1.22	KOX_01150(max5)  KOX_01150(max5)  KOX_02715  KOX_07630(cyaA)  KOX_21345  KOX_27220  KOX_23845(purT)/KOX_27160(purN)  KOX_23845(purT)	atp -> amp + ppi datp -> damp + ppi dgtp -> dgmp + ppi atp -> camp + ppi da -> camp + ppi da -> cam + mbd imp + nad -> nadh + xmp fthf + gar <-> fgam + thf atp + formate + gar <-> adp + fgam + pi
NUTP6 NUTP8 NUTP7 ADNCYC DANDA IMPDH PRGNFT	Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (GTP) adenylate cyclase Deoxyadenosine deaminase IMP dehydrogenase phosphoribosylglycinamide formyttransferse glycinamide ribonucleotide transformylasse phosphoribosylaminoimidacolec arboxamide fromyttransferse phosphoribosylaminoimidacolec arboxamide fromyttransferse phosphoribosylaminoimidacolec arboxamide fromyttransferse	3.6.1.8 3.6.1.19 4.6.1.1 3.5.4.4 11.1.1.2.05 2.1.2.2	KOX_01150(max5)  KOX_07150(max5)  KOX_072715  KOX_07630(cyaA)  KOX_21945  KOX_27220  KOX_23845(pur1)/KOX_27160(purN)	atp -> amp + ppi datp -> damp + ppi datp -> dgmp + ppi atp -> camp + ppi da -> camp + ppi da -> din + mb4 imp + nad -> nadh + xmp fthf + gar <-> fgam + thf
NUTP6 NUTP7 ADNCYC DANDA IMPDH PRGNFT GARTFM	Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (dGTP) adenylate cyclase Deoxyadenosine deaminase IMP dehydrogenase phosphoribosyldyicinamide formyttransferase glycinamide ribonucleotide transformytasase phosphoribosylaminoimidazolec arboxamide formytransferase glutamine phosphoribosyldiphosphate	3.6.18 3.6.18 3.6.119 4.6.11 3.5.44 1.1.1205 2.1.22	KOX_01150(max5)  KOX_01150(max5)  KOX_02715  KOX_07630(cyaA)  KOX_21345  KOX_27220  KOX_23845(purT)/KOX_27160(purN)  KOX_23845(purT)	atp -> amp + ppi datp -> damp + ppi dgtp -> dgmp + ppi atp -> camp + ppi da -> camp + ppi da -> cam + mbd imp + nad -> nadh + xmp fthf + gar <-> fgam + thf atp + formate + gar <-> adp + fgam + pi
NUTP6 NUTP7 ADNCYC DANDA IMPDH PRGMFT GARTFM PRAZCFT	Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (GGTP) adenylate cyclase Deoxyadenosine deaminase IMP dehydrogenase phosphoribosyldyicinamide formytransferase glycinamide fibonucleotide transformylase phosphoribosylaminoimidazolec arboxamide formytransferase glytamide formytransferase glytamine	3.6.18 3.6.119 4.6.11 3.5.44 1.1.1.205 2.1.22	KOX_01150(maxG)  KOX_01150(maxG)  KOX_02715  KOX_07630(cyaA)  KOX_21345  KOX_27220  KOX_23845(purT)/KOX_27160(purN)  KOX_23845(purT)  KOX_08025(purH)	atp -> amp + ppi datp -> damp + ppi dgtp -> dgmp + ppi atp -> camp + ppi da >> cin + nh4 imp + nad -> nadh + xmp fthf + gar <>> fgam + thf atp + formate + gar <>> adp + fgam + pi fthf + aicar <>> fprica + thf
NUTP6 NUTP7 ADNCYC DANDA IMPDH PRGMFT GARTFM PRAZCFT GLUPRPAT	Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (AGTP) adenylate cyclase Deoxyadenosine deaminase IMP delydrogenase phosphoribosylglycinamide formyttransferase glycinamide ribonucleotide transformylase phosphoribosylaminoimidazolec arboxamide formyttransferase glutamine phosphoribosylaminoimidazolea arboxamide formyttransferase glutamine phosphoribosylaminoimidazolea arboxamide formyttransferase adenylsuccinate lyase adenylsuccinate lyase	36.18 3.6.19 4.6.11 3.5.44 1.1.1.205 2.1.22 2.1.23 2.4.2.14 4.3.22 4.3.22	KOX_01150(maxG)  KOX_021150(maxG)  KOX_02715  KOX_07630(cyaA)  KOX_21245  KOX_27220  KOX_23845(pur1)/KOX_27160(purN)  KOX_23845(pur1)  KOX_08025(purH)  KOX_060550	atp -> amp + ppi datp -> damp + ppi dgtp -> dgmp + ppi atp -> dgmp + ppi atp -> dgmp + ppi da -> din + nb4 imp + nad -> nadh + xmp fthf + gar <> -> fgam + thf atp + formate + gar <>> adp + fgam + pi fthf + aicar <>> fprica + thf gln + prpp -> glu + ppi + pram
NUTP6 NUTP8 NUTP7 ADNCYC DANDA IMPOH PRGNFT GARTFM PRAZCFT GLUPRPAT ADSUCL1	Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (GTP) and adenylate cyclase Deoxyadenosine deaminase IMP dehydrogenase phosphoribosyldyicinamide formyltransferase glycinamide ribonucleotide transformylase phosphoribosyldyicinamide phosphoribosyldyicinamide ribonucleotide transformylase adeoximide formyltransferase glutamine phosphoribosyldiphosphate amidotransferase adenylsuccinate lyase adenylsuccinate lyase phosphoribosyldminoimidazoles uccinocarboxamide synthase	36.18 3.6.19 4.6.11 3.5.44 1.1.1.205 2.1.22 2.1.23 2.4.2.14 4.3.22 4.3.22	KOX_01150(maxG)  KOX_01150(maxG)  KOX_02715  KOX_07630(cyaA)  KOX_21945  KOX_2220  KOX_23845(pur1)/KOX_27160(purN)  KOX_23845(pur1)/KOX_27160(purN)  KOX_08025(purH)  KOX_08025(purH)  KOX_08025(purH)	atp >> amp + ppi datp >> damp + ppi datp >> damp + ppi dgtp >> dgmp + ppi atp -> camp + ppi da >> dan + nb4 mp + nad >> nadh + xmp fthf + gar <>> fgam + thf atp + formate + gar <>> adp + fgam + pi fthf + aicar <>> fprica + thf gln + prpp -> glu + ppi + pram asuc <>> amp + fum
NUTP6 NUTP8 NUTP7 ADNCYC DANDA IMPOH PRGNET GARTEM PRAZCET GLUPRPAT ADSUCL1 ADSUCL2	Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (GTP) adenylate cyclase daenylate cyclase Deoxyadenosine deaminase IRM dehydrogenase phosphoribosyldyicinamide fromyttransferase glycinamide ribonucleotide transformylase phosphoribosylaminoimidazoles phosphoribosyldiphosphate amidotransferase glutamine phosphoribosyldiphosphate amidotransferase adenylsuccinate lyase adenylsuccinate lyase adenylsuccinate lyase adenylsuccinate lyase	3.6.18 3.6.119 4.6.11 3.5.44 1.1.1.205 2.1.22 2.1.23 2.4.2.14 4.3.2.2 4.3.2.2	KOX_01150(mazG)  KOX_02715  KOX_07630(cyaA)  KOX_27245  KOX_27220  KOX_23845(purT)/KOX_27160(purN)  KOX_23845(purT)/KOX_27160(purN)  KOX_08025(purH)  KOX_08025(purH)  KOX_08025(purH)	atp -> amp + ppi datp -> damp + ppi dgtp -> dgmp + ppi atp -> camp + ppi da -> cin + nb4 imp + rad -> nadh + xmp tthf + gar <-> fgam + thf atp + formate + gar <-> adp + fgam + pi tthf + aicar <-> fprica + thf gln + prpp -> glu + ppi + pram asuc <-> amp + fum saicar <-> alcar + fum
NUTP6 NUTP8 NUTP7 ADNCYC DANDA IMPOH PRGNET GARTFM PRAZCFT GLUPRPAT ADSUCL1 ADSUCL2 PRASUCS	Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (AGTP) nucleoside-triphosphatase (AGTP) adenylate cyclase Deoxyadenosine deaminase IMP dehydrogenase phosphoribosyldyicnamide from	36.18 36.18 36.119 46.11 35.44 1.11.205 2.1.22 2.1.23 2.4.2.14 4.3.22 4.3.22 6.3.26	KOX_01150(mazG)  KOX_02715  KOX_07630(cyaA)  KOX_27245  KOX_27220  KOX_23845(purT)/KOX_27160(purN)  KOX_23845(purT)/KOX_27160(purN)  KOX_23845(purT)  KOX_08025(purH)  KOX_26550  KOX_17535  KOX_17535  KOX_27090	atp -> amp + ppi datp -> damp + ppi dgtp -> dgmp + ppi atp -> camp + ppi ds -> camp + ppi ds -> cin + mb4 imp + rad -> nadh + xmp tthf + gar <-> fgam + thf atp + formate + gar <-> adp + fgam + pi tthf + aicar <-> fprica + thf gln + prpp -> glu + ppi + pram asuc <-> amp + fum saicar <-> aicar + fum cair + asp + atp -> saicar + adp + pi
NUTP6 NUTP8 NUTP7 ADNCYC DANDA IMPDH PRGNFT GARTFM PRAZCFT GLUPRPAT ADSUCL1 ADSUCL2 PRASUCS PRAIZS PRGCS ADSUCS	Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (AGTP) adenylate cyclase Deoxyadenosine deaminase IMP dehydrogenase phosphoribosyldyicnamide formyttransferase glycinamide ribonucleotide transformylase phosphoribosyldiphosphate amidotransferase glutamine phosphoribosyldiphosphate amidotransferase adenylsuccinate lyase adenylsuccinate lyase adenylsuccinate lyase phosphoribosyldiphosphate synthase phosphoribosylgylaminoimidazoles ynthase phosphoribosylgylaminoimidazole synthase phosphoribosylgylicniamide synthase adenylsuccinate synthase adenylsuccinate synthase adenylsuccinate synthase	36.18 36.18 36.19 46.11 35.44 1.11205 2.122 2.123 2.4.214 4.3.22 4.3.22 6.3.26 6.3.31 6.3.44	KOX_01150(maxG)  KOX_01150(maxG)  KOX_02715  KOX_07630(cyaA)  KOX_21245  KOX_27220  KOX_23845(pur1)/KOX_27160(purN)  KOX_23845(pur1)/KOX_27160(purN)  KOX_08025(purH)  KOX_08025(purH)  KOX_17535  KOX_17535  KOX_17535  KOX_27090  KOX_27155  KOX_27090  KOX_27155  KOX_08020  KOX_08030	atp >> amp + ppi datp >> damp + ppi datp >> damp + ppi dgtp >> damp + ppi atp >> camp + ppi da >> din + mb4 min + ada >> nadh + xmp fthf + gar <>> fgam + thf atp + formate + gar <>> adp + fgam + pi fthf + aicar <>> fprica + thf gin + prpp >> glu + ppi + pram aauc <>> amp + fum saicar <>> aicar + fum cair + asp + atp >> saicar + adp + pi atp + fpram >> adp + air + pi atp + fpram >> adp + air + pi
NUTP6 NUTP8 NUTP7 ADNCYC DANDA IMPDH PRGNET GARTEM PRAZCET GLUPRPAT ADSUCL1 ADSUCL2 PRASUCS PRAIZS PRGCS ADSUCS GMPS	Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (GTP) adenylate cyclase Deoxyadenosine deaminase IMP dehydrogenase phosphoribosylglycinamide formyltransferase glycinamide ribonucleotide transformylates phosphoribosylaminoimidazolec arboxamide formyltransferase glutamine phosphoribosyldiphosphate amidotransferase adenylsuccinate lysae adenylsuccinate lysae adenylsuccinate lysae phosphoribosylaminoimidazole synthase phosphoribosylaminoimidazole synthase phosphoribosylaminoimidazole synthase phosphoribosylaminoimidazole synthase adenylsuccinate synthase shosphoribosylaminoimidazole synthase adenylsuccinate synthase GMP synthase	36.18 36.18 36.119 46.11 35.44 1.11.205 2.1.22 2.1.23 2.4.2.14 4.3.22 4.3.22 6.3.26 6.3.31 6.3.4.13 6.3.4.4 6.3.5.2	KOX_01150(mazG)  KOX_02715  KOX_07630(cyaA)  KOX_27240  KOX_27220  KOX_23845(pur1)(KOX_27160(purh))  KOX_23845(pur1)(KOX_27160(purh))  KOX_23845(pur1)  KOX_08025(purh)  KOX_17535  KOX_17535  KOX_07090  KOX_27155  KOX_08020  KOX_08030  KOX_08030  KOX_08030  KOX_08030  KOX_08030	atp >> amp + ppi  datp >> damp + ppi  datp >> damp + ppi  dgtp >> dgmp + ppi  atp -> camp + ppi  da >> din + nb4  imp + rad >> nadh + xmp  tthf + gar <>> fgam + thf  atp + formate + gar <>> adp + fgam + pi  tthf + aicar <>> fprica + thf  gln + prpp >> glu + ppi + pram  asuc <>> amp + fum  saicar <>> aicar + fum  cair + asp + atp -> saicar + adp + pi  atp + fpram -> adp + air + pi  atp + gly + pram <>> adp + air + pi  atp + gly + pram <>> adp + air + pi  atp + gly + pram <>> adp + air + pi  atp + gly + pram <>> adp + air + pi  atp + gly + pram <>> adp + air + pi  atp + gly + pram <>> adp + air + pi  atp + gly + pram <>> adp + gly + pi  atp + gly + pram <>> auc + gdp + pi  atp + gly + mp >> auc + gdp + pi  atp + gly + mp >> auc + gdp + pi  atp + gly + mp >> auc + gdp + pi  atp + gly + mp >> auc + gdp + pi
NUTP6 NUTP8 NUTP7 ADNCYC DANDA IMPDH PRGNFT GARTFM PRAZCFT GLUPRPAT ADSUCL1 ADSUCL2 PRASUCS PRAIZS PRGCS ADSUCS	Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (GTP) adenylate cyclase Deoxyadenosine deaminase IMP dehydrogenase phosphoribosylglycinamide formyltransferase glycinamide ribonucleotide transformylates phosphoribosyldiphosphate amidotransferase phosphoribosyldiphosphate amidotransferase glutamine phosphoribosyldiphosphate amidotransferase adenylsuccinate lysse phosphoribosyldiphosphate amidotransferase phosphoribosyldiphosphate phosphoribosyldiphosphate phosphoribosyldiphosphate phosphoribosyldiphosphate phosphoribosyldiphosphate adenylsuccinate lysse phosphoribosyldiphosphate in the phosphate phosphoribosyldiphosphate phosphoribosyldiphosphate in the phosphate phosphoribosyldiphosphate in the phosphate phosphoribosyldiphosphate in the phosphate phosphoribosyldiphosphate in the phosphoribosyldiphosphate in the phosphate phosphoribosyldiphosphate in the ph	36.18 36.18 36.19 46.11 35.44 1.11205 2.122 2.123 2.4.214 4.3.22 4.3.22 6.3.26 6.3.31 6.3.44	KOX_01150(maxG)  KOX_01150(maxG)  KOX_02715  KOX_07630(cyaA)  KOX_21245  KOX_27220  KOX_23845(pur1)/KOX_27160(purN)  KOX_23845(pur1)/KOX_27160(purN)  KOX_08025(purH)  KOX_08025(purH)  KOX_17535  KOX_17535  KOX_17535  KOX_27090  KOX_27155  KOX_27090  KOX_27155  KOX_08020  KOX_08030	atp > amp + ppi datp > damp + ppi datp > damp + ppi dgtp >> dgmp + ppi atp -> dgmp + ppi da >> dam + ppi da >> dam + ppi da >> dam + mbd minp + mad >> nadm + xmp fthf + gar <>> fgam + thf atp + formate + gar <>> adp + fgam + pi fthf + aicar <<>> fprica + thf gln + prop -> glu + ppi + pram asuc <>> amp + fum saicar <>> aicar + fum cair + asp + atp >> saicar + adp + pi atp + fpram -> adp + air + pi atp + fpram -> adp + gar + pi asp + gtp + pram <>> adu + gdp + pi asp + gtp + pram <>> adu + gdp + pi asp + gtp + pram <>> adu + gdp + pi asp + gtp + pram <>> adu + gdp + pi
NUTP6 NUTP8 NUTP7 ADNCYC DANDA IMPDH PRGNET GARTEM PRAZCET GLUPRPAT ADSUCL1 ADSUCL2 PRASUCS PRAIZS PRGCS ADSUCS GMPS	Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (AGTP) adenylate cyclase Deoxyadenosine deaminase IMP dehydrogenase phosphoribosyldyicamide fromyltransferase glycinamide ribonucleotide transformylates phosphoribosyldiphosphate amidotransferase adenylsucrinate lyase adenylsucrinate lyase adenylsucrinate lyase adenylsucrinate lyase adenylsucrinate lyase adenylsucrinate lyase adenylsucrinate synthase phosphoribosyldyminoimidazoles ynthase phosphoribosyldycinamide synthase adenylsucrinate synthase GMP synthase phosphoribosyldycinamidine synthase phosphoribosylformylglycinamidine synthase phosphoribosylformylglycinamidine synthase phosphoribosylformylglycinamidine synthase phosphoribosylformylglycinamidine synthase	36.18 36.18 36.119 46.11 35.44 1.11.205 2.1.22 2.1.23 2.4.2.14 4.3.22 4.3.22 6.3.26 6.3.31 6.3.4.13 6.3.4.4 6.3.5.2	KOX_01150(mazG)  KOX_02150(mazG)  KOX_02715  KOX_07630(cyaA)  KOX_21945  KOX_2220  KOX_23845(purT)/KOX_27160(purN)  KOX_23845(purT)/KOX_27160(purN)  KOX_23845(purT)  KOX_08025(purH)  KOX_26550  KOX_17535  KOX_17535  KOX_17535  KOX_277090  KOX_27155  KOX_27155  KOX_27090  KOX_08020  KOX_08020  KOX_08020  KOX_08030  KOX_08030  KOX_08040  KOX_08040  KOX_08050  KOX_080600  KOX_07495	atp >> amp + ppi  datp >> damp + ppi  datp >> damp + ppi  dgtp >> dgmp + ppi  atp -> camp + ppi  da >> din + nb4  imp + rad >> nadh + xmp  tthf + gar <>> fgam + thf  atp + formate + gar <>> adp + fgam + pi  tthf + aicar <>> fprica + thf  gln + prpp >> glu + ppi + pram  asuc <>> amp + fum  saicar <>> aicar + fum  cair + asp + atp -> saicar + adp + pi  atp + fpram -> adp + air + pi  atp + gly + pram <>> adp + air + pi  atp + gly + pram <>> adp + air + pi  atp + gly + pram <>> adp + air + pi  atp + gly + pram <>> adp + air + pi  atp + gly + pram <>> adp + air + pi  atp + gly + pram <>> adp + air + pi  atp + gly + pram <>> adp + gly + pi  atp + gly + pram <>> auc + gdp + pi  atp + gly + mp >> auc + gdp + pi  atp + gly + mp >> auc + gdp + pi  atp + gly + mp >> auc + gdp + pi  atp + gly + mp >> auc + gdp + pi
NUTP6 NUTP8 NUTP7 ADNCYC DANDA IMPOH PRGNET GARTEM PRAZCET GLUPRPAT ADSUCL1 ADSUCL2 PRASUCS PRAIZS PRGCS ADSUCS GMPS PREGAS	Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (AGTP) adenylate cyclase Deoxyadenosine deaminase IMP dehydrogenase phosphoribosyldyinamide fromyttransferase glycinamide ribonucleotide transformylase phosphoribosyldiphosphate amidotransferase adenylsucriante lyase adenylsucriante synthase phosphoribosyldycinamide synthase GMP synthase phosphoribosylformylglycinamidine synthase phosphoribosylformylglycinamidine synthase phosphoribosylamionimidazole carboxylase 5-(carboxyamino)imidazole carboxylase 5-(carboxyamino)imidazole	36.18 36.18 36.119 46.11 35.44 1.11.205 2.1.22 2.1.23 2.4.2.14 4.3.22 4.3.22 6.3.26 6.3.31 6.3.413 6.3.52 6.3.53	KOX_01150(mazG)  KOX_01150(mazG)  KOX_02715  KOX_07630(cyaA)  KOX_21945  KOX_27220  KOX_23845(purT)/KOX_27160(purN)  KOX_23845(purT)/KOX_27160(purN)  KOX_23845(purT)  KOX_08025(purH)  KOX_17535  KOX_17535  KOX_17535  KOX_27090  KOX_27155  KOX_27155  KOX_27155  KOX_27090  KOX_27155  KOX_08020  KOX_08020  KOX_08030/KOX_26875/KOX_27215(guaA)  KOX_27495  KOX_13195	atp -> amp + ppi datp -> damp + ppi datp -> damp + ppi dgtp -> dgmp + ppi atp -> camp + ppi da -> din + nb4 imp + nad -> nadh + xmp tthf + gar <-> fgam + thf atp + formate + gar <-> adp + fgam + pi tthf + aicar <-> fprica + thf  gln + prpp -> glu + ppi + pram asuc <-> amp + fum saicar <-> aicar + fum cair + asp + atp -> saicar + adp + pi atp + fpram -> adp + air + pi atp + gly + pram <-> adp + apr + pi atp + gly + pram <-> adp + gar + pi atp + gly + pram <-> adp + gar + pi atp + gly + man <-> adp + gar + pi atp + gly + xmp -> amp + glu + gmp + ppi atp + gln + xmp -> amp + glu + gmp + ppi atp + fgam + gln -> adp + fpram + glu + pi atp + fgam + gln -> adp + fpram + glu + pi
NUTP6 NUTP8 NUTP7 ADNCYC DANDA IMPOH PRGNET GARTEM PRAZCET GLUPRPAT ADSUCL1 ADSUCL2 PRASUCS PRAIZS PRGCS ADSUCS GMP5 PREGAS AIRC CAIZM	Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (AGTP) adenylate cyclase Deoxyadenosine deaminase IRMP dehydrogenase phosphoribosylglycinamide from	36.18 3.6.18 3.6.19 4.6.11 3.5.44 1.11.205 2.1.22 2.1.23 2.4.2.14 4.3.22 4.3.22 6.3.2.6 6.3.3.1 6.3.4.13 6.3.5.2 6.3.5.2 6.3.5.3 6.3.4.18 5.4.99.18	KOX_01150(mazG)  KOX_02715  KOX_07630(cyaA)  KOX_21945  KOX_2720  KOX_23845(pur1)(KOX_27160(purN))  KOX_23845(pur1)(KOX_27160(purN))  KOX_23845(pur1)  KOX_08025(purH)  KOX_08025(purH)  KOX_08025(purH)  KOX_08020  KOX_07090  KOX_27155  KOX_27090  KOX_08020  KOX_08020  KOX_08020  KOX_08020  KOX_08030  KOX_27495  KOX_13195  KOX_13200	atp >> amp + ppi datp >> damp + ppi datp >> damp + ppi dgtp >> dgmp + ppi atp -> camp + ppi da >> din + nb4 imp + nad >> nadh + xmp tthf + gar <>> fgam + thf atp + formate + gar <>> adp + fgam + pi tthf + aicar <>> piu + ppi + pram asuc <>> amp + fum saicar <>> aicar + fum cair + asp + atp -> saicar + adp + pi atp + fpram -> adp + air + pi atp + fpram -> adp + air + pi atp + gly + pram <>> adp + apr + pi atp + gly + pram <>> adp + apr + pi atp + gly + pram <>> adp + gar + pi atp + gly + may >> auc + gdp + pi atp + gln + xmp >> amp + glu + gmp + ppi atp + fgam + gln -> adp + fpram + glu + pi air + atp + hco3 -> caiz + adp + pi caiz <>> cair
NUTP6 NUTP8 NUTP7 ADNCYC DANDA IMPDH PRGNET GARTEM PRAZCET GLUPRPAT ADSUCL1 ADSUCL2 PRASUCS PRAIZS PRGCS ADSUCS GMPS PREGAS AIRC CAIZM ADPRT2	Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (GTP) and adenylate cyclase Deoxyadenosine deaminase IMP dehydrogenase phosphoribosylglycinamide formyltransferase glycinamide ribonucleotide transformylase phosphoribosylaminoimidazolec arboxamide formyltransferase glutamine phosphoribosyldiphosphata amidotransferase glutamine phosphoribosyldiphosphata amidotransferase glutamine phosphoribosyldiphosphata amidotransferase adenylsuccinate lyase adenylsuccinate lyase adenylsuccinate lyase adenylsuccinate synthase phosphoribosyldiphosphatic synthase adenylosuccinate synthase phosphoribosyldiphosphoribosylgipcinamidie synthase phosphoribosylaminoimidazole ribonucleotide mutase adenine	36.18 36.18 36.19 46.11 35.44 1.11.205 2.1.22 2.1.23 2.4.2.14 4.3.22 4.3.22 6.3.26 6.3.31 6.3.413 6.3.52 6.3.52 6.3.53 6.3.418 5.4.99.18 2.4.2.7	KOX_01150(mazG)  KOX_02150(mazG)  KOX_02715  KOX_07630(cyaA)  KOX_21945  KOX_2220  KOX_23845(purT)/KOX_27160(purN)  KOX_23845(purT)/KOX_27160(purN)  KOX_23845(purT)  KOX_08025(purH)  KOX_26550  KOX_17535  KOX_17535  KOX_17535  KOX_277090  KOX_27155  KOX_27155  KOX_27499  KOX_08000  KOX_08000  KOX_08000  KOX_08000  KOX_18000	atp > amp + ppi datp > damp + ppi datp > damp + ppi dgtp >> dgmp + ppi atp -> camp + ppi da >> din + nb4 imp + rad >> nadh + xmp tthf + gar <>> fgam + thf atp + formate + gar <>> adp + fgam + pi tthf + aicar <>> fprica + thf  gln + prpp >> glu + ppi + pram asuc <>> amp + fum saicar <>> aicar + fum cair + asp + atp >> saicar + adp + pi atp + fpram >> adp + air + pi atp + fpram >> adp + air + pi atp + gly + pram <>> adp + apr + pi atp + gly + pram <>> adp + apr + pi atp + gly + pram <>> adp + pr atp + gly + pram <>> adp + pr atp + gly + ram <>> adp + pr atp + gly + ram <>> adp + pr atp + fgam + gln >> adp + fpram + glu + pr atp + fgam + gln >> adp + fpram + glu + pr atr + transpar air + atr + bro3 >> caiz + adp + pi caiz <>> cair aicar + ppi <>> Sa4ic + prpp
NUTP6 NUTP8 NUTP7 ADNCYC DANDA IMPOH PRGNET GARTEM PRAZCET GLUPRPAT ADSUCL1 ADSUCL2 PRASUCS PRAIZS PRGCS ADSUCS GMP5 PREGAS AIRC CAIZM	Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (GTP) and adenylate cyclase Deoxyadenosine deaminase IMP dehydrogenase phosphoribosylglycinamide formyltransferase glycinamide ribonucleotide transformylase phosphoribosylaminoimidazolec arboxamide formyltransferase glutamine phosphoribosyldiphosphata amidotransferase glutamine phosphoribosyldiphosphata amidotransferase adenylsuccinate lyase adenylsuccinate lyase adenylsuccinate lyase adenylsuccinate significant control of the control of	36.18 3.6.18 3.6.19 4.6.11 3.5.44 1.11.205 2.1.22 2.1.23 2.4.2.14 4.3.22 4.3.22 6.3.2.6 6.3.3.1 6.3.4.13 6.3.5.2 6.3.5.2 6.3.5.3 6.3.4.18 5.4.99.18	KOX_01150(mazG)  KOX_02715  KOX_07630(cyaA)  KOX_21945  KOX_2720  KOX_23845(pur1)(KOX_27160(purN))  KOX_23845(pur1)(KOX_27160(purN))  KOX_23845(pur1)  KOX_08025(purH)  KOX_08025(purH)  KOX_08025(purH)  KOX_08020  KOX_07090  KOX_27155  KOX_27090  KOX_08020  KOX_08020  KOX_08020  KOX_08020  KOX_08030  KOX_27495  KOX_13195  KOX_13200	atp >> amp + ppi datp >> damp + ppi datp >> damp + ppi dgtp >> dgmp + ppi atp -> camp + ppi da >> din + nb4 imp + nad >> nadh + xmp tthf + gar <>> fgam + thf atp + formate + gar <>> adp + fgam + pi tthf + aicar <>> piu + ppi + pram asuc <>> amp + fum saicar <>> aicar + fum cair + asp + atp -> saicar + adp + pi atp + fpram -> adp + air + pi atp + fpram -> adp + air + pi atp + gly + pram <>> adp + apr + pi atp + gly + pram <>> adp + apr + pi atp + gly + pram <>> adp + gar + pi atp + gly + may >> auc + gdp + pi atp + gln + xmp >> amp + glu + gmp + ppi atp + fgam + gln -> adp + fpram + glu + pi air + atp + hco3 -> caiz + adp + pi caiz <>> cair
NUTP6 NUTP8 NUTP7 ADNCYC DANDA IMPDH PRGNET GARTEM PRAZCET GLUPRPAT ADSUCL1 ADSUCL2 PRASUCS PRAIZS PRGCS ADSUCS GMPS PREGAS AIRC CAIZM ADPRT2	Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (AGTP) adenylate cyclase Deoxyadenosine deaminase IMP dehydrogenase phosphoribosylghyinamide fromyttransferase glycinamide ribonucleotide transformylase phosphoribosyldiphosphate amidotransferase glutamine phosphoribosyldiphosphate amidotransferase adenylsuccinate lyase adenylsuccinate lyase adenylsuccinate lyase adenylsuccinate lyase phosphoribosylaminoimidazoles uccinocarboxamide synthase phosphoribosylghycinamide synthase phosphoribosylghycinamide synthase GMP synthase phosphoribosylformylglycinamidica synthase phosphoribosylformylglycinamidica synthase phosphoribosylformylglycinamidica synthase phosphoribosylformylglycinamidica phosphoribosylformylglycinamidical phosphoribosylformylglycinamidical carboxylase 5-(carboxyamino)imidazole ribonucleotide mutase adenine phosphoribosyltransferase adenine	36.18 36.18 36.19 46.11 35.44 1.11.205 2.1.22 2.1.23 2.4.2.14 4.3.22 4.3.22 6.3.26 6.3.31 6.3.413 6.3.52 6.3.52 6.3.53 6.3.418 5.4.99.18 2.4.2.7	KOX_01150(mazG)  KOX_02150(mazG)  KOX_02715  KOX_07630(cyaA)  KOX_21945  KOX_2220  KOX_23845(purT)/KOX_27160(purN)  KOX_23845(purT)/KOX_27160(purN)  KOX_23845(purT)  KOX_08025(purH)  KOX_26550  KOX_17535  KOX_17535  KOX_17535  KOX_277090  KOX_27155  KOX_27155  KOX_27499  KOX_08000  KOX_08000  KOX_08000  KOX_08000  KOX_18000	atp > amp + ppi datp > damp + ppi datp > damp + ppi dgtp >> dgmp + ppi atp -> camp + ppi da >> din + nb4 imp + rad >> nadh + xmp tthf + gar <>> fgam + thf atp + formate + gar <>> adp + fgam + pi tthf + aicar <>> fprica + thf  gln + prpp >> glu + ppi + pram asuc <>> amp + fum saicar <>> aicar + fum cair + asp + atp >> saicar + adp + pi atp + fpram >> adp + air + pi atp + fpram >> adp + air + pi atp + gly + pram <>> adp + apr + pi atp + gly + pram <>> adp + apr + pi atp + gly + pram <>> adp + pr atp + gly + pram <>> adp + pr atp + gly + ram <>> adp + pr atp + gly + ram <>> adp + pr atp + fgam + gln >> adp + fpram + glu + pr atp + fgam + gln >> adp + fpram + glu + pr atr + transpar air + atr + bro3 >> caiz + adp + pi caiz <>> cair aicar + ppi <>> Sa4ic + prpp
NUTP6 NUTP8 NUTP7 ADNCYC DANDA IMPOH PRGNET GARTEM PRAZCET GLUPRPAT ADSUCL1 ADSUCL2 PRASUCS PRAIZS PRGCS ADSUCS GMPS PREGAS AIRC CAIZM ADPRT2 ADPRT3	Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (AGTP) adenylate cyclase Deoxyadenosine deaminase IMP dehydrogenase phosphoribosylate phosphoribosylate phosphoribosylate phosphoribosylate phosphoribosylate phosphoribosylate phosphoribosylate amidotransferase adenylsuccinate lyase adenylsuccinate lyase adenylsuccinate lyase adenylsuccinate lyase adenylsuccinate synthase phosphoribosylaminoimidazoles uccinocarboxamide synthase phosphoribosylaminoimidazole synthase adenylsuccinate synthase GMP synthase phosphoribosylghycinamidine synthase phosphoribosylformylghycinamidine synthase phosphoribosylaminoimidazole raboxylase S-(carboxyamino)imidazole ribonucleotide mutase adenine phosphoribosyltransferase adenine	36.18 36.18 36.19 46.11 35.44 11.11.205 21.22 21.23 24.214 43.22 43.22 63.26 63.31 63.413 63.44 63.52 63.53 63.418 54.99.18 24.27 24.27	KOX_01150(mazG)  KOX_02715  KOX_07630(cyaA)  KOX_27245  KOX_2726  KOX_23845(purT)/KOX_27160(purN)  KOX_23845(purT)/KOX_27160(purN)  KOX_23845(purT)  KOX_08025(purH)  KOX_26550  KOX_17535  KOX_17535  KOX_17535  KOX_277090  KOX_27155  KOX_27090  KOX_27155  KOX_27090  KOX_27155  KOX_27090  KOX_27155  KOX_13305  KOX_13305  KOX_13305  KOX_13305  KOX_13305  KOX_13305  KOX_13305	atp > amp + ppi datp > damp + ppi datp > damp + ppi dgtp >> dgmp + ppi atp -> camp + ppi da >> din + nb4 imp + nad >> nadn + xmp tthf + gar <>> fgam + thf atp + formate + gar <>> adp + fgam + pi tthf + aicar <>> fprica + thf  gln + prpp >> glu + ppi + pram asuc <>> amp + fum saicar <>> aicar + fum cair + asp + atp >> saicar + adp + pi atp + fpram >> adp + air + pi atp + fpram >> adp + air + pi atp + gly + pram <>> adp + apr + pi atp + gly + pram <>> adp + gar + pi atp + gly + pram <>> adp + gar + pi atp + gly + pram <>> adp + gar + pi atp + gln + xmp >> amp + glu + gmp + ppi atp + fgam + gln >> adp + fpram + glu + pi air + atp + kco3 >> caiz + adp + pi caiz <>> cair aicar + ppi <>> Satic + prpp gmp + ppi <>> gn + prpp
NUTP6 NUTP8 NUTP7 ADNCYC DANDA IMPOH PRGNET GARTEM PRAZCET GLUPRPAT ADSUCL1 ADSUCL2 PRASUCS PRAIZS PRGCS ADSUCS GMP5 PREGAS AIRC CAIZM ADPRT2 ADPRT3 NUDPK9 NUDPK10	Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) and adenylate cyclase Deoxyadenosine deaminase IMP dehydrogenase phosphorbosyldynamide fromyttransferase glycinamide ribonucleotide transformylase phosphorbosyldiphosphate amidotransferase glutamine phosphorbosyldiphosphate amidotransferase adenylsuccinate lyase adenylsuccinate lyase adenylsuccinate lyase phosphorbosyldiphosphate amidotransferase adenylsuccinate lyase adenylsuccinate lyase phosphorbosyldynimioimidazoles uccinocarboxamide synthase phosphorbosyldynimioimidazole synthase of the synthase phosphorbosyldynimioimidazole synthase phosphorbosyldynimioimidazole rynthase phosphorbosyldynimioimidazole rynthase phosphorbosyldynimioimidazole rabonucleotide mutase adenine phosphorbosyltransferase adenine adenine phosphorbosyltransferase adenine a	3.6.18 3.6.18 3.6.119 4.6.11 3.5.44 1.11.205 2.1.22 2.1.23 2.4.2.14 4.3.22 4.3.22 6.3.26 6.3.31 6.3.4.13 6.3.4.14 6.3.5.2 6.3.5.3 6.3.4.18 5.4.99.18 2.4.2.7 2.4.2.7 2.7.4.6 2.7.4.6	KOX_01150(mazG)  KOX_02715  KOX_07630(cyaA)  KOX_21945  KOX_2720  KOX_23845(pur1)  KOX_23845(pur1)  KOX_23845(pur1)  KOX_23845(pur1)  KOX_23845(pur1)  KOX_26550  KOX_17535  KOX_17535  KOX_17535  KOX_27090  KOX_27155  KOX_27290  KOX_281355  KOX_27290  KOX_281355  KOX_17355  KOX_27155  KOX_27156  K	atp >> amp + ppi datp >> damp + ppi atp -> camp + ppi da >> dan + nbd imp + mad >> nadh + xmp tthf + gar <>> fgam + thf atp + formate + gar <>> adp + fgam + pi tthf + aicar <>> fprica + thf  gln + prpp >> glu + ppi + pram asuc <>> amp + fum saicar <>> aicar + fum cair + asp + atp -> saicar + adp + pi atp + fpram >> adp + air + pi atp + fpram >> adp + air + pi atp + fpram >> adp + air + pi atp + fpram >> adp + air + pi atp + fpram >> adp + air + pi atp + glu + pma +> adp + pi atp + glu + pma +> adp + pi atp + glu + xmp >> amp + glu + gmp + ppi atp + fgam + gln -> adp + fpram + glu + pi air + atp + bco3 -> caiz + adp + pi caiz <-> cair aicar + ppi <>> Safic + prpp gmp + ppi <>> gn + prpp atp + didp <>> adp + ditp atp + idp <>> adp + ditp
NUTP6 NUTP8 NUTP7 ADNCYC DANDA IMPOH PRGNET GARTEM PRAZCET GLUPRPAT ADSUCL1 ADSUCL2 PRASUCS PRAIZS PRAGCS ADSUCS GMP5 PREGAS AIRC CAIZM ADPRT2 ADPRT3 NUDPK9	Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (GTP) adenyiate cyclase Deoxyadenosine deaminase IMP dehydrogenase phosphoribosylglycinamide formyttransferase glycinamide ribonucleotide transformylase phosphoribosyldiphosphata amidotransferase glutamine phosphoribosyldiphosphata amidotransferase adenylsuccinate lyase adenylsuccinate lyase adenylsuccinate lyase adenylsuccinate lyase phosphoribosyldiphosphata amidotransferase adenylsuccinate lyase adenylsuccinate lyase adenylsuccinate lyase adenylsuccinate synthase phosphoribosyldiphosphaticsyldiphosphoribosyldiphosphoribosyldiphosphoribosyldiphosphoribosyldiphosphoribosyldiphosphoribosyldiphosphoribosyldiphosphoribosyldiphosphoribosyldiphosphoribosyldiphosphoribosyldiphosphoribosyldiphosphoribosyldiphosphoribosyldiphosphoribosyldiphosphoribosyldiphosphate kinase (ATP-GDP) nucleoside-diphosphate kinase (ATP-GDP) adenine	3.6.18 3.6.18 3.6.19 4.6.11 3.5.44 1.11.205 2.1.22 2.1.23 2.4.2.14 4.3.22 4.3.22 6.3.2.6 6.3.31 6.3.4.13 6.3.4.4 6.3.5.2 6.3.5.3 6.3.4.18 5.4.99.18 2.4.2.7 2.4.2.7 2.7.4.6	KOX_01150(mazG)  KOX_02115  KOX_02715  KOX_07630(cyaA)  KOX_21945  KOX_2220  KOX_23845(purT)/KOX_27160(purN)  KOX_23845(purT)/KOX_27160(purN)  KOX_23845(purT)  KOX_08025(purH)  KOX_26550  KOX_17535  KOX_17535  KOX_07090  KOX_27155  KOX_08020  KOX_27195  KOX_08020  KOX_27495  KOX_08030  KOX_27495  KOX_13305  KOX_13005  KOX_13005  KOX_13005  KOX_13005  KOX_13025  KOX_13025  KOX_12290(ndk)  KOX_27290(ndk)  KOX_27290(ndk)	atp >> amp + ppi  datp >> damp + ppi  datp >> damp + ppi  datp >> damp + ppi  atp >> camp + ppi  da >> din + mb4  imp + rad >> nadh + xmp  fthf + gar <>> fgam + thf  atp + formate + gar <>> adp + fgam + pi  fthf + aicar <>> fprica + thf  gln + prpp >> glu + ppi + pram  asuc <>> amp + fum  saicar <>> aicar + fum  cair + asp + atp >> saicar + adp + pi  atp + fpram >> adp + air + pi  atp + fpram >> adp + air + pi  atp + gly + pram <>> adp + gar + pi  atp + gly + pram <>> adp + pram + glu + pi  atp + gly + xmp >> amp + glu + gmp + ppi  atp + gln + xmp >> amp + glu + gmp + ppi  atp + fgam + gln >> adp + fpram + glu + pi  air + atp + bco3 >> caiz + adp + pi  caiz <>> cair  aicar + ppi <>> Safic + prpp  gmp + ppi <>> gn + prpp  atp + didp <>> adp + ditp  atp + idp <>> adp + ditp  atp + idp <>> adp + ditp  atp + idp <>> adp + ditp  atp + pi <>> adp + ditp
NUTP6 NUTP8 NUTP7 ADNCYC DANDA IMPOH PRGNET GARTEM PRAZCET GLUPRPAT ADSUCL1 ADSUCL2 PRASUCS PRAIZS PRGCS AURC GMPS PREGAS AIRC CAIZM ADPRT2 ADPRT3 NUDPK19 NUDPK10 ADPRT4 PYK1 PYK2	Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (GTP) adenine deside-triphosphatase (GTP) adenine deside-triphosphatase (GTP) adenine deside-triphosphatase phosphoribosylgyicinamide fromyttransferase glycinamide ribonucleotide transformylase phosphoribosylaminoimidazolec arboxamide formyttransferase glutamine phosphoribosyldiphosphata amidotransferase glutamine phosphoribosyldiphosphata amidotransferase adenyfsuccinate lyase adenyfsuccinate lyase adenyfsuccinate lyase adenyfsuccinate of the deside synthase phosphoribosyldiphosphaticolide synthase glutamine deside synthase phosphoribosyldiphosphaticolide synthase glutamidine synthase phosphoribosyldiphosphaticolide deside-diphosphaticolide mutase adenine phosphoribosylaminoimidazole carboxylase science deside-diphosphate kinase (ATP-GDP) nucleoside-diphosphate kinase pyruvate kinase pyruvate kinase pyruvate kinase pyruvate kinase	36.18 36.18 36.19 46.11 35.44 1.11.205 2.1.22 2.1.23 2.4.2.14 4.3.22 4.3.22 4.3.22 6.3.26 6.3.31 6.3.4.13 6.3.5.2 6.3.5.3 6.3.4.18 5.4.99.18 2.4.2.7 2.7.4.6 2.7.4.6 2.7.4.6 2.7.4.6 2.7.1.40 2.7.1.40	KOX_01150(maxG)  KOX_0215  KOX_07630(cyaA)  KOX_12945  KOX_27220  KOX_23845(pur1)(KOX_27160(purN))  KOX_23845(pur1)(KOX_27160(purN))  KOX_23845(pur1)  KOX_08025(purH)  KOX_08025(purH)  KOX_08025(purH)  KOX_08020  KOX_071555  KOX_27090  KOX_07155  KOX_07	atp >> amp + ppi  datp >> damp + ppi  datp >> damp + ppi  datp >> damp + ppi  atp >> camp + ppi  da >> din + mb4  imp + rad >> nadh + xmp  tthf + gar <>> fgam + thf  atp + formate + gar <>> adp + fgam + pi  tthf + aicar <>> fprica + thf  gln + prpp >> glu + ppi + pram  ascu <>> amp + fum  saicar <>> aicar + fum  cair + asp + atp >> saicar + adp + pi  atp + fpram >> adp + air + pi  atp + fpram >> adp + air + pi  atp + gly + pram <>> adp + gar + pi  atp + gly + pram <>> adp + pri  atp + gly + pram <>> adp + pri  atp + gln + xmp >> amp + glu + gmp + ppi  atp + gln + xmp >> amp + glu + ppi  atp + fgam + gln >> adp + fpram + glu + pi  air + atp + hco3 -> caiz + adp + pi  caiz <>> cair  aicar + ppi <>> Salic + prpp  gmp + ppi <>> gn + prpp  atp + didp <>> adp + ditp  atp + idp <>> adp + ditp  atp + idp <>> adp + ditp  atp + pry <> dadp + prp  datp + pry <>> adp + prp  datp + pry <>> dadp + prp
NUTP6 NUTP8 NUTP7 ADNCYC DANDA IMPOH PRGNFT GARTFM PRAZCFT GLUPRPAT ADSUCL1 ADSUCL2 PRASUCS PRAIZS PRAIZS PRAIZS PRACS ADSUCS GMPS PREGAS AIRC CAIZM ADPRT2 ADPRT3 NUDPK9 NUDPK10 ADPRT4 PYK1	Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) and adenylate cyclase Deoxyadenosine deaminase IRM dehydrogenase phosphorbosyldynamide formyltransferase glycinamide ribonucleotide transformylase phosphorbosyldiphosphate amidotransferase glutamine phosphorbosyldiphosphate amidotransferase adenylsucriante lyase adenylsucriante lyase adenylsucriante lyase adenylsucriante lyase phosphorbosyldiphosphate amidotransferase adenylsucriante lyase adenylsucriante lyase adenylsucriante lyase adenylsucriante lyase adenylsucriante lyase adenylsucriante synthase (DMP synthase phosphorbosyldyniniominidazole synthase phosphorbosylminiomidazole carboxylase S-(carboxyamino)imidazole ribonucleotide mutase adenine phosphorbosylminiomidazole ribonucleotide mutase adenine phosphorbosylminiomidazole ribonucleotide mutase (ATP-GDP) nucleoside-diphosphate kinase (ATP-GDP) adenine phosphorbosyltransferase adenine phosphorbosyltransferase private kinase private kinase private kinase	3.6.18 3.6.18 3.6.119 4.6.11 3.5.44 1.11.205 2.1.22  2.1.23 2.4.2.14 4.3.2.2 4.3.2.2 6.3.2.6 6.3.3.1 6.3.4.4 6.3.5.2 6.3.5.3 6.3.4.18 5.4.9.9.18 2.4.2.7 2.7.4.6 2.7.4.6 2.7.4.6 2.7.4.6 2.7.4.6 2.7.4.6 2.7.1.40	KOX_01150(maxG)  KOX_01150(maxG)  KOX_02715  KOX_07630(cyaA)  KOX_21345  KOX_22345(pur1)/KOX_27160(purN)  KOX_23845(pur1)/KOX_27160(purN)  KOX_08025(purH)  KOX_17535  KOX_17535  KOX_17535  KOX_27155  KOX_27155  KOX_27155  KOX_27155  KOX_27155  KOX_27155  KOX_27155  KOX_18020  KOX_27155  KOX_18020  KOX_27155  KOX_18020  KOX_18020  KOX_18020  KOX_18020  KOX_18020  KOX_18020  KOX_18025	atp > amp + ppi  datp > damp + ppi  da > dan + ppi  da > dan + ppi  da > dan + mbd  imp + mad > madh + xmp  fithf + gar <> pgam + thf  atp + formate + gar <> padp + fgam + pi  fithf + aicar <>> fprica + thf  gln + prop >> glu + ppi + pram  asuc <> pam + fum  saicar <> pam + fum  saicar <> pam + atp >> saicar + adp + pi  atp + fpram >> adp + pi  atp + fpram >> adp + gar + pi  asp + gtp + pram <>> adp + gar + pi  asp + gtp + pram >> auc + gdp + pi  atp + gln + xmp >> amp + glu + gmp + ppi  atp + gln + xmp >> adp + fpram + glu + pi  air + atp + hco3 >> caiz + adp + pi  aicar <> pam + pi  aicar <> pam + pi  air + atp + co3 >> caiz + adp + pi  aicar <> pam + pi  air + atp + co3 >> caiz + adp + pi  air <= caiz <>> cair  aicar <> pam + pi <>> adp + ditp  amp + ppi <>> adp + ditp  amp + ppi <>> adp + ditp  amp + ppi <>> adp + ppp  datp + pyr <>> gdp + pep  datp + pyr <>> gdp + pep  datp + pyr <>> gdp + pep  datp + ppr <>> gdp + pep  datp + ppr <>> gdp + pep  datp + ppr <>> gdp + pep
NUTP6 NUTP8 NUTP7 ADNCYC DANDA IMPOH PRGNFT GARTFM PRAZCFT GLUPRPAT ADSUCL1 ADSUCL2 PRASUCS PRAIZS PRAIZS PRAIZS ADSUCS GMPS PREGAS AIRC CAIZM ADPRT2 ADPRT3 NUDPK9 NUDPK10 ADPRT4 PYK1 PYK2 PYK2 PYK3	Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) and adenylate cyclase Deoxyadenosine deaminase IRM dehydrogenase phosphorbosyldynamide formyltransferase glycinamide ribonucleotide transformylase phosphorbosyldiphosphate amidotransferase glutamine phosphorbosyldiphosphate amidotransferase adenylsuccinate lyase adenylsuccinate lyase adenylsuccinate lyase adenylsuccinate lyase phosphorbosyldiphosphate amidotransferase adenylsuccinate lyase adenylsuccinate lyase adenylsuccinate lyase adenylsuccinate synthase phosphorbosyldiphosphate synthase GMP synthase phosphorbosyldiphosphate initial carbosylase 5-(carboxyamino)imidazole ribonucleotide mutase adenine phosphorbosylaminimidazole ribonucleotide mutase adenine phosphorbosylaminimidazole ribonucleotide mutase adenine phosphorbosylaminimidazole ribonucleotide diphosphate kinase (ATP-GDP) adenine phosphorbosylaminimidazole ribonucleotide-diphosphate kinase phosphorbosylaminimidazole ribonucleotide-diphosphate kinase (ATP-GDP) adenine phosphorbosylaminimidazole ribonucleotide-diphosphate kinase phosphorbosylaminimidazole ribonucleotide-diphosphate kinase phosphorbosylaminimidazole ribonucleotide-diphosphate kinase phosphorbosylaminimidazole ribonucleotide-diphosphate kinase adenylate kinase adenylate kinase adenylate kinase adenylate kinase adenylate kinase	3.6.18 3.6.18 3.6.119 4.6.11 3.5.44 1.11.205 2.1.22  2.1.23 2.4.2.14 4.3.22 4.3.22 6.3.2.6 6.3.3.1 6.3.4.4 6.3.5.2 6.3.5.3 6.3.4.18 5.4.99.18 2.4.2.7 2.7.4.6 2.7.4.6 2.7.4.6 2.7.4.6 2.7.1.40 2.7.1.40	KOX_01150(maxG)  KOX_0215  KOX_07630(cyaA)  KOX_12945  KOX_27220  KOX_23845(pur1)(KOX_27160(purN))  KOX_23845(pur1)(KOX_27160(purN))  KOX_23845(pur1)  KOX_08025(purH)  KOX_08025(purH)  KOX_08025(purH)  KOX_08020  KOX_071555  KOX_27090  KOX_07155  KOX_07	atp >> amp + ppi  datp >> damp + ppi  datp >> damp + ppi  datp >> damp + ppi  atp >> camp + ppi  da >> din + mb4  imp + rad >> nadh + xmp  tthf + gar <>> fgam + thf  atp + formate + gar <>> adp + fgam + pi  tthf + aicar <>> fprica + thf  gln + prpp >> glu + ppi + pram  ascu <>> amp + fum  saicar <>> aicar + fum  cair + asp + atp >> saicar + adp + pi  atp + fpram >> adp + air + pi  atp + fpram >> adp + air + pi  atp + gly + pram <>> adp + gar + pi  atp + gly + pram <>> adp + pri  atp + gly + pram <>> adp + pri  atp + gln + xmp >> amp + glu + gmp + ppi  atp + gln + xmp >> amp + glu + ppi  atp + fgam + gln >> adp + fpram + glu + pi  air + atp + hco3 -> caiz + adp + pi  caiz <>> cair  aicar + ppi <>> Salic + prpp  gmp + ppi <>> gn + prpp  atp + didp <>> adp + ditp  atp + idp <>> adp + ditp  atp + idp <>> adp + ditp  atp + pry <> dadp + prp  datp + pry <>> adp + prp  datp + pry <>> dadp + prp
NUTP6 NUTP8 NUTP7 ADNCYC DANDA IMPDH PRGNET GARTEM PRAZCET GLUPRPAT ADSUCL1 ADSUCL2 PRASUCS PRAIZS PRAIZS PREGAS AIRC CAIZM ADPRT2 ADPRT3 NUDPK10 ADPRT4 PYK1 PYK2 PYK2 PYK2 PYK2 PYK2 PYK2 PYK2 PYK2	Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (GTP) adenine deside-triphosphatase (GTP) adenine deside-triphosphatase (GTP) adenine deside-triphosphatase phosphoribosylgyicinamide formyttransferase glycinamide ribonucleotide transformylase phosphoribosylaminoimidazolea arboxamide formyttransferase glutamine phosphoribosyldiphosphata amidotransferase glutamine phosphoribosyldiphosphata amidotransferase adenyfsuccinate lyase adenyfsuccinate lyase adenyfsuccinate was adenyfsuccinate selection of the deside succincarboxamide synthase phosphoribosyldyaminoimidazoles ynthase phosphoribosyldyaminoimidazole synthase adenyfosuccinate synthase GMP synthase phosphoribosyldromydgycinamidine synthase phosphoribosyldromydgycinamidine synthase adenine phosphoribosyldromydgycinamidine synthase phosphoribosyldromydgycinamidine synthase adenine gwithase adenine (ATP-GDP) nucleoside-diphosphate kinase (ATP-GDP) nucleoside-diphosphate kinase pyruvate kinase pyruvate kinase pyruvate kinase pyruvate kinase pyruvate kinase	36.18 36.18 36.119 46.11 35.44 11.11.205 21.22 21.23 24.214 43.22 43.22 63.26 63.31 63.413 63.42 63.52 63.53 63.418 54.99.18 24.27 27.46 27.46 24.28 27.140 27.140 27.140 27.140	KOX_01150(marG)  KOX_01150(marG)  KOX_02715  KOX_07630(cyaA)  KOX_21345  KOX_27240  KOX_23845(purT)/KOX_27160(purN)  KOX_08025(purH)  KOX_08025(purH)  KOX_26550  KOX_17535  KOX_17535  KOX_27990  KOX_27995  KOX_27155  KOX_27990  KOX_28030  KOX_280300  KOX_2	atp >> amp + ppi  datp >> dmp + ppi  datp datp datp datp datp datp  datp + formate + gar <-> adp + fgam + pi  fithf + aicar <-> fprica + thf  gln + prpp >> glu + ppi + pram  ascu <-> amp + fum  saicar <-> aicar + fum  cair + asp + atp >> saicar + adp + pi  atp + fgram -> adp + air + pi  atp + fgram -> adp + air + pi  atp + gly + pram <-> adp + apr + pi  atp + gly + pram <-> adp + pri  atp + gln + xmp >> amp + glu + gmp + ppi  atp + gln + xmp >> amp + glu + ppi  atp + fgam + gln >> adp + fpram + glu + pi  air + atp + hco3 -> caiz + adp + pi  caiz <-> cair  aicar + ppi <-> Safic + prpp  gmp + ppi <-> gn + prpp  atp + didp <-> adp + ditp  atp + idp <-> adp + itp  amp + ppi <-> adp + ppp  datp + pyr <-> dadp + pep  ddp + ppr <-> gdp + pep  ddp + ppr <-> gdp + pep  ddp + ppr <-> gdp + pep  ddp + ppr <-> ddp + pep  ddp + ppr + odpq + ppr  ddp + ddp <-> adp + ppr  ddp + ppr <-> ddp + pep  ddp + ppr <-> gdp + pep  ddp + ppr <-> ddp + pep  ddp + ppr <-> ddp + ppr  ddp + ddp <-> adp + ppr  ddp + ppr <-> adp + datp <->
NUTP6 NUTP8 NUTP7 ADNCYC DANDA IMPOH PRGNFT GARTFM PRAZCFT GLUPRPAT ADSUCL1 PRASUCS PRAIZS PRAGCS ADSUCS GMPS PREGAS AIRC CAIZM ADPRT2 ADPRT3 NUDPK9 NUDPK10 ADPRT4 PPX1 PYX2 PYX2 PYX3 ADNCYC1	Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (GTP) adenine daenylate cyclase Deoxyadenosine deaminase IMP dehydrogenase phosphoribosylglycinamide formyttransferase glycinamide ribonucleotide transformylase phosphoribosyldiphosphata amidotransferase glutamine phosphoribosyldiphosphata amidotransferase glutamine phosphoribosyldiphosphata amidotransferase adenylsuccinate lyase adenylsuccinate lyase adenylsuccinate lyase hosphoribosyldiphosphata amidotransferase adenylsuccinate lyase phosphoribosyldiphosphatiacole synthase phosphoribosyldiphosphaticosyldiphosphoribosyldiphos	36.18 36.18 36.18 36.19 46.11 35.44 1.11205 2.1.22  2.1.23 2.4.2.14 4.3.2.2 4.3.2.2 4.3.2.2 6.3.3.1 6.3.4.3 6.3.4.4 6.3.5.3 6.3.4.8 5.4.99.18 2.4.2.7 2.7.4.6 2.7.4.6 2.7.4.6 2.7.1.40	KOX_01150(marG)  KOX_01150(marG)  KOX_02715  KOX_07630(cyaA)  KOX_21345  KOX_27240  KOX_23845(purT)/KOX_27160(purN)  KOX_08025(purH)  KOX_08025(purH)  KOX_26550  KOX_17535  KOX_17535  KOX_27590  KOX_27999  KOX_27155  KOX_27990  KOX_28030/KOX_26875/KOX_27215(guaA)  KOX_28030	atp > amp + ppi  datp > damp + ppi  atp - camp + ppi  da > dain + mbd  mp - mad > madh + xmp  tthf + gar <> adp + tgam + pi  tthf + aicar <> fprica + thf  gln + prpp -> glu + ppi + pram  asuc <> amp + fum  asuc <> amp + fum  asuc <> aicar + tum  cair + asp + atp > saicar + adp + pi  atp + fpram >> adp + gar + pi  atp + gly + pram <> adp + gar + pi  asp + gtp + imp >> asuc + gdp + pi  atp + gly + xmp >> amp + glu + gmp + ppi  atp + glh + xmp >> amp + glu + gmp + ppi  air + atp + bco3 >> caiz + adp + pi  caiz <> cair  aicar + ppi <> Saicic + prpp  gmp + ppi <> gn + prpp  atp + didp <> adp + ditp  atp + idp <> adp + ditp  atp + gdp + grap + pp  datp + grap <> adp + ditp  amp + ppi <> adp + tip  amp + ppi <> adp + tip  amp + ppi <> adp + pp  datp + ppr <> adp + pp  datp + ppr <> datp + pp  datp + ppr <> datp + pp  datp + ppr <> datp + pp  datp + pp >> adp + pp
NUTP6 NUTP8 NUTP7 ADNCYC DANDA IMPDH PRGNFT GARTFM PRAZCFT GLUPRPAT ADSUCL1 ADSUCL2 PRASUCS PRAIZS PRGCS GMPS PRFGAS AIRC CAIZM ADPRT2 ADPRT3 NUDPK10 ADPRT4 PYK1 PYK2 PYK2 PYK2 PYK2 ADNCYC1 23CNPDE1 23CNPDE1 23CNPDE2 GSK	Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (GTP) adenine daenylate cyclase Deoxyadenosine deaminase IMP dehydrogenase phosphoribosylglycinamide formyttransferase glycinamide ribonucleotide transformylase phosphoribosyldiphosphata amidotransferase glutamine phosphoribosyldiphosphata amidotransferase adenylsuccinate lyase adenylsuccinate lyase adenylsuccinate lyase adenylsuccinate lyase phosphoribosylaminoimidazoles uccinocarboxamide synthase phosphoribosylaminoimidazoles ynthase phosphoribosylaminoimidazoles ynthase gamen denylsuccinate synthase GMP synthase phosphoribosylgivanimoimidazoles ynthase phosphoribosylgivanimoimidazoles ynthase GMP synthase phosphoribosylgivanimoimidazole ribonucleotide mutase adenine phosphoribosyltransferase nucleoside diphosphoribosyltransferase nucleoside-diphosphate kinase (ATP-GDP) nucleoside-diphosphate kinase pyruvate kinase pyruvate kinase pyruvate kinase adenylate kinase insine/guanosine kinase kinase adeninase kinase adeninase insine/guanosine kinase kinase adeninase insine/guanosine kinase kinase adeninase insine/guanosine kinase kinase adeninase kinase adeninas	3.6.18 3.6.18 3.6.119 4.6.11 3.5.44 1.11.205 2.1.22 2.1.23 2.4.2.14 4.3.22 4.3.22 4.3.22 6.3.26 6.3.31 6.3.4.13 6.3.5.2 6.3.5.3 6.3.4.18 5.4.9.18 2.4.2.7 2.7.4.6 2.7.4.6 2.7.4.6 2.7.4.6 2.7.1.40 2.7.1.	KOX_01150(mazG)  KOX_01150(mazG)  KOX_02715  KOX_07630(cyaA)  KOX_21945  KOX_22845(purT)(KOX_27160(purN))  KOX_23845(purT)(KOX_27160(purN))  KOX_23845(purT)  KOX_08025(purH)  KOX_26550  KOX_17535  KOX_17535  KOX_17535  KOX_17535  KOX_27155  KOX_27155  KOX_272900  KOX_2845(purT)  KOX_08020  KOX_08020  KOX_08020  KOX_08020  KOX_08020  KOX_08020  KOX_13355  KOX_13305  KOX_13305  KOX_13200	atp >> amp + ppi  datp >> amp + ppi  datp >> damp + ppi  datp >> damp + ppi  datp >> damp + ppi  da >> dam + mbd  atp + formate + gar <>> adp + fgam + pi  fthf + aicar <>> fgam + thf  dp + prpp >> glu + ppi + pram  asuc <>> amp + fum  saicar <>> aicar + fum  cair + asp + atp >> saicar + adp + pi  atp + fpram -> adp + air + pi  atp + fpram -> adp + air + pi  atp + gly + pram <>> adp + gar + pi  atp + gly + pram <>> adp + pri  atp + gly + pram >> amp + glu + gmp + ppi  atp + gly + mp >> arp + glu + gmp + ppi  atp + fpram >> adp + air + pi  atp + gly + ram <>> adp + air + pi  atp + gly + pram <>> adp + pram + glu + ppi  atp + gly + pram >> adp + fpram + glu + pi  atp + fgam + gln >> adp + fpram + glu + pi  atp + fgam + gln >> adp + fpram + glu + pi  atr + atp + bco3 -> caiz + adp + pi  caiz <>> cair  aicar + ppi <>> Safic + prpp  gmp + ppi <>> adp + ditp  atp + didp <>> adp + ditp  atp + pyr <>> adp + prp  gtp + pyr <>> adp + ppp  gtp + pyr <>> ddp + pep  gtp + pyr <>> gdp + pep  gtp + gmp + ppi  23camp >> 3amp  gm + atp <>> gmp + adp
NUTP6 NUTP8 NUTP7 ADNCYC DANDA IMPOH PRGNFT GARTFM PRAZCFT GLUPRPAT ADSUCL1 ADSUCL2 PRASUCS PRAIZS PRAIZS PRAIZS ADSUCS GMPS PREGS ADSUCS GMPS ADSUCS ADPRT2 ADPRT3 ADPRT2 ADPRT3 ADPRT4 PYK1 PYK2 PYK2 PYK3 ADNCYC1 23CNPDE1	Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) and adenylate cyclase Deoxyadenosine deaminase IRM dehydrogenase phosphorbosyldynamide formyltransferase glycinamide ribonucleotide transformylase phosphorbosyldiphosphate amidotransferase glutamine phosphorbosyldiphosphate amidotransferase adenylsuccinate lyase adenylsuccinate lyase adenylsuccinate lyase adenylsuccinate lyase adenylsuccinate synthase phosphorbosyldyminoimidazoles uccinocarboxamide synthase phosphorbosyldyminoimidazole synthase phosphorbosyldyminoimidazole synthase GMP synthase phosphorbosyldyninoimidazole synthase phosphorbosyldycinamidine synthase phosphorbosyldycinamidine synthase phosphorbosyldiphosphorbosyldransferase adenylase (ATP-GDP) adenine phosphorbosyltransferase (ATP-GDP) adenine phosphorbosyltransferase phosphorbosyltransferase phosphorbosyltransferase phosphorbosyltransferase pyruvate kinase pyruvate kinase pyruvate kinase pyruvate kinase adenylate cyclase 2;3-cyclic-nucleotide 2-phosphodiesterase 2;3-cyclic-nucleotide 2-phosphodiesterase inosine/guanosine kinase inosine/guanosi	3.6.18 3.6.18 3.6.18 3.6.19 4.6.11 3.5.44 1.11205 2.1.22  2.1.23 2.4.214 4.3.22 4.3.22 6.3.26 6.3.31 6.3.44 6.3.52 6.3.53 6.3.418 5.4.99.18 2.4.27 2.7.4.6 2.7.4.6 2.7.4.6 2.7.1.40 2.7	KOX_01150(maxG)  KOX_01150(maxG)  KOX_02715  KOX_07630(cyaA)  KOX_21345  KOX_22345(pur1)/KOX_27160(purN)  KOX_23845(pur1)/KOX_27160(purN)  KOX_08025(purH)  KOX_08025(purH)  KOX_17535  KOX_17535  KOX_17535  KOX_27155  KOX_27155  KOX_27155  KOX_27155  KOX_27155  KOX_27155  KOX_27155  KOX_13035  KOX_13055  KOX_27250(xoX_28870  KOX_27250(xoX_28870  KOX_27250(xoX_28870  KOX_27250(xoX_28870  KOX_27250(xoX_28870  KOX_27250(xoX_28870  KOX_27250(xoX_28870  KOX_27250(xoX_28870  KOX_13060  KOX_09030(cpdB)  KOX_09030(cpdB)  KOX_13060  KOX_13060  KOX_13060  KOX_13060	atp > amp + ppi  datp > amp + ppi  datp > damp + ppi  datp > damp + ppi  datp > damp + ppi  da > dam + ppi  da > dam + ppi  da > dam + mbd  imp + mad > nadm + xmp  fithf + gar <> pgam + thf  atp + formate + gar <> padp + fgam + pi  fithf + aicar <>> fprica + thf  gln + prop >> glu + ppi + pram  asuc <> pam + fum  saicar <> pi - pricar + fum  cair + asp + atp > saicar + adp + pi  atp + fpram >> adp + gar + pi  atp + gpram >> adp + gar + pi  atp + gpram >> adp + gar + pi  asp + gtp + imp >> asuc + gdp + pi  atp + gln + xmp >> amp + glu + gmp + ppi  atp + gln + xmp >> adp + glr + ppi  atp + gln + xmp >> adp + fpram + glu + pi  atp + fpam + gln >> adp + fpram + glu + pi  atp + gar + gpr <> pricar + ppi  atp + gar + gpr <> pricar + ppi  atp + gar + gr <> pricar + ppi  atp + gar + gr <> pricar + ppi  atp + gar + gr <> pricar + ppi  atp + gar + gr <> pricar + ppi  atp + gar + gr <> pricar + ppi  atp + didp <>> adp + ditp  atp + didp <>> adp + ditp  atp + dap <>> adp + ppp  datp + ppr <>> dadp + ppp  gtp + ppr <>> gdp + ppp  datp + ppr <>> gdp + ppp  datp + gar >> gdp + ppr  atp + dadp = gdp <= pricar + gdp <= pp  dadp + ppp > gdp + ppr  atp + dadp = gdp <= pricar + gdp <= pp  dadp + ppp > gdp + ppr  datp + pr <> pp > ddp + ppp  datp + gr <> gdp + ppr  datp + gdp <> gr >> gdp + gr <> gdp + ppr  datp + gr <> gdp + ppr <> gdp + ppr  datp + gr <> gdp + ppr <> gdp <> gdp + ppr <> gdp > <
NUTP6 NUTP8 NUTP7 ADNCYC DANDA IMPOH PRGNFT GARTFM PRAZCFT GLUPRPAT ADSUCL1 ADSUCL2 PRASUCS PRAIZS PRAIZS PRAIZS PRAIZS PRAIZS ADSUCS GMPS PREGAS AURC CAIZM ADPRT2 ADPRT3 NUDPK9 NUDPK10 ADPRT4 PYK1 PYK2 PYK3 ADNCYCL 23CNPDE1 23CNPDE1 23CNPDE2 GSK INSK GMPRD ADDA	Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) and adenylate cyclase Deoxyadenosine deaminase IMP dehydrogenase phosphorbosyldynamide fromyttransferase glycinamide ribonucleotide transformylase phosphorbosyldiphosphate amidotransferase adenylase complexionation of the phosphorbosyldynamiomidazolec adenylasucrante lyase phosphorbosylaminomidazoles synthase phosphorbosylaminomidazole synthase GMP synthase phosphorbosylaminomidazole robnoucleotide mutase adenylasucrante lyase synthase phosphorbosylaminomidazole ribonucleotide mutase adenine phosphorbosylaminomidazole ribonucleotide mutase (ATP-GDP) adenine phosphorbosylarnasferase phosphorbosylarnasferase phosphorbosylarnasferase phosphorbosylare kinase (ATP-GDP) adenine phosphorbosylare kinase pyruvate kinase pyruvate kinase pyruvate kinase pyruvate kinase pyruvate kinase adenylate cyclase 2,3-cyclic-nucleotide 2-phosphodiesterase inosine/guanosine kinase inosine/guanosine kinase inosine/guanosine kinase inosine/guanosine kinase inosine/guanosine kinase adenine deaminase adenine deaminase	3.6.18 3.6.18 3.6.18 3.6.19 4.6.11 3.5.44 1.11205 2.1.22 2.1.23 2.4.2.14 4.3.22 4.3.22 6.3.2.6 6.3.3.1 6.3.4.13 6.3.4.4 6.3.5.2 6.3.5.3 6.3.4.18 5.4.9.18 2.4.2.7 2.7.4.6 2.7.1.40 3.1.4.16	KOX_01150(maxG)  KOX_01150(maxG)  KOX_02715  KOX_07630(cyaA)  KOX_21345  KOX_22345(pur1)/KOX_27160(purN)  KOX_23845(pur1)/KOX_27160(purN)  KOX_08025(purH)  KOX_17535  KOX_17535  KOX_17535  KOX_27155  KOX_27155  KOX_27155  KOX_27155  KOX_27155  KOX_27155  KOX_27155  KOX_18020  KOX_27155  KOX_18020  KOX_27155  KOX_18020  KOX_27155  KOX_18020  KOX_27155  KOX_27155  KOX_27155  KOX_18020  KOX_27155  KOX_18020  KOX_27155  KOX_18020  KOX_27155  KOX_18020  KOX_18020	atp > amp + ppi  datp > amp + ppi  datp > damp + ppi  datp > damp + ppi  datp > damp + ppi  da > dam + ppi  da > dam + ppi  da > dam + mbd  imp + mad > madh + xmp  fithf + gar <> pgam + thf  atp + formate + gar <> padp + fgam + pi  fithf + aicar <>> fprica + thf  gln + prop >> glu + ppi + pram  asuc <> pam + fum  saicar <> pam + fum  saicar <> pam + fum  saicar <> pam + atp > saicar + adp + pi  atp + fpram >> adp + air + pi  atp + gpram >> adp + gar + pi  asp + gpp + imp >> asuc + gdp + pi  atp + gln + xmp >> amp + glu + gmp + ppi  atp + gln + xmp >> adp + glr + pri  atp + fpam + gln >> adp + fpram + glu + pi  atp + fpam + gln >> adp + fpram + glu + pi  atp + gar + ghr >> glr + pri  atp + gar + ppi <>> glr + pri  atp + gar + glr + grap + glr + pri  atp + gar + glr + grap + glr + pri  atp + gar + glr + grap + glr + pri  atp + gar + glr + grap + glr + pri  atp + gar + glr + grap + glr + grap + glr + pri  atp + glr + grap + glr
NUTP6 NUTP8 NUTP7 ADNCYC DANDA IMPOH PRGNFT GARTFM PRAZCFT GLUPRPAT ADSUCL1 ADSUCL2 PRASUCS PRAIZS PRAIZS PRAIZS PRAIZS ADSUCS GMP5 PREGAS AIRC CAIZM ADPRT2 ADPRT3 NUDPK9 NUDPK10 ADPRT4 PYK1 PYK2 PX3 ADNCYC1 23CNPDE1 23CNPDE1 23CNPDE1 23CNPDE2 GSK GMPRD ADDA SADT1	Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (AGTP) adenylate cyclase Deoxyadenosine deaminase IRM dehydrogenase phosphoribosylghycinamide formyttransferase glycinamide ribonucleotide transformylase phosphoribosylghycinamide adenylate cyclase phosphoribosyldiphosphate amidotransferase glutamine phosphoribosyldiphosphate amidotransferase adenylsuccinate lyase adenylsuccinate lyase adenylsuccinate lyase adenylsuccinate lyase hosphoribosylaminoimidazoles uccinocarboxamide synthase phosphoribosylaminoimidazole synthase adenylsuccinate synthase GMP synthase GMP synthase GMP synthase formylsuccinate synthase GMP synthase phosphoribosylghycinamidic synthase phosphoribosylsminoimidazole robonucleotide mutase adenylate cyclase (ATP-GDP) nucleoside-tiphosphate kinase (ATP-GDP) adenine phosphoribosyltransferase pyruvate kinase pyruvate kinase pyruvate kinase pyruvate kinase adenylate cyclase 2:3-cyclic-nucleotide 2'phosphoribosyltransferase pyruvate kinase adenylate cyclase 2:3-cyclic-nucleotide 2'phosphoficiansie kinase inosine/Quanosine kinase	3.6.18 3.6.18 3.6.18 3.6.119 4.6.11 3.5.44 1.11.205 2.1.22 2.1.23 2.4.2.14 4.3.22 4.3.22 4.3.22 6.3.2.6 6.3.3.1 6.3.4.4 6.3.5.2 6.3.5.3 6.3.4.13 6.3.4.4 6.3.5.2 2.7.4.6 2.7.4.6 2.7.4.6 2.7.4.6 2.7.4.6 2.7.4.6 2.7.4.6 2.7.4.6 3.1.4.16	KOX_01150(maxG)  KOX_01150(maxG)  KOX_02715  KOX_07630(cyaA)  KOX_21945  KOX_27220  KOX_23845(purT)(KOX_27160(purN))  KOX_23845(purT)(KOX_27160(purN))  KOX_23845(purT)  KOX_08025(purH)  KOX_26550  KOX_17535  KOX_17535  KOX_17535  KOX_17535  KOX_27155  KOX_27155  KOX_272900  KOX_28870  KOX_28870  KOX_28870  KOX_28870  KOX_27290(ndk)  KOX_13025  KOX_13025  KOX_17290(ndk)  KOX_27290(ndk)  KOX_1806(ndk)  KOX_1806(ndk)  KOX_1808(ndk)  KOX_1808(ndk)  KOX_1808(ndk)  KOX_1808(ndk)  KOX_1808(ndk)  KOX_1808(ndk)  KOX_13660  KOX_13660  KOX_13660  KOX_13660  KOX_13660  KOX_13600	atp >> amp + ppi  datp >> amp + ppi  datp >> damp + ppi  datp >> damp + ppi  datp >> damp + ppi  da >> dam + mbd  imp + mad >> madh + xmp  fthf + gar <>> fgam + thf  atp + formate + gar <>> adp + fgam + pi  fthf + aicar <>> fprica + thf  gln + prpp >> glu + ppi + pram  asuc <>> amp + fum  saicar <>> aicar + fum  cair + asp + atp >> air + pi  atp + fpram >> adp + gar + pi  asp + gtp + imp >> asuc + gdp + pi  atp + gfp + pram <>> adp + gar + pi  asp + gtp + imp >> asuc + gdp + pi  atp + gfp + xmp >> adp + glu + gmp + ppi  atp + gfp + xmp >> adp + fpram + glu + pi  atp + fgam + gln >> adp + fpram + glu + pi  atp + fgam + gln >> adp + fpram + glu + pi  atp + fgam + gln >> adp + fpram + glu + pi  atr + ppi <>> Safic + prpp  gmp + ppi <>> gn + prpp  atp + idp <>> adp + ditp  amp + ppi <>> ad + prp  datp + gr <>> gdp + pep  dgdp + pep > gdp + pep  dgdp + pep > gdp + pry  atp + damp <>> adp + dadp  gmp > adp + dadp  gmp > adp + dadp  gmp > adp >> samp  23camp >> 3amp  gm + atp <>> gmp + adp  gmp + nadp + nad  atp + sod >> ppi + nad  atp + sod >> ppi + nad  atp + sod >> ppi + aps
NUTP6 NUTP8 NUTP7 ADNCYC DANDA IMPOH PRGNET GARTEM PRAZCET GLUPRPAT ADSUCL1 ADSUCL2 PRASUCS PRAIZS PRGCS AURC CAIZM ADPRT3 NUDPK10 ADPRT4 PYK1 PYK2 PYK2 PYK2 PYK2 PYK2 ADNCYC1 23CNPDE1 23CNPDE1 23CNPDE2 GSK INSK INSK GMPRD ADDA ADDA ADDA ADDA ADDA ADDA ADDA A	Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (GTP) adenyiate ycylase Deoxyadenosine deaminase IMP dehydrogenase phosphoribosylglycinamide fromyttransferase glycinamide ribonucleotide transformylase phosphoribosylglycinamide adenyiate ychosphoribosyldiphosphate amidotransferase adenysuccinate lyase adenysuccinate lyase adenysuccinate lyase adenysuccinate lyase adenysuccinate lyase adenysuccinate synthase phosphoribosyldiphosphate amidotransferase adenysuccinate synthase adenysuccinate synthase phosphoribosyldiphosphate synthase phosphoribosyldiphosphate synthase GMP synthase phosphoribosyldiphosphate synthase GMP synthase phosphoribosyldiphosphate synthase indepolice synthase (application of the synthase synthase in the synthase phosphoribosyldiphosphate synthase (ATP-GDP) adenine phosphoribosyltransferase adenine phosphoribosyltransferase phosphoribosyltransferase adenine phosphoribosyltransferase adenine phosphoribosyltransferase adenine phosphoribosyltransferase adenine phosphoribosyltransferase adenine phosphoribosyltransferase adenine (ATP-GDP) adenine phosphoribosyltransferase pyruvate kinase pyruvate kinase pyruvate kinase adenydute kinase adenydute kinase adenydute kinase adenydute kinase adenydute kinase adenydute kinase adeninie deaminase adeninie deaminase adeninie deaminase adenine dea	36.18 36.18 36.18 36.18 36.19 46.11 35.44 11.11.205 21.22 21.23 24.214 43.22 43.22 43.22 63.26 63.31 63.413 63.42 63.52 63.53 63.44 63.52 63.53 63.44 63.52 24.27 27.46 27.46 27.46 27.40 27.14	KOX_01150(maxG)  KOX_02715  KOX_07630(cyaA)  KOX_21945  KOX_2720  KOX_23845(pur1)  KOX_23845(pur1)  KOX_23845(pur1)  KOX_23845(pur1)  KOX_26550  KOX_17535  KOX_17535  KOX_17535  KOX_17535  KOX_27155  KOX_27155  KOX_27155  KOX_27155  KOX_272090  KOX_28870  KOX_28870  KOX_272090  KOX_28870  KOX_272090  KOX_27200  KOX	atp >> amp + ppi  datp >> dmp + ppi  da >> dm + ppi  da >> dm + ppi  da >> dm + mbd  imp + mad >> nadm + xmp  fthf + gar <>> fgam + thf  atp + formate + gar <>> adp + fgam + pi  fthf + aicar <>> fprica + thf  gln + prpp >> glu + ppi + pram  asuc <>> amp + fum  saicar <>> aicar + fum  cair + asp + atp >> saicar + adp + pi  atp + fpram -> adp + air + pi  atp + fpram -> adp + air + pi  atp + gly + pram <>> adp + gar + pi  atp + gly + pram <>> adp + pri  atp + gly + pram <>> adp + pri  atp + gly + pram <>> adp + pri  atp + gly + pram <>> adp + pri  atp + gly + pram <>> adp + pri  atp + gly + pram <>> adp + pri  atp + gly + pram <>> adp + pri  atp + gly + primp >> asuc + gdp + pi  atp + gly + primp >> adp + fpram + glu + pi  atp + fgam + gln >> adp + fpram + glu + pi  atp + fgam + gln >> adp + fpram + glu + pi  atr + atp + bco3 -> caiz + adp + pi  caiz <>> cair  aicar + ppi <>> Safic + prpp  gmp + ppi <>> gn + prpp  atp + didp <>> adp + ditp  atp + idp <>> adp + ditp  atp + pyr <>> gdp + pep  gtp - pyr <>> gdp + pep  gtp + pyr <>> gdp + pep  gtp - pyr <>> gdp + pep  gtp + pyr <>> pop + ppi  22cmp >> 3gmp  gun + atp <>> mp + ppi  adv + pyr + pyr  adv + pyr + pyr + pyr  adv + py
NUTP6 NUTP8 NUTP7 ADNCYC DANDA IMPOH PRGNET GARTEM PRAZCET GLUPRPAT ADSUCL1 ADSUCL2 PRASUCS PRAIZS PRGCS ADSUCS GMP5 PREGAS AIRC CAIZM ADPRT2 ADPRT3 NUDPK9 NUDPK10 ADPRT4 PYK1 PYK2 PYK2 PYK3 PYK1 PYK2 PYK3 ADNCYC1 23CNPD61 23CNPD61 23CNPD61 23CNPD61 23CNPD61 23CNPD61 CGMPR6 ADDA SADT1 UREA SHISOUH ALLTD	Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (GTP) adenylate yeldae Deoxyadenosine deaminase IMP dehydrogenase phosphoribosylglycinamide fromyltransferase glycinamide ribonucleotide transformylase phosphoribosyldiphosphate amidotransferase glutamine phosphoribosyldiphosphate amidotransferase glutamine phosphoribosyldiphosphate amidotransferase adenylsuccinate lyase adenylsuccinate lyase adenylsuccinate lyase adenylsuccinate selection of the phosphoribosyldiphosphate amidotransferase adenylsuccinate synthase adenylsuccinate synthase phosphoribosyldiphosphate synthase GMP synthase phosphoribosyldiphosphate synthase GMP synthase phosphoribosyldiphosphate synthase GMP synthase phosphoribosyldiphosphoribosyldiphosphoribosyldiphosphoribosyldiphosphoribosyldiransferase nucleoside-diphosphate kinase phosphoribosyltransferase phosphoribosyltransferase privarete kinase privarete kinase privarete kinase privarete kinase privarete kinase adenylate kinase adenyla	36.18 36.18 36.18 36.18 36.119 46.11 35.44 11.11.205 21.22 21.23 24.214 43.22 43.22 63.26 63.31 63.413 63.43 63.44 63.52 63.53 63.44 63.52 24.27 2.7.46 2.7.46 2.7.46 2.7.140 3.5.15 3.5.217 3.5.35 3.5.35	KOX_01150(maxG)  KOX_01150(maxG)  KOX_02715  KOX_07630(cyaA)  KOX_21945  KOX_27220  KOX_23845(pur1)  KOX_23845(pur1)  KOX_23845(pur1)  KOX_23845(pur1)  KOX_26550  KOX_17535  KOX_17535  KOX_17555  KOX_17555  KOX_27090  KOX_27155  KOX_27155  KOX_27155  KOX_27155  KOX_272090  KOX_28155  KOX_28150  KOX_28	atp >> amp + ppi  datp >> dmp + ppi  da >> dm + ppi  da >> dm + ppi  da >> dm + mbd  imp + mad >> nadh + xmp  fthf + gar <>> fgam + thf  atp + formate + gar <>> adp + fgam + pi  fthf + aicar <>> fprica + thf  gln + prpp >> glu + ppi + pram  asuc <>> amp + fum  saicar <>> aicar + fum  cair + asp + atp >> saicar + adp + pi  atp + fpram >> adp + air + pi  atp + gly + pram <>> adp + air + pi  atp + gly + pram <>> adp + ajr + pi  atp + gly + pram <>> adp + pi  atp + gly + pram <>> adp + pi  atp + gly + pram <>> adp + pi  atp + gly + pram <>> adp + pi  atp + gly + pram <>> adp + pi  atp + gly + pram <>> adp + pi  atp + gly + pram <>> adp + pi  atp + gly + pram <>> adp + pi  atp + gly + smp >> auc + gdp + pi  atp + gly + smp >> adp + fpram + glu + pi  atp + fgam + gln -> adp + fpram + glu + pi  air + atp + bco3 -> caiz + adp + pi  caiz <>> cair  aicar + ppi <>> 5afic + prpp  gmp + ppi <>> gn + prpp  atp + didp <>> adp + ditp  atp + idp <>> adp + ditp  atp + idp <>> adp + ditp  atp + pyr <>> gdp + pep  dgdp + pep > dgtp + pyr  atp + damp >> adp + dadp  22cmp >> 3gmp  22cmp >> 3gmp  gm + atp <> gmp + adp  ins + atp <> imp + adp
NUTP6 NUTP8 NUTP7 ADNCYC DANDA IMPOH PRGNFT GARTFM PRAZCFT GLUPRPAT ADSUCL1 ADSUCL2 PRASUCS PRAIZS PRAGCS ADSUCS GMPS PREGAS AIRC CAIZM ADPRT2 ADPRT3 NUDPK9 NUDPK10 ADPRT4 PYK1 PYK2 PYK3 ADNCYC1 23CNPDE1 23CNPDE1 23CNPDE1 23CNPDE2 GSK INSK GMPRD ADDA ADDA ADDA ADDA ADDA ADDA ADDA A	Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (GTP) adenine adenylate cyclase Deoxyadenosine deaminase IMP dehydrogenase phosphoribosylglycinamide formyttransferase glycinamide ribonucleotide transformylase phosphoribosylglycinamide adenylate carboxamide formyttransferase glutamine phosphoribosyldiphosphata amidotransferase glutamine phosphoribosyldiphosphata amidotransferase adenylsuccinate lyase adenylsuccinate lyase adenylsuccinate lyase phosphoribosyldiphosphata amidotransferase adenylsuccinate synthase phosphoribosyldiphosphatae synthase phosphoribosyldiphosphaticsold synthase adenylsuccinate synthase GMP synthase phosphoribosyldiphosphoribosylformylglycinamidine synthase GMP synthase phosphoribosylformylglycinamidine synthase adenine phosphoribosylformylglycinamidine synthase adenine phosphoribosylformylglycinamidine synthase adenine phosphoribosylformylglycinamidine phosphoribosylformylglycinamidine synthase adenine phosphoribosylformylglycinamidiazole ribonucleotide rutase adenine phosphoribosylformylglycinamidiazole ribonucleotide synthase adenine phosphoribosylformylglycinamidiazole rutase adenine phosphoribosylformylglycinamidiazole rutase synthase adenine phosphoribosylformylglycinamidiazole rutase synthase synt	36.18 36.18 36.18 36.18 36.119 46.11 35.44 11.11.205 21.22 21.23 24.214 43.22 43.22 43.22 63.26 63.31 63.413 63.42 63.52 63.53 63.44 63.52 24.27 27.46 27.46 27.46 24.28 27.140 27.153 27.27 35.35	KOX_01150(marS)  KOX_01150(marS)  KOX_02715  KOX_07630(cyaA)  KOX_21945  KOX_221945  KOX_22345(pur1)/KOX_27160(purN)  KOX_23845(pur1)/KOX_27160(purN)  KOX_23845(pur1)  KOX_08025(pur1+)  KOX_08025(pur1+)  KOX_27655  KOX_17535  KOX_17535  KOX_27990  KOX_27990  KOX_279155  KOX_27990  KOX_28000/KOX_26875/KOX_27215(guaA)  KOX_27155  KOX_1300  KOX_13000/KOX_26875/KOX_27215(guaA)  KOX_1300  KOX_13000/KOX_26875/KOX_27215(guaA)  KOX_13005  KOX_13005  KOX_13005  KOX_13005  KOX_13005  KOX_27990(ndk)  KOX_27950(KOX_23870  KOX_27550(KOX_23870  KOX_27550(KOX_23870  KOX_27550(KOX_23870  KOX_13050(gaA)  KOX_06030(cpdb)  KOX_06030(cpdb)  KOX_13060  KOX_13060	atp >> amp + ppi  datp >> damp + ppi  datp >> camp + ppi  da >> dan + mbd  atp + formate + gar <>> adp + fgam + pi  fthf + aicar <>> fprica + thf  gln + prpp >> glu + ppi + pram  asuc <>> amp + fum  saicar <>> aicar + tum  cair + asp + atp >> saicar + adp + pi  atp + gly + pram <>> adp + gar + pi  asp + gtp + imp >> asuc + gdp + pi  atp + gly + pram <>> adp + gar + pi  asp + gtp + imp >> asuc + gdp + pi  atp + gln + smp >> amp + glu + gmp + ppi  atp + gln + smp >> amp + glu + pi  air + atp + bco3 >> caiz + adp + pi  caiz <>> cair  aicar + ppi <>> Salic + prpp  gmp + ppi <>> gn + prpp  datp + gpr <>> gdp + pep  datp + pyr <>> dadp > pep  gtp + pyr <>> gdp + pep  datp + pyr <>> dadp > pep  gtp + pyr <>> gdp + pep  datp + pyr <>> dadp > pep  gtp + pyr <>> gdp + pep  datp + pyr <> gdp + pep  datp + pyr <>> gmp + pi  23camp > 3amp  gm + adp <>> gmp + adp  ins + atp <> long + ph  dath > long + lond  ath > sod > pi+ ph  dath > long + lond  ath > sod > pi+ ph  dath > long + lond  ath > sod > pi+ ph  dath > long + lond  dath > long + lond  ath > sod > pi+ ph  dath > long + lond
NUTP6 NUTP8 NUTP7 ADNCYC DANDA IMPOH PRGNET GARTEM PRAZCET GLUPRPAT ADSUCL1 ADSUCL2 PRASUCS PRAIZS PRGCS ADSUCS GMP5 PREGAS AIRC CAIZM ADPRT2 ADPRT3 NUDPK9 NUDPK10 ADPRT4 PYK1 PYK2 PYK2 PYK3 PYK1 PYK2 PYK3 ADNCYC1 23CNPD61 23CNPD61 23CNPD61 23CNPD61 23CNPD61 23CNPD61 CGMPR6 ADDA SADT1 UREA SHISOUH ALLTD	Purine metabolism	nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) nucleoside-triphosphatase (ATP) and adenylate cyclase Decoyadenosine deaminase IRM dehydrogenase phosphorbosylghoribosylghoribosylghoribosylghoribosylghoribosylghoribosylghoribosylghoribosylghoribosylghoribosylghoribosylghoribosylghoribosylghoribosylghoribosylghoribosylghoribosylghoribosylghosphate amidotransferase glutamine phosphorbosylghiomiomidazoles adenylsuccinate lyase phosphorbosylghiomiomidazoles ynthase phosphorbosylghiomiomidazole synthase GMP synthase phosphorbosylghiomiomidazole cynthase (SMP synthase phosphorbosylforibosylfransferase adenylate cynthase phosphorbosylfransferase phosphorbosylfransferase adenine phosphorbosyltransferase adenine phosphoribosyltransferase phosphoribosyltransferase phosphoribosyltransferase pyruvate kinase sadenylate cyclica-nucleotide 2° phosphodisetrase 2°,3°-cyclic-nucleotide 2° phosphodisetrase 2°,3°-cyclic-nucleotide 2° phosphodisetrase 2°,3°-cyclic-nucleotide 2° phosphodisetrase 2°,3°-cyclic-nucleotide 2° phosphodisetrase 3°,3°-cyclic-nucleotide 3° phosphodisetrase 3°,3°-cyclic-nucleotide 3°	36.18 36.18 36.18 36.18 36.119 46.11 35.44 11.11.205 21.22 21.23 24.214 43.22 43.22 43.22 63.26 63.31 63.413 63.42 63.52 63.53 63.44 63.52 24.27 27.46 27.46 27.46 24.28 27.140 27.153 27.27 35.35	KOX_01150(marS)  KOX_01150(marS)  KOX_02715  KOX_07630(cyaA)  KOX_21945  KOX_2729  KOX_23845(purl)/KOX_27160(purN)  KOX_23845(purl)/KOX_27160(purN)  KOX_08025(purl+)  KOX_08025(purl+)  KOX_08025(purl+)  KOX_076990  KOX_27155  KOX_17535  KOX_27999  KOX_27999  KOX_273155  KOX_17355  KOX_27999  KOX_27990(mill)  KOX_27495  KOX_13195  KOX_13100  KOX_13025  KOX_13200  KOX_13025  KOX_27290(mill)  KOX_13025  KOX_27290(mill)  KOX_13025  KOX_27290(mill)  KOX_13025  KOX_2729(mill)  KOX_13035  KOX_27290(mill)  KOX_13035  KOX_2729(mill)  KOX_13035  KOX_13056  KOX_2729(mill)  KOX_13060  KOX	atp >> amp + ppi  datp >> dmp + ppi  da >> dm + ppi  da >> dm + ppi  da >> dm + mbd  imp + mad >> nadh + xmp  fthf + gar <>> fgam + thf  atp + formate + gar <>> adp + fgam + pi  fthf + aicar <>> fprica + thf  gln + prpp >> glu + ppi + pram  asuc <>> amp + fum  saicar <>> aicar + fum  cair + asp + atp >> saicar + adp + pi  atp + fpram >> adp + air + pi  atp + gly + pram <>> adp + air + pi  atp + gly + pram <>> adp + ajr + pi  atp + gly + pram <>> adp + pi  atp + gly + pram <>> adp + pi  atp + gly + pram <>> adp + pi  atp + gly + pram <>> adp + pi  atp + gly + pram <>> adp + pi  atp + gly + pram <>> adp + pi  atp + gly + pram <>> adp + pi  atp + gly + pram <>> adp + pi  atp + gly + smp >> auc + gdp + pi  atp + gly + smp >> adp + fpram + glu + pi  atp + fgam + gln -> adp + fpram + glu + pi  air + atp + bco3 -> caiz + adp + pi  caiz <>> cair  aicar + ppi <>> 5afic + prpp  gmp + ppi <>> gn + prpp  atp + didp <>> adp + ditp  atp + idp <>> adp + ditp  atp + idp <>> adp + ditp  atp + pyr <>> gdp + pep  dgdp + pep > dgtp + pyr  atp + damp >> adp + dadp  22cmp >> 3gmp  22cmp >> 3gmp  gm + atp <> gmp + adp  ins + atp <> imp + adp

		allantoin transport in via protor	,		
ALLTNtr	Putative Transporters	symport			alltn_e + hext <-> alltn
ARGORNt	Putative Transporters	arginine/ornithine antiporter acetoacetate transport via			arg_e + orn <-> arg + orn_e
ACACt	Putative Transporters	proton symport			acac_e + hext <-> acac
BUTtr	Putative Transporters	Butyrate transport via proton			1boh_e + hext <-> 1boh
		symport, reversible D-galactarte transport via			
GALCTtr	Putative Transporters	proton symport, reversible			dgal_e + hext <-> dgal
DGLUCAt	Putative Transporters	D-glucarate transport via			dgluca_e + hext <-> dgluca
		proton symport, reversible 3-phenylpropionate transport			
PPPNtr	Putative Transporters	via proton symport, reversible			hext + pppn_e <-> pppn
		3-(3-hydroxyphenyl)propionate			
HPPPNtr	Putative Transporters	transport via proton symport, reversible			3hpppn_e + hext <-> 3hpppn
		3-hydroxycinnamic acid			
HCINNMtr	Putative Transporters	transport via proton symport,			3hcinnm_e + hext <-> 3hcinnm
		reversible			
GLUABUTt	Putative Transporters	4-aminobutyrate/glutamate antiport			gaba + glu_e <-> gaba_e + glu
ALAtr	Putative Transporters	L-alanine reversible transport			ala e + hext <-> ala
715111	ratative riansporters	via proton symport			dia_c - frent dia
URAtr	Putative Transporters	uracil transport in via proton symport, reversible			hext + ura_e <-> ura
GLYBtr	Putative Transporters	Glycine betaine transport via			qlyb_e + hext <-> qlyb
GLIBII	rutative transporters	proton symport, reversible			giyo_e + next <-> giyo
CHLabc	Putative Transporters	choline transport via ABC system			atp + choline_e -> adp + choline + pi
		Glycine betaine transport via			
GLYBabc	Putative Transporters	ABC system			atp + glyb_e -> adp + glyb + pi
TARTRt	Putative Transporters	Tartrate/succinate antiporter			succ + tartr_e <-> succ_e + tartr
SUCCabc	Putative Transporters	Succinate transport via ABC system			atp + succ_e -> adp + pi + succ
GUAt2	Putative Transporters	guanine transport in via proton			qn_e + hext -> qn
GUALZ	rutative transporters	symport			gn_e + next -> gn
XANt2	Putative Transporters	xanthine transport in via protor symport	1		hext + xan_e -> xan
IDONOX	Alternate Carbon Metabolism	L-Idonate:NAD oxidoreductase		KOX_00855	idon + nad <-> 5dhgluc + nadh
IDONOXp	Alternate Carbon Metabolism	L-Idonate:NADP oxidoreductase		KOX_00855	idon + nadp <-> 5dhgluc + nadph
5KDGR	Alternate Carbon Metabolism	5-keto-D-gluconate 5- reductase	1.1.1.169	KOX_00845/KOX_12365	5dhgluc + nadph <-> gluc + nadp
PCT4	Alternate Carbon Metabolism	propionate CoA-transferase	2.8.3.1	KOX_02010	ppcoa + succ -> ppa + succoa
5DHGOX	Alternate Carbon Metabolism	5-dehydro-D-gluconate:NADP+	1.1.1.215	KOX_05560	25dhglucn + nadh -> 5dhgluc + nad
		2-oxidoreductase 5-dehydro-D-gluconate:NADP+		_	
5DHGOXp	Alternate Carbon Metabolism	2-oxidoreductase	1.1.1.215	KOX_05560	25dhglucn + nadph -> 5dhgluc + nadp
THMDS	Pyrimidine metabolism	thymidylate synthase	2.1.1.45	KOX_01605(thyA)	dump + metthf -> dhf + dtmp
THMDPP	Pyrimidine metabolism	thymidine phosphorylase uracil	2.4.2.4	KOX_10310(deoA)	pi + thymd <-> dr1p + thym
URAPRT	Pyrimidine metabolism	phosphoribosyltransferase	2.4.2.9	KOX_27140	prpp + ura <-> ppi + ump
CYTDK1	Pyrimidine metabolism	cytidylate kinase (CMP)	2.7.4.14	KOX_16005(cmk)	atp + cmp <-> adp + cdp
CYTDK2	Pyrimidine metabolism	cytidylate kinase (dCMP)	2.7.4.14	KOX_16005(cmk)	atp + dcmp <-> adp + dcdp
UMPK	Pyrimidine metabolism	UMP kinase	2.7.4.14	KOX_16005(cmk)	atp + ump <-> adp + udp
NUDPK2	Pyrimidine metabolism	nucleoside-diphosphate kinase (ATP:UDP)	2.7.4.6	KOX_27290(ndk)	atp + udp <-> adp + utp
NUDPK3	Pyrimidine metabolism	nucleoside-diphosphate kinase	2.7.4.6	KOX 27290(ndk)	atp + cdp <-> adp + ctp
NODERS	r yrimidine metabolism	(ATP:CDP)	2.7.4.0	KOX_27290(lidk)	atp + cap <-> aup + ctp
NUDPK4	Pyrimidine metabolism	nucleoside-diphosphate kinase (ATP:dTDP)	2.7.4.6	KOX_27290(ndk)	atp + dtdp <-> adp + dttp
NUDPK6	Desirability and the lines	nucleoside-diphosphate kinase	2.7.4.6	KOX_27290(ndk)	
NUDPK6	Pyrimidine metabolism	(ATP:dUDP)	2.7.4.6	KOX_2/290(ndk)	atp + dudp <-> adp + dutp
NUDPK7	Pyrimidine metabolism	nucleoside-diphosphate kinase (ATP:dCDP)	2.7.4.6	KOX_27290(ndk)	atp + dcdp <-> adp + dctp
DTMPK	Pyrimidine metabolism	dTMP kinase	2.7.4.9	KOX_17315(tmk)	atp + dtmp <-> adp + dtdp
NUTD1		5'-nucleotidase (dUMP)	3.1.3.5	KOX_01045(surE)/KOX_10270/KOX_13075(ushA)/	dump -> du + pi
NOTEL	Pyrimidine metabolism	5 -Hucleotidase (dolvir)	3.1.3.3	KOX_26410	
NUTD2	Pyrimidine metabolism	5'-nucleotidase (UMP)	3.1.3.5	KOX_01045(surE)/KOX_10270/KOX_13075(ushA)/ KOX_26410	ump -> pi + uri
AUTED	B	EL LUCL (ICME)	2425	KOX_28410 KOX_01045(surE)/KOX_10270/KOX_13075(ushA)/	
NUTD3	Pyrimidine metabolism	5'-nucleotidase (dCMP)	3.1.3.5	KOX 26410	dcmp -> dc + pi
NUTD4	Pyrimidine metabolism	5'-nucleotidase (CMP)	3.1.3.5	KOX_01045(surE)/KOX_10270/KOX_13075(ushA)/	cmp -> cytd + pi
NUTD4	Pyrimidine metabolism	5'-nucleotidase (CMP)	3.1.3.5	KOX_01045(surE)/KOX_10270/KOX_13075(ushA)/ KOX_26410	crip -> cytu + pi
NUTD4 NUTD5	Pyrimidine metabolism  Pyrimidine metabolism	5'-nucleotidase (CMP) 5'-nucleotidase (dTMP)	3.1.3.5 3.1.3.5	KOX_01045(surE)/KOX_10270/KOX_13075(ushA)/	crip -> cytu + pi
				KOX_01045(surE)/KOX_10270/KOX_13075(ushA)/ KOX_26410 KOX_01045(surE)/KOX_10270/KOX_13075(ushA)/	cmp-> cytu + pi
NUTD5 CTDA DCTPDA1	Pyrimidine metabolism Pyrimidine metabolism Pyrimidine metabolism	5'-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase	3.1.3.5 3.5.4.1 3.5.4.13	KOX_01045(surE)/KOX_10270/KOX_13075(ushA)/ KOX_26410 KOX_01045(surE)/KOX_10270/KOX_13075(ushA)/ KOX_26410 KOX_04555/KOX_14050 KOX_04555/KOX_14050 KOX_25240(dcd)	dtmp -> cytu + pr  dtmp -> pi + thymd  ct -> nh4 + ura  dctp -> dutp + nh4
NUTD5 CTDA DCTPDA1 DCTPDA2	Pyrimidine metabolism Pyrimidine metabolism Pyrimidine metabolism Pyrimidine metabolism	5'-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase	3.1.3.5 3.5.4.1 3.5.4.13 3.5.4.13	KOX_01045(surE)/KOX_10270/KOX_13075(ushA)/ KOX_26410 KOX_01045(surE)/KOX_10270/KOX_13075(ushA)/ KOX_041045(surE)/KOX_10270/KOX_13075(ushA)/ KOX_04555/KOX_14050 KOX_25240(dcd) KOX_25240(dcd)	dtmp -> cytu + pi  dtmp -> pi + thymd  ct -> nh4 + ura  dtcp -> dutp + nh4  ctp -> utp + nh4
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP	Pyrimidine metabolism Pyrimidine metabolism Pyrimidine metabolism Pyrimidine metabolism Pyrimidine metabolism	5'-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase	3.1.3.5 3.5.4.1 3.5.4.13 3.5.4.13 3.6.1.23/3.6.1.19	KOX, 01045(surE)/KOX_10270/KOX_13075(ushA)/ KOX_26410 KOX_01045(surE)/KOX_10270/KOX_13075(ushA)/ KOX_26410 KOX_04555/KOX_14050 KOX_0555/KOX_14050 KOX_0555/KOX_14050 KOX_0555/KOX_14050 KOX_0555/KOX_14050	dtmp -> pi + thymd  ct -> nh4 + ura  dctp -> dutp + nh4  ctp -> utp + nh4  dutp -> dump + ppi
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8	Pyrimidine metabolism Pyrimidine metabolism Pyrimidine metabolism Pyrimidine metabolism Pyrimidine metabolism Pyrimidine metabolism	5'-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase	31.35 35.41 35.413 35.413 36.123/3.6119 24.21	KOX_0104/SusE_I/KOX_10270/KOX_13075(ushA)/ KOX_56410 KOX_01045(usE_I/KOX_10270/KOX_13075(ushA)/ KOX_56410 KOX_04555/KOX_14050 KOX_04555/KOX_14050 KOX_0455/KOX_14050 KOX_05240(dcd) KOX_05955(dut)/KOX_02715 KOX_10320(debD)	$\begin{array}{llllllllllllllllllllllllllllllllllll$
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP	Pyrimidine metabolism Pyrimidine metabolism Pyrimidine metabolism Pyrimidine metabolism Pyrimidine metabolism	5'-nucleotidase (dTMP)  Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase uridylate kinase (dUMP)	3.1.3.5 3.5.4.1 3.5.4.13 3.5.4.13 3.6.1.23/3.6.1.19	KOX, 01045(surE)/KOX_10270/KOX_13075(ushA)/ KOX_26410 KOX_01045(surE)/KOX_10270/KOX_13075(ushA)/ KOX_26410 KOX_04555/KOX_14050 KOX_0555/KOX_14050 KOX_0555/KOX_14050 KOX_0555/KOX_14050 KOX_0555/KOX_14050	dtmp -> pi + thymd  ct -> nh4 + ura  dctp -> dutp + nh4  ctp -> utp + nh4  dutp -> dump + ppi
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8	Pyrimidine metabolism Pyrimidine metabolism Pyrimidine metabolism Pyrimidine metabolism Pyrimidine metabolism Pyrimidine metabolism	S'-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase punine nucleoside phosphorylase uridylate kinase (dUMP) dihydroortate dehydrogenase	31.35 35.41 35.413 35.413 36.123/3.6119 24.21	KOX_0104/SusE_I/KOX_10270/KOX_13075(ushA)/ KOX_56410 KOX_01045(usE_I/KOX_10270/KOX_13075(ushA)/ KOX_56410 KOX_04555/KOX_14050 KOX_04555/KOX_14050 KOX_0455/KOX_14050 KOX_05240(dcd) KOX_05955(dut)/KOX_02715 KOX_10320(debD)	$\begin{array}{llllllllllllllllllllllllllllllllllll$
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1	Pyrimidine metabolism	S'-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase uridylate kinase (dUMP) dilhydroorotate dehydrogenase (tumarate)	31.3.5 35.4.1 35.4.13 35.4.13 36.123/3.6.119 24.2.1 27.4.9 13.98.1	KOX_01045(surl)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surl)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surl)/KOX_10270/KOX_13075(ushA)/ KOX_6455(kOX_14050) KOX_6455(kOX_14050) KOX_25240(dect) KOX_25240(dect) KOX_10240(dect) KOX_13240(dect) KOX_13240(dect) KOX_13240(dect) KOX_13245(dect)	dmp >> pi+ thymd  ct >> nN4 + ura  dctp >> dutp + nN4  dctp >> utp + nN4  dutp >> dump + ppi  du+ pi <> drip + ura  atp + dump <>> adp + dudp  doroa + fum <>> oroa + succ
NUTD5 CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROAD	Pyrimidine metabolism	5'-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase urilylate kinase (dUMP) dlhydroorotate dehydrogenase (umarate) aspartate carbamoyltransferase orotate	31.3.5 35.4.1 35.4.13 35.4.13 36.123/3.6.119 24.2.1 27.4.9 13.98.1	KOX_01045surE)/KOX_10270/KOX_13075(ushA)/ KOX_01045surE)/KOX_10270/KOX_13075(ushA)/ KOX_01045surE)/KOX_10270/KOX_13075(ushA)/ KOX_04555/KOX_14050 KOX_025240(dect) KOX_05240(dect) KOX_05253(dect) KOX_05253(dect) KOX_10320(dect) KOX_10320(dect) KOX_17315(mkc) KOX_16135 KOX_09285/KOX_09290(pyrB)	dmp >> pi + thymd  ct >= nh4 + ura  dcp >> dutp + nh4  dutp >> dutp + nh4  dutp >> dump + ppi  du + pi <> dr1p + ura  atp + dump <>> adp + dudp  doroa + fum <>> oroa + succ  asp + cap >> casp >> pi
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROAD ASPCBT OROPRT	Pyrimidine metabolism	5'-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase uridylate kinase (dUMP) dilydcoorotate dehydrogenase (fumarate) aspartate carbamoyltransferase orotate	3.1.35 3.5.413 3.5.413 3.5.413 3.6.123/3.6.119 2.4.21 2.7.49 13.98.1 2.1.32 2.4.210	KOX_01045curE)/KOX_10270/KOX_13075(ushA)/ KOX_26410 KOX_01045(surE)/KOX_10270/KOX_13075(ushA)/ KOX_66410 KOX_04555/KOX_14050 KOX_15240(odc) KOX_05955(dut)/KOX_02715 KOX_10320(decD) KOX_1535(mk) KOX_11315(mk) KOX_16135 KOX_09285/KOX_09290(pyr8) KOX_05965	dtp > pi + thymd  ct > nN4 + ura  dtp > dup + nN4  dtp > dup + nN4  dup > dup + nN4  dup > dump + pi  du + pi <> dr1p + ura  atp + dump <> adp + dudp  doroa + fum <> oroa + succ  asp + cap > casep + pi  omp + ppi <> oroa + prpp
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROAD ASPCBT OROPRT DHORT	Pyrimidine metabolism	5'-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase urilylate kinase (dUMP) dlhydroorotate dehydrogenase (umarate) aspartate carbamoyltransferase orotate	3.135 3.5.41 3.5.413 3.5.413 3.6.123/3.6119 2.4.21 2.7.49 1.3.98.1 2.1.32 2.4.210 3.5.23	KCX, 01045(surl)/KCX, 10.270/KCX, 13.075(ushA)/ KCX, 01045(surl)/KCX, 10.270/KCX, 13.075(ushA)/ KCX, 01045(surl)/KCX, 10.270/KCX, 13.075(ushA)/ KCX, 25440(scd) KCX, 25240(scd) KCX, 10.320(scd) KCX, 10.320(scd) KCX, 10.320(scd) KCX, 11.315(mk) KCX, 16.315 KCX, 0.5958/KCX, 09.290(py#8) KCX, 0.5958/KCX, 09.290(py#8) KCX, 0.5958/KCX, 17.195	dtmp >> pi + thymd  dtmp >> pi + thymd  dtmp >> pi + thymd  dtmp >> dutp + nb4  ctp >> dutp + nb4  ctp >> dutp + nb4  dutp >> dump + ppi  du + pi <>> dr1p + ura  atp -< dump <>> adp + dudp  doroa + fum <>> oroa + succ  asp + cap >> casep + pi  omp + ppi <>> oroa + prpp  doroa <>> casep + cap >> casep + pi  omp + ppi <>> oroa + prpp  doroa <>> casep + cap >> oroa + prpp
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROAD ASPCBT DHORT DHORT	Pyrimidine metabolism	5'-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase uritylate kinase (dUMP) dilhydroorotate dehydrogenase (tumarate) aspartate carbamoyltransferase orotate phosphoribosyltransferase dilhydroorotase orotidine-5'-phosphate decarboxylase	3.135 3.541 3.5413 3.5413 3.6.123/3.6.119 2.421 2.749 13.981 2.132 2.4210 3.523 4.1123	KOX_01045(surla)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surla)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surla)/KOX_10270/KOX_13075(ushA)/ KOX_04555(kOX_14050) KOX_2524(dect) KOX_2524(dect) KOX_05255(surl, KOX_02715 KOX_10320(dest)) KOX_17315(tmk) KOX_16135 KOX_09285/KOX_09290(pyr8) KOX_05965 KOX_05965 KOX_09185/KOX_17195 KOX_018440	dmp >> pi+ thymd  ct >> nh4 + ura  dctp >> dutp + nh4  ct >> utp + nh4  dutp >> dutp + nh4  dutp >> dutp + nh4  dutp >> dutp + nh  dutp >> dutp + chr  dutp >> dutp + chr  atp + dump +> adp + dudp  doroa + fum <> oroa + succ  asp + cap >> casp + pi  omp + ppi <> oroa + prp  doroa <> casp  omp >> co2 + ump
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROAD ASPCBT OROPRT DHORT OMPDC CTPS	Pyrimidine metabolism	5'-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase uridylate kinase (dUMP) dilhydroorotate dehydrogenase (tumarate) sapartate carbamoyltransferase orotatie phosphoribosyltransferase dilhydroorotase orotidine-5'-phosphate decarboxylase CTP synthase (glutamine)	3.1.35 3.5.41 3.5.413 3.5.413 3.6.123/3.6.119 2.4.21 2.7.49 1.3.98.1 2.1.32 2.4.2.10 3.5.2.3 4.1.1.23 6.3.4.2	KOX_01045susE)/KOX_10270/KOX_13075(ushA)/ KOX_01045susE)/KOX_10270/KOX_13075(ushA)/ KOX_01045susE)/KOX_10270/KOX_13075(ushA)/ KOX_02450(kdc) KOX_025240(kdc) KOX_025240(kdc) KOX_025240(kdc) KOX_02525(kdc)/KOX_02715 KOX_10320(kdc)D KOX_10320(kdc)D KOX_10320(kdc)D KOX_17315(mk) KOX_09285/KOX_09290(pyrB) KOX_09285/KOX_09290(pyrB) KOX_09285/KOX_07195 KOX_07185/KOX_17195 KOX_018440 KOX_01145(pyrG)	cmp > y(u = y)  dtmp > pi + thymd  ct > nh4 + ura  dtp > dutp + nh4  ctp > utp + nh4  dutp > dump + ppi  du + pi <> dr1p + ura  atp + dump <> adp + dudp  doroa + fum <> oroa + succ  asp + cap -> cassp + pi  omp + ppi <> oroa + prpp  doroa <> cassp  omp > co2 + ump  atp + gin + utp > adp + ctp + giu + pi
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROAD ASPCBT DHORT DHORT URIDK2 URIDK2 URIDK2 URIDK3	Pyrimidine metabolism Pyrimidine metabolism	5'-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase uridylate kinase (dUMP) dihydroorotate dehydrogenase (tumarate) aspartate carbamoyltransferase orotate phosphoribosyltransferase dihydroorotate doihydroorotate phosphoribosyltransferase orotidine-5'-phosphate decarbosylsae CTP synthase (glutamine) uridylate kinase	31.35 35.41 35.413 35.413 36.123/36.119 24.21 27.49 13.98.1 21.32 24.210 35.23 41.123 63.42 27.422	KCX_01045(surls)/KCX_10270/KCX_13075(ushA)/ KCX_26410 KCX_01045(surls)/KCX_10270/KCX_13075(ushA)/ KCX_01045(surls)/KCX_10270/KCX_13075(ushA)/ KCX_0455(xCX_1405) KCX_2524(dcct) KCX_2524(dcct) KCX_1524(dcct) KCX_1525(dch/KCX_02715 KCX_10320(dcst) KCX_17315(tmk) KCX_16135 KCX_09285/KCX_09290(pyr8) KCX_059565 KCX_09185/KCX_17195 KCX_18440 KCX_011445(pyr6) KCX_11445(pyr6)	dmp >> pi+ thymd  ct >> nh4 + ura  dctp >> dutp + nh4  ct >> utp + nh4  dutp >> dutp + nh4  dutp >> dutp + nh4  dutp >> dutp + nh  dutp >> dutp + chr  dutp >> dutp + chr  atp + dump +> adp + dudp  doroa + fum <> oroa + succ  asp + cap >> casp + pi  omp + ppi <> oroa + prp  doroa <> casp  omp >> co2 + ump
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROAD ASPCBT DHORT OMPDC CTPS URIDK2 DHPM CYTDA	Pyrimidine metabolism	5'-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase uridylate kinase (dUMP) dilhydroorotate dehydrogenase (tumarate) sapartate carbamoyltransferase orotatie phosphoribosyltransferase dilhydroorotase orotidine-5'-phosphate decarboxylase CTP synthase (glutamine)	31.35 35.41 35.413 36.123/36.119 24.21 27.49 13.98.1 21.32 24.210 35.23 41.123 63.42 27.422 35.22 35.24	KOX_01045(surla)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surla)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surla)/KOX_10270/KOX_13075(ushA)/ KOX_04555(kOX_14050) KOX_25440(scd.) KOX_25440(scd.) KOX_153240(scd.) KOX_11315(mik) KOX_16135 KOX_05985/KOX_09290(pyr8) KOX_05985/KOX_09290(pyr8) KOX_05985 KOX_09185/KOX_17195 KOX_018440 KOX_011445(pyr6) KOX_11445(pyr6) KOX_11445(pyr6) KOX_10455(pyr1) KOX_25270 KOX_04555(KOX_14050)	dmp > pi + thymd  dtmp > pi + thymd  dtmp > pi + thymd  dtmp > dutp + nh4  dtp > dutp + nh4  dtp > dutp + nh4  dutp > dump + ppi  du + pi <> dr1p + ura  atp + dump <> adp + dudp  dorna + fum <> orna + succ  asp + cap > casep + pi  omp + ppi <> orna + prpp  dorna <> casep  mp > co2 + ump  atp + dup + orna + prp  dorna <> casep  mp > co2 + ump  atp + ump <> adp + udp > dp + pi + pi  atp + ump <> adp + udp  Sedhu <> 3urdpp  Sem <> x > 3urdpp  Sem <> x > sucp
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROAD ASPCBT OROPRT DHORT OMPDC CTPS URIDK2 DIFFM CYTDA DIFFM CYTDA DIFFM DIF	Pyrimidine metabolism	5'-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase uridylate kinase (dUMP) dihydroorotate dehydrogenase (tumarate) aspartate carbamoyltransferase orotate phosphoribosyltransferase dihydroorotase cortidine-5'-phosphate decarboxylase CTP symthase (glutamine) uridylate kinase dihydroorytaine deaminase dihydropytimidinase cytosine deaminase dihydropytimidinase	31.35 3.5.41 3.5.413 3.5.413 3.6.123/3.6.119 2.4.21 2.7.49 13.98.1 2.1.32 2.4.210 3.5.23 3.5.23 4.11.23 6.3.42 2.7.422 3.5.22 3.5.23 3.5.22 3.5.23 3.5.24 3.5.25	KOX_01045(surE)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surE)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surE)/KOX_10270/KOX_13075(ushA)/ KOX_04555,KOX_14050 KOX_15240(dcd) KOX_0555(dcd)/KOX_02715 KOX_10320(decd) KOX_10320(decd) KOX_10320(decd) KOX_16135 KOX_09285,KOX_09290(pyrB) KOX_0566 KOX_05665 KOX_05965	dmp > pi + thymd  ct > nN4 + ura  dtp > dutp + nN4  ct > nty + nN4  dtp > dutp + nN4  dutp > dump + ppi  du + pi <> drlp + ura  atp + dump <> adp + dudp  doroa + fum <> oroa + succ  asp + cap > cassp + pi  omp + ppi <> oroa + prpp  doroa <> cassp  omp > cap > cassp + ura  atp + dum + ura  atp = dump + ura  store + ura
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROAD ASSCBT OROPRT DHORT OMPDC CTPS URIDK2 DHPM CVTDA DHPMD URIK	Pyrimidine metabolism	5-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase uridylate kinase (dUMP) dihydroorotate dehydrogenase (tumarate) asparlate carbamoyltransferase orotate phosphoribosyltransferase dihydroorotase cordidine-5'-phosphate decarbosylase CTP synthase (glytutamine) uridylate kinase dihydropyrimidinase cytosine deaminase dihydropyrimidinase votroline kinase dihydropyrimidinase uridine kinase (GTP)	3.1.35 3.5.41 3.5.413 3.6.123/3.6.119 2.4.21 2.7.49 13.98.1 2.1.32 2.4.210 3.5.23 4.1.123 6.3.42 2.7.422 3.5.22 3.5.41 3.5.23 4.1.134 6.3.42 2.7.422 3.5.23	KOX_01045(surE)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surE)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surE)/KOX_10270/KOX_13075(ushA)/ KOX_04555(kOX_14050) KOX_04555(kOX_14050) KOX_15240(dect) KOX_15240(dect) KOX_151315(mik) KOX_16135 KOX_09285/KOX_09290(pyr8) KOX_05985 KOX_09285/KOX_09290(pyr8) KOX_05985 KOX_09185/KOX_17195 KOX_18140 KOX_01145(pyr6) KOX_11445(pyr6) KOX_11445(pyr6) KOX_01455(pyr14) KOX_023270 KOX_04555(KOX_14050) KOX_023250	tmp >> pi + thymd  ttmp >> pi + thymd  ttmp >> pi + thymd  ttmp >> dutp + nh4  ttp >> dutp + nh4  ttp >> dutp + nh4  dutp >> dump + ppi  du + pi <>> dr1p + ura  atp + dump <>> adp + dudp  doroa + fum <>> oroa + succ  asp + cap >> casp + pi  omp + ppi <>> oroa + prpp  doroa <>> casp + up  somp >> co2 + ump  atp + ump <>> adp + udp  somp >> co2 + ump  somp >> co2 + ump  somp >> co3 + ump  som <>> sucp >>
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROAD ASPCBT OROPRT DHORT OMPDC CTPS URIDK2 DHPM CYTDA DHPMD URIK CYTDA	Pyrimidine metabolism	5'-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase uridylate kinase (dUMP) dihydroorotate dehydrogenase (tumarate) aspartate carbamoyltransferase orotate phosphoribosyltransferase dihydroorotase cortidine-5'-phosphate decarboxylase CTP symthase (glutamine) uridylate kinase dihydroorytaine deaminase dihydropytimidinase cytosine deaminase dihydropytimidinase	31.35 3.5.41 3.5.413 3.5.413 3.6.123/3.6.119 2.4.21 2.7.49 13.981 2.1.32 2.4.210 3.5.23 4.1.123 6.3.42 2.7.422 3.5.22 3.5.24 3.5.21 3.5.21 3.5.21 3.5.21 3.5.22 2.7.422 3.5.22 2.7.438	KOX_01045(surla)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surla)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surla)/KOX_10270/KOX_13075(ushA)/ KOX_04555(xOX_14050) KOX_15240(dcd) KOX_15240(dcd) KOX_15240(dcd) KOX_15240(dcd) KOX_15245(dcd) KOX_15245(dcd) KOX_15245(dcd) KOX_15245(dcd) KOX_15245(dcd) KOX_16135 KOX_09285/KOX_09290(pyrla) KOX_05965 KOX_05965 KOX_05965 KOX_05965 KOX_05965 KOX_05965 KOX_05965 KOX_11455(pyrl) KOX_11455(pyrl) KOX_11455(pyrl) KOX_11455(pyrl) KOX_12270 KOX_04555(KOX_14050) KOX_15245 KOX_05245 KOX_15245	dmp >> pi+ thymd  ct >= nh4 + ura  dcp >> dutp + nh4  ct >> th4 + ura  dcp >> dutp + nh4  dutp >> dump + ppi  du+ pi <> dr2p + ura  atp + dump <>> adp + dudp  doraa + fum <>> oraa + succ  asp + cap >> caasp + pi  omp + ppi <>> oraa + prp  doraa <>> caasp + cap >> caap  omp >> ca2 + ump  atp + gin + utp >> adp + ctp + glu + pi  atp + ump <>> adp + utp  Sishu <>> 3urdpp  Smc <>> thym + nh4  Sishu <>> such yet + pi  syd + ump  cyd + gtp >= vmp + ydp
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROAD ASSCBT OROPRT DHORT OMPDC CTPS URIDK2 DHPM CVTDA DHPMD URIK	Pyrimidine metabolism	5'-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase uridylate kinase (dUMP) dihydroorotate dehydrogenase (tumarate) asparlate carbamoyltransferase orotate phosphoribosyltransferase dihydroorotase corotate phosphoribosyltransferase dihydroorotase dihydroorotase corotidase phosphoribosyltransferase orotidase phosphoribosyltransferase orotidine-5'-phosphate decarbosylase CTP synthase (glutamine) uridylate kinase dihydropyrimidinase cytosine deaminase dihydropyrimidinase uridine kinase (GTP) rytidnie kinase (GTP) ribonucleoside-triphosphate reductase	3.1.35 3.5.41 3.5.413 3.6.123/3.6.119 2.4.21 2.7.49 13.98.1 2.1.32 2.4.210 3.5.23 4.1.123 6.3.42 2.7.422 3.5.22 3.5.41 3.5.23 4.1.134 6.3.42 2.7.422 3.5.23	KOX_01045(surE)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surE)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surE)/KOX_10270/KOX_13075(ushA)/ KOX_04555(kOX_14050) KOX_04555(kOX_14050) KOX_15240(dect) KOX_15240(dect) KOX_151315(mik) KOX_16135 KOX_09285/KOX_09290(pyr8) KOX_05985 KOX_09285/KOX_09290(pyr8) KOX_05985 KOX_09185/KOX_17195 KOX_18140 KOX_01145(pyr6) KOX_11445(pyr6) KOX_11445(pyr6) KOX_01455(pyr14) KOX_023270 KOX_04555(KOX_14050) KOX_023250	tmp >> pi + thymd  ttmp >> pi + thymd  ttmp >> pi + thymd  ttmp >> dutp + nh4  ttp >> dutp + nh4  ttp >> dutp + nh4  dutp >> dump + ppi  du + pi <>> dr1p + ura  atp + dump <>> adp + dudp  doroa + fum <>> oroa + succ  asp + cap >> casp + pi  omp + ppi <>> oroa + prpp  doroa <>> casp + up  somp >> co2 + ump  atp + ump <>> adp + udp  somp >> co2 + ump  somp >> co2 + ump  somp >> co3 + ump  som <>> sucp >>
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROAD ASPCBT OROPRT DHORT OMPDC CTPS URIDK2 DHPM CYTDA DHPMD URIK CYTDA	Pyrimidine metabolism	5-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase uridylate kinase (dUMP) dihydroorotate dehydrogenase (tumarate) asparlate carbamoyltransferase orotate phosphoribosyltransferase dihydroorotase cortotate phosphoribosyltransferase orotidine-5'-phosphate decarbosylsae CTP synthase (glylutamine) uridylate kinase dihydropyrimidinase cytosine deaminase dihydropyrimidinase uridine kinase (GTP) cytdine kinase (GTP)	31.35 3.5.41 3.5.413 3.5.413 3.6.123/3.6.119 2.4.21 2.7.49 13.981 2.1.32 2.4.210 3.5.23 4.1.123 6.3.42 2.7.422 3.5.22 3.5.24 3.5.21 3.5.21 3.5.21 3.5.21 3.5.22 2.7.422 3.5.22 2.7.438	KOX_01045(surla)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surla)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surla)/KOX_10270/KOX_13075(ushA)/ KOX_04555(xOX_14050) KOX_15240(dcd) KOX_15240(dcd) KOX_15240(dcd) KOX_15240(dcd) KOX_15245(dcd) KOX_15245(dcd) KOX_15245(dcd) KOX_15245(dcd) KOX_15245(dcd) KOX_16135 KOX_09285/KOX_09290(pyrla) KOX_05965 KOX_05965 KOX_05965 KOX_05965 KOX_05965 KOX_05965 KOX_05965 KOX_11455(pyrl) KOX_11455(pyrl) KOX_11455(pyrl) KOX_11455(pyrl) KOX_12270 KOX_04555(KOX_14050) KOX_15245 KOX_05245 KOX_15245	dmp >> pi+ thymd  ct >= nh4 + ura  dcp >> dutp + nh4  ct >> th4 + ura  dcp >> dutp + nh4  dutp >> dump + ppi  du+ pi <> dr2p + ura  atp + dump <>> adp + dudp  doraa + fum <>> oraa + succ  asp + cap >> caasp + pi  omp + ppi <>> oraa + prp  doraa <>> caasp + cap >> caap  omp >> ca2 + ump  atp + gin + utp >> adp + ctp + glu + pi  atp + ump <>> adp + utp  Sishu <>> 3urdpp  Smc <>> thym + nh4  Sishu <>> such yet + pi  syd + ump  cyd + gtp >= vmp + ydp
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROAD ASPCBT OROPRT DHORT OMPDC CTPS URIDK2 DIFIPM CYTDA DIFIPM CYTDA DIFIPM CYTDA RNTPR3 RNTPR4	Pyrimidine metabolism	5'-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase uridylate kinase (dUMP) dihydroorotate dehydrogenase (tumarate) asparlate carbamoyltransferase orotate phosphoribosyltransferase dihydroorotase corotate phosphoribosyltransferase dihydroorotase dihydroorotase corotidase phosphoribosyltransferase orotidase phosphoribosyltransferase orotidine-5'-phosphate decarbosylase CTP synthase (glutamine) uridylate kinase dihydropyrimidinase cytosine deaminase dihydropyrimidinase uridine kinase (GTP) rytidnie kinase (GTP) ribonucleoside-triphosphate reductase	3.1.35 3.5.41 3.5.413 3.5.413 3.6.123/3.6.119 2.4.2.1 2.7.4.9 1.3.98.1 2.1.3.2 2.4.2.10 3.5.2.3 4.1.1.2.3 6.3.4.2 2.7.4.2.2 3.5.2.2 3.5.4.1 3.5.2.2 2.7.4.2.2 3.5.2.1 3.5.4.1 3.5.2.2 2.7.1.4.8 2.7.1.4.8 1.17.4.2	KOX_01045(surla/KOX_10270/KOX_13075(ushA)/ KOX_01045(surla/KOX_10270/KOX_13075(ushA)/ KOX_01045(surla/KOX_10270/KOX_13075(ushA)/ KOX_0455(kox_10405) KOX_0455(kox_10405) KOX_0455(kox_10405) KOX_0455(kox_10405) KOX_10320(deb0) KOX_17315(tmk) KOX_16135 KOX_09285/KOX_09290(pyr8) KOX_05965 KOX_05965 KOX_09185/KOX_17195 KOX_018440 KOX_01145(pyr0) KOX_11445(pyr0) KOX_01145(pyr0) KOX_0145(pyr0) KOX_02570 KOX_04555(KOX_14050) KOX_059230 KOX_09230	dmp >> pi+ thymd  ct >> nN4 + ura  dctp >> dutp + nN4  ct >> tutp + nN4  dutp >> dutp + nN4  dutp >> dump + ppi  du+ pi <> dr1p + ura  atp + dump <>> adp + dudp  doroa + fum <>> oroa + succ  asp + dap >> casp + pi  omp + ppi <> oroa + prpp  doroa <>> casp + ap >> casp + pi  omp + ppi <> oroa + prpp  doroa <>> casp + ap >> casp + pi  som + up <>> adp + utp >> adp + ctp + glu + pi  atp + uff <>> adp + utp >> adp + utp  Schlu <>> 3urdpp  Schu <>> 3urdpp  Smc <>> thym + nN4  Schlt <>> 3udb  gt + uff >> adp + utp  opt + glp + uff >> adp + utp  opt + glp + uff >> adp + utp  opt + glp + uff >> adp + utp  opt + glp + uff >> adp + utp  opt + glp + uff >> adp + utp  opt + glp + oros + glp + utp  opt + uff >> adp + utp  opt + glp + oros + glp + utp  opt + glp + oros + glp + utp  opt + glp + oros + glp + utp  opt + glp + oros + glp + utp  opt + glp + utp + oros + glp + utp  opt + utp + vtp + oros + glp + utp  opt + utp + vtp + utp  opt + vtp + vtp + vtp + vtp + vtp + vtp  opt + vtp
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROAD ASPCBT OROPRT DHORT OMPDC CTPS URIDK2 DIFINA URIDK2 DIFINA CYTDA DIFINA DIFINA CYTDA DIFINA CYTDA RNTPR3	Pyrimidine metabolism	5'-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase indigate kinase (dIMP) dihydroorotate dehydrogenase (tumarate) aspartate carbamoyltransferase orotate phosphoribosyltransferase dihydroorotate corotate phosphoribosyltransferase dihydroorotate corotate phosphoribosyltransferase dihydroorotate corotidine-5'-phosphate decarbosylase CTP synthase (glutamine) uridylate kinase dihydropyrimidinase uridine kinase (GTP) rytdine kinase (GTP) rytdine kinase (GTP) ribonucleoside-triphosphate reductase ribonucleoside-triphosphate reductase Uridine triphosphate pyrophosphoyldrolase	3.1.35 3.5.41 3.5.413 3.5.413 3.6.123/3.6.119 2.4.2.1 2.7.4.9 1.3.98.1 2.1.3.2 2.4.2.1.0 3.5.2.3 4.1.1.2.3 6.3.4.2 2.7.4.2.2 3.5.2.2 3.5.4.1 3.5.2.2 2.7.1.4.8 1.7.1.4.8 1.7.1.4.8	KOX_01045(surla)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surla)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surla)/KOX_10270/KOX_13075(ushA)/ KOX_04555(xOX_14050) KOX_05240(dech) KOX_052540(dech) KOX_15340(dech) KOX_15340(dech) KOX_15315(tmk) KOX_16135 KOX_05285/KOX_09290(pyrla) KOX_05965 KOX_05985/KOX_079290(pyrla) KOX_18440 KOX_01145(pyrla) KOX_0145(pyrla) KOX_0145(pyrla) KOX_0145(pyrla) KOX_0455(syKOX_14050) KOX_05220 KOX_05220	dmp >> pi+ thymd  ct >= nh4 + ura  dcp >> dup+ nh4  ct >> th4 + ura  dcp >> dup+ nh4  dup >> dump+ ppi  du+ pi<>> dr2p+ ura  atp + dump <>> adp+ dudp  doroa + fum <>> oroa + succ  asp + cap >> casp >> pi  omp+ ppi <>> oroa + prpp  doroa <>> casp >> cap >> cap >> cap >> tp  omp + ppi <>> oroa + prpp  doroa <>> casp >> cap >> cap >> tp  omp <> co2 + ump  atp + gin + up >> adp + ctp + glu + pi  atp + ump <>> adp + ump  steful <>> succ  sin + ump <>> adp + ump  steful <>> succ  sin + ump <>> up  sin + up
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROAD ASPCBT OROPRT DHORT OMPDC CTPS URIDK2 DIFIPM CYTDA DIFIPM CYTDA DIFIPM CYTDA RNTPR3 RNTPR4	Pyrimidine metabolism	5-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphonylase uridylate kinase (dUMP) dihydroorotate dehydrogenase (tumarate) aspartate carbamoyltransferase orotate phosphoribosyltransferase dihydroorotase corotate phosphoribosyltransferase dihydroorotase corotate phosphoribosyltransferase orotidine-5'-phosphate decarboxylsae dihydrooryimidinase dihydropyrimidinase dihydropyrimidinase uridine kinase (GTP) cytdine kinase (GTP) cy	3.1.35 3.5.41 3.5.413 3.5.413 3.6.123/3.6.119 2.4.2.1 2.7.4.9 1.3.98.1 2.1.3.2 2.4.2.10 3.5.2.3 4.1.1.2.3 6.3.4.2 2.7.4.2.2 3.5.2.2 3.5.4.1 3.5.2.2 2.7.4.2.2 3.5.2.1 3.5.4.1 3.5.2.2 2.7.1.4.8 2.7.1.4.8 1.17.4.2	KOX_01045(surla/KOX_10270/KOX_13075(ushA)/ KOX_01045(surla/KOX_10270/KOX_13075(ushA)/ KOX_01045(surla/KOX_10270/KOX_13075(ushA)/ KOX_0455(kox_10405) KOX_0455(kox_10405) KOX_0455(kox_10405) KOX_0455(kox_10405) KOX_10320(deb0) KOX_17315(tmk) KOX_16135 KOX_09285/KOX_09290(pyr8) KOX_05965 KOX_05965 KOX_09185/KOX_17195 KOX_018440 KOX_01145(pyr0) KOX_11445(pyr0) KOX_01145(pyr0) KOX_0145(pyr0) KOX_02570 KOX_04555(KOX_14050) KOX_059230 KOX_09230	dmp >> pi+ thymd  ct >> nN4 + ura  dctp >> dutp + nN4  ct >> tutp + nN4  dutp >> dutp + nN4  dutp >> dump + ppi  du+ pi <> dr1p + ura  atp + dump <>> adp + dudp  doroa + fum <>> oroa + succ  asp + dap >> casp + pi  omp + ppi <> oroa + prpp  doroa <>> casp + ap >> casp + pi  omp + ppi <> oroa + prpp  doroa <>> casp + ap >> casp + pi  som + up <>> adp + utp >> adp + ctp + glu + pi  atp + uff <>> adp + utp >> adp + utp  Schlu <>> 3urdpp  Schu <>> 3urdpp  Smc <>> thym + nN4  Schlt <>> 3udb  gt + uff >> adp + utp  opt + glp + uff >> adp + utp  opt + glp + uff >> adp + utp  opt + glp + uff >> adp + utp  opt + glp + uff >> adp + utp  opt + glp + uff >> adp + utp  opt + glp + oros + glp + utp  opt + uff >> adp + utp  opt + glp + oros + glp + utp  opt + glp + oros + glp + utp  opt + glp + oros + glp + utp  opt + glp + oros + glp + utp  opt + glp + utp + oros + glp + utp  opt + utp + vtp + oros + glp + utp  opt + utp + vtp + utp  opt + vtp + vtp + vtp + vtp + vtp + vtp  opt + vtp
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROAD ASPCBT OROPRT DHORT OMPDC CTPS URIDK2 DIPM CYTDA DIPM CYTDA DIPMM CYTDA DIPMM CYTDA RNTPR3 RNTPR4 URITPP	Pyrimidine metabolism	S'-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase individual kinase (dIMP) dilydrocrotate dehydrogenase (tumarate) aspartate carbamoyltransferase orotate phosphoribosyltransferase dilydrocrotase corotate phosphoribosyltransferase dilydrocrotase corotidine-5'-phosphate decarbosylase CTP synthase (glutamine) uridylate kinase dilydropyrimidinase dilydropyrimidinase dilydropyrimidinase uridine kinase (GTP) cytotine kinase dilydropyrimidinase uridine byrophosphoridinase dilydropyrimidinase dilydropyrimidinase uridine byrophosphoridinase dilydropyrimidinase dilydropyrimidi	3.1.3.5 3.5.4.1 3.5.4.13 3.5.4.13 3.5.4.13 3.6.1.23/3.6.1.19 2.4.2.1 2.7.4.9 1.3.98.1 2.1.3.2 2.4.2.1.0 3.5.2.2 3.5.2.2 3.5.2.2 3.5.4.1 3.5.2.2 2.7.4.2.2 3.5.2.1 3.5.4.1 3.5.2.2 2.7.1.4.8 1.7.7.4.2 1.7.7.4.2 3.6.1.19	KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_0455(kox_0210)/KOX_10270/KOX_13075(ushA)/ KOX_0455(kox_0210)/KOX_10270(kox_0210)/KOX_10230(deat)/ KOX_10230(deat)/KOX_102715 KOX_10230(deat)/KOX_102715 KOX_0450(deat)/KOX_102715 KOX_0450(deat)/KOX_102715 KOX_0450(deat)/KOX_102715 KOX_05965 KOX_05966 KOX_05966 KOX_05966 KOX_05966 KOX_05966	dmp >> pi+ thymd  ct >> nN4 + ura  dctp >> dutp + nN4  ct >> nN4 + ura  dctp >> dutp + nN4  dutp >> dutp + nN4  dutp >> dump + ppi  du + pi <> drlp + ura  atp + dump <>> adp + dudp  doroa + fum <>> oroa + succ  asp + cap >> casp + pi  omp + ppi <>> oroa + prpp  doroa <>> casp + cap >> casp + pi  omp + ppi <>> oroa + prpp  doroa <>> casp >> adp + utp  atp + gin + utp >> adp + ctp + glu + pi  atp + utp <>> adp + utp  Sidhu <>> 3urdpp  Sidhu <>> 3urdpp  Sidhu <>> 3urdpp  Sidhu <>> 3urdpp  ste <>> the <>> the <>> the <>> the <>> the >y oth  sidh + utp <>> adp + utp  cyt + cytho >> dutp + oth  sidh + cytho >> dutp + oth  cyth + vin >> adp + utp  cyth + utp >> dutp + oth  sidh + cytho >> comp + gdb  ctp + rth >> dutp + oth  utp >> thu + oth  u
NUTDS CTDA DCTPPA1 DCTPPA2 DUTPOP PUNPP8 URIDK1 DOROAD ASPCBT OROPRT DHORT OMPDC CTPS URIDK2 DHPMD URIDK2 DHPMD URIK CVTDK RNTPR3 RNTPR4 URITPP	Pyrimidine metabolism	5-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphonylase uridylate kinase (dUMP) dihydroorotate dehydrogenase (tumarate) aspartate carbamoyltransferase orotate phosphoribosyltransferase dihydroorotase corotate phosphoribosyltransferase dihydroorotase corotate phosphoribosyltransferase orotidine-5'-phosphate decarboxylsae dihydrooryimidinase dihydropyrimidinase dihydropyrimidinase uridine kinase (GTP) cytdine kinase (GTP) cy	3.1.3.5 3.5.4.1 3.5.4.13 3.5.4.13 3.5.4.13 3.6.1.23/3.6.1.19 2.4.2.1 2.7.4.9 1.3.98.1 2.1.3.2 2.4.2.10 3.5.2.3 4.1.1.2.3 6.3.4.2 2.7.4.2.2 3.5.2.1 3.5.2.2 3.5.4.1 3.5.2.2 2.7.1.4.8 1.7.7.4.2 1.7.7.4.2 3.6.1.1.9 3.6.1.1.9	KOX_01045(surla/KOX_10270/KOX_13075(ushA)/ KOX_01045(surla/KOX_10270/KOX_13075(ushA)/ KOX_01045(surla/KOX_10270/KOX_13075(ushA)/ KOX_04555(kOX_14050) KOX_04555(kOX_14050) KOX_15240(sich) KOX_16135 KOX_05965 KOX_05965 KOX_05965 KOX_05965 KOX_05965 KOX_05965 KOX_11455(siph) KOX_01145(siph) KOX_01145(siph) KOX_01145(siph) KOX_01145(siph) KOX_01145(siph) KOX_01245(siph) KOX_02520 KOX_25245 KOX_25245 KOX_25245 KOX_05230 KOX_02715 KOX_02715	dmp >> pi + thymd  ct >= nh4 + ura  dctp >> dutp + nh4  ct >> nh4 + ura  dctp >> dutp + nh4  dutp >> dump + ppi  du + pi <> drtp + ura  atp + dump + ppi  dorna + fum <<> orna + pup  dorna + fum <<> orna + pup  dorna + fum <<> orna + pup  dorna + fum <>> orna + pup  dorna <> casp > casp + pi  omp + pi <<> orna + prpp  dorna <>> casp + udp  stb + utp >> adp + udp  stb + utp >> adp + udp  stb + utp >> dutp  stb + utp >> dutp + utp  stb + utp + utp  stb + utp + utp  stb + utp + utp + utp + utp  stb + utp + utp + utp + utp  stb + utp + u
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROADD ASPCBT OMPDC CTPS URIDK2 DHPM CYTDA DHPMD URIK CYTDA DHPMD URIK CYTDK RNTPR3 RNTPR4 URITPP CYTDDA1	Pyrimidine metabolism	5-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase uridylate kinase (dUMP) dihydroorotate dehydrogenase (tumarate) aspartate carbamoyltransferase orotate phosphoribosyltransferase dihydroorotase orotate phosphoribosyltransferase dihydroorotase curidine-5'-phosphate decarbosylase CTP synthase (glytutamine) uridylate kinase dihydropyrimidinase ctytosine deaminase dihydropyrimidinase uridine kinase (GTP) cytdine kinase dihydropyrimidinase uridine kinase cytosine deaminase cytotine deaminase cytidine deaminase cytidine deaminase cytidine deaminase cytidine deaminase cytidine deaminase cytidine deaminase	3.1.35 3.5.41 3.5.413 3.5.413 3.6.123/3.6.119 2.4.21 2.7.49 1.3.98.1 2.1.32 2.4.210 3.5.23 4.1.123 6.3.42 2.7.422 3.5.22 3.5.41 3.5.22 2.7.422 3.5.22 3.5.41 3.5.23 4.1.17.42 3.6.119 3.6.119 3.6.119	KOX_01045(surl)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surl)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surl)/KOX_10270/KOX_13075(ushA)/ KOX_04555/KOX_14050 KOX_05955(kurl)/KOX_02715 KOX_10320(deat) KOX_15135(mk) KOX_16135 KOX_05955(kurl)/KOX_09290(pyr8) KOX_05955(kurl)/KOX_09290(pyr8) KOX_05956(kurl)/KOX_09290(pyr8) KOX_05965 KOX_059715 KOX_02715 KOX_059715	dmp >> pi+ thymd  ct >> nM+ wra  dctp >> dutp + nM4  ct >> nM+ wra  dctp >> dutp + nM4  dutp >> dutp + nM4  dutp >> dump + ppi  du+ pi <> drlp + ura  atp + dump <>> adp + dudp  doroa + fum <>> oroa + succ  asp + dap >> casp + pi  omp + ppi <>> oroa + prpp  doroa <>> casp + pi  omp + ppi <>> oroa + prpp  doroa <>> casp >> adp + utp  atp + gin + utp >> adp + ctp + glu + pi  atp + utp <>> adp + utp  Scidiu <>> 3urdpp  Smc <>> thym + nM4  Scidit <>> 3udp  tp + uti >> adp + utp  cyt + glp + uti >> adp + utp  cyt + glp + oroa + prp  ddt > glp + utp >> dutp + otp  ddt + gtp >> cmp + gdp  ctp + rthio >> dutp + othio  utp + rthio >> dutp + othio  utp >> ump + ppi  dttp >> dutp >> ump + ppi  dttp >> dutp + pi  dttp >> dutp + nM4  dc -> du + nM4  dc -> du + nM4
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROAD ASPCBT OMPDC CTPS URIDK2 DHPMC CYTDA DHPMC VYTDA DHPMD URIK CYTDA DHPMD CYTDAA URITPP	Pyrimidine metabolism	5'-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase indylate kinase (dUMP) dilydrocrotate dehydrogenase (tumarate) aspartate carbamoyltransferase orotate phosphoribosyltransferase drilydrocrotate corotate phosphoribosyltransferase drilydrocrotase corotate phosphoribosyltransferase drilydrocrotase corotidine-5'-phosphate decarboxylase dilydropyrimidinase dilydropyrimidinase dilydropyrimidinase dilydropyrimidinase dilydropyrimidinase unificate kinase (GTP) cytidine kinase (GTP) prophosphorydrolase Deoxythymidine triphosphate prophosphorydrolase Deoxythymidine triphosphate prychosphophydrolase cytidine deaminase cytidine deaminase 2,3'-cyclic-nucleotide 2'- phosphodiesterase	3.1.3.5 3.5.4.1 3.5.4.1 3.5.4.1 3.5.4.1 3.6.1.2.3.6.1.19 2.4.2.1 2.7.4.9 1.3.98.1 2.1.3.2 2.4.2.10 3.5.2.3 4.1.1.2.3 6.3.4.2 2.7.4.2.2 3.5.2.2 3.5.4.1 3.5.2.2 2.7.4.2.2 3.5.4.1 3.5.2.2 2.7.1.4.8 2.7.1.4.8 1.17.4.2 3.6.1.1.9 3.6.1.1.9 3.6.1.1.9 3.6.1.1.9 3.6.1.1.9 3.6.1.1.9 3.6.1.1.9	KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_04555(kOX_14050) KOX_04555(kOX_14050) KOX_15240(dect) KOX_1533(dect) KOX_17315(mik) KOX_16135 KOX_05965 KOX_09285/KOX_09290(pyr8) KOX_01832(dect) KOX_17315(mik) KOX_16145(pyr6) KOX_018440 KOX_01145(pyr6) KOX_01445(pyr6) KOX_01455(pyr1) KOX_22700 KOX_05965 KOX_05975 KOX_05975 KOX_05975 KOX_05975 KOX_05975 KOX_05775 KOX_05775 KOX_05975 KOX_05975 KOX_05930 KOX_05775 KOX_05930(cpd8)	dmp >> pi+ thymd  ct >> nM+ +ura  dctp >> dutp + nM4  ct >> nM+ +ura  dctp >> dutp + nM4  ct >> dump + ppi  du+ pi <> dr1p + ura  atp + dump <>> adp + dudp  doroa + fum <>> oroa + succ  asp + cap >> casp + pi  omp + ppi <>> oroa + prpp  doroa <>> casp + pi  omp + ppi <>> oroa + prpp  doroa <>> casp >> adp + utp  atp + dim <>> oroa + prpp  doroa <>> casp >> oroa + prpp  doroa <>> casp + oroa + prpp  doroa <>> casp >> oroa + prpp  doroa <>> cap >> oroa + prpp  doroa <>> oroa + prpp  doroa <>> cap >> oroa + prpp  doroa <>> oroa +
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROAD ASPCBT OROPRT DHORT OMPDC CTPS URIDK2 DHPM CYTDA DHPMD URIK CYTDA DHPMD URIK CYTDA DHPMD URIK CYTDA URITPP DTTPP DTTPP CYTDDA1 CYTDDA1	Pyrimidine metabolism	5-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase uridylate kinase (dUMP) dihydroorotate dehydrogenase (tumarate) aspartate carbamoyltransferase orotate phosphoribosyltransferase dihydroorotase orotate phosphoribosyltransferase dihydroorotase curidine-5'-phosphate decarbosylase CTP synthase (glytutamine) uridylate kinase dihydropyrimidinase ctytosine deaminase dihydropyrimidinase uridine kinase (GTP) cytdine kinase dihydropyrimidinase uridine kinase cytosine deaminase cytotine deaminase cytidine deaminase cytidine deaminase cytidine deaminase cytidine deaminase cytidine deaminase cytidine deaminase	3.1.35 3.5.41 3.5.413 3.5.413 3.5.413 3.6.123/3.6.119 2.4.2.1 2.7.4.9 13.98.1 2.1.32 2.4.2.10 3.5.2.3 4.1.1.23 6.3.4.2 2.7.4.2 2.7.4.2 3.5.2.2 3.5.4.1 3.5.2.2 2.7.1.4.8 2.7.1.4.8 1.17.4.2 3.6.1.19 3.6.1.19 3.6.1.19 3.6.1.19 3.6.1.19	KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_04555(kOX_14050) KOX_04555(kOX_14050) KOX_15340(scd) KOX_1533(sde) KOX_17315(mik) KOX_16135 KOX_05965 KOX_09285/KOX_09290(pyr8) KOX_17315(mik) KOX_16135 KOX_05965 KOX_05965 KOX_05965 KOX_05965 KOX_05965 KOX_05965 KOX_05965 KOX_05965 KOX_05965 KOX_14545(pyr6) KOX_01145(pyr6) KOX_01145(pyr6) KOX_01145(pyr6) KOX_1455(pyr4) KOX_02370 KOX_05955 KOX_05930 KOX_05930 KOX_05930 KOX_07715 KOX_07715 KOX_07715 KOX_07715 KOX_07715 KOX_07715	dmp >> pi+ thymd  ct >> nM+ wra  dctp >> dutp + nM4  ct >> nM+ wra  dctp >> dutp + nM4  dutp >> dutp + nM4  dutp >> dump + ppi  du+ pi <> drlp + ura  atp + dump <>> adp + dudp  doroa + fum <>> oroa + succ  asp + dap >> casp + pi  omp + ppi <>> oroa + prpp  doroa <>> casp + pi  omp + ppi <>> oroa + prpp  doroa <>> casp >> adp + utp  atp + gin + utp >> adp + ctp + glu + pi  atp + utp <>> adp + utp  Scidiu <>> 3urdpp  Smc <>> thym + nM4  Scidit <>> 3udp  tp + uti >> adp + utp  cyt + glp + uti >> adp + utp  cyt + glp + oroa + prp  ddt > glp + utp >> dutp + otp  ddt + gtp >> cmp + gdp  ctp + rthio >> dutp + othio  utp + rthio >> dutp + othio  utp >> ump + ppi  dttp >> dutp >> ump + ppi  dttp >> dutp + pi  dttp >> dutp + nM4  dc -> du + nM4  dc -> du + nM4
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROAD ASPCBT OMPDC CTPS URIDK2 DHPMC CYTDA DHPMC VYTDA DHPMD URIK CYTDA DHPMD CYTDAA URITPP	Pyrimidine metabolism	5-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase uridylate kinase (dUMP) dihydroorotate dehydrogenase (tumarate) aspartate carbamoyltransferase orotate phosphoribosyltransferase dihydroorotase cortotate phosphoribosyltransferase dihydroorotase cortotate phosphoribosyltransferase orotidine-5'-phosphate decarbosylase CTP synthase (glytuamine) uridylate kinase dihydropyrimidinase ctytosine deaminase dihydropyrimidinase uridine kinase (GTP) cytdine kinase (Josephosphorydrolase prophosphorydrolase prophosphorydrolase cytdine deaminase cyt	3.1.3.5 3.5.4.1 3.5.4.1 3.5.4.1 3.5.4.1 3.6.1.2.3.6.1.19 2.4.2.1 2.7.4.9 1.3.98.1 2.1.3.2 2.4.2.10 3.5.2.3 4.1.1.2.3 6.3.4.2 2.7.4.2.2 3.5.2.2 3.5.4.1 3.5.2.2 2.7.4.2.2 3.5.4.1 3.5.2.2 2.7.1.4.8 2.7.1.4.8 1.17.4.2 3.6.1.1.9 3.6.1.1.9 3.6.1.1.9 3.6.1.1.9 3.6.1.1.9 3.6.1.1.9 3.6.1.1.9	KOX, 01045(surla)/KOX, 10.270/KOX, 13.075(ushA)/ KOX, 26410 KOX, 26410 KOX, 01045(surla)/KOX, 10.270/KOX, 13.075(ushA)/ KOX, 26450 KOX, 26450 KOX, 26450 KOX, 25440(scd.) KOX, 25240(scd.) KOX, 10.1323(sed.) KOX, 10.1323(sed.) KOX, 11.315(mik) KOX, 16.135 KOX, 09285/KOX, 09290(pyr8) KOX, 10.91285/KOX, 09290(pyr8) KOX, 10.91285/KOX, 17.195 KOX, 18440 KOX, 01145(pyr6) KOX, 11445(pyr6) KOX, 1145(pyr6) KOX, 1145(pyr6	dmp >> pi+ thymd  ct >> nN4 + ura  dctp >> dutp + nN4  ct >> nN4 + ura  dctp >> dutp + nN4  dutp >> dutp + nN4  dutp >> dump + ppi  du + pi <> drlp + ura  atp + dump <>> adp + dudp  doroa + fum <>> oroa + succ  asp + dap >> casp + pi  omp + ppi <>> oroa + prpp  doroa <>> casp + ap >> casp + pi  omp + ppi <>> oroa + prpp  doroa <>> casp >> adp + utp  atp + gin + utp >> adp + ctp + glu + pi  atp + utp <>> adp + utp  Schlu <>> 3urdpp  Smc <>> thym + nN4  Schlu <>> 3urdpp  pt + uti >> adp + utp  cytd + gtp >> cmp + gdp  ctp + rhio >> ddp + ottp + ottio  utp + rhio >> dutp + othio  utp + utip >> utp + othio  utp >> ump + ppi  dttp >> utp + ppi  dttp >> utp + ppi  dttp >> dutp + othio  utp >> ump + ppi  dttp >> dutp + othio  dtp >> dutp + othio  dtp >> dutp + othio  23ccmp >> 3cmp  23ccmp >> 3cmp
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROAD ASPCBT OROPRT DHORT OMPDC CTPS URIDK2 DHHM CYTDA DHHM CYTDA RNTPR3 RNTPR4 URITPP DTTPP CYTDDA1 CYTDDA1 CYTDDA1 CYTDDA2 23CNPDE4 DURIDK	Pyrimidine metabolism	5'-nucleotidase (dTMP) Cytosine deaminase dCIP deaminase dCIP deaminase dUTP diphosphatase purine nucleoside phosphorylase uridylate kinase (dIMP) dilydroorotate dehydrogenase (tumarate) aspartate carbamoyltransferase orotate phosphoribosyltransferase dilydroorotase corotate phosphoribosyltransferase dilydroorotase corotate phosphoribosyltransferase dilydroorotase corotidine-5'-phosphate decarbooylase CTP synthase (glutamine) uridylate kinase dilydropyrimidinase utidhe kinase dilydropyrimidinase utidhe kinase (GTP) cytidine kinase (Uridine triphosphate prophosphoribydrolase Deoxyltymidine triphosphate prophosphoribydrolase Deoxyltymidine deaminase 2,3'-cyclic-nucleotide 2'- phosphodiesterase 2,3'-cyclic-nucleotide 2'- phosphodiesterase deoxyuridine kinase (ATP-Deoxyuridine)	3.1.3.5 3.5.4.1 3.5.4.1 3.5.4.1 3.5.4.1 3.5.4.1 3.6.1.2.3/3.6.1.19 2.4.2.1 2.7.4.9 1.3.98.1 2.1.3.2 2.4.2.10 3.5.2.3 4.1.1.2.3 6.3.4.2 2.7.4.2 2.7.4.2 3.5.2.2 3.5.2.1 3.5.4.1 3.5.2.2 2.7.1.4.8 2.7.1.4.8 2.7.1.4.8 2.7.1.4.9 3.6.1.1.9 3.6	KOX, 01045(surla)/KOX, 10.270/KOX, 13.075(ushA)/ KOX, 26410 KOX, 26410 KOX, 01045(surla)/KOX, 10.270/KOX, 13.075(ushA)/ KOX, 26450 KOX, 26450 KOX, 26450 KOX, 26450 KOX, 25240(dech KOX, 25240(dech KOX, 13.15(mh) KOX, 16135 KOX, 10320(dech) KOX, 17315(mh) KOX, 16135 KOX, 09285/KOX, 09290(pyr8) KOX, 09885/KOX, 09290(pyr8) KOX, 09185/KOX, 17195 KOX, 18440 KOX, 01145(pyr6) KOX, 11445(pyr6) KOX, 11455(pyr6) KOX, 11455(pyr6) KOX, 123270 KOX, 123270 KOX, 12455(pyr6) KOX, 25245 KOX, 25245 KOX, 25245 KOX, 25245 KOX, 25215 KOX, 25215 KOX, 25715 KOX, 25715 KOX, 25715 KOX, 26930(pyr8) KOX, 26930(pyr8) KOX, 25715 KOX, 26930(pyr8) KOX, 25715 KOX, 26930(pyr8) KOX, 26930(pyr8) KOX, 26930(pyr8) KOX, 25715 KOX, 26930(pyr8) KOX, 2	dmp >> pi+ thymd  ct >> nN4 + ura  dctp >> dutp + nN4  ct >> nN4 + ura  dctp >> dutp + nN4  dutp >> dutp + nN4  dutp >> dump + ppi  du + pi <> drlp + ura  atp + dump <>> adp + dudp  doroa + fum <>> oroa + succ  asp + dap >> casp + pi  omp + ppi <>> oroa + prpp  doroa <>> casp + pi  omp + ppi <>> oroa + prpp  doroa <>> casp + adp + ctp + glu + pi  atp + urb <> adp + utp >> adp + utp  \$56dhu <>> 3urdpp  \$56mu <>> 3urdpp <>> 3urdpp  \$56mu <>> 3urdpp <>> 3urdpp  \$56mu <>> 3urdpp <>> 3urdpp   \$50mu <>> 3urdpp <>> 3urdpp   \$50mu <>> 3urdpp <>> 3urdpp   \$50mu <>> 3urdpu <>> 3urdpu   \$50mu <>> 3urdpu
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROAD ASPCBT OMPDC CTPS URIDK2 DHORT OMPDC CTPS URIDK2 DHPM CYTDA DHPMD URIK CYTDA DHPMD URIK CYTDK RNTPR3 RNTPR4 URITPP DTTPP CYTDDA1 CYTDDA1 CYTDDA1 CYTDDA2 23CNPDE4	Pyrimidine metabolism	5-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase uridylate kinase (dUMP) dihydroorotate dehydrogenase (tumarate) aspartate carbamoyltransferase orotate phosphoribosyltransferase dihydroorotase cortotate phosphoribosyltransferase dihydroorotase cortotate phosphoribosyltransferase orotidine-5'-phosphate decarbosylase CTP synthase (glytuamine) uridylate kinase dihydropyrimidinase ctytosine deaminase dihydropyrimidinase uridine kinase (GTP) cytdine kinase (Josephosphorydrolase prophosphorydrolase prophosphorydrolase cytdine deaminase cyt	3.1.3.5 3.5.4.1 3.5.4.1 3.5.4.1 3.5.4.1 3.6.1.2.3/3.6.1.19 2.4.2.1 2.7.4.9 13.98.1 2.1.3.2 2.4.2.10 3.5.2.3 4.1.1.2.3 6.3.4.2 2.7.4.2.2 3.5.2.2 3.5.4.1 3.5.2.2 2.7.4.2.2 3.5.4.1 3.5.2.2 2.7.4.2.2 3.6.1.1.9	KOX, 01045(surla)/KOX, 10.270/KOX, 13.075(ushA)/ KOX, 26410 KOX, 26410 KOX, 01045(surla)/KOX, 10.270/KOX, 13.075(ushA)/ KOX, 26450 KOX, 26450 KOX, 26450 KOX, 25440(scd.) KOX, 25240(scd.) KOX, 10.1323(sed.) KOX, 10.1323(sed.) KOX, 11.315(mik) KOX, 16.135 KOX, 09285/KOX, 09290(pyr8) KOX, 10.91285/KOX, 09290(pyr8) KOX, 10.91285/KOX, 17.195 KOX, 18440 KOX, 01145(pyr6) KOX, 11445(pyr6) KOX, 1145(pyr6) KOX, 1145(pyr6	dmp >> pi+ thymd  ct >> nN4 + ura  dctp >> dutp + nN4  ct >> nN4 + ura  dctp >> dutp + nN4  dutp >> dutp + nN4  dutp >> dump + ppi  du + pi <> drlp + ura  atp + dump <>> adp + dudp  doroa + fum <>> oroa + succ  asp + dap >> casp + pi  omp + ppi <>> oroa + prpp  doroa <>> casp + ap >> casp + pi  omp + ppi <>> oroa + prpp  doroa <>> casp >> adp + utp  atp + gin + utp >> adp + ctp + glu + pi  atp + utp <>> adp + utp  Schlu <>> 3urdpp  Smc <>> thym + nN4  Schlu <>> 3urdpp  pt + uti >> adp + utp  cytd + gtp >> cmp + gdp  ctp + rhio >> ddp + ottp + ottio  utp + rhio >> dutp + othio  utp + utip >> utp + othio  utp >> ump + ppi  dttp >> utp + ppi  dttp >> utp + ppi  dttp >> dutp + othio  utp >> ump + ppi  dttp >> dutp + othio  dtp >> dutp + othio  dtp >> dutp + othio  23ccmp >> 3cmp  23ccmp >> 3cmp
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROAD ASPCBT OMOPDC CTPS URIDK2 DHORT OMPDC CTPS URIDK2 DHPM CYTDA DHPMC URIK CYTDA DHPMD URIK CYTDK RNTPR3 RNTPR4 URITPP DTTPP CYTDDA1 CYTDDA2 23CNPDE3 23CNPDE4 DURIDK URIPP	Pyrimidine metabolism	5-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase uridylate kinase (dUMP) dihydroorotate dehydrogenase (tumarate) aspartate carbamoyltransferase orotate phosphoribosyltransferase dihydroorotase cortotate phosphoribosyltransferase dihydroorotase curidine-5'-phosphate decarbosylase CTP synthase (glottamine) uridylate kinase dihydropyrimidinase ctytosine deaminase dihydropyrimidinase uridine kinase (GTP) cytdine kinase dihydropyrimidinase uridine kinase (GTP) cytdine kinase (JP) cytdine kinase cytosine deaminase cytoline deaminase cytidine deaminase cytidine deaminase cytidine deaminase cytidine deaminase cytidine deaminase cytidine deaminase (JRP)-posophohydrolase logical cytidine deaminase (JPP)-posophoholiseterase deoxyuridine kinase (ATP-Thymidine) uridine phosphonylase	3.1.3.5 3.5.4.1 3.5.4.1 3.5.4.1 3.5.4.1 3.5.4.1 3.6.1.2.3.6.1.19 2.4.2.1 2.7.4.9 1.3.98.1 2.1.3.2 2.4.2.1 3.5.2.3 4.1.1.2.3 6.3.4.2 2.7.4.2.2 3.5.2.2 3.5.4.1 3.5.2.2 2.7.4.2.2 3.5.2.2 3.5.4.1 3.5.2.2 2.7.1.4.8 2.7.1.4.8 1.17.4.2 3.6.1.19 3.6.1.19 3.5.4.5 3.5.4.5 3.1.4.1.6 2.7.1.2.1 2.7.1.2.1 2.7.1.2.1 2.7.1.2.1 2.4.2.3	KOX_01045(surl)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surl)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surl)/KOX_10270/KOX_13075(ushA)/ KOX_0455(surl)/KOX_10270/KOX_13075(ushA)/ KOX_0455(surl)/KOX_04016(surl)/KOX_	dmp >> pi + thymd  ct >> nh4 + ura  dctp >> dutp + nh4  ct >> thy + nh4  dutp >> dutp + pi  du + pi <> drlp + ura  atp + dump <>> adp + dudp  doroa + fum <>> oroa + succ  asp + ap >> casp + pi  omp + ppi <>> oroa + prp  doroa <>> casp  omp -> co2 + ump  atp + ump <>> adp + ctp + glu + pi  atp + ump <>> adp + utp >> adp + ttp + glu + pi  atp + ump <>> oroa + succ  some <>> thym + nh4  Sofith <>> 3udopb  sofith <>> 3udopb  sofith <>> by + uri >> adp + utp + pi  sofith <>> by + uri >> adp + utp  sofith <>> by + uri >> adp + utp  sofith <>> by + uri >> adp + utp  sofith <>> by + uri >> adp + utp  sofith <>> by + uri >> adp + utp  sofith <>> by + uri >> adp + utp  sofith <>> by + uri >> adp + utp  sofith <>> by + uri >> adp + utp  sofith <>> by + uri >> adp + utp  sofith <>> by + uri >> adp + utp  sofith <>> by + uri >> adp + utp  sofith <>> by + uri >> adp + utp  sofith <>> by + uri >> adp + utp  sofith <>> by + uri >> adp + utp  sofith <>> by + uri >> adp + utp  sofith <>> by + uri >> adp + utp  sofith <>> by + uri >> adp + utp  sofith <>> by + uri >> adp + utp  sofith <>> by + uri >> adp + utp  sofith <>> by + uri >> adp + utp  sofith <>> by + uri >> adp + utp  sofith <>> by + uri >> adp + utp  sofith <>> by + uri >> adp + utp  sofith <>> by + uri >> adp + utp  sofith <>> by + uri >> adp + utp  sofith <>> by + uri >> adp + utp  sofith <>> by + utp  sofith <
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROAD ASPCBT OROPRT DHORT OMPDC CTPS URIDK2 DHPM CYTDA DHPMD URIK CYTDA DHPMD URIK CYTDK RNTPR3 RNTPR4 URITPP DTTPP CYTDDA1 CYTDDA2 23CNPDE3 23CNPDE4 DURIDK THYMDK URIPP LURIDK THYMDK URIPP	Pyrimidine metabolism	5'-nucleotidase (dTMP) Cytosine deaminase dCIP deaminase dCIP deaminase dUTP diphosphatase purine nucleoside phosphorylase urilylate kinase (dIMP) dilydroorotate dehydrogenase (tumarate) aspartate carbamoyltransferase orotate phosphoribosyltransferase dilydroorotase arbosyltransferase orotate phosphoribosyltransferase dilydroorotase corotate phosphoribosyltransferase dilydroorotase corotidine-5'-phosphate decarbosylase CTP synthase (glutamine) uridylate kinase dilydropyrimidinase uridylate kinase dilydropyrimidinase uridne kinase (dilydropyrimidinase uridne kinase (GTP) cytidine kinase (GTP) cytidine kinase (GTP) cytidine kinase (GTP) tribosphotate pryophosphotydrolase Deoxyltymidine triphosphate prophosphotydrolase Deoxyltymidine deaminase 2,3'-cyclic-nucleotide 2'- phosphodiseterase 2,3'-cyclic-nucleotide 2'- phosphodiseterase deoxyuridne kinase (ATP-Deoxyuridne) deoxyuridne kinase (ATP-Thymigridne) uridine phosphonylase	3.1.3.5 3.5.4.1 3.5.4.1 3.5.4.13 3.5.4.13 3.6.1.23/3.6.1.19 2.4.2.1 2.7.4.9 13.98.1 2.1.3.2 2.4.2.10 3.5.2.2 3.5.2.2 3.5.2.2 3.5.4.1 3.5.2.2 2.7.4.2 2.7.4.2 3.6.1.19 3.6.1.19 3.6.1.19 3.5.4.5 3.1.4.16 3.1.4.16 2.7.1.21 2.7.2.2 2.4.2.3 3.6.1.8	KOX_01045(surls)/KOX_10270/KOX_13075(subhA)/ KOX_01045(surls)/KOX_10270/KOX_13075(subhA)/ KOX_01045(surls)/KOX_10270/KOX_13075(subhA)/ KOX_04555(kOX_14050) KOX_05955(sulf)/KOX_02715 KOX_10320(desD) KOX_17315(mk) KOX_10325(sulf)/KOX_02715 KOX_05955(sulf)/KOX_02715 KOX_05955(sulf)/KOX_02715 KOX_05965 KOX_09185/KOX_17195 KOX_05965 KOX_09185/KOX_17195 KOX_05965 KOX_05966 KOX_05	dmp > pi+ thymd  ct > nM+ wra  dtp > dup + nM4  ct > nM+ wra  dtp > dup + nM4  dtp > dup + nM4  dup > dump + ppi  du+ pi < dr1p + ura  atp + dump <> adp + dudp  doroa + fum <> oroa + succ  asp + cap > casp + pi  omp + ppi <> oroa + prpp  doroa <> casp + oroa + prpp  doroa <> casp > adp + dup + glu + pi  atp + gln + utp > adp + ctp + glu + pi  atp + ump <> adp + ump  stef + ump <> adp + ump  stef + ump <> adp + ump  stef + ump  stef + upp <> to + pi  stef + ump  stef + upp <> to + pi  stef + ump  stef + upp  stef + thio > dutp  tup + uth > dup + othio  utp > ump + ppi  dttp > dump + adp  dt > dx + ppi  dt + ppi < sup + upp  stef > upp + upp  stef > upp + upp  dttp > ump + ppi  dttp > dump + ppi  dttp > dump + adp  dt + atp > dump + adp  du + atp > dump + adp  thym + atp > dump + adp  thym + atp > dump + adp  uri + pi <> um + r1p  dudp, < vump + sipp
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROAD ASPCBT OMOPDC CTPS URIDK2 DHORT OMPDC CTPS URIDK2 DHIPM CYTDA DHIPM CYTDA DHIPM CYTDA DHIPM CYTDA DHIPM CYTDA CYTDAL CYTD	Pyrimidine metabolism  Pyrimidine Pyrimidine  P	5-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase uridylate kinase (dUMP) dihydroorotate dehydrogenase (tumarate) aspartate carbamoyltransferase orotate phosphoribosyltransferase orotate ceraboxylase CTP synthase (glutamine) uridylate kinase dihydropyrimidinase ctytosine deaminase dihydropyrimidinase uridine kinase (GTP) cytodine deaminase cytidine deaminase cytidine deaminase cytidine deaminase cytidine deaminase cytidine deaminase (ZTP-Cytolic-nucleotide 2 - phosphodiesterase deoxyuridine deoxyuridine kinase (ATP-Thymidine) uridine phosphorylase ATP diphosphatase ATP diphosphatase	3.1.3.5 3.5.4.1 3.5.4.1 3.5.4.13 3.5.4.13 3.6.1.2.3.6.1.19 2.4.2.1 2.7.4.9 1.3.98.1 2.1.3.2 2.4.2.1 2.7.4.9 3.5.2.3 4.1.1.2.3 6.3.4.2 2.7.4.2.2 3.5.2.2 3.5.4.1 3.5.2.2 2.7.4.2.2 3.5.2.1 3.5.4.1 3.5.2.2 2.7.1.4.8 3.6.1.1.9 3.6.1.1.9 3.6.1.1.9 3.6.1.1.9 3.6.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.	KOX_01045(surl)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surl)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surl)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surl)/KOX_10270/KOX_13075(ushA)/ KOX_05955(kox_1/KOX_02715 KOX_10320(sled) KOX_11315(mk) KOX_16135 KOX_09285/KOX_09290(pyr8) KOX_05956(shi/KOX_07295) KOX_05965 KOX_09285/KOX_09290(pyr8) KOX_05965 KOX_09185/KOX_17195 KOX_18440 KOX_01145(pyr6) KOX_1145(pyr6) KOX_123270 KOX_04555/KOX_14050 KOX_25245 KOX_029230 KOX_05965 KOX_05966 KOX_05966 KOX_05966 KOX_05966 KOX_05966 KOX_05966 KOX_05966 KOX_05966 KOX_05966 KOX_059666 KOX_059666 KOX_059666 KOX_059666 KOX_059666 KOX_059666 KOX_0596666 KOX_0596666 KOX_059666666 KOX_059666666666666666666666666666666666666	thip >> pi+ thymd  ct >> nN4 + ura  dctp >> dutp + nN4  ct >> nN4 + ura  dctp >> dutp + nN4  ct >> tup + nN4  dutp >> dutp + nN4  dutp >> dutp + pi  du + pi <>> drlp + ura  atp + dump +> adp + dudp  doroa + fum <>> oroa + succ  asp + ga >> casp + pi  omp + ppi <>> oroa + prp  doroa <>> casp  omp -> co2 + ump  atp + gin + utp >> adp + ctp + glu + pi  atp + ump <>> adp + utp  Softu <>> 3urdp  Softu <>> 3urdp  Softu <>> 3urdp  Softu <>> 3urdp  try + uri >> gdp + ump  cyld + glp >> cmp + pdp  ctp + rthio >> ddp + othio  utp + rthio >> dutp + othio  utp > tmp + ppi  ddr >> utp + pri  ddr >> dump + ppi  ddr >> utp + pri  ddr >> dump + ppi  ddr +> dr >> dump + adp  utp + uri >> dump + ppi  ddr +> dr >> dump + adp  try + atp >> dump + adp  try + atp >> dump + adp  uri + pi <>> ura + rlp  udg _e >> ump + glp  utg _e >> ump + glp  tutp => uri + ppi
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROAD ASPCBT OROPRT DHORT OMPDC CTPS URIDK2 DHPM CYTDA DHPMD URIK CYTDA DHPMD URIK CYTDK RNTPR3 RNTPR4 URITPP DTTPP CYTDDA1 CYTDDA2 23CNPDE3 23CNPDE4 DURIDK THYMDK URIPP LURIDK THYMDK URIPP	Pyrimidine metabolism	5'-nucleotidase (dTMP) Cytosine deaminase dCIP deaminase dCIP deaminase dUTP diphosphatase purine nucleoside phosphorylase urikylate kinase (dIMP) dilydroorotate dehydrogenase (tumarate) aspartate carbamoyltransferase orotate phosphoribosyltransferase dilydroorotase arbosyltransferase orotate phosphoribosyltransferase dilydroorotase corotate phosphoribosyltransferase dilydroorotase corotidine-5'-phosphate decarbosylase CTP synthase (glutamine) uridylate kinase dilydropyrimidinase uridylate kinase dilydropyrimidinase uridne kinase (dilydropyrimidinase uridne kinase (GTP) cytidine kinase (GTP) cytidine kinase (GTP) cytidine kinase (GTP) tribonucleoside-triphosphate reductase luridne kinase (GTP) tribonucleoside-triphosphate prophosphorlydrolase Deoxyltymidine triphosphate pyrophosphorlydrolase 2,3'-cyclic-nucleotide 2'- phosphodiseterase deoxyuridne kinase (ATP-Deoxyuridne) deoxyuridne inase (ATP-Thymigridne) uridine phosphonylase ATP diphosphorlase	3.1.3.5 3.5.4.1 3.5.4.1 3.5.4.13 3.5.4.13 3.6.1.23/3.6.1.19 2.4.2.1 2.7.4.9 13.98.1 2.1.3.2 2.4.2.10 3.5.2.2 3.5.2.2 3.5.2.2 3.5.4.1 3.5.2.2 2.7.4.2 2.7.4.2 3.6.1.19 3.6.1.19 3.6.1.19 3.5.4.5 3.1.4.16 3.1.4.16 2.7.1.21 2.7.2.2 2.4.2.3 3.6.1.8	KOX_01045(surls)/KOX_10270/KOX_13075(sushA)/ KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_0455(surls)/KOX_10270/KOX_13075(ushA)/ KOX_05955(surls)/KOX_02715 KOX_10320(desD) KOX_17315(mk) KOX_06925(surls)/KOX_02715 KOX_06925(surls)/KOX_0715 KOX_06925(surls)/KOX_0715 KOX_069285/KOX_069290(pyrls) KOX_05965 KOX_069185/KOX_17195 KOX_05965 KOX_06185/KOX_17195 KOX_05965 KOX_05965 KOX_06185/KOX_17195 KOX_05965 KOX_0715 KOX_0715 KOX_0715 KOX_0715 KOX_0715 KOX_0715 KOX_0715 KOX_0715 KOX_073030 KOX_07305/KOX_07765 KOX_07305(kOX_07165) KOX_0715(kOX_07165) KOX_073030 KOX_073030 KOX_073030 KOX_07305/KOX_07765 KOX_07305(kOX_015)(maxG) KOX_0115(longarG)	dmp > pi + thymd  ct > nM4 + ura  dcp > dup + nM4  ct > nM4 + ura  dcp > dup + nM4  dup > dup + nM4  dup > dup + pi  du + pi <> dr1p + ura  atp + dump <> adp + dudp  doroa + fum <> oroa + succ  asp + cap > casp + pi  omp + ppi <> oroa + prpp  doroa <> casp > casp + pi  omp + ppi <> oroa + prpp  doroa <> casp + unp  atp + dip + up > adp + ctp + glu + pi  atp + unp <> adp + udp  Softhu <> 3urdpp  Softhu <> 3urdpp  Softhu <> but + pi  Softhu <> but + pi  softhu > but + pi  softhu + pi  soft
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROAD ASPCBT OROPRT DHORT OMPDC CTPS URIDK2 DIPPM CYTDA DIPPM CYTDA DIPPM URIK CYTDK RNTPR3 RNTPR4 URITPP DTTPP CYTDDA1 CYTDDA2 23CNPDE3 23CNPDE4 DURIDK THYMDK URIPP ATPDP1 ATPDP2 ATPDP2 ATPDP3	Pyrimidine metabolism	5'-nucleotidase (dTMP) Cytosine deaminase dCIP deaminase dCIP deaminase dUTP diphosphatase purine nucleoside phosphonylase uridylate kinase (dIMP) dilydroorotate dehydrogenase (tumarate) aspartate carbamoyltransferase orotate phosphoribosyltransferase dilydroorotase orotate phosphoribosyltransferase dilydroorotase orotidine-5'-phosphate decarbosylase CIP synthase (glutamine) uridylate kinase dilydropyrimidinase utidhe kinase dilydropyrimidinase utidhe kinase (GTP) cytdine kinase (JTP) didne triphosphate reductase Uridine triphosphate reductase Uridine triphosphate prophospholydrolase Deoxyltymidine triphosphate prophospholydrolase 2,3'-cyclic-nucleotide 2'- phosphodiseterase 2,3'-cyclic-nucleotide 2'- phosphodiseterase deoxyuridine kinase (ATP-thymidine) deoxyuridine kinase (ATP-thymidine) uridine phosphonylase ATP diphosphatase	3.1.35 3.5.41 3.5.413 3.5.413 3.5.413 3.6.123/3.6.119 2.4.2.1 2.7.4.9 1.3.98.1 2.1.3.2 2.4.2.10 3.5.2.3 4.1.1.2.3 6.3.4.2 2.7.4.2.2 3.5.2.2 3.5.2.2 3.5.4.1 3.5.2.2 2.7.1.4.8 2.7.1.4.8 1.17.4.2 3.6.1.19 3.6.1.19 3.6.1.19 3.6.1.19 3.6.1.19 3.5.4.5 3.5.4.5 3.1.4.1.6 2.7.1.2.1 2.7.1.2.1 2.7.1.2.1 2.7.1.2.1 2.7.2.2 3.6.1.8 3.6.1.8 3.6.1.8 3.6.1.8 3.6.1.8	KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_0455(surls)/KOX_10270/KOX_13075(ushA)/ KOX_15136(surls)/KOX_02715 KOX_1315(mk) KOX_16135 KOX_16145(surls)/KOX_05155(surls)/KOX_16135 KOX_05965 KOX_05965 KOX_05965 KOX_05965 KOX_05965 KOX_05965 KOX_05965 KOX_05965 KOX_05965 KOX_18145(surls)/KOX_17195 KOX_18140 KOX_1145(surls)/KOX_01145(surls)/KOX_1145(surls)/KOX_1145(surls)/KOX_1145(surls)/KOX_1145(surls)/KOX_1145(surls)/KOX_01145(surl	dmp >> pi + thymd  ct >= nN4 + ura  dctp >> dutp + nN4  ct >> nN4 + ura  dctp >> dutp + nN4  ct >> tup + nN4  dutp >> dump + ppi  du + pi <> dr1p + ura  atp + dump <>> adp + dudp  doroa + fum <>> oroa + succ  asp + cap >> cassp + pi  omp + ppi <<>> oroa + prpp  ddoroa <>> cassp + udp  somp >> cas + ump  atp + gln + utp >> adp + ctp + glu + pi  atp + ump <>> adp + udp  softhu <>> advodb  stofthu <>> advodb  stofthu <>> advodb  stofthu <>> dutp  stofthu <>> du
NUTDS CITDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROAD ASPCBT OROPET DHORT OMPDC CIPS URIDK2 DHIPM CYTDA DHIPM URIK CYTDA DHIPM URITP DTTPP CYTDA1 CYTDDA2 23CNPDE3 23CNPDE4 DURIDK THYMDK URIPP ATPDP1 ATPDP2 ATPDP2 ATPDP3 NUTP9 NUTP10	Pyrimidine metabolism	5-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase uridylate kinase (dUMP) dilhydrooriotate dehydrogenase (tumarate) aspartate carbamoyltransferase orotidate phosphoribosyltransferase dilhydrooriotate dehydrogenase (tumarate) aspartate carbamoyltransferase orotidate phosphoribosyltransferase orotidine-5'-phosphate decarbosylase CTP synthase (glotamine) uridylate kinase dilhydropyrimidinase cytosine deaminase dilhydropyrimidinase uridine kinase (GTP) cytodine kinase (GTP) cytodine kinase (GTP) cytosine deaminase dilhydropyrimidinase uridine kinase (GTP) cytosine deaminase cytosine deaminase cytidine deaminase (ATP-Deoxyuridine) deoxyuridine) deoxyuridine kinase (ATP-thymidine) uridine phosphonylase ATP diphosphatase ATP diphosphatase ATP diphosphatase ATP diphosphatase ATP diphosphatase NJC diphosphatase NJ	3.1.3.5 3.5.4.1 3.5.4.1 3.5.4.1 3.5.4.1 3.5.4.1 3.6.1.2.3.6.1.19 2.4.2.1 2.7.4.9 1.3.8.1 2.1.3.2 2.4.2.1 2.7.4.2 3.5.2.3 4.1.1.23 6.3.4.2 2.7.4.2 3.5.2.2 3.5.4.1 3.5.2.2 3.5.4.1 3.5.2.2 3.5.4.1 3.5.2.2 3.5.4.1 3.5.2.2 3.5.4.1 3.5.2.2 3.6.1.19	KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_05955(suls)/KOX_02715 KOX_13135(mk) KOX_16135 KOX_05956(suls)/KOX_079290(pyrls) KOX_16135 KOX_05966 KOX_09185/KOX_17195 KOX_18464 KOX_05966 KOX_09185/KOX_17195 KOX_18464 KOX_1145(pyrl) KOX_1145(pyrl) KOX_1145(pyrl) KOX_1145(pyrl) KOX_1145(pyrl) KOX_02327 KOX_02327 KOX_02320 KOX_02320 KOX_03230 KOX_0715 KOX_0715 KOX_0715 KOX_09330(pdl) KOX_23303 KOX_07405/KOX_07765 KOX_0115(maxG)	dmp > pi + thymd  ct > nM4 + ura  dcp > dup + nM4  ct > nM4 + ura  dcp > dup + nM4  dup > dup + nM4  dup > dup + pi  du + pi <> dr1p + ura  atp + dump <> adp + dudp  doroa + fum <> oroa + succ  asp + cap > casp + pi  omp + ppi <> oroa + prpp  doroa <> casp > casp + pi  omp + ppi <> oroa + prpp  doroa <> casp + unp  atp + dip + up > adp + ctp + glu + pi  atp + unp <> adp + udp  Softhu <> 3urdpp  Softhu <> 3urdpp  Softhu <> but + pi  Softhu <> but + pi  softhu > but + pi  softhu + pi  soft
NUTDS CTDA DCTPPA1 DCTPPA2 DUTPOP PUNPP8 URIDK1 DOROAD ASPCBT OROPRT DHORT OMPDC CTPS URIDK2 DHPM CVTDA URIDK2 DHPM CVTDA RNTPR3 RNTPR4 URITPP DTTPP CVTDDA1 CVTDDA2 23CNPDE3 23CNPDE4 DURIDK THYMDK URIPP ATPOP1 ATPOP2 AT	Pyrimidine metabolism	5'-nucleotidase (dTMP) Cytosine deaminase dCITP deaminase dCITP deaminase dUTP diphosphatase purine nucleoside phosphorylase urilylate kinase (dUMP) dilydroorotate dehydrogenase (tumarate) aspartate carbamoyltransferase orotate phosphoribosyltransferase dilydroorotase orotate phosphoribosyltransferase dilydroorotase orotatie phosphoribosyltransferase dilydropyrimidinase uridne kinase (dilydropyrimidinase uridne kinase (GTP) cytidine kinase (dilydropyrimidinase uridne kinase (GTP) cytidine kinase (dilydropyrimidinase uridne kinase (TP) phosphodise-triphosphate pvrophosphohydrolase cytidine deaminase 2,3'-cyclic-nucleotide 2' phosphodiseterase cleonyuridne deonyuridne	3.1.3.5 3.5.4.1 3.5.4.13 3.5.4.13 3.5.4.13 3.6.1.23/3.6.1.19 2.4.2.1 2.7.4.9 13.98.1 2.1.3.2 2.4.2.10 3.5.2.3 3.5.2.3 4.1.1.2.3 4.3.2.2 2.7.4.2.2 3.5.2.1 3.5.2.2 2.7.4.2.2 3.5.2.1 3.5.2.2 2.7.4.2.2 3.5.4.1 1.7.4.2 1.7.4.2 3.6.1.19 3.6.1.19 3.5.4.5 3.1.4.1.6 2.7.1.2.1 2.7.1.2.1 2.7.2.1 2.7.2.1 2.7.2.2 2.7.2.2 3.5.4.3 3.5.4.5 3.5.4.5 3.6.1.8 3.6.1.8 3.6.1.8 3.6.1.8	KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_0455(surls)/KOX_10270/KOX_13075(ushA)/ KOX_15136(surls)/KOX_02715 KOX_1315(mk) KOX_16135 KOX_16145(surls)/KOX_05155(surls)/KOX_16135 KOX_05965 KOX_05965 KOX_05965 KOX_05965 KOX_05965 KOX_05965 KOX_05965 KOX_05965 KOX_05965 KOX_18145(surls)/KOX_17195 KOX_18140 KOX_1145(surls)/KOX_01145(surls)/KOX_1145(surls)/KOX_1145(surls)/KOX_1145(surls)/KOX_1145(surls)/KOX_1145(surls)/KOX_01145(surl	dmp >> pi + thymd  ct >= nN4 + ura  dctp >> dutp + nN4  ct >> nN4 + ura  dctp >> dutp + nN4  ct >> tup + nN4  dutp >> dump + ppi  du + pi <> dr1p + ura  atp + dump <>> adp + dudp  doroa + fum <>> oroa + succ  asp + cap >> cassp + pi  omp + ppi <>> oroa + prpp  ddoroa <>> cassp + udp  somp >> casp + udp  somp >> cap + udp  softh <>> adp + udp  softh <>> softh <>> softh <>> ura  atp + dum + nN4  softh <>> oroa + prpp  ddoroa <>> casp + udp  softh <>> adp + udp  softh <>> adp + udp  softh <>> adp + udp  softh <>> addb + udp  softh <>> udp + pi  softh <>> addb + udp  softh <>> addb + udp  softh <
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROAD ASPCBT OROPRT DHORT OMPDC CTPS URIDK2 DIPPM CYTDA DIPPM DTTPP DTTPP DTTPP CYTDDA1 CYTDDA2 23CNPDE4 DURIDK THYMOK URIPP ATPDP1 ATPDP2 ATPDP3 NUTP9 NUTP10 ALHD1 PPS	Pyrimidine metabolism	5'-nucleotidase (dTMP) Cytosine deaminase dCIP deaminase dCIP deaminase dUTP diphosphatase purine nucleoside phosphorylase urilydate kinase (dUMP) dilydroorotate dehydrogenase (tumarate) asparate carbamoyltransferase orotate phosphoribosyltransferase dilydroorotase orotate phosphoribosyltransferase dilydroorotase orotate phosphoribosyltransferase orotidine-5'-phosphate ocarboxylase CTP synthase (glutamine) uridylate kinase dilydropyrimidinase utindipate virilydropyrimidinase (ATP-Deoxyrimidine) deoxyrimidine virilydropyrimidinase ATP diphosphatase	3.1.35 3.5.41 3.5.413 3.5.413 3.6.123/3.6.119 2.4.2.1 2.7.4.9 1.3.98.1 2.1.3.2 2.4.2.10 3.5.2.3 4.1.1.2.3 6.3.4.2 2.7.4.2.2 3.5.2.2 3.5.4.1 3.5.2.2 2.7.4.2.2 3.5.4.1 3.5.2.2 2.7.1.4.8 1.7.7.4.2 3.6.1.19	KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_26410 KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_04555/KOX_14050 KOX_25240(dech) KOX_125240(dech) KOX_125240(dech) KOX_12535(surls)/KOX_02715 KOX_10320(desD) KOX_17315(mik) KOX_10325 KOX_05955 KOX_09385/KOX_09290(pyrls) KOX_05965 KOX_09385/KOX_17195 KOX_05965 KOX_09385/KOX_17195 KOX_18400 KOX_1145(pyrls) KOX_1145(pyrls) KOX_15445 KOX_23270 KOX_0555/KOX_14050 KOX_125245 KOX_02320 KOX_02715 KOX_02715 KOX_02715 KOX_05715 KOX_09030(cpdls) KOX_09030(cpdls) KOX_07045(kOX_01150(maxC) KOX_01150(maxC) KOX_01150(m	dmp > pi + thymd  ct > nM4 + ura  dcp > dup + nM4  ct > nM4 + ura  dcp > dup + nM4  dup > dup + nM4  dup > dup + pi  du + pi <> dr1p + ura  atp + dump <> adp + dudp  doroa + fum <> oroa + succ  asp + cap > casp + pi  omp + ppi <> oroa + prpp  doroa <> casp + adp + dup  atp + gin + utp > adp + ctp + glu + pi  atp + ump <> adp + udp  Sishu <> 3urdpp  Sishu <> 3urdpp  Sishu <> 3urdpp  Sishu <> 3urdpp  Sishu <> butp + utp  syd + gtp > ump  syd + gtp > ump  syd + gtp > cmp + gdp  ctp + rhio > ddp + othio  utp + ump + psi  dtp > dump + ppi  dtp > dump + adp  butp > dump + adp  butp + un + adp  utr + pi <> ura + rlp  udup, <> ump + ppi  ctp + rhio > dutp + adp  tur + pi <> ura + rlp  udup, <> ump + ppi  ctp + vmp +
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROAD ASPCBT OROPT DHORT OMPDC CTPS URIDK2 DHPM CYTDA DHPM CYTDA DHPMD URIK CYTDA DHPMD URIK CYTDK RNTPR3 RNTPR4 URITPP DTTPP CYTDDA1 CYTDDA2 23CNPDE3 23CNPDE4 DURIDK THYMDK URIPP ATPOP1 ATPOP2 ATPOP2 ATPOP2 ATPOP2 ATPOP2 ATPOP2 NUTP9 NUTP10 ALHD1	Pyrimidine metabolism	5-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase uridylate kinase (dUMP) dilhydroortotate dehydrogenase (tumarate) aspartate carbamoyltransferase orotate phosphoribosyltransferase orotate carboxylase CTP synthase (glottamine) uridylate kinase dilhydropyrimidinase ctytosine deaminase dilhydropyrimidinase uridine kinase (GTP) cytoline kinase (GTP) cytoline kinase (GTP) cytosine deaminase uridine kinase (GTP) posphosphohydrolase Deoxythymidine prophosphohydrolase Deoxythymidine prophosphohydrolase cytidine deaminase zytidine deaminase zylidine deamin	3.1.3.5 3.5.4.1 3.5.4.1 3.5.4.13 3.5.4.13 3.6.1.2.3.6.1.19 2.4.2.1 2.7.4.9 13.98.1 2.1.3.2 2.4.2.1 2.7.4.9 3.5.2.3 4.1.1.2.3 6.3.4.2 2.7.4.2.2 3.5.2.2 3.5.4.1 3.5.2.2 2.7.4.2.2 3.5.2.1 3.5.4.1 3.5.2.2 2.7.1.4.8 2.7.1.4.8 2.7.1.4.8 2.7.1.4.8 2.7.1.4.8 2.7.1.4.8 2.7.1.4.8 2.7.1.4.8 2.7.1.4.8 2.7.1.4.8 2.7.1.4.8 2.7.1.4.8 2.7.1.4.8 2.7.1.4.8 2.7.1.4.8 2.7.1.4.8 3.6.1.19 3.6.1.19 3.6.1.19 3.6.1.19 3.6.1.19 3.6.1.10 3.	KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_05955(kox_10x0X_02715 KOX_10320(sled) KOX_11315(mk) KOX_16135 KOX_09285/KOX_09290(pyrls) KOX_05956(surl,WOX_07290(pyrls) KOX_05965 KOX_09285/KOX_09290(pyrls) KOX_05965 KOX_09285/KOX_17195 KOX_18440 KOX_11455(pyrl) KOX_12715 KOX_11455(pyrl) KOX_2270 KOX_10455(pyrl) KOX_2270 KOX_02928 KOX_05965 KOX_05965 KOX_05965 KOX_05965 KOX_05965 KOX_05965 KOX_05966 KOX_07965 KOX_01150(max6)	dmp >> pi + thymd  ct >> nh4 + ura  dctp >> dutp + nh4  ct >> thy + nh4  dutp >> dutp + pi  du + pi <>> drlp + ura  atp + dump <>> adp + dudp  doroa + fum <>> oroa + succ  asp + ga >> casp + pi  omp + ppi <>> oroa + prp  doroa <>> casp  omp -> co2 + ump  atp + gin + utp >> adp + ctp + glu + pi  atp + ump <>> adp + utp  Sodiu <>> 3urdpp  Som <>> such + usp <>> such + usp <>> oron  py dr + gly >> oron + ppi  ctp + thio >> dutp + othio  utp + thio >> dutp + othio  utp + thio >> dutp + othio  utp > tmp + ppi  ddt >> dutp + othio  utp > tmp + ppi  ddt >> dutp + dutp + adp  utp + all >> dutp + othio  utp + thio >> dutp + othio  utp + thio >> dutp + othio  utp + thio >> dutp + othio  utp > tmp + ppi  ddt >> dutp + dutp + adp  thym + atp >> dump + adp  thym + atp >> dump + adp  thym + atp >> dump + ppi  tup e >> ump + glp  tup e >> ump + ppi  ctp >> cmp + ppi  dctp >> cmp + ppi  dctp >> dctp >> mp + ppi  dctp >> mp + ppi  dctp >> dctp >> mp + ppi
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROAD ASPCBT OROPRT DHORT OMPDC CTPS URIDK2 DIPPM CYTDA DIPPM DTTPP DTTPP DTTPP CYTDDA1 CYTDDA2 23CNPDE4 DURIDK THYMOK URIPP ATPDP1 ATPDP2 ATPDP3 NUTP9 NUTP10 ALHD1 PPS	Pyrimidine metabolism	5'-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase urilydate kinase (dUMP) dilydroorotate dehydrogenase (tumarate) aspartate carbamoyltransferase orotate phosphoribosyltransferase dilydroorotase corotate phosphoribosyltransferase dilydroorotase orotatie phosphoribosyltransferase orotidine-5'-phosphate decarboxylase CTP synthase (glutamine) urilydate kinase dilydropyrimidinase urilydate kinase dilydropyrimidinase urilne kinase dilydropyrimidinase urilne kinase (GTP) cytidine kinase (TP) sponybosphohydrolase posoyhoyhdrolase posoyhoyhdrolase posoyhoyhdrolase posoyhoyhdrolase pyrophosphohydrolase pyrophosphohydrolase pyrophosphohydrolase cytidine deaminase cytidine deaminase cytidine deaminase cytidine deaminase cytidine deaminase deoxyuridine kinase (ATP-Benoyuridine) deoxyuridine deoxyuridine kinase (ATP-Benoyuridine) deoxyuridine	3.1.35 3.5.41 3.5.413 3.5.413 3.6.123/3.6.119 2.4.2.1 2.7.4.9 1.3.98.1 2.1.3.2 2.4.2.10 3.5.2.3 4.1.1.2.3 6.3.4.2 2.7.4.2.2 3.5.2.2 3.5.4.1 3.5.2.2 2.7.4.2.2 3.5.4.1 3.5.2.2 2.7.1.4.8 1.7.7.4.2 3.6.1.19	KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_26410 KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_04555/KOX_14050 KOX_25240(dech) KOX_125240(dech) KOX_125240(dech) KOX_12535(surls)/KOX_02715 KOX_10320(desD) KOX_17315(mik) KOX_10325 KOX_05955 KOX_09385/KOX_09290(pyrls) KOX_05965 KOX_09385/KOX_17195 KOX_05965 KOX_09385/KOX_17195 KOX_18400 KOX_1145(pyrls) KOX_1145(pyrls) KOX_15445 KOX_23270 KOX_0555/KOX_14050 KOX_125245 KOX_02320 KOX_02715 KOX_02715 KOX_02715 KOX_05715 KOX_09030(cpdls) KOX_09030(cpdls) KOX_07045(kOX_01150(maxC) KOX_01150(maxC) KOX_01150(m	dmp > pi + thymd  ct > nM4 + ura  dcp > dup + nM4  ct > nM4 + ura  dcp > dup + nM4  dup > dup + nM4  dup > dup + pi  du + pi <> dr1p + ura  atp + dump <> adp + dudp  doroa + fum <> oroa + succ  asp + cap > casp + pi  omp + ppi <> oroa + prpp  doroa <> casp + adp + dup  atp + gin + utp > adp + ctp + glu + pi  atp + ump <> adp + utp  Sidhu <> 3urdpp  Sidhu <> 3urdpp  Sidhu <> 3urdpp  Sidhu <> butp + utp  sidh + utp <> butp  sidh + utp <> butp  sidh + utp  sidh
NUTDS CITDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROAD ASPCBT OROPET DHORT OMPDC CIPS URIDK2 DHIPM CYTDA DHIPM URIK CYTDA DHIPM CYTDA DHIPM DTTPP CYTDA1 CYTDA2 23CNPDE3 23CNPDE4 DURIDK THYMDK URIPP ATPOP1 ATPOP2 ATPOP2 ATPOP3 NUTP9 NUTP10 ALHD1 PPS LALDR	Pyrimidine metabolism	5-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase uridylate kinase (dUMP) dilhydrooriotate dehydrogenase (tumarate) aspartate carbamoyltransferase orotidate phosphoribosyltransferase orotidate phosphoribosyltransferase orotidate phosphoribosyltransferase orotidate corbidate	3.1.3.5 3.5.4.1 3.5.4.1 3.5.4.13 3.5.4.13 3.6.1.23/3.6.1.19 2.4.2.1 2.7.4.9 13.98.1 2.1.3.2 2.4.2.10 3.5.2.2 2.4.2.10 3.5.2.2 3.5.2.2 3.5.2.2 3.5.2.1 3.5.2.2 2.7.4.2.8 1.7.7.2 1.7.7.2 1.7.7.2 1.7.7.2 1.7.7.2 1.7.7.2 1.7.7.2 1.7.7.2 1.7.7.2 3.6.1.19 3.5.4.5 3.6.1.8	KOX, 1045(surl)/KOX, 10270/KOX, 13075(ushA)/ KOX, 26410 KOX, 26410 KOX, 1045(surl)/KOX, 10270/KOX, 13075(ushA)/ KOX, 1045(surl)/KOX, 10270/KOX, 13075(ushA)/ KOX, 1045(surl)/KOX, 10400 KOX, 10455(koX), 14050 KOX, 15315(mk) KOX, 16135 KOX, 16135 KOX, 16136 KOX, 1613	dmp >> pi+ thymd  ct >> nh4 + ura  dctp >> dup+ nh4  ct >> th4 + ura  dctp >> dup+ nh4  dup >> dup+ nh4  dup >> duph ppi  du + pi <>> drlp + ura  atp + dump <>> adp + dudp  doroa + fum <>> oroa + succ  asp + ga >> casp + pi  omp + ppi <>> oroa + prp  doroa <>> casp  omp >> co2 + ump  atp + gin + utp >> adp + ctp + glu + pi  atp + ump <>> adp + utp  Sodhu <>> 3urdpp  Som <>> to >> to + up  Sodhu <>> sudp + up  ydd + gtp >> mp + pi  to + up <>> dp + up  ydd + gtp >> mp + pi  to + up <>> dp + up  ydd + gtp >> mp + pi  to + thio >> dutp + othio  utp + rthio >> dutp + othio  utp + rthio >> dutp + othio  utp > tmp + ppi  ddt >> durp + pi  dd + atp >> dump + adp  thy + pi <> ump + glp  utg, => ump + glp  tup, => ump + glp  tup, => ump + ppi  dctp >> dup + ppi  dctp >> dup + ppi  dctp >> ump + ppi
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROAD ASPCBT OROPT DHORT OMPDC CTPS URIDK2 DHIPM CYTDA DHIPM URITPP DTTPP CYTDA1 CYTDA2 23CNPDE3 23CNPDE4 DURIDK THYMDK URIPP ATPOP1 ATPOP2 ATPOP2 ATPOP2 ATPOP2 ATPOP2 ATPOP3 NUTP9 NUTP10 ALHD1 PPS LALDR HAGTH	Pyrimidine metabolism Pyrimide Metabolism Pyri	5-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase uridylate kinase (dUMP) dilhydrooriotate dehydrogenase (tumarate) aspartate carbamoyltransferase orotidate phosphoribosyltransferase orotidate phosphoribosyltransferase orotidate phosphoribosyltransferase orotidate corbosyltransferase orotidate phosphoribosyltransferase orotidate phosphoribosyltransferase orotidate carboxylase CTP synthase (glottamine) uridylate kinase dilhydropyrimidinase cytosine deaminase dilhydropyrimidinase uridne kinase (GTP) cytodine kinase (GTP) cytosine kinase (dilhydropyrimidinase uridne kinase (GTP) cytosine cytosine deaminase cytidine deaminase cytidine deaminase cytidine deaminase cytidine deaminase cytidine deaminase (ATP-Cheoxyuridine) deoxyuridine kinase (ATP-Cheoxyuridine) deoxyuridine kinase (ATP-Thymidine) uridine phosphosphatase ATP diphosphatase ATP diphosphat	3.1.35 3.5.41 3.5.413 3.5.413 3.5.413 3.6.123/3.6.119 2.4.21 2.7.49 13.98.1 2.1.32 2.4.21 2.7.49 3.5.23 4.1.123 6.3.42 2.7.422 3.5.22 3.5.41 3.5.21 3.5.41 3.5.22 3.6.14 3.6.119 3.5.45 3.6.119 3.5.45 3.1.416 2.7.121 2.4.23 3.6.18 3.6.18 3.6.18 3.6.18 3.6.18 3.6.18 3.6.18 3.6.18 3.6.18	KOX_01045(surl_)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surl_)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surl_)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surl_)/KOX_10270/KOX_13075(ushA)/ KOX_05955(kox_10x0X_02715 KOX_10320(sled) KOX_11315(mk) KOX_16135 KOX_09325/KOX_09290(py#B) KOX_05955 KOX_09325/KOX_09290(py#B) KOX_05955 KOX_09325/KOX_17195 KOX_18440 KOX_01145(pyrb) KOX_1145(pyrb) KOX_12370 KOX_104555/KOX_14050 KOX_22370 KOX_02320 KOX_02320 KOX_02320 KOX_02715 KOX_25715 KOX_25715 KOX_25715 KOX_25715 KOX_25930 KOX_09330(pydB) KOX_09330(pydB) KOX_09330(pydB) KOX_09330(pydB) KOX_09330(pydB) KOX_09330(pydB) KOX_09330(pydB) KOX_09330(pydB) KOX_1935(kox_07765 KOX_01150(maxC) KOX_01150(maxC) KOX_01150(maxC) KOX_01150(maxC) KOX_00375 KOX_00375 KOX_00375 KOX_0030665 KOX_01150(maxC) KOX_0030666 KOX_01150(maxC) KOX_0030666 KOX_01150(maxC) KOX_0030666 KOX_01150(maxC) KOX_003666 KOX_01150(maxC) KOX_003666 KOX_01150(maxC)	dmp > pi + thymd  ct > nN4 + ura  dtmp > dtmp > pi + thymd  ct > nN4 + ura  dtp > dup + nN4  ct >> tup + nN4  dutp >> dump + ppi  du + pi <> dr1p + ura  atp + dump <> adp + dudp  doroa + fum <> oroa + succ  asp + cap >> cassp + pi  omp + ppi <> oroa + prpp  ddoroa <> cassp + pi  omp + ppi <<> oroa + prpp  ddoroa <> cassp > cap + udp  stell + utp >> adp + ctp + glu + pi  atp + ump <> adp + udp  stell + utp >> adp + udp  stell + utp >> adp + utp  stell + utp >> dup  stell + utp -> utp >> utp  stell + utp -> utp >> utp >> utp  stell + utp -> utp >> utp >> utp  stell + utp -> utp >> utp >> utp >> utp  stell + utp -> utp >> utp >> utp  stell + utp -> utp -> utp >> utp ->
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPPP PUNPP8 URIDK1 DOROAD ASPCBT OROPRT DHORT OMPDC CTPS URIDK2 DHPM CYTDA DHPM CYTDA DHPMD TITPP CYTDDA1 CYTDDA2 23CNPDE4 DURIDK THYMDK URIUPP ATPOP1 AT	Pyrimidine metabolism	5'-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase urilydate kinase (dUMP) dilydroorotate dehydrogenase (tumarate) aspartate carbamyltransferase orotate phosphoribosyltransferase dilydroorotase corotate phosphoribosyltransferase dilydroorotase orotidine-5'-phosphate decarboxylase CTP synthase (glutamine) urilydate kinase dilydropyrimidinase utrilydropyrimidinase utrilopytimidinase utrilopytimidinase dilydropyrimidinase utrilopse trilopse trilopse phosphoryboyboyboyboyboyboyboyboyboyboyboyboyboy	3.1.35 3.5.41 3.5.413 3.5.413 3.5.413 3.6.123/3.6.119 2.4.2.1 2.7.4.9 1.3.98.1 2.1.3.2 2.4.2.10 3.5.2.3 4.1.1.2.3 6.3.4.2 2.7.4.2.2 3.5.2.2 3.5.2.2 3.5.4.1 3.5.2.2 2.7.1.4.8 2.7.1.4.8 1.17.4.2 3.6.1.19	KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_26410 KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_04555(xOX_14050) KOX_125240(scle) KOX_125240(scle) KOX_125240(scle) KOX_12535(surls)/KOX_02715 KOX_10320(desD) KOX_11315(mik) KOX_16135 KOX_05965 KOX_098185/KOX_17195 KOX_05965 KOX_098185/KOX_17195 KOX_05965 KOX_059230 KOX_059230 KOX_059230 KOX_05715 KOX_05715 KOX_05715 KOX_05715 KOX_05715 KOX_059330(cpdB) KOX_09330(cpdB) KOX_09330(cpdB) KOX_09330(cpdB) KOX_09330(cpdB) KOX_050665 KOX_01150(maxG) KOX_011	dmp > pi + thymd  ct > nM4 + ura  dctp > dutp + nM4  ct > nM4 + ura  dctp > dutp + nM4  dctp > dutp + nM4  dutp > dutp + pi  dut + pi < drip + ura  atp + dump <> adp + dudp  doroa + fum <> oroa + succ  asp + cap > casp + pi  omp + ppi <> oroa + prpp  doroa > casp + oroa + prpp  doroa > coz + ump  atp + gin + utp > adp + ctp + glu + pi  atp + ump <> adp + utp  Sidhu <> 3 urdpp  Smc <> t thym + nM4  Sidht <> 3 urdpp  smc <> t thym + nM5  Sidht <> 3 urdpp  smc <> thym + nM5  Sidht <> 3 urdpp  smc <> thym + nM4  Sidht <> 3 urdpp  smc <> thym + nM4  Sidht <> 3 urdpp  smc <> thym + nM4  Sidht <> 3 urdpp  smc <> thym + nM4  Sidht <> 3 urdpp  smc <> thym + nM4  Sidht <> 3 urdpp  smc <> thym + nM4  Sidht <> 3 urdpp  smc <> thym + nM4  Sidht <> 3 urdpp  smc <> thym + nM4  Sidht <> 3 urdpp  smc <> thym + nM4  Sidht <> 3 urdpp  smc <> thym + nM4  Sidht <> 3 urdpp  smc <> thym + nM4  Sidht <> 3 urdpp  smc <> thym + nM4  Sidht <> 3 urdpp  smc <> thym + nM4  Sidht <> 3 urdpp  smc <> thym + nM4  Sidht <> 3 urdpp  smc <> thym + nM4  Sidht <> 3 urdpp  smc <> thym + nM4  sidtp > ump + ppi  dtp > ump + ppi  dtp > du + atp > dump + adp  thym + atp > dump + adp  thym + atp > dump + padp  utp + pi <> ump + ppi  dtp + or ump +
NUTDS CITDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROADD ASPCBT OROPET DHORT OMPDC CIPS URIDK2 DHIPM CYTDA DHIPM URIK CYTDA DHIPM CYTDA DHIPM DTTPP CYTDA1 CYTDA2 23CNPDE3 23CNPDE4 DURIDK THYMDK URIPP ATPOP1 ATPOP2 ATPOP3 ATPOP3 NUTP9 NUTP10 ALHD1 PPS LALDR HAGTH MGXS LGTTHL MIGRD	Pyrimidine metabolism Pyrimide Metabolism Pyrivavate Metabolism Pyrivavate Metabolism Pyrivavate Metabolism Pyruvate Metabolism	5-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase uridylate kinase (dUMP) dilhydrooriotate dehydrogenase (tumarate) aspartate carbamoyltransferase orotidate phosphoribosyltransferase orotidate phosphoribosyltransferase orotidate phosphoribosyltransferase orotidate carboxylase CTP synthase (glottamine) uridylate kinase dilhydropyrimidinase cytosine deaminase dilhydropyrimidinase cytosine deaminase dilhydropyrimidinase uridine kinase (GTP) cytodine kinase (GTP) cytodine kinase (GTP) cytodine kinase (GTP) cytosine deaminase uridine kinase (GTP) cytosine deaminase cytidine cominatione cytidine cominatio	3.1.3.5 3.5.4.1 3.5.4.1 3.5.4.1 3.5.4.1 3.5.4.1 3.5.4.1 3.6.1.2.3.6.1.19 2.4.2.1 2.7.4.9 1.3.9.8.1 2.1.3.2 2.4.2.1 2.7.4.2 3.5.2.3 4.1.1.23 6.3.4.2 2.7.4.2 3.5.2.2 3.5.4.1 3.5.2.2 3.5.4.1 3.5.2.2 3.5.4.1 3.5.2.2 3.5.4.1 3.5.2.2 3.5.4.1 3.5.2.2 3.6.1.19 3.6.1.19 3.6.1.19 3.6.1.19 3.6.1.19 3.6.1.19 3.6.1.10 2.7.1.2.1	KOX, 1045(surl)/KOX, 10270/KOX, 13075(ushA)/ KOX, 26410 KOX, 26410 KOX, 26400 KOX, 26400 KOX, 26400 KOX, 26450 KOX, 26450 KOX, 26400 KOX, 26450 KOX, 26400 KOX, 26400 KOX, 26400 KOX, 26400 KOX, 26400 KOX, 26400 KOX, 16400	dmp > pi + thymd  ct > nN4 + ura  dcp > dutp + nN4  ct > nN4 + ura  dcp > dutp + nN4  dutp > dutp + nN4  dutp > dutp + pi  du + pi <> drLp + ura  atp + dump <> adp + dudp  doroa + fum <> oroa + succ  asp + cap > cassp + pi  omp + ppi <> oroa + prpp  doroa <> cassp  omp > co2 + ump  atp + gln + utp > adp + ctp + glu + pi  atp + ump <> adp + udp  Steful <> 3 aduch  steful <> aduch  steful
NUTDS CITDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROAD ASPCBT OROPET DHORT OMPDC CIPS URIDK2 DHIPM CYTDA DHIPM URIK CYTDA DHIPM CYTDA DHIPM DTTPP CYTDA1 CYTDA2 23CNPDE3 23CNPDE4 DURIDK THYMDK URIPP ATPOP1 ATPOP2 ATPOP2 ATPOP3 NUTP9 NUTP10 ALHD1 PPS LALDR HAGTH MGXS LGTTHL	Pyrimidine metabolism	5'-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase urilydate kinase (dUMP) dilydroorotate dehydrogenase (tumarate) aspartate carbamyltransferase orotate phosphoribosyltransferase dilydroorotase corotate phosphoribosyltransferase dilydroorotase orotidine-5'-phosphate decarboxylase CTP synthase (glutamine) urilydate kinase dilydropyrimidinase utrilydropyrimidinase utrilopytimidinase utrilopytimidinase dilydropyrimidinase utrilopse trilopse trilopse phosphoryboyboyboyboyboyboyboyboyboyboyboyboyboy	3.1.3.5 3.5.4.1 3.5.4.1 3.5.4.1 3.5.4.1 3.5.4.1 3.5.4.1 3.6.1.2.3.6.1.19 2.4.2.1 2.7.4.9 1.3.8.1 2.1.3.2 2.4.2.1 2.7.4.2 3.5.2.3 4.1.1.23 6.3.4.2 2.7.4.2 3.5.2.2 3.5.4.1 3.5.2.2 3.5.4.1 3.5.2.2 3.5.4.1 3.5.2.2 3.5.4.1 3.5.2.2 3.5.4.1 3.5.2.2 3.6.1.19 3.6.	KOX, 1045(surl)/KOX, 10270/KOX, 13075(ushA)/ KOX, 26410 KOX, 26410 KOX, 26400 KOX, 26400 KOX, 26400 KOX, 26450 KOX, 26400 KOX, 26450 KOX, 26400 KOX, 26450 KOX, 26400 KOX, 26400 KOX, 17315(mk) KOX, 16135 KOX, 16360 KOX, 16385(KOX, 17395 KOX, 18440 KOX, 16135 KOX, 16385 KOX, 16386 KOX, 26300 KOX, 2	dmp > pi + thymd  ct > nN4 + ura  dctp > dutp + nN4  ct > nN4 + ura  dctp > dutp + nN4  dutp > dutp + nN4  dutp > dutp + pi  du + pi <> drLp + ura  atp + dump <> adp + dudp  doroa + fum <> oroa + succ  asp + cap > cassp + pi  omp + ppi <> oroa + prpp  doroa <> cassp  omp > co2 + ump  atp + gln + utp > adp + ctp + glu + pi  atp + ump <> adp + udp  Steful <> 3 dudb  gtp + utr > gdp + utp  Steful <> 3 dudb  gtp + utr > gdp + utp  Steful <> 3 dudb  gtp + utr > gdp + utp  Steful <> 3 dudb  gtp + utr > gdp + utp  Steful <> 3 dudb  gtp + utr > gdp + utp  Steful <> 3 dudb  gtp + utr > gdp + utp  Steful <> 3 dudb  gtp + utr > gdp + utp  Steful <> 3 dudb  gtp + utr > gdp + utp  Steful <> 3 dudb  gtp + utr > gdp + utp  Steful <> 3 dudb  gtp + utr > gdp + utp  Steful <> 3 dudb  gtp + utr > sqb + utp  Steful <> 3 dudb  gtp + utr > gdp + utp  Steful <> 3 dudb  gtp + utr + pi <> dutp + steful  utp > thmp + ppi  dttp > dtmp + ppi  dttp > dtmp + ppi  dty > dtmp + adp  thym + atp > dump + adp  thym + atp > dump + adp  thym + atp > dump + gdp  utg => ump + ppi  ctg => cmp + ppi  dtdp > dtp > dmp + pp + pi  llaid = nadh <> 1zppd-R + nad  ltg > gt + lac  dap > mtg + pi  rgt + mtg > ltg
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROAD ASPCBT OROPT DHORT OMPDC CTPS URIDK2 DHPM CYTDA DHPMC CYTDA DHPMC CYTDA DHPMC CYTDA DHPMD CYTDA DHPMD CYTDA DHPMD CYTDA DHPMD TITPP DTTPP CYTDDA1 CYTDDA1 CYTDDA2 23CNPDE3 23CNPDE4 DURIDK THYMDK URIPP ATPOP1 ATPOP1 ATPOP2 ATPOP3 NUTP9 NUTP10 ALHD1 PPS LALDR HAGTH MGXS LGTTHL MGXS LGTTHL MTGRD ALCDET ALCD	Pyrimidine metabolism Pyrimide Metabolism Pyrivate Metabolism Pyrivated Metabolism	5'-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase urikylate kinase (dUMP) dilhydroorotate dehydrogenase (tumarate) aspartate carbamoyltransferase orotate phosphoribosyltransferase dilhydroorotase orotate phosphoribosyltransferase dilhydroorotase orotatie phosphoribosyltransferase dilhydroorotase dilhydroorytimidinase uridine kinase (dilydropyrimidinase uridine kinase (GTP) cytdine kinase (GTP) cytdine kinase (GTP) cytdine kinase (dilydropyrimidinase uridine kinase (dilydropyrimidinase pyrophosphohydrolase powythydrolase powythydrolase powythydrolase powythydrolase pyrophosphohydrolase cytdine deaminase 2,3'-cyclic -nucleotide 2'- phosphodissterase 2,3'-cyclic -nucleotide 2'- phosphodissterase (ATP-Deoxyuridine) decoyuridine kinase (ATP-Deoxyuridine) decoyuridine kinase (ATP-Thymidine) uridine phosphorylase ATP diphosphatase ATP dipho	3.1.35 3.5.41 3.5.413 3.5.413 3.5.413 3.6.123/3.6.119 2.4.2.1 2.7.4.9 13.98.1 2.1.32 2.4.2.10 3.5.2.3 4.1.1.23 6.3.4.2 2.7.4.2 2.7.4.2 3.5.2.2 3.5.2.1 3.5.4.1 3.5.2.2 2.7.1.4.8 2.7.1.4.8 2.7.1.4.8 2.7.1.4.8 2.7.1.4.8 2.7.1.4.8 2.7.1.4.8 2.7.1.4.8 2.7.1.4.8 2.7.1.4.8 2.7.1.4.8 2.7.1.8 3.6.1.19 3.6.1.	KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_26410 KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_04555(xOX_14050) KOX_125240(scle) KOX_125240(scle) KOX_125240(scle) KOX_1253(surls)/KOX_02715 KOX_10320(desD) KOX_11315(mik) KOX_16135 KOX_09385/KOX_09290(pyrls) KOX_05965 KOX_09385/KOX_17195 KOX_05965 KOX_09385/KOX_17195 KOX_05965 KOX_01150(maxG) KOX_01150(	dmp > pi + thymd  ct > nM4 + ura  dctp > dutp + nM4  ct > nM4 + ura  dctp > dutp + nM4  dctp > dutp + nM4  dutp > dutp + pi  du + pi <> drlp + ura  atp + dump <> adp + dudp  doroa + fum <> oroa + succ  asp + cap > casp + pi  omp + ppi <> oroa + prpp  doroa > casp + pi  omp + ppi <> oroa + prpp  doroa > casp = adp + utp  atp + ufp > adp + ctp + glu + pi  atp + ufp > adp + utp  Schlu <> 3urdpp  Smc <> thym + nM4  Schlu <> 3urdpp  Smc <> thym + nM4  Schlu <> 3udpp  gt + uf > 3udp + utp  gt + uf > 3pd + utp  gt - utp  gt + utp  gt
NUTDS CITDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROADA ASPCBT OROPET DHORT OMPDC CTPS URIDK2 DHIPM CYTDA DHIPM CYTDA DHIPM URIK CYTDA DHIPM DTIPP CYTDA1 CYTDA2 23CNPDE4 DURIDK THYMDK URIPP ATPOP1 ATPOP2 ATPOP2 ATPOP3 NUTP9 NUTP1 ALIDI HAGTH MGXS LGTTHL MGCRD ALCDE ALC	Pyrimidine metabolism Pyrimide Metabolism	5-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase uridylate kinase (dUMP) dlihydroortoate dehydrogenase (tumarate) aspartate carbamoyltransferase orotidate phosphoribosyltransferase orotidate phosphoribosyltransferase orotidate phosphoribosyltransferase orotidate carboxylase CTP synthase (glottamine) uridylate kinase dlihydrooprimidinase cytosine deaminase dlihydropyrimidinase cytosine deaminase dlihydropyrimidinase uridne kinase (GTP) cytodine kinase (GTP) cytodine kinase (GTP) cytodine kinase (GTP) cytodine kinase (GTP) cytosine deaminase cytodine deaminase cytodine deaminase cytidine deaminase (ATP-Deoxyuridine) deoxyuridine) deoxyuridine kinase (ATP-Deoxyuridine) deoxyuridine kinase (ATP-Deoxyuridine) deoxyuridine kinase (ATP-Diphosphatase ATP diphosphatase ATP dip	3.1.3.5 3.5.4.1 3.5.4.1 3.5.4.1 3.5.4.1 3.5.4.1 3.5.4.1 3.5.4.1 3.5.4.1 2.7.4.9 1.3.9.1 2.1.3.2 2.4.2.1 2.7.4.9 3.5.2.3 4.1.1.23 6.3.4.2 2.7.4.2 3.5.2.2 3.5.2.1 3.5.4.1 3.5.2.2 3.5.4.1 3.5.2.2 3.5.4.1 3.5.2.2 3.5.4.1 3.5.2.2 3.5.4.1 3.5.2.2 3.6.1.19 3.6.1.19 3.6.1.19 3.6.1.19 3.6.1.19 3.6.1.10 3.1.4.1.6 2.7.1.2.1 2.7.1.2.1 2.7.2.2 2.7.1.2.1 2.7.2.2 2.7.1.2.1 2.7.2.2 2.7.1.2.1 2.7.2.2 2.7.1.2.1 2.7.2.2 2.7.1.2.1 2.7.2.2 2.7.1.2.1 2.7.2.2 2.7.2 2.7.2 2.7.2 2.7.2 2.7.2 2.7.2 2.7.2 2.7.2 2.7.2 2.7.2 2.7.2 2.7.2 2.7.2 2.7.2 2.7.2 2.7	KOX, 1045(surla)/KOX, 10270/KOX, 13075(ushA)/ KOX, 26410 KOX, 26410 KOX, 26400 KOX, 26400 KOX, 26450 KOX, 12315(mk) KOX, 16135 KOX, 16326 KOX, 26326 KOX,	dmp >> pi+ thymd  ct >= nM+ wra  dctp >> dutp + nM4  ct >> nM+ wra  dctp >> dutp + nM4  dutp >> dump + ppi  du+ pi <> drLp + ura  atp + dump <>> adp + dudp  doroa + fum <>> oroa + succ  asp + cap >> casp p  omp + ppi <<> oroa + prpp  doroa <>> casp p  omp >> co2 + ump  atp + gln + utp >> adp + ctp + glu + pi  atp + ump <>> adp + udp  Steful <>> 3 dudb  steful <> 3 dudb  steful <>> 3 dudb  steful <> 3 dudb  steful <
NUTDS CTDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROAD ASPCBT OROPT DHORT OMPDC CTPS URIDK2 DHPM CYTDA DHPMC CYTDA DHPMC CYTDA DHPMC CYTDA DHPMD CYTDA DHPMD CYTDA DHPMD CYTDA DHPMD TITPP DTTPP CYTDDA1 CYTDDA1 CYTDDA2 23CNPDE3 23CNPDE4 DURIDK THYMDK URIPP ATPOP1 ATPOP1 ATPOP2 ATPOP3 NUTP9 NUTP10 ALHD1 PPS LALDR HAGTH MGXS LGTTHL MGXS LGTTHL MTGRD ALCDET ALCD	Pyrimidine metabolism Pyrimide Metabolism Pyrivate Metabolism Pyrivated Metabolism	5'-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase urikylate kinase (dUMP) dilhydroorotate dehydrogenase (tumarate) aspartate carbamoyltransferase orotate phosphoribosyltransferase dilhydroorotase orotate phosphoribosyltransferase dilhydroorotase orotatie phosphoribosyltransferase dilhydroorotase dilhydroorytimidinase uridine kinase (dilydropyrimidinase uridine kinase (GTP) cytdine kinase (GTP) cytdine kinase (GTP) cytdine kinase (dilydropyrimidinase uridine kinase (dilydropyrimidinase pyrophosphohydrolase powythydrolase powythydrolase powythydrolase powythydrolase pyrophosphohydrolase cytdine deaminase 2,3'-cyclic -nucleotide 2'- phosphodissterase 2,3'-cyclic -nucleotide 2'- phosphodissterase (ATP-Deoxyuridine) decoyuridine kinase (ATP-Deoxyuridine) decoyuridine kinase (ATP-Thymidine) uridine phosphorylase ATP diphosphatase ATP dipho	3.1.35 3.5.41 3.5.413 3.5.413 3.5.413 3.6.123/3.6.119 2.4.2.1 2.7.4.9 13.98.1 2.1.32 2.4.2.10 3.5.2.3 4.1.1.23 6.3.4.2 2.7.4.2 2.7.4.2 3.5.2.2 3.5.2.1 3.5.4.1 3.5.2.2 2.7.1.4.8 2.7.1.4.8 2.7.1.4.8 2.7.1.4.8 2.7.1.4.8 2.7.1.4.8 2.7.1.4.8 2.7.1.4.8 2.7.1.4.8 2.7.1.4.8 2.7.1.4.8 2.7.1.8 3.6.1.19 3.6.1.	KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_26410 KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_01045(surls)/KOX_10270/KOX_13075(ushA)/ KOX_04555(xOX_14050) KOX_125240(scle) KOX_125240(scle) KOX_125240(scle) KOX_1253(surls)/KOX_02715 KOX_10320(desD) KOX_11315(mik) KOX_16135 KOX_09385/KOX_09290(pyrls) KOX_05965 KOX_09385/KOX_17195 KOX_05965 KOX_09385/KOX_17195 KOX_05965 KOX_01150(maxG) KOX_01150(	dmp > pi + thymd  ct > nM4 + ura  dctp > dutp + nM4  ct > nM4 + ura  dctp > dutp + nM4  dctp > dutp + nM4  dutp > dutp + pi  du + pi <> drlp + ura  atp + dump <> adp + dudp  doroa + fum <> oroa + succ  asp + cap > casp + pi  omp + ppi <> oroa + prpp  doroa > casp + pi  omp + ppi <> oroa + prpp  doroa > casp = adp + utp  atp + ufp > adp + ctp + glu + pi  atp + ufp > adp + utp  Schlu <> 3urdpp  Smc <> thym + nM4  Schlu <> 3urdpp  Smc <> thym + nM4  Schlu <> 3udpp  gt + uf > 3udp + utp  gt + uf > 3pd + utp  gt - utp  gt + utp  gt
NUTDS CITDA DCTPDA1 DCTPDA2 DUTPDP PUNPP8 URIDK1 DOROADA ASPCBT OROPET DHORT OMPDC CTPS URIDK2 DHIPM CYTDA DHIPM CYTDA DHIPM URIK CYTDA DHIPM DTIPP CYTDA1 CYTDA2 23CNPDE4 DURIDK THYMDK URIPP ATPOP1 ATPOP2 ATPOP2 ATPOP3 NUTP9 NUTP1 ALIDI HAGTH MGXS LGTTHL MGCRD ALCDE ALC	Pyrimidine metabolism Pyrimide Metabolism	S*-nucleotidase (dTMP) Cytosine deaminase dCTP deaminase dCTP deaminase dCTP deaminase dUTP diphosphatase purine nucleoside phosphorylase uridylate kinase (dUMP) dilhydroorotate dehydrogenase (tumarate) asparate carbamyltransferase orotate phosphoribosyltransferase dilhydroorotase orotate phosphoribosyltransferase dilhydroorotase orotatie phosphoribosyltransferase orotatie phosphoribosyltransferase orotatie phosphoribosyltransferase orotatie phosphoribosyltransferase orotatie phosphoribosyltransferase orotatie phosphoribosyltransferase orotatie oridylate kinase (GTP) orytdine kinase dilhydropyrimidinase uridine kinase (GTP) cytdine	3.1.3.5 3.5.4.1 3.5.4.1 3.5.4.1 3.5.4.1 3.5.4.1 3.5.4.1 3.5.4.1 3.5.4.1 2.7.4.9 1.3.9.1 2.1.3.2 2.4.2.1 2.7.4.9 3.5.2.3 4.1.1.23 6.3.4.2 2.7.4.2 3.5.2.2 3.5.2.1 3.5.4.1 3.5.2.2 3.5.4.1 3.5.2.2 3.5.4.1 3.5.2.2 3.5.4.1 3.5.2.2 3.5.4.1 3.5.2.2 3.6.1.19 3.6.1.19 3.6.1.19 3.6.1.19 3.6.1.19 3.6.1.10 3.1.4.1.6 2.7.1.2.1 2.7.1.2.1 2.7.2.2 2.7.1.2.1 2.7.2.2 2.7.1.2.1 2.7.2.2 2.7.1.2.1 2.7.2.2 2.7.1.2.1 2.7.2.2 2.7.1.2.1 2.7.2.2 2.7.1.2.1 2.7.2.2 2.7.2 2.7.2 2.7.2 2.7.2 2.7.2 2.7.2 2.7.2 2.7.2 2.7.2 2.7.2 2.7.2 2.7.2 2.7.2 2.7.2 2.7.2 2.7	KOX, 1045(surla)/KOX, 10270/KOX, 13075(ushA)/ KOX, 26410 KOX, 26410 KOX, 26400 KOX, 26400 KOX, 26450 KOX, 12315(mk) KOX, 16135 KOX, 16326 KOX, 26326 KOX,	dmp >> pi+ thymd  ct >= nM+ wra  dctp >> dutp + nM4  ct >> nM+ wra  dctp >> dutp + nM4  dutp >> dump + ppi  du+ pi <> drLp + ura  atp + dump <>> adp + dudp  doroa + fum <>> oroa + succ  asp + cap >> casp p  omp + ppi <<> oroa + prpp  doroa <>> casp p  omp >> co2 + ump  atp + gln + utp >> adp + ctp + glu + pi  atp + ump <>> adp + udp  Steful <>> 3 dudb  steful <> 3 dudb  steful <>> 3 dudb  steful <> 3 dudb  steful <

PTA	Pyruvate Metabolism	phosphotransacetylase	2.3.1.8	KOX_26440	accoa + pi <-> actp + coa
ACKA PCT1	Pyruvate Metabolism Pyruvate Metabolism	acetate kinase propionate CoA-transferase	2.7.2.1 2.8.3.1	KOX_01540/KOX_26435 KOX_02010	ac + atp <-> actp + adp accoa + ppa <-> ac + ppcoa
APPS2	Pyruvate Metabolism	acylphosphatase	3.6.1.7	KOX_16295	actp -> ac + pi
ACS ALHD1p	Pyruvate Metabolism  Pyruvate Metabolism	acetyl-CoA synthetase aldehyde dehydrogenase	6.2.1.1 1.2.1.3	KOX_08465	ac + atp + coa -> accoa + amp + ppi acal + nadp -> ac + nadph
r	•	(acetaldehyde, NAD)		KOX_09770/KOX_15225/KOX_15975/KOX_16885	r
PFL	Pyruvate Metabolism	formate C-acetyltransferase	2.3.1.54	pfID)	pyr + coa -> formate + accoa
POX2	Pyruvate Metabolism	pyruvate dehydrogenase (quinone)	1.2.5.1	KOX_15775	pyr + uq -> ac + uqh2 + co2
PTA2	Pyruvate Metabolism	phosphotransacetylase 5-amino-6-(5-		KOX_27005(eutD)	accoa + pi <-> actp + coa
A6PRAUR	Rivoflavin metabolism	phosphoribosylamino)uracil	1.1.1.193	KOX_12575(ribD)	a6rp5p + nadph -> a6rp5p2 + nadp
FLVRp	Rivoflavin Metabolism	reductase riboflavin reductase (NADP)	1.5.1.30	KOX_07820(fre)	nadph + ribflav -> nadp + rbflvrd
FLVR	Rivoflavin Metabolism	riboflavin reductase (NAD) 6,7-dimethyl-8-ribityllumazine	1.5.1.30	KOX_07820(fre)	nadh + ribflav -> nad + rbflvrd
DMLZS	Rivoflavin metabolism	synthase	2.5.1.78	KOX_12580(ribH)	a6rp + db4p -> dmlz + pi
RBFS APPT	Rivoflavin metabolism Rivoflavin metabolism	riboflavin synthase acid phosphatase	2.5.1.9 3.1.3.2	KOX_22155 KOX_08315(aphA)/KOX_14030/KOX_18070	2 dmlz -> a6rp + ribflav fmn -> ribflav + pi
RBFK FMNANT	Rivoflavin metabolism Rivoflavin metabolism	riboflavin kinase	2.7.1.26 2.7.7.2	KOX_10525 KOX_10525	atp + ribflav -> adp + fmn
		FMN adenylyltransferase diaminohydroxyphosphoribosyl		_	atp + fmn -> fad + ppi
DHPPRAP	Rivoflavin metabolism	aminopryrimidine deaminase (25drapp)	3.5.4.26	KOX_12575(ribD)	25drapp -> a6rp5p + nh4
DHB4PS	Rivoflavin metabolism	3,4-Dihydroxy-2-butanone-4-	4.1.99.12	KOX_03025(ribB)	rl5p -> db4p + formate
GTPCHII	Rivoflavin metabolism	phosphate synthase GTP cyclohydrolase II	3.5.4.25	KOX_18420(ribA)	gtp -> 25drapp + formate + ppi
		Nicotinate-nucleotide			
NNDMBZPT	Rivoflavin metabolism	dimethylbenzimidazole phosphoribosyltransferase	2.4.2.21	KOX_01340(cobT)	dmbzid + nacn -> 5prdmbz + nac
PMPP	Rivoflavin metabolism	pyrimidine phosphatase alpha-ribazole 5-phosphate	3.1.3		a6rp5p2 -> a6rp + pi
RZ5PP	Rivoflavin metabolism	phosphatase	3.1.3.73	KOX_14245	5prdmbz -> pi + rdmbzi
FMNRDp	Rivoflavin metabolism	NADPH-dependent FMN reductase	1.5.1.38	KOX_16130	fmn + nadph -> fmnh2 + nadp
FMNRD	Rivoflavin metabolism	NADH-dependent FMN	1.5.1.41	KOX_07820(fre)	fmn + nadh -> fmnh2 + nad
SELNPS	Selenocompound metabolism	reductase Selenophosphate synthase	2.7.9.3	KOX_18075	atp + seld -> amp + pi + selnp
CYSGS1 CYSGS2	Selenocompound metabolism Selenocompound metabolism	cystathionine gamma-synthase cystathionine gamma-synthase		KOX_07310 KOX_07310	ahser + scys -> sllct + ac
CYSGS3	Selenocompound metabolism Selenocompound metabolism	cystathionine gamma-synthase cystathionine gamma-synthase		KOX_07310 KOX_07310	shser + scys -> sllct + succ phser + scys -> sllct + pi
CYSTBL3	Selenocompound metabolism	cystathionine beta-lyase	4.4.1.8	KOX_02875/KOX_21920	sllct -> shcys + nh4 + pyr
ADHC2 SADMET	Selenocompound metabolism Selenocompound metabolism	adenosylhomocysteinase S-adenosylmethionine	3.3.1.1 2.5.1.6	KOX_24860 KOX_02650	seadseh -> adn + shcys atp + smet -> pi + ppi + seasmet
METTRSS	Selenocompound metabolism	synthetase methionyl-tRNA synthetase	6.1.1.10	KOX_25560(metG)	atp + smet + trnamet -> amp + ppi + selmtrna
CYSST4	Selenocompound metabolism	cysteine synthase	2.5.1.47	KOX_12795/KOX_18690/KOX_26835/KOX_26885	aser + seld -> scys + ac
SULFR	Selenocompound metabolism	sulfite reductase (NADPH)	1.8.1.9	cysM) KOX 15885	selt + 3 nadp -> seld + 3 nadph
ADSLFK2	Selenocompound metabolism	adenylyl-sulfate kinase	2.7.1.25	KOX_01075	atp + aseInt -> adp + ppadsel
SMTTGH	Selenocompound metabolism	5- methyltetrahydropteroyltrigluta	2.1.1.14	KOX_07750/KOX_08065(metH)/KOX_21350/KOX_ 21375	chor + Emtels > cmet + tels
SWITGIT	Selenocompound metabolism	matehomocysteine methyltransferase	2.1.1.14	21375	ancys + annigiu -> aniet + tgiu
CYSTHL	Selenocompound metabolism	cystathionine gamma-lyase	4.4.1.1	KOX_02800	smet -> metseln + nh4 + obut
SELNCYS1	Selenocompound metabolism	selenocysteine lyase L-seryl-tRNA(Ser)	2.8.1.7/4.4.1.16	KOX_18715/KOX_22770	mslencys -> pyr + nh4 + metseln
STRNAST	Selenocompound metabolism	seleniumtransferase	2.9.1.1	KOX_02440/KOX_05740/KOX_09190	sectrna + selnp -> selncystrna + pi
SELNCYS2 THRDOX	Selenocompound metabolism Selenocompound metabolism	selenocysteine lyase thioredoxin reductase (NADPH)	4.4.1.16 1.8.1.9	KOX_18715/KOX_22770 KOX_15885	scys + fadh2 <-> seld + fad + ala metselnt + 2 nadph -> metseln + 2 nadp
SELTOXR	Selenocompound metabolism	selenite:reduced acceptor	1.97.1.9	KOX_21550/KOX_23285	selnt + fadh2 -> selt + fad
SELTGLUT	Selenocompound metabolism	oxidoreductase spontaneous			selt + 4 rgt -> selngluth + ogt
SELNGLUT	Selenocompound metabolism	spontaneous alpha,alpha-trehalose-			selngluth + rgt -> gluthsel + ogt
TRHPS	Starch and sucrose metabolism	phosphate synthase (UDP-	2.4.1.15	KOX_24010	g6p + udpg -> tre6p + udp
AMMALT1	Starch and sucrose metabolism	forming) Amylomaltase (maltotriose)	2.4.1.25	KOX_04675(malQ)	mlt + mlttr -> glc + mltttr
AMMALT2 AMMALT3	Starch and sucrose metabolism	Amylomaltase (maltotetraose)	2.4.1.25	KOX_04675(malQ)	mlt + mltttr -> glc + maltpt
AMMALT4	Starch and sucrose metabolism Starch and sucrose metabolism	Amylomaltase (maltopentaose) Amylomaltase (maltohexaose)	2.4.1.25	KOX_04675(malQ) KOX_04675(malQ)	mlt + maltpt -> glc + mlthx mlt + mlthx -> glc + malthp
TRH6PP TREHL	Starch and sucrose metabolism Starch and sucrose metabolism	trehalose-phosphatase alpha,alpha-trehalase	3.1.3.12 3.2.1.28	KOX_24015 KOX_05310(treF)/KOX_23470(treA)	tre6p -> pi + tre tre -> 2 glc
TREHLe	Starch and sucrose metabolism	alpha,alpha-trehalase	3.2.1.28	KOX_05310(treF)/KOX_23470(treA)	tre_e -> 2 glc_e
GLCGP1 GLCGP2	Starch and sucrose metabolism Starch and sucrose metabolism	glycogen phosphorylase glycogen phosphorylase	2.4.1.1	KOX_04680/KOX_04715 KOX_04680/KOX_04715	starch + pi -> amylose + g1p qlycogen + pi -> q1p
GLCBRAN2	6. 1. 1	1,4-alpha-glucan branching			
GLUBRANZ	Starch and sucrose metabolism	enzyme (glycogen -> bglycogen)	2.4.1.18	KOX_04735	glycogen -> bglycogen
MLTGCT	Starch and sucrose metabolism	maltose alpha-D- glucosyltransferase	5.4.99.16	KOX_22195	tre_e <-> mlt_e
LEVANS	Starch and sucrose metabolism	levanase	3.2.1.65	KOX_13550	levan_mn <-> levan_m + levan_n
FRUFSD	Starch and sucrose metabolism	beta-fructofuranosidase	3.2.1.26	KOX_01765/KOX_07150/KOX_13360 KOX_00740/KOX_01670/KOX_18370/KOX_21960, KOX_23455/KOX_25615	suc6p <-> fru + g6p
GLUSDASE1			3.2.1.21	KOX_23455/KOX_25615	glusd -> glc
GLUSDASE2	Starch and sucrose metabolism	beta-glucosidase			
	Starch and sucrose metabolism	beta-glucosidase	3.2.1.21	KOX_23455/KOX_25615 KOX_00740/KOX_01670/KOX_18370/KOX_21960, KOX_23455/KOX_25615	cellobiose -> 2 glc
GLUSDASE3			3.2.1.21 3.2.1.21	KOX_00740/KOX_01670/KOX_18370/KOX_21960,	cellobiose -> 2 glc
GLUSDASE3 ENDOGLUC	Starch and sucrose metabolism	beta-glucosidase beta-glucosidase endoglucanase		KOX_00740/KOX_01670/KOX_18370/KOX_21960, KOX_23455/KOX_25615 KOX_00740/KOX_01670/KOX_18370/KOX_21960, KOX_23455/KOX_25615	cellobiose -> 2 glc
	Starch and sucrose metabolism Starch and sucrose metabolism	beta-glucosidase	3.2.1.21	KOX_00740/KOX_01670/KOX_18370/KOX_21960,	cellulose_n -> 2 glc cellulose_n -> cellulose_n_1 + glc
ENDOGLUC	Starch and sucrose metabolism  Starch and sucrose metabolism  Starch and sucrose metabolism	beta-glucosidase beta-glucosidase endoglucanase glucose-1-phosphate adenylytransferase glycogen synthase/starch	3.2.1.21 3.2.1.4	KOX_00740/KOX_01670/KOX_18370/KOX_21960, KOX_23455/KOX_25615	cellulose_n -> cellulose_n_1 + glc cellulose_n -> cellulose_n_1 + cellulose_n
ENDOGLUC G1PADTRA GLYSYN1	Starch and sucrose metabolism	beta-glucosidase beta-glucosidase endoglucanase glucose-1-phosphate adenylyltransferase	3.2.1.21 3.2.1.4 2.7.7.27 2.4.1.21	KOX_00740/KOX_01570/KOX_18370/KOX_21960, KOX_23455/KOX_25615 KOX_04725(glgC) KOX_04720(glgA)	cellulose_n -> 2 glc  cellulose_n -> cellulose_n_1 + glc  cellulose_n -> cellulose_n_1 + celluloise  atp + g1p -> adpglc + ppi  adpglc -> glycogen + adp
ENDOGLUC G1PADTRA	Starch and sucrose metabolism Starch and sucrose metabolism Starch and sucrose metabolism Starch and sucrose metabolism	beta-glucosidase beta-glucosidase endoglucanase glucose-1-phosphate adenylytransferase glycogen synthase/starch synthase glycogen synthase/starch synthase	3.2.1.21 3.2.1.4 2.7.7.27	KOX_00740/kOX_01670/kOX_18370/kOX_21960, KOX_23455/kOX_25615 KOX_04725(glgC)	cellulose_n -> 2 glc  cellulose_n -> cellulose_n_1 + glc  cellulose_n -> cellulose_n_1 + cellulose atp + g1p -> adpglc + ppi
ENDOGLUC G1PADTRA GLYSYN1	Starch and sucrose metabolism	beta-glucosidase beta-glucosidase endoglucanase glucose-1-phosphate adenyiyftransferase glycogen synthase/starch synthase synthase glycogen synthase/starch synthase maltose-6-phosphate glucosidase/trehalose-6- glucosidase/trehalose-6-	3.2.1.21 3.2.1.4 2.7.7.27 2.4.1.21	KOX_00740/KOX_01570/KOX_18370/KOX_21960, KOX_23455/KOX_25615 KOX_04725(glgC) KOX_04720(glgA)	cellulose_n -> 2 glc  cellulose_n -> cellulose_n_1 + glc  cellulose_n -> cellulose_n_1 + celluloise  atp + g1p -> adpglc + ppi  adpglc -> glycogen + adp
ENDOGLUC G1PADTRA GLYSYN1 GLYSYN2 TRE6PH	Starch and sucrose metabolism	beta-glucosidase beta-glucosidase endoglucanase glucose-1-phosphate adenylytransferase glycogen synthase/starch synthase glycogen synthase/starch synthase maltose-6-phosphate	32.121 32.14 27.727 24.121 24.121 32.1.122/32.1.93	KOX_00740/KOX_01670/KOX_18370/KOX_21960, KOX_23455/KOX_25615  KOX_04726/glgC) KOX_04726/glgA)  KOX_04720(glgA)  KOX_04720(glgA)	cellulose_n -> 2 glc  cellulose_n -> cellulose_n_1 + glc  cellulose_n -> cellulose_n_1 + cellobiose  atp + g1p -> adpglc + ppi  adpglc -> glycogen + adp  adpglc -> amylose + adp  tre6p -> glc + g6p
ENDOGLUC G1PADTRA GLYSYN1 GLYSYN2 TRE6PH MLT6PG	Starch and sucrose metabolism	beta-glucosidase beta-glucosidase endoglucanase glucose-1-phosphate adenylyftranferase glycogen synthase/starch synthase glycogen synthase/starch synthase glycogen synthase/starch synthase glycogen synthase/starch synthase glycosidase/trehalose-6-phosphate glucosidase/trehalose-6-phosphate glucosidase maltose-6-phosphate glucosidase	32.121 32.14 2.7.727 24.121 24.121 3.21.122/3.21.93	KOX_00740;KOX_01670;KOX_18370;KOX_21960, KOX_23455;KOX_25615  KOX_04725(glgC)  KOX_04720(glgA)  KOX_04720(glgA)  KOX_04720(glgA)  KOX_046480;KOX_09255	cellulose_n -> 2 glc  cellulose_n -> cellulose_n_1 + glc  cellulose_n -> cellulose_n_1 - cellulose  atp + g1p -> adpglc + ppi  adpglc -> glycogen + adp  adpglc -> amylose + adp  tre6p -> glc + g6p  mit6p <-> glc + g6p
ENDOGLUC G1PADTRA GLYSYN1 GLYSYN2 TRE6PH MLT6PG AMDS4	Starch and sucrose metabolism	beta-glucosidase beta-glucosidase endoglucanase glucose-1-phosphate adenylyftranferase glycogen symthase/starch symthase maltose-6-phosphate glucosidase (trehalose-6-phosphate glucosidase (trehalose-6-phosphate glucosidase amidiase amidiase phenylacetaldehyde	32.121 32.14 2.7.727 2.4.121 2.4.121 3.2.1.122/3.2.193 3.2.1.122 3.5.14	KOX_00748/KOX_01670/KOX_18370/KOX_21960, KOX_23455/KOX_25615 KOX_04725(g)gC) KOX_04725(g)gA) KOX_04720(g)gA) KOX_04720(g)gA) KOX_06480/KOX_09255 KOX_06480 KOX_09850/KOX_13720/KOX_20510	cellobiose -> 2 glc  cellulose_n -> cellulose_n_1 + glc  cellulose_n -> cellulose_n_1 + cellobiose  atp + g1p -> adpglc + ppi  adpglc -> glycogen + adp  adpglc -> arnylose + adp  tre6p -> glc + g6p  mlt6p <-> glc + g6p  pheact -> pac + nh4
ENDOGLUC G1PADTRA GLYSYN1 GLYSYN2 TRE6PH MLT6PG AMDS4 PHEALDD	Starch and sucrose metabolism Styrene degradation Styrene degradation	beta-glucosidase beta-glucosidase endoglucanase glucose-1-phosphate adenylyftransferase glycogen synthase/starch synthase synthase glycogen synthase/starch synthase maltose-6-phosphate glucosidase/trehalose-6- phosphate hydrolase maltose-6-phosphate glucosidase amidiase amidiase dehydrogenase	32.121 32.14 2.7.727 24.121 24.121 32.1122/3.2.193 32.1122 3.5.14 1.2.139	KOX_00748/KOX_01570/KOX_18370/KOX_21960, KOX_23455/KOX_25615 KOX_04725(g)gC) KOX_04725(g)gA) KOX_04720(g)gA) KOX_04720(g)gA) KOX_06480/KOX_09255 KOX_06480 KOX_09850/KOX_13720/KOX_20510 KOX_19195	cellulose_n -> 2 glc  cellulose_n -> cellulose_n_1 + glc  cellulose_n -> cellulose_n_1 - cellulose  atp + g1p -> adpglc + ppi  adpglc -> glycogen + adp  adpglc -> amylose + adp  tre6p -> glc + g6p  mit6p <-> glc + g6p
ENDOGLUC GIPADTRA GLYSYN1 GLYSYN2 TRE6PH MLT6PG AMDS4 PHEALDD PHEACTHL	Starch and sucrose metabolism Styrene degradation Styrene degradation Styrene degradation	beta-glucosidase beta-glucosidase endoglucanase glucose-1-phosphate adenyiyftransferase glycogen synthase/starch synthase synthase glycogen synthase/starch synthase maltose-6-phosphate glucosidase/trehalose-6- phosphate hydrolase maltose-6-phosphate glucosidase amidase dlucosidase amidase dehydrogenase 2-phenylacetalidehyde dehydrogenase 2-phenylacetamide hydro-lyase (nitrile-forming)	32.121 32.14 2.7.27 2.4.121 2.4.121 3.2.1122/3.2.1.93 3.2.1122 3.5.14 1.2.1.39 4.2.1.84	KOX_00740/KOX_01670/KOX_18370/KOX_21960, KOX_23455/KOX_25615  KOX_04725(g)gC)  KOX_04720(g)gA)  KOX_04720(g)gA)  KOX_04720(g)gA)  KOX_06480/KOX_09255  KOX_06480  KOX_06850/KOX_13720/KOX_20510  KOX_19195  KOX_20500/KOX_20505	cellobiose -> 2 glc  cellulose_n -> cellulose_n_1 + glc  cellulose_n -> cellulose_n_1 + cellobiose  atp + g1p -> adpglc + ppi  adpglc -> glycogen + adp  adpglc -> amylose + adp  trefip -> glc + g6p  mlt6p <-> glc + g6p  pheact -> pac + nh4  pacald + nad -> pac + nadh  pheacnit -> pheact
ENDOGLUC G1PADTRA GLYSYN1 GLYSYN2 TRE6PH MLT6PG AMDS4 PHEALDD PHEACTHL ACLMHL	Starch and sucrose metabolism Styrene degradation Styrene degradation Styrene degradation Styrene degradation	beta-glucosidase beta-glucosidase endoglucanase glucose-1-phosphate adenylytranferase glycogen synthase/starch synthase glycogen synthase/starch synthase natlose-6-phosphate glucosidase/trehalose-6- phosphate hydrolase maltose-6-phosphate glucosidase/trehalose-6- phosphate hydrolase amidose glucosidase/trehalose-6- glucosidase/trehalose-6- phosphate hydrolase amidose-6-phosphate glucosidase aridase	32.121 32.14 2.7.27 24.121 24.121 32.1122/32.193 32.1122 3.5.14 12.139 42.184 42.184	KOX_00740/KOX_01670/KOX_18370/KOX_21960, KOX_23455/KOX_25615  KOX_04726/glgC) KOX_04720/glgA) KOX_04720/glgA) KOX_04720/glgA) KOX_06480/KOX_09255  KOX_06480 KOX_09850/KOX_13720/KOX_20510 KOX_19195  KOX_20500/KOX_20505 KOX_20500/KOX_20505	cellulose_n -> 2 glc  cellulose_n -> cellulose_n_1 + glc  cellulose_n -> cellulose_n_1 + cellobiose  atp + g1p -> adpglc + ppi  adpglc -> glycogen + adp  adpglc -> amylose + adp  tre6p -> glc + g6p  milt6p -> glc + g6p  pheact -> pac + nh4  pheacnit -> pheact  aconit -> admi
ENDOGLUC GIPADTRA GLYSYN1 GLYSYN2 TRE6PH MLT6PG AMDS4 PHEALDD PHEACTHL ACLMHL AMDS5 PCT3	Starch and sucrose metabolism Styrene degradation	beta-glucosidase beta-glucosidase endoglucanase glucose-1-phosphate adenylytranferasa glycogen synthase/starch synthase maltose-6-phosphate glucosidase/trehaloze-6- phosphate hydrolase maltose-6-phosphate glucosidase/trehaloze-6- phosphate hydrolase maltose-6-phosphate glucosidase/trehaloze-6- phosphate hydrolase maltose-6-phosphate glucosidase midase glucosidase midase glucosidase midase ardiade dehydrogenase chylaricetamide hydro-lyase (nitrile-forming) acnylamide hydro-lyase amidase propionate CoA-transferase	32.121 32.14 2.7.27 24.121 24.121 32.1122/32.193 32.1122 35.14 12.139 42.184 42.184 35.14 28.31	KOX_C0740/KOX_O1670/KOX_18370/KOX_21960, KOX_23455/KOX_25615  KOX_04726/glgC) KOX_04726/glgA) KOX_04720/glgA) KOX_04720/glgA) KOX_06480/KOX_09255  KOX_06480 KOX_19195  KOX_09850/KOX_13720/KOX_20510 KOX_19195  KOX_20500/KOX_20505 KOX_20580/KOX_20505 KOX_08880/KOX_13720/KOX_20510 KOX_00880/KOX_13720/KOX_20510 KOX_00880/KOX_13720/KOX_20510 KOX_00880/KOX_13720/KOX_20510 KOX_00800/KOX_13720/KOX_20510 KOX_00800/KOX_13720/KOX_20510	cellulose_n -> 2 glc  cellulose_n -> cellulose_n_1 + glc  cellulose_n -> cellulose_n_1 + cellobiose  atp + g1p -> adpglc + ppi  adpglc -> glycogen + adp  adpglc -> amylose + adp  tre6p -> glc + g6p  mittp <-> glc + g6p  mittp <-> glc + n4  pheact -> pac + nh4  pheach + ad -> pac + nadh  pheacnit -> pheact  aconit -> aclm  adm -> propen + nh4  lactca + ac -> llac +> accoa
ENDOGLUC GIPADTRA GLYSYN1 GLYSYN2 TRE6PH MLT6PG AMD54 PHEALDD PHEACTHL ACLMHL AMD55 PCT3 SLFR	Starch and sucrose metabolism Styrene degradation	beta-glucosidase beta-glucosidase endoglucanase glucose-1-phosphate adenyiyftransferase glycogen synthase/starch synthase synthase glycogen synthase/starch synthase glucosidase/trehalose-6-phosphate glucosidase/trehalose-6-phosphate glucosidase amidose-6-phosphate glucosidase-6-phosphate glucosidase-6-phospha	32121 3214 27.727 24.121 24.121 32.1122/32.193 32.1122/35.14 12.139 42.184 42.184 43.514 28.31 18.12	KOX_00748/KOX_01670/KOX_18370/KOX_21960, KOX_23455/KOX_25615 KOX_04725(g)g/C) KOX_04725(g)g/A) KOX_04720(g)g/A) KOX_04720(g)g/A) KOX_06480/KOX_09255 KOX_06480 KOX_09850/KOX_13720/KOX_20510 KOX_19195 KOX_20500/KOX_20505 KOX_20500/KOX_20505 KOX_0650/KOX_20505 KOX_0650/KOX_205010 KOX_021010 KOX_01115/KOX_01120(cys)	cellulose_n -> 2 glc  cellulose_n -> cellulose_n_1 + glc  cellulose_n -> cellulose_n_1 + celluloise  atp + glp -> adpglc + ppi  adpglc -> glycogen + adp  adpglc -> amylose + adp  tre6p -> glc + g6p  mit6p <-> glc + g6p  pheact -> pac + nh4  pacalid + nad -> pac + nadh  pheacnit -> pheact  aconit -> aclm
ENDOGLUC GIPADTRA GLYSYN1 GLYSYN2 TRE6PH MLT6PG AMDS4 PHEALDD PHEACTHL ACLMHL AMDS5 PCT3	Starch and sucrose metabolism Styrene degradation	beta-glucosidase  beta-glucosidase  endoglucanase glucose-1-phosphate adenyiyftransferase glycogen synthase/starch synthase synthase glycogen synthase/starch synthase maltose-6-phosphate glucosidase/trehalose-6- phosphate hydrolase maltose-6-phosphate glucosidase amidase amidase dehydrogenase 2-phenylacetalidehyde dehydrogenase 2-phenylacetamide hydro-lyase (nitrile-forming) acnylamide hydro-lyase sulfite reductase phosphoadenylyl-sulfate reductase (thioredoxin)	32.121 32.14 2.7.27 24.121 24.121 32.1122/32.193 32.1122 35.14 12.139 42.184 42.184 35.14 28.31	KOX_00740,KOX_01670,KOX_18370,KOX_21960, KOX_23455,KOX_25615  KOX_04720[g]gA)  KOX_04720[g]gA)  KOX_04720[g]gA)  KOX_06480,KOX_09255  KOX_06480  KOX_09850,KOX_13720,KOX_20510  KOX_19195  KOX_20500,KOX_20505  KOX_20500,KOX_20505  KOX_00500,KOX_20505  KOX_00500,KOX_20505  KOX_00500,KOX_20505  KOX_00500,KOX_20505  KOX_00500,KOX_20505  KOX_00500,KOX_20505  KOX_00500,KOX_20505  KOX_01110,KOX_01120(c)ys1)  KOX_011116,KOX_01120(c)ys1)	cellobiose -> 2 glc  cellulose_n -> cellulose_n_1 + glc  cellulose_n -> cellulose_n_1 + cellobiose  atp + g1p -> adpglc + ppi  adpglc -> glycogen + adp  adpglc -> amylose + adp  trefip -> glc + g6p  mlt6p <-> glc + g6p  mlt6p <-> plc + nh4  pacald + nad -> pac + nh4  pacald + nad -> pac + nadh  pheacnit -> pheact  aconit -> propen + nh4  lactoa + ac -> llac + accoa  3 andh + so3 -> N2s + 3 nadp  paps + rthio -> pap + so3 + othio
ENDOGLUC GIPADTRA GLYSYN1 GLYSYN2 TRE6PH MLT6PG AMDS4 PHEALDD PHEACTHL ACLMHL AMDS5 PCT3 SLFR PASR1 ADSLFX1 BPNT	Starch and sucrose metabolism Styrene degradation	beta-glucosidase  beta-glucosidase  endoglucanase glucose-1-phosphate adenylyftransferase glycogen synthase/starch synthase synthase glycogen synthase/starch synthase maltose-6-phosphate glucosidase/trehalose-6- phosphate hydrolase maltose-6-phosphate glucosidase amidase amidase dehydrogenase 2-phenylacetalidehyde dehydrogenase 2-phenylacetamide hydro-lyase (nitrile-forming) acnylamide hydro-lyase sulfitar enductase propionate CoA-transferase sulfite reductase phosphoadenylyl-sulfate reductase (thioredoxin) adenylyl-sulfate kinase	32.121 32.14 27.727 24.121 24.121 32.1122/32.193 32.1122 35.14 12.139 42.184 42.184 42.184 35.14 28.31 18.12 18.48 27.125 31.137	KOX_0740,KOX_01670,KOX_18370,KOX_21960, KOX_23455,KOX_25615  KOX_04725(g)gC)  KOX_04720(g)gA)  KOX_04720(g)gA)  KOX_04720(g)gA)  KOX_05480,KOX_09255  KOX_05480  KOX_09850,KOX_13720,KOX_20510  KOX_19195  KOX_20500,KOX_20505  KOX_20500,KOX_20505  KOX_20500,KOX_20505  KOX_0540,KOX_01120(c)ys1)  KOX_01115,KOX_01120(c)ys1)  KOX_01115  KOX_01075  KOX_00595	cellobiose -> 2 glc  cellulose_n -> cellulose_n_1 + glc  cellulose_n -> cellulose_n_1 + cellobiose  atp + g1p -> adpglc + ppi  adpglc -> glycogen + adp  adpglc -> amylose + adp  tre6p -> glc + g6p  mit6p <-> glc + g6p  mit6p <-> plc + y6p  pheact -> pac + nhd  pacald + nad -> pac + nadh  pheacnit -> pheact  aconit -> aclm  adm -> propen + nhd  lactoa + ac -> llac + accoa  3 nadph + so3 -> b2s + 3 nadp  paps + rthio -> paps + so3 + othio  aps + atp -> adp + paps  pap +> mph pi
ENDOGLUC GIPADTRA GLYSYN1 GLYSYN2 TRE6PH MLT6PG AMDS4 PHEALDD PHEACTHL ACLMHL AMDS5 PCT3 SLFR PASR1 ADSLFK1 BPNT1 BPNT2	Starch and sucrose metabolism Styrene degradation	beta-glucosidase  beta-glucosidase  endoglucanase glucose-1-phosphate adenylytransferase glycogen synthase/starch synthase glycogen synthase/starch synthase glucosidase/trehalose-6- phosphate hydrolase maltose-6-phosphate glucosidase/trehalose-6- phosphate hydrolase maltose-6-phosphate glucosidase/trehalose-6- phosphate hydrolase maltose-6-phosphate glucosidase/trehalose-6- phosphate hydrolase amidase 2-phenylacetaldehyde dehydrogenase 2-phenylacetamide hydro-lyase (nitrile-forming) acrylamide rydro-lyase suffite reductase \$7.5-bisphosphate nucleotidase \$7.5-bisphosphate nucleotidase	32.121 32.14 2.7.27 2.4.121 2.4.121 3.2.1122/3.2.193 3.2.1122 3.5.1.4 1.2.139 4.2.184 4.2.184 3.5.1.4 1.8.12 1.8.48 2.7.125 3.1.37 3.1.37	KOX_00740/KOX_01670/KOX_18370/KOX_21960, KOX_23455/KOX_25615  KOX_04726(glgC)  KOX_04726(glgA)  KOX_04720(glgA)  KOX_06480/KOX_09255  KOX_06480/KOX_13720/KOX_20510  KOX_19195  KOX_20500/KOX_20505  KOX_06580/KOX_13720/KOX_20510  KOX_01115/KOX_01120(cys1)  KOX_01115/KOX_01120(cys1)  KOX_01075  KOX_00305	cellobiose -> 2 glc  cellulose_n -> cellulose_n 1 + glc  cellulose_n -> cellulose_n 1 + cellobiose  atp + g1p -> adpglc + ppi  adpglc -> glycogen + adp  adpglc -> amylose + adp  tre6p -> glc + g6p  mit6p -> glc + g6p  pheact -> pac + nh4  pacald + nad -> pac + nadh  pheacnit -> pheact  aconit -> aclm  adm -> propen + nh4  latctoa + ac -> llac -> accoa  3 nadph + so3 -> h2s + 3 nadp  paps + ethio -> pap + so3 -> othio  aps + atp -> adp + paps  pap -> amp + pi  paps -> aps -> pi
ENDOGLUC GIPADTRA GLYSYN1 GLYSYN2 TRE6PH MLT6PG AMDS4 PHEALDD PHEACTHL ACLMHL AMDS5 PCT3 SLFR PASR1 ADSLFX1 BPNT	Starch and sucrose metabolism Styrene degradation	beta-glucosidase  beta-glucosidase  endoglucanase glucose-1-phosphate adenylyftransferase glycogen synthase/starch synthase synthase glycogen synthase/starch synthase maltose-6-phosphate glucosidase/trehalose-6- phosphate hydrolase maltose-6-phosphate glucosidase amidase amidase dehydrogenase 2-phenylacetalidehyde dehydrogenase 2-phenylacetamide hydro-lyase (nitrile-forming) acnylamide hydro-lyase sulfitar enductase propionate CoA-transferase sulfite reductase phosphoadenylyl-sulfate reductase (thioredoxin) adenylyl-sulfate kinase	32.121 32.14 27.727 24.121 24.121 32.1122/32.193 32.1122/32.193 42.139 42.184 42.184 42.184 35.14 28.31 18.12 18.48 27.125 31.37 31.37 31.37	KOX_0740,KOX_01670,KOX_18370,KOX_21960, KOX_23455,KOX_25615  KOX_04725(g)gC)  KOX_04720(g)gA)  KOX_04720(g)gA)  KOX_04720(g)gA)  KOX_05480,KOX_09255  KOX_05480  KOX_09850,KOX_13720,KOX_20510  KOX_19195  KOX_20500,KOX_20505  KOX_20500,KOX_20505  KOX_20500,KOX_20505  KOX_0540,KOX_01120(c)ys1)  KOX_01115,KOX_01120(c)ys1)  KOX_01115  KOX_01075  KOX_00595	cellobiose -> 2 glc  cellulose_n -> cellulose_n_1 + glc  cellulose_n -> cellulose_n_1 + cellobiose  atp + g1p -> adpglc + ppi  adpglc -> glycogen + adp  adpglc -> amylose + adp  tre6p -> glc + g6p  mit6p <-> glc + g6p  mit6p <-> plc + y6p  pheact -> pac + nhd  pacald + nad -> pac + nadh  pheacnit -> pheact  aconit -> aclm  adm -> propen + nhd  lactoa + ac -> llac + accoa  3 nadph + so3 -> b2s + 3 nadp  paps + rthio -> paps + so3 + othio  aps + atp -> adp + paps  pap +> mph pi
ENDOGLUC G1PADTRA GLYSYN1 GLYSYN2 TRE6PH MLT6PG AMD54 PHEALDD PHEACTHL ACLMHL AMD55 PCT3 SLFR PASR1 ADSLFK1 BPN12 TAUDO GLUTPEPT	Starch and sucrose metabolism Styrene degradation	beta-glucosidase beta-glucosidase endoglucanase glucose-1-phosphate adenyyltransferase glycogen synthase/starch synthase synthase glycogen synthase/starch synthase glycogen synthase/starch synthase maltose-6-phosphate glucosidase/trehalose-6- phosphate lydrolase maltose-6-phosphate glucosidase/trehalose-6- glucosidase/trehalose-6- amidose delydrogenase 2-phenylacetainde hydro-lyase (mitrile-forming) acylamide hydro-lyase suffite reductase phosphoadenylyf-sulfate reductase (phosphoadenylyf-sulfate kinase 3/5-bisphophate nucleotidase 3/5-bisphophate nucleotidase 3/5-bisphophate nucleotidase 3/5-bisphophate nucleotidase 3/5-bisphophate nucleotidase 3/5-bisphophate nucleotidase	32121 3214 27.727 24.121 24.121 32.1122/32.193 32.1122/32.193 42.184 42.184 42.184 43.514 28.31 18.12 18.42 28.31 18.12 18.43 27.125 31.37	KOX_0748/KOX_01670/KOX_18370/KOX_21960, KOX_23455/KOX_25615 KOX_04725(g)gC) KOX_04720(g)gA) KOX_04720(g)gA) KOX_06480/KOX_09255 KOX_06480 KOX_09850/KOX_13720/KOX_20510 KOX_191915 KOX_0500/KOX_20505 KOX_0500/KOX_20505 KOX_0500/KOX_13720/KOX_20510 KOX_01110 KOX_01110 KOX_01110 KOX_01110 KOX_01110 KOX_01110 KOX_01110 KOX_0110005 KOX_0115/KOX_00015 KOX_00015 KOX_00015 KOX_01200(c)u1/KOX_16795 KOX_01370(c)u1/KOX_16795	cellulose_n -> 2 glc  cellulose_n -> cellulose_n_1 + glc  cellulose_n -> cellulose_n_1 + cellobiose  atp + glp -> adpglc + ppi  adpglc -> glycogen + adp  adpglc -> amylose + adp  tre6p -> glc + g6p  mit6p> glc + g6p  mit6p> pac + nh4  pacald + nad -> pac + nadh  pheacnt -> pheact  acont -> adm  adm -> propen + nh4  lactcos + ac -> liac + accoa  3 nadph + sod -> h2s + 3 nadp  paps + thio -> pap + sod + orbio  aps + atp -> adp + paps  pap -> amp + pi  paps -> amp + pi  paps -> aps + pi  add -> collection -> col
ENDOGLUC GIPADTRA GLYSYN1 GLYSYN2 TRE6PH MLT6PG AMD54 PHEALDD PHEACTHL ACLMHL AMD55 PCT3 SLFR PASR1 ADSLFK1 BPN12 TAUDO GLUTPEPT TRAKGTA	Starch and sucrose metabolism Styrene degradation Suffur Metabolism Taurine and Hypotaurine metabolism	beta-glucosidase  beta-glucosidase  endoglucanase glucose-1-phosphate adenyiyftransferase glycopen synthase/starch synthase synthase glycopen synthase/starch synthase glycopen synthase/starch synthase maltose-6-phosphate glucosidase/trehalose-6- phosphate hydroiase maltose-6-phosphate glucosidase amidase amidase amidase phenylacetamide hydroi-yase (nitrile-forming) acnylamide hydroi-yase glycomide synthamide syntha	32121 3214 27.727 24.121 24.121 32.1122/32.193 32.1122/32.193 42.184 42.184 42.184 43.5.14 28.31 18.12 18.42 28.31 31.37	KOX, 2014A(KOX, 201570/KOX, 18370/KOX, 21960, KOX, 23455/KOX, 25615) KOX, 24725(glgC) KOX, 24720(glgA) KOX, 04720(glgA) KOX, 06480/KOX, 29255 KOX, 06480/KOX, 29255 KOX, 26580/KOX, 13720/KOX, 20510 KOX, 191995 KOX, 20500/KOX, 20505 KOX, 20500/KOX, 20505 KOX, 20500/KOX, 20505 KOX, 20110/KOX, 20110/KOX, 20110 KOX, 20110 KOX, 20110/KOX, 20110/KOX, 20110/KOX, 20110 KOX, 20110/KOX, 20110/KOX, 20110/KOX, 20110 KOX, 20110/KOX, 20110/	cellulose_n -> 2 glc  cellulose_n -> cellulose_n_1 + glc  cellulose_n -> cellulose_n_1 + cellobiose  atp + glp -> adpglc + ppi  adpglc -> glycogen + adp  adpglc -> amylose + adp  tre6p -> glc + g6p  mit6p> glc + g6p  mit6p> pac + nh4  pacald + nad -> pac + nadh  pheacnt -> pheact  acont -> aclm  adm -> propen + nh4  lactcoa + ac -> liac + accoa  3 nadph + soa -> h2s + 3 nadp  paps + thio -> pap + so3 + othio  aps + atp -> adp + paps  pap >> amp + pi  paps >> amp + pi  paps >> amp + pi  paps >> aps pi  alt = cellulose_n -> cellulose_n
ENDOGLUC G1PADTRA GLYSYN1 GLYSYN2 TRE6PH MLT6PG AMD54 PHEALDD PHEACTHL ACLMHL AMD55 PCT3 SLFR PASR1 ADSLFK1 BPN12 TAUDO GLUTPEPT	Starch and sucrose metabolism Styrene degradation	beta-glucosidase beta-glucosidase endoglucanase glucose-1-phosphate adenyiyftransferase glycogen synthase/starch synthase synthase glycogen synthase/starch synthase glycogen synthase/starch synthase maltose-6-phosphate glucosidase/trehalose-6- phosphate hydrolase maltose-6-phosphate glucosidase amidase amidase amidase amidase dehydrogenase 2-phenylacetamide hydro-lyase (nitrile-forming) acylamide hydro-lyase suffice reductase phosphoadenylyl-sulfate reductase phosphoadenylyl-sulfate kinase 3/5-bisphosphate nucleotidase 3/5-bisphosphate nucleotidase 3/5-bisphosphate nucleotidase 3/5-bisphosphate nucleotidase 3/5-bisphosphate nucleotidase anima-glutamyltranspeptidase taurine-2-oxoglutarate transaminase thämine-phosphate diphosphonylase	32121 3214 27.727 24.121 24.121 32.1122/32.193 32.1122/32.193 42.184 42.184 42.184 43.514 28.31 18.12 18.42 28.31 18.12 18.43 27.125 31.37	KOX_0748/KOX_01670/KOX_18370/KOX_21960, KOX_23455/KOX_25615 KOX_04725(g)gC) KOX_04720(g)gA) KOX_04720(g)gA) KOX_06480/KOX_09255 KOX_06480 KOX_09850/KOX_13720/KOX_20510 KOX_191915 KOX_0500/KOX_20505 KOX_0500/KOX_20505 KOX_0500/KOX_20505 KOX_01110/KOX_01120(c)g5) KOX_01110 KOX_01110 KOX_01110 KOX_01110 KOX_01110 KOX_01100 KOX_01150 KOX_	cellulose_n -> 2 glc  cellulose_n -> cellulose_n_1 + glc  cellulose_n -> cellulose_n_1 + cellobiose  atp + glp -> adpglc + ppi  adpglc -> glycogen + adp  adpglc -> amylose + adp  tre6p -> glc + g6p  mit6p> glc + g6p  mit6p> pac + nh4  pacald + nad -> pac + nadh  pheacnt -> pheact  acont -> adm  adm -> propen + nh4  lactcos + ac -> liac + accoa  3 nadph + sod -> h2s + 3 nadp  paps + thio -> pap + sod + orbio  aps + atp -> adp + paps  pap -> amp + pi  paps -> amp + pi  paps -> aps + pi  add -> collection -> col
ENDOGLUC GIPADTRA GLYSYN1 GLYSYN2 TRE6PH MLT6PG AMD54 PHEALDD PHEACTHL ACLMHL AMD55 PCT3 SLFR PASR1 ADSLFK1 BPN12 TAUDO GLUTPEPT TRAKGTA	Starch and sucrose metabolism Styrene degradation Sulfur Metabolism Sulfur Metabolism Sulfur Metabolism Taurine and Hypotaurine metabolism Taurine and Hypotaurine metabolism Taurine and Hypotaurine metabolism	beta-glucosidase beta-glucosidase endoglucanase glucose-1-phosphate adenylytransferase glycogen synthase/starch synthase glycogen synthase/starch synthase glycogen synthase/starch synthase maltose-6-phosphate glucosidase/trehalose-6- phosphate hydrolase maltose-6-phosphate glucosidase/trehalose-6- phosphate hydrolase amidase amidase phenylacetalidehyde dehydrogenase 2-phenylacetamide hydro-lyase (nitrile-formiga) acnylamide hydro-lyase amidase propionate CoA-transferase sulfine reductase phosphoademylyi-sulfate transaminase	32121 3214 27.727 24.121 24.121 32.1122/32.193 32.1122/32.193 42.184 42.184 42.184 43.5.14 28.31 18.12 18.42 28.31 31.37	KOX, 2014A(KOX, 201570/KOX, 18370/KOX, 21960, KOX, 23455/KOX, 25615) KOX, 24725(glgC) KOX, 24720(glgA) KOX, 04720(glgA) KOX, 06480/KOX, 29255 KOX, 06480/KOX, 29255 KOX, 26580/KOX, 13720/KOX, 20510 KOX, 191995 KOX, 20500/KOX, 20505 KOX, 20500/KOX, 20505 KOX, 20500/KOX, 20505 KOX, 20110/KOX, 20110/KOX, 20110 KOX, 20110 KOX, 20110/KOX, 20110/KOX, 20110/KOX, 20110 KOX, 20110/KOX, 20110/KOX, 20110/KOX, 20110 KOX, 20110/KOX, 20110/	cellulose_n -> 2 glc  cellulose_n -> cellulose_n_1 + glc  cellulose_n -> cellulose_n_1 + cellobiose  atp + glp -> adpglc + ppi  adpglc -> glycogen + adp  adpglc -> amylose + adp  tre6p -> glc + g6p  mit6p> glc + g6p  mit6p> pac + nh4  pacald + nad -> pac + nadh  pheacnt -> pheact  aconit -> adm  adm -> propen + nh4  lactca + ac -> liac + accoa  3 nadph + so3 -> h2s + 3 nadp  paps + tribi -> pap + so3 + orbio  aps + atp -> adp + paps  pap -> amp + pi  paps -> amp + pi  paps -> aps + pi  adg -> 2 + taur -> aacald + co2 + so3 + succ  pept + glutaur -> glupept + taur  taur + akg -> sulald + glu
ENDOGLUC GIPADIRA GLYSYN1 GLYSYN2 TRE6PH MLT6PG AMDS4 PHEALDD PHEACTHL ACLMHL AMDS5 PCT3 SLFR PASR1 ADSLEK1 BPNT BPNT TAUDO GLUTPEPT TRAKGTA THMPDP HMPMK HETHZK	Starch and sucrose metabolism Styrene degradation	beta-glucosidase beta-glucosidase endoglucanase glucose-1-phosphate adenylytransferase glycogen synthase/starch synthase glycogen synthase/starch synthase glycogen synthase/starch synthase maltose-6-phosphate glucosidase/trehalose-6- phosphate hydrolase maltose-6-phosphate glucosidase/trehalose-6- phosphate hydrolase maltose-6-phosphate glucosidase/trehalose-6- phosphate hydrolase maltose-6-phosphate glucosidase amidase phenylacetalidehyde dehydrogenase p-pospinate-CoA-transferase sulfite reductase phosphoadenylyf-sulfate reductase (thoredoxin) adenylyf-sulfate kinase 3,5-bsphosphate nucleotidase 3,5-bsphosphate nucleotidase Taurine dioxygenase gamma-glutamytranspeptidase taurine2-oxoglutarate transaminase thiamine-phosphate diphosphonylase kinase (ATP) hydroxyethythiazole kinase	32.121 32.14 27.727 24.121 24.121 32.1122/32.193 32.1122 35.14 12.139 42.184 42.184 42.184 42.184 28.31 18.12 18.48 27.125 3.137 114.1117 23.22 26.155 25.13 27.149 27.150	KOX_00740,ROX_01670/KOX_18370/KOX_21960, KOX_23455/ROX_25615  KOX_04726[g]c] KOX_04726[g]gA) KOX_04720[g]gA) KOX_06480/KOX_09255  KOX_06480/KOX_13720/KOX_20510 KOX_19195  KOX_20500/KOX_20505 KOX_20500/KOX_20505 KOX_20500/KOX_13720/KOX_20510 KOX_01115/KOX_01120(cysl) KOX_01115/KOX_01120(cysl) KOX_011075 KOX_01075 KOX_04780[ggtf/KOX_16795 KOX_04780[ggtf/KOX_16795 KOX_07505	cellulose_n -> 2 glc  cellulose_n -> cellulose_n_1 + glc  cellulose_n -> cellulose_n_1 + cellobiose  atp + g1p -> adpglc + ppi  adpglc -> glycogen + adp  adpglc -> amylose + adp  tre6p -> glc + g6p  mit6p <-> glc + g6p  mit6p <-> glc + g6p  pheact -> pac + nh4  pacald + nad -> pac + nadh  pheacnit -> pheact  aconit -> acon  adm -> propen + nh4  lactoa + ac -> llac + accoa  3 andph + so3 -> h2s + soadp  paps + rthio -> pap + so3 + othio  aps + at +> adp + paps  pap > amp + p1  adg + o2 + taur -> aacald + co2 + so3 + succ  pept + glutaur -> glupept + taur  taur + akg -> sulad + glu  ahnpp + thzp -> ppi + thmp  ahn + atp -> dampm + adp  4mhetz + atp -> taup + taup
ENDOGLUC G1PADTRA GLYSYN1 GLYSYN2 TRE6PH MLT6PG AMD54 PHEALDD PHEACTHL ACLMHL AMD55 PCT3 SLFR PASR1 ADSLFK1 BPN12 TAUDO GLUTPEPT TRAKGTA THMPDP HMPMK HETHZK THMPK	Starch and sucrose metabolism Styrene degradation Styren	beta-glucosidase beta-glucosidase endoglucanase glucose-1-phosphate adenyiyftransferase glycogen synthase/starch synthase synthase glycogen synthase/starch synthase maltose-6-phosphate glucosidase/trehalose-6- phosphate hydrolase maltose-6-phosphate glucosidase amidase amidase amidase dehydrogenase 2-phenylacetaindle hydro-lyase (nitrile-forming) acylamide hydro-lyase synthase propionate CoA-transferase sulfite reductase phosphoadenylyl-sulfate reductase (1)5-bisphosphate nucleotidase 3,5-bisphosphate nucleotidase 3,5-bisphosphate nucleotidase 3,5-bisphosphate nucleotidase 3,5-bisphosphate nucleotidase taurine—2-oxoglutarate transaminase thämine-phosphate diphosphonyjonidie kinase (ATP) hydroveethythiazole kinase hydrosynthikazole kinase hydrosynthikazole kinase hydrosynthikazole kinase hydrosynthikazole kinase hydrosynthikazole kinase hydrosynthyfivarole kinase hydrosyethythiazole kinase thämine-phosphate kinase	32.121 32.14 27.727 24.121 24.121 32.1122/32.193 32.1122 35.14 12.139 42.184 42.184 43.514 28.31 18.12 18.12 18.13 13.17 31.37	KOX, 2013/A(KOX, 2015/0)/KOX, 18370/KOX, 21960, KOX, 23455/KOX, 25615  KOX, 24725(glgC)  KOX, 24720(glgA)  KOX, 04720(glgA)  KOX, 06480/KOX, 29255  KOX, 06480/KOX, 29255  KOX, 26580/KOX, 13720/KOX, 20510  KOX, 19199  KOX, 20500/KOX, 20505  KOX, 20500/KOX, 20505  KOX, 20500/KOX, 20505  KOX, 20500/KOX, 20505  KOX, 20111/KOX, 20110/KOX, 20110  KOX, 20110  KOX, 20110  KOX, 20110  KOX, 20110  KOX, 20110  KOX, 20117  KOX, 20035  KOX, 12300(auD)  KOX, 213775  KOX, 207960  KOX, 25505	cellulose_n -> 2 glc  cellulose_n -> cellulose_n_1 + glc  cellulose_n -> cellulose_n_1 + cellobiose  atp + glp -> adpglc + ppi  adpglc -> glycogen + adp  adpglc -> amylose + adp  tre6p -> glc + g6p  mit6p> glc + g6p  mit6p> glc + g6p  pheact -> pac + nh4  pacalid + nad -> pac + nadh  pheacnit -> pheact  aconit -> aclm  adm -> propen + nh4  lactica + ac -> lia + accoa  3 nadph + so 3 -> h2s + 3 nadp  paps + rthio -> pap + so 3 + othio  aps + alp -> adp + paps  pap -> amp + pi  paps -> amp + pi  paps -> amp + pi  paps -> glc + g6p  ahmp + thrp -> papi + thmp  ahm + atp -> sualid + glu  ahmp + thrp -> ppi + thmp  ahm + atp -> dap + thmp  atp + thmp -> adp + thmp  atp + thmp  atp + thmp  adp -> adp + thmp
ENDOGLUC GIPADIRA GLYSYN1 GLYSYN2 TRE6PH MLT6PG AMDS4 PHEALDD PHEACTHL ACLMHL AMDS5 PCT3 SLFR PASR1 ADSLFK1 BPNT BPNT2 TAUDO GLUTPEPT TRAKGTA THMPDP HMPMK HETHZK THMPK PMPMK	Starch and sucrose metabolism Styrene degradation Styrene despradation Styrene degradation Styrene degrada	beta-glucosidase beta-glucosidase endoglucanase glucose-1-phosphate adenyiyftransferase glycogen synthase/starch synthase synthase glycogen synthase/starch synthase maltose-6-phosphate glucosidase/trehalose-6- phosphate hydrolase maltose-6-phosphate glucosidase amidase amidase amidase dehydrogenase 2-phenylacetamide hydro-lyase (nitrile-forming) acnylamide hydro-lyase glidase synthase propionate CoA-transferase sulfite reductase phosphoadenylyl-sulfate reductase phosphoadenylyl-sulfate kinase 3.5-bisphosphate nucleotidase 3.5-bisphosphate nucleotidase 3.5-bisphosphate nucleotidase 3.5-bisphosphate nucleotidase taurine—2-oxoglutarate transaminase thämine-phosphate diphosphonylaridine kinase (ATP) hydrovgethylthiazole kinase phosphomethylpyrimidine kinase (ATP) hydrovgethylthiazole kinase phosphomethylpyrimidine kinase	32.121 32.14 27.727 24.121 24.121 32.1122/32.193 32.1122 3.5.14 12.139 42.184 42.184 42.184 3.5.14 2.8.31 1.8.12 1.8.48 2.7.125 3.137 3.13	KOX_00740,ROX_01670/KOX_18370/KOX_21960, KOX_23455/ROX_25615  KOX_04726[g]c] KOX_04726[g]gA) KOX_04720[g]gA) KOX_06480/KOX_09255  KOX_06480/KOX_13720/KOX_20510 KOX_19195  KOX_20500/KOX_20505 KOX_20500/KOX_20505 KOX_20500/KOX_13720/KOX_20510 KOX_01115/KOX_01120(cysl) KOX_01115/KOX_01120(cysl) KOX_011075 KOX_01075 KOX_04780[ggtf/KOX_16795 KOX_04780[ggtf/KOX_16795 KOX_07505	cellulose_n -> 2 glc  cellulose_n -> cellulose_n_1 + glc  cellulose_n -> cellulose_n_1 + cellobiose  atp + glp -> adpglc + ppi  adpglc -> glycogen + adp  adpglc -> amylose + adp  tre6p -> glc + g6p  mit6p> glc + g6p  mit6p> plc + g6p  pheact -> pac + nh4  pacald + nad -> pac + nadh  pheacnit -> pheact  aconit -> aclm  adm -> propen + nh4  lactoa + ac -> llac + accoa  3 nadph + so3 -> bx 5 + 3 nadp  paps + rthio -> paps + paps  pap -> amp + pap  paps -> amp + pa  paps -> amp + pa  paps -> aps + pi  adsy -> cell + taur -> accald + co2 + so3 + succ  pept + glutaur -> glupept + taur  taur + akg -> sulaid + glu  ahmpp + thxp -> ppi + thmp  ahm + atp -> dampm + adp  4mhetz + atp -> thxp + adp  atp + thmp -> adp + thmpp  4ampm + atp -> ahmpp + adp
ENDOGLUC G1PADTRA GLYSYN1 GLYSYN2 TRE6PH MLT6PG AMD54 PHEALDD PHEACTHL ACLMHL AMD55 PCT3 SLFR PASR1 ADSLFK1 BPN12 TAUDO GLUTPEPT TRAKGTA THMPDP HMPMK HETHZK THMPK	Starch and sucrose metabolism Styrene degradation Styren	beta-glucosidase beta-glucosidase endoglucanase glucose-1-phosphate adenylytransferase glycogen synthase/starch synthase glycogen synthase/starch synthase maltose-6-phosphate glucosidase/trehalose-6- phosphate hydrolase maltose-6-phosphate glucosidase/trehalose-6- phosphate hydrolase maltose-6-phosphate glucosidase/trehalose-6- phosphate hydrolase maltose-6-phosphate glucosidase/trehalose-6- phosphate hydrolase maltose-6-phosphate glucosidase amidase phenylacetamide hydro-lyase (nitrile-formig) acrylamide hydro-lyase amidase propionate CoA-transferase sulfite reductase phosphoadenyly-sulfate reductase (thioredoxin) adenyly-sulfate kinase phosphoadenyly-sulfate kinase gamma-glutanytranspeptidase taurine2-oxoglutarate transaminase thiamine-phosphate kinase (ATP) hydroxyethylprimidine kinase (ATP) hydroxyethylpyrimidine kinase (ATP) hydroxyethylpyrimidine kinase	32.121 32.14 27.727 24.121 24.121 32.1122/32.193 32.1122 35.14 12.139 42.184 42.184 43.514 28.31 18.12 18.12 18.13 13.17 31.37	KOX, 2013/A(KOX, 2015/0)/KOX, 18370/KOX, 21960, KOX, 23455/KOX, 25615  KOX, 24725(glgC)  KOX, 24720(glgA)  KOX, 04720(glgA)  KOX, 06480/KOX, 29255  KOX, 06480/KOX, 29255  KOX, 26580/KOX, 13720/KOX, 20510  KOX, 19199  KOX, 20500/KOX, 20505  KOX, 20500/KOX, 20505  KOX, 20500/KOX, 20505  KOX, 20500/KOX, 20505  KOX, 20111/KOX, 20110/KOX, 20110  KOX, 20110  KOX, 20110  KOX, 20110  KOX, 20110  KOX, 20110  KOX, 20117  KOX, 20035  KOX, 12300(auD)  KOX, 213775  KOX, 207960  KOX, 25505	cellulose_n -> 2 glc  cellulose_n -> cellulose_n_1 + glc  cellulose_n -> cellulose_n_1 + cellobiose  atp + glp -> adpglc + ppi  adpglc -> glycogen + adp  adpglc -> amylose + adp  tre6p -> glc + g6p  mit6p> glc + g6p  mit6p> glc + g6p  pheact -> pac + nh4  pacalid + nad -> pac + nadh  pheacnit -> pheact  aconit -> aclm  adm -> propen + nh4  lactica + ac -> lia + accoa  3 nadph + so 3 -> h2s + 3 nadp  paps + rthio -> pap + so 3 + othio  aps + alp -> adp + paps  pap -> amp + pi  paps -> amp + pi  paps -> amp + pi  paps -> glc + g6p  ahmp + thrp -> papi + thmp  ahm + atp -> sualid + glu  ahmp + thrp -> ppi + thmp  ahm + atp -> dap + thmp  atp + thmp -> adp + thmp  atp + thmp  atp + thmp  adp -> adp + thmp
ENDOGLUC GIPADIRA GLYSYN1 GLYSYN2 TRE6PH MLT6PG AMDS4 PHEALDD PHEACTHL ACLMHL AMDS5 PCT3 SLFR PASR1 ADSLEXL BPNT BPNT2 TAUDO GLUTPEPT TRAKGTA THMPDP HMPMK HETHZK THMPK THMPK	Starch and sucrose metabolism Styrene degradation Styrene degradat	beta-glucosidase beta-glucosidase endoglucanase glucose-1-phosphate adenylytransferase glycogen synthase/starch synthase synthase glycogen synthase/starch synthase maltose-6-phosphate glucosidase/trehalose-6- phosphate hydrolase maltose-6-phosphate glucosidase/strehalose-6- phosphate hydrolase maltose-6-phosphate glucosidase amidase amidase dehydrogenase synthase phosphate hydrol-yase (nitrile-forming) acrylamide hydro-lyase amidase propionate CoA-transferase sulfile reductase phosphoadenylyl-sulfate reductase (thioredoxin) adenylyl-sulfate kinase phosphoadenylyl-sulfate kinase phosphoadenylyl-sulfate kinase phosphoadenylyl-sulfate kinase transaminase tinamine-phosphate nucleotidase 3-5-bisphosphate nucleotidase taurine2-oxoglutarate transaminase tinamine-phosphate kinase hydrosynethythiziaole kinase thiamine-phosphate kinase thiamine-phosphate kinase thiamine-phosphatese thiamine kinase thiamine kinase thiamine kinase	32121 3214 27.727 24.121 24.121 32.1122/32.193 32.1122 35.14 12.139 42.184 42.184 42.184 42.184 28.31 18.12 18.48 27.125 31.37 31.37 114.1117 23.22 26.155 25.13 27.149 27.150 27.416 27.47 31.3.	KOX_00740,ROX_01670/KOX_18370/KOX_21960, KOX_23455/ROX_25615  KOX_04726[g]c] KOX_04720[g]gA) KOX_04720[g]gA) KOX_06480/KOX_09255  KOX_06480/KOX_13720/KOX_20510 KOX_19195  KOX_20500/KOX_20505 KOX_20500/KOX_20505 KOX_20500/KOX_20505 KOX_00500/KOX_20505 KOX_00500/KOX_13720/KOX_20510 KOX_01110 KOX_01075 KOX_01110 KOX_01075 KOX_01120/KOX_0120/KOX_0120 KOX_0117675 KOX_017575 KOX_01775 KOX_07960 KOX_25505 KOX_25505 KOX_25505 KOX_25505 KOX_25505	cellulose_n -> 2 glc  cellulose_n -> cellulose_n_1 + cellulose atp + g1p -> adpglc + ppi  adpglc -> glycogen + adp  adpglc -> glycogen + adp  adpglc -> amylose + adp  trefip -> glc + g6p  milt6p -> glc + g6p  milt6p -> glc + g6p  pheact -> pac + mh4  pacald + nad -> pac + nadh  pheacnit -> pheact  aconit -> acim  adm -> propen + nh4  lactoa + ac -> liac + accoa  3 nadph + so3 -> h2s + s nadp  paps + rthio -> pap + so3 + othio  aps + atp -> adp + paps  pap -> amp + pi  paps -> ags + pi  adg + o2 + taur -> aacald + co2 + so3 + succ  pept + glutaur -> glupept + taur  taur + akg -> sulald + glu  ahmpp + thrp -> ppi + thmp  ahm + atp -> tmpp + adp  4mmpm + adp -> adp + pap  patp + mhe -> adp  4mmpm + adp -> tmpp + adp  thiamin + pi -<> tmpp
ENDOGLUC GIPADIRA GLYSYN1 GLYSYN2 TRE6PH MLT6PG AMDS4 PHEALDD PHEACTHL ACLMHL AMDS5 PCT3 SLFR PASR1 ADSLFK1 BPNT BPNT2 TAUDO GLUTPEPT TRAKGTA THMPDP HMPMK HETHZK THMPK THMPK THMR THMR THMR THMR THMB	Starch and sucrose metabolism Styrene degradation Styren	beta-glucosidase beta-glucosidase endoglucanase glucose-1-phosphate adenylyftransferase glycogen synthase/starch synthase synthase glycogen synthase/starch synthase maltose-6-phosphate glucosidase/trehalose-6- phosphate hydrolase maltose-6-phosphate glucosidase/trehalose-6- phosphate hydrolase maltose-6-phosphate glucosidase amidase amidase amidase aphenylacetalidehyde dehydrogende dehydrogende services phosphate hydro-lyase (nitrile-forming) acrylamide hydro-lyase propionate CoA-transferase sulfite reductase phosphoadenylyl-sulfate reductase (thioredoxin) adenylyl-sulfate kinase phosphoadenylyl-sulfate kinase phosphoadenylyl-sulfate kinase gamma-glutamyltranspeptidase taurine—2-oxoglutarate transaminase thiamine-phosphate kinase hydrosynethylyprimidine kinase (ATP) hydrosyethylprimidine kinase phosphoadenylyprimidine kinase thiamine-phosphate kinase thiamine-phosphate kinase thiamine iknase thiamine kinase thiamine kinase thiamine kinase thiamine kinase thiamine kinase	32.121 32.14 2.7.727 2.4.121 2.4.121 3.2.1122/3.2.193 3.2.1122 3.5.14 1.2.139 4.2.184 4.2.184 4.2.184 2.8.31 1.8.12 1.8.48 2.7.125 3.1.37 1.14.11.17 2.3.22 2.6.155 2.5.13 2.7.149 2.7.150 2.7.416 2.7.47 3.1.3. 2.7.189 undear reaction	KOX_00740/KOX_01670/KOX_18370/KOX_21960, KOX_23455/KOX_25615  KOX_04726[g]c] KOX_04726[g]gA) KOX_04720[g]gA) KOX_06480 KOX_06480 KOX_06480/KOX_13720/KOX_20510 KOX_19195  KOX_20500/KOX_20505 KOX_20500/KOX_20505 KOX_20500/KOX_20505 KOX_20500/KOX_20505 KOX_20500/KOX_20505 KOX_0010 KOX_01115/KOX_01120(kysl) KOX_01100 KOX_01075 KOX_011075 KOX_01120(kysl) KOX_017355(kysl) KOX_1237076 KOX_1237076 KOX_123705 KOX_123506 KOX_123705	cellulose_n -> 2 glc  cellulose_n -> cellulose_n_1 + cellobiose  atp + g1p -> adpglc + ppi  adpglc -> glycogen + adp  adpglc -> glycogen + adp  adpglc -> amylose + adp  treëp -> glc + g6p  mit6p <-> glc + g6p  mit6p <-> glc + g6p  pheact -> pac + mhd  pacald + nad -> pac + nadh  pheacnit -> pheact  aconit -> acon  adm -> propen + nhd  lactca + ac -> liac + accoa  3 nadph + so 3 -> h2z + 3 nadp  paps + rthio -> pap + so3 + othio  aps + atp -> adp + paps  pap -> amp + pi  paps -> ags + pi  adsy + o2 + taur -> aacald + co2 + so3 + succ  pept + glutaur -> glupept + taur  taur + adg -> sulald + glu  ahmpp + thrp -> ppi + thmp  ahm + atp -> 4ampm + adp  4mmpm + atp -> adp + mpp  thamin + pi <-> thmp  thamin + pi <-> thmp  thamin + pi <-> thmp  thamin + pi <> thmp  tair -> ahm  atp + cys + dx6p + byr >> 4bbza + thzp + ala + amp + co2 + ppi
ENDOGLUC GIPADIRA GLYSYN1 GLYSYN2 TRE6PH MLT6PG AMDS4 PHEALDD PHEACTHL ACLMHL AMDS5 PCT3 SLFR PASR1 ADSLFR1 BPN17 TAUDO GLUTPEPT TRAKGTA THMPDP HMPMK HETHZK THMPK PMPMK THIMPT THIMK THMB	Starch and sucrose metabolism Styrene degradation Styrene degradat	beta-glucosidase  beta-glucosidase  endoglucanase glucose-1-phosphate adenyiyftransferase glycopen synthase/starch synthase synthase glycopen synthase/starch synthase maltose-6-phosphate glucosidase/strehalose-6-phosphate plucosidase/strehalose-6-phosphate glucosidase amidase amidase amidase amidase amidase amidase phenylacetamide hydro-lyase (nitrile-formiga) acn/amide hydro-lyase suffice reductase phosphoadenyiyf-suffate reductase phosphoadenyiyf-suffate reductase phosphoadenyiyf-suffate reductase phosphoadenyiyf-suffate reductase phosphoadenyiyf-suffate reductase glucosidase amidase propionate CoA-transferase suffite reductase phosphoadenyiyf-suffate reductase glycopabate nucleotidase 3.5°-bisphosphate nucleotidase 3.5°-bisphosphate nucleotidase aturine—2-oxoglutarate transaminase transaminase thiamine-phosphate diphosphonylase hydroymethyfpyrimidine kinase (ATP) hydrovethyfthiazole kinase phosphatase thiamine biosynthesis protein ThiC thiaxole phosphate synthesis Thiamin hydrodase	32121 3214 27.727 24.121 24.121 32.1122/32.193 32.1122/32.193 42.184 42.184 42.184 43.5.14 28.31 18.12 18.12 18.13 13.17 31.37	KOX_0704A(KOX_01670)KOX_18370/KOX_21960, KOX_23455/KOX_25615 KOX_04725(g)gC) KOX_04720(g)gA) KOX_04720(g)gA) KOX_06480/KOX_09255 KOX_06480 KOX_09850/KOX_13720/KOX_20510 KOX_19199 KOX_0500/KOX_20505 KOX_069850/KOX_13720/KOX_20510 KOX_01115/KOX_01120(c)g1) KOX_01110 KOX_01115/KOX_01120(c)g1) KOX_0113775 KOX_06035 KOX_12300(c)g1) KOX_04780(g)g1/KOX_16795 KOX_07960 KOX_25505 KOX_25505 KOX_25505 KOX_25505 KOX_25505 KOX_25505 KOX_25505 KOX_17355(c)hik)	cellulose_n -> 2 glc  cellulose_n -> cellulose_n_1 + glc  cellulose_n -> cellulose_n_1 + cellobiose  atp + glp -> adpglc + ppi  adpglc -> glycogen + adp  adpglc -> amylose + adp  ttre6p -> glc + g6p  mit6p> glc + g6p  mit6p> plc + g6p  pheact -> pac + nh4  pacald + nad -> pac + nadh  pheacnit -> pheact  aconit -> aclm  adm -> propen + nh4  latcoa + ac -> liac + accoa  3 nadph + so3 -> h2s + 3 nadp  paps + rthio -> paps + paps  pap -> amp + pi  paps -> amp + pi  paps -> aps + pi  akg + o2 + taur -> aacald + co2 + so3 + succ  pept + glutaur -> glupept + taur  taur + akg -> sulaid + glu  ahmpp + thzp -> ppi + thmp  ahm + atp -> dampm + adp  4mhetz + atp -> thzp + adp  atp + thmp -> adp + thmpp  4ampm + atp -> ahmpp + adp  thamin + atp -> thmp
ENDOGLUC GIPADIRA GLYSYN1 GLYSYN2 TRE6PH MLT6PG AMDS4 PHEALDD PHEACTHL ACLMHL AMDS5 PCT3 SLFR PASR1 ADSLFK1 BPNT BPNT2 TAUDO GLUTPEPT TRAKGTA THMPDP HMPMK HETHZK THMPK THMPK THMR THMR THMR THMR THMB	Starch and sucrose metabolism Styrene degradation Styren	beta-glucosidase  beta-glucosidase  endoglucanase glucose-1-phosphate adenyiyftransferase glycopen synthase/starch synthase synthase glycopen synthase/starch synthase maltose-6-phosphate glucosidase/strehalose-6-phosphate plucosidase/strehalose-6-phosphate glucosidase amidase amidase amidase amidase amidase amidase amidase behyrio-glacetaldehyde dehydrogenase 2-phenylacetamide hydro-lyase (nitrile-formig) acn/amide hydro-lyase sumidase propionate (OA-transferase sulfite reductase phosphoadenylyf-sulfate reductase (phosphoadenylyf-sulfate kinase 3',5-bisphosphate nucleotidase 3',5-bisphosphate nucleotidase 3',5-bisphosphate nucleotidase 3',5-bisphosphate nucleotidase alimine-phosphate transaminase thämine-phosphate diphosphonylase hydroymethyfpyrimidine kinase kinase (ATP) hydrovgethyfthiazole kinase phosphatase thämine biosynthesis protein Thic thiaxole phosphate synthesis Thiamin hydrolase 2-hydrosy-5-methyl-cic,is- muconate 2-Osc-5-methyl-cic,is- muconate 2-Osc-5-methyl-cic,is-	32.121 32.14 2.7.727 2.4.121 2.4.121 3.2.1122/3.2.193 3.2.1122 3.5.14 1.2.139 4.2.184 4.2.184 4.2.184 3.5.14 2.8.31 1.8.12 1.8.48 2.7.125 3.137 3.1.37 1.1411.17 2.3.22 2.6.155 2.5.13 2.7.149 2.7.150 2.7.416 2.7.47 3.1.3. 2.7.189 unclear reaction 3.5.99.2	KOX_00740/KOX_01670/KOX_18370/KOX_21960, KOX_23455/KOX_25615  KOX_04726[g]c] KOX_04726[g]gA) KOX_04720[g]gA) KOX_06480 KOX_06480 KOX_06480/KOX_13720/KOX_20510 KOX_19195  KOX_20500/KOX_20505 KOX_20500/KOX_20505 KOX_20500/KOX_20505 KOX_20500/KOX_20505 KOX_20500/KOX_20505 KOX_0010 KOX_01115/KOX_01120(kysl) KOX_01100 KOX_01075 KOX_011075 KOX_01120(kysl) KOX_017355(kysl) KOX_1237076 KOX_1237076 KOX_123705 KOX_123506 KOX_123705	cellulose_n -> 2 glc  cellulose_n -> cellulose_n_1 + cellobiose  atp + g1p -> adpglc + ppi  adpglc -> glycogen + adp  adpglc -> glycogen + adp  adpglc -> amylose + adp  treëp -> glc + g6p  mit6p <-> glc + g6p  mit6p <-> glc + g6p  pheact -> pac + mhd  pacald + nad -> pac + nadh  pheacnit -> pheact  aconit -> acon  adm -> propen + nhd  lactca + ac -> liac + accoa  3 nadph + so 3 -> h2z + 3 nadp  paps + rthio -> pap + so3 + othio  aps + atp -> adp + paps  pap -> amp + pi  paps -> ags + pi  adsy + o2 + taur -> aacald + co2 + so3 + succ  pept + glutaur -> glupept + taur  taur + adg -> sulald + glu  ahmpp + thrp -> ppi + thmp  ahm + atp -> 4ampm + adp  4mmpm + atp -> adp + mpp  thamin + pi <-> thmp  thamin + pi <-> thmp  thamin + pi <-> thmp  thamin + pi <> thmp  tair -> ahm  atp + cys + dx6p + byr >> 4bbza + thzp + ala + amp + co2 + ppi
ENDOGLUC GIPADIRA GLYSYN1 GLYSYN2 TRE6PH MLT6PG AMDS4 PHEALDD PHEACTHL ACLMHL AMDS5 PCT3 SLFR PASR1 ADSLFX1 BPNT BPNT2 TAUDO GLUTPEPT TRAKGTA THMPDP HMPMK HETHZK THMPK THMPK THMR THMR THMR THMR THMB	Starch and sucrose metabolism Styrene degradation Styren	beta-glucosidase beta-glucosidase endoglucanase glucose-1-phosphate adenylytransferase glycogen synthase/starch synthase synthase glycogen synthase/starch synthase maltose-6-phosphate glucosidase/trehalose-6- phosphate hydrolase maltose-6-phosphate glucosidase/trehalose-6- phosphate hydrolase maltose-6-phosphate glucosidase amidase amidase amidase amidase phenylacetalidehyde dehydrogenate glucosidase synthase phenylacetamide hydro-lyase (nitrile-forming) acrylamide hydro-lyase amidase propionate CoA-transferase sulfite reductase phosphoadenyly1-sulfate reductase (thioredoxin) adenyly1-sulfate kinase phosphoadenyly1-sulfate kinase phosphoadenyly1-sulfate kinase gamma-glutamyltranspeptidase taurine -2-coxoglutarate transaminase thaimine-phosphate kinase thiamine-phosphate kinase thiamine-phosphate kinase thiamine-phosphate kinase thiamine iknase thiamine kinase	32.121 32.14 2.7.727 2.4.121 2.4.121 3.2.1122/3.2.193 3.2.1122 3.5.14 1.2.139 4.2.184 4.2.184 3.5.14 2.8.31 1.8.12 1.8.48 2.7.125 3.137 3.1.37 1.14.11.17 2.3.22 2.6.155 2.5.13 2.7.149 2.7.150 2.7.416 2.7.47 3.1.3. 2.7.189 unclear reaction 3.5.99.2 5.3.2-	KOX_00740,ROX_01670/KOX_18370/KOX_21960, KOX_23455/ROX_25615  KOX_04725(g)gC) KOX_04720(g)gA) KOX_04720(g)gA) KOX_06480/KOX_09255  KOX_06480 KOX_06480/KOX_13720/KOX_20510 KOX_19195  KOX_20500/KOX_20505 KOX_20500/KOX_20505 KOX_20500/KOX_20505 KOX_02500/KOX_20505 KOX_0010 KOX_01115/KOX_01120(kysl) KOX_0110 KOX_01075 KOX_011075 KOX_01120(kysl) KOX_01170 KOX_01175 KOX_01175 KOX_01175 KOX_12300(tauD) KOX_04780(ggt)/KOX_16795 KOX_12506 KOX_25505 KOX_25505 KOX_25505 KOX_25505 KOX_12590 KOX_17355(thiK) KOX_17355(thiK) KOX_17355(thiK) KOX_17365	cellulose_n -> 2 glc  cellulose_n -> cellulose_n_1 + glc  cellulose_n -> cellulose_n_1 + cellobiose  atp + g1p -> adpglc + ppi  adpglc -> glycogen + adp  adpglc -> amylose + adp  trefip -> glc + g6p  milt6p -> glc + g6p  milt6p -> glc + g6p  pheact -> pac + nh4  pacald + nad -> pac + nadh  pheacnit -> pheact  aconit -> aclm  adm -> propen + nh4  lactca + ac -> llac + accoa  3 nadph + so3 -> h2s +3 nadp  paps + rthio -> pap + so3 + othio  aps + atp -> adp + paps  pap -> amp + pi  paps -> aps + pi  ads + o2 + taur -> aacald + co2 + so3 + succ  pept + glutaur -> glupept + taur  taur + akg -> sulaid + glu  ahmpp + thrp -> ppi + thmp  ahm + atp -> 4ampm + adp  4mhetz + atp -> thrp + adp  atp + mp -> adp + thrp -> adp  thiamin + pi -> thmp + adp  thiamin + pi -> thmp + adp  atir -> ahm  atp + cys + dx5p + tyr -> 4hbza + thzp + ala + amp + co2 + ppi  thiamin -> ahm + 4mhetz

4H2OVA	Toluene and Xylene degradation	4-hydroxy 2-oxovalerate	4.1.3.39	KOX_22670	hohx -> propanal + pyr
NITRDT1	Trinitrotoluene degradation	aldolase nitroreductase	1		tnittol + 2 nadh -> 4hlmdnit + 2 nad
NITRDT2	Trinitrotoluene degradation	nitroreductase	1,-,-,-	KOX_13625/KOX_15665/KOX_22095	tnittol + 2 nadh -> 2hlmdnit + 2 nad
CARMNOXD	Trinitrotoluene degradation	carbon-monoxide dehydrogenase	1.2.99.2		24danit -> 24da6hat
TRPPA1 TRPPA2	Tryptophan metabolism		4.1.99.1 4.1.99.1	KOX_09730(tnaA) KOX_09730(tnaA)	trp <-> indole + nh4 + pyr
IDPD	Tryptophan metabolism Tryptophan metabolism	Tryptophanase (L-cysteine) indolepyruvate decarboxylase	4.1.1.74	KOX_26745	cys -> indole + h2s + pyr idpyr -> i3aa + co2
ALHD8	Tryptophan metabolism	aldehyde dehydrogenase (NAD+)	1.2.1.3	KOX_00375	i3aa + nad -> i3ac + nadh
ALHD9	Tryptophan metabolism	aldehyde dehydrogenase	12.13	KOX 00375	Shiaa + nad -> Shiac + nadh
CATL	Tryptophan metabolism	(NAD+) catalase	1.11.1.6/1.11.1.21	KOX 18225(katE)/KOX 26215/KOX 20220	2 3han + 2 o2 -> cvn + 2 h2o2
OGDH3	Tryptophan metabolism	2-oxoglutarate dehydrogenase	1.2.4.2	KOX_14590(sucA)	2oad + nad + coa -> glutcoa + co2 + nadh
ID3ACTHL		E1 component	42104		id3act -> idactn
	Tryptophan metabolism	Indole-3-acetamide hydro-lyase 4-hydroxyphenylacetate-3-			
4HPHEA1	Tyrosine metabolism	hydroxylase	1.14.14.9	KOX_10010(hpaC)/KOX_10015	hpheac + o2 + nadh -> 34dhpheac + nad
4HPHEA2	Tyrosine metabolism	4-hydroxyphenylacetate-3- hydroxylase	1.14.14.9	KOX_10010(hpaC)/KOX_10015	4hpheac + o2 + nadh -> 34dhpheac + nad
MNAO3	Tyrosine metabolism	monoamine oxidase	1.4.3.21	KOX_19410(tynA)	o2 + tym -> 4hac + h2o2 + nh4
34DHPACD	Tyrosine metabolism	3,4-dihydroxyphenylacetate 2,3- dioxygenase	1.13.11.15	KOX_10045	34dhpheac + o2 <-> 5cm2hmsa
5CM2HMSAD	Tyrosine metabolism	5-carboxymethyl-2- hydroxymuconic-semialdehyde	12160	KOX_10050	Scm2hmsa + nad <-> Scm2hm + nadh
SCMZHMSAD	Tyrosine metabolism	dehydrogenase	1.2.1.60	KOX_10050	5cmznmsa + nad <-> 5cmznm + nadn
CARHM1	Tyrosine metabolism	5-carboxymethyl-2- hydroxymuconate isomerase	5.3.3.10		5cm2hm -> 5c2o3e
		5-oxopent-3-ene-1,2,5-			
5C2O3EI	Tyrosine metabolism	tricarboxylate decarboxylas isomerase	4.1.1.68	KOX_10055/KOX_10060	5c2o3e -> 2hhpdd + co2
2HHPDDI	Tyrosine metabolism	2-hydroxyhepta-2,4-diene-1,7-	4.1.1.68/5.3.3	KOX_10055/KOX_10060	2hhpdd <-> 2o3e
ACDH2	Tyrosine metabolism	dioate isomerase acyl dehydratase	4.2.1		2hhpdd -> 24dhhepd
ACDH3	Tyrosine metabolism	acyl dehydratase 2,4-dihydroxyhept-2-ene-1,7-	4.2.1		2o3e -> 24dhhepd
DHHED1	Tyrosine metabolism	z,4-ainyaroxynept-z-ene-1,7- dioic acid aldolase	4.1.2	KOX_10030	24dhhepd -> sucsal + pyr
MALAAC	Tyrosine metabolism	maleylacetoacetate isomerase	5.2.1.2	KOX_25680	4maac -> 4faac
4HPHED1	Tyrosine metabolism	4-hydroxyphenylpyruvate dioxygenase	1.13.11.27		4hpp + o2 -> homogen + co2
ASPAM5 MNAO15	Tyrosine metabolism Tyrosine metabolism	aspartate aminotransferase monoamine oxidase	2.6.1.1 1.4.3.21	KOX_16370 KOX_19410(tynA)	akg + tyr <-> 4hpp + glu dopa + o2 -> 34dhpac + nh4 + h2o2
ALCDd	Tyrosine metabolism	alcohol dehydrogenase	1.1.1.1	KOX_19595/KOX_20090/KOX_23025	34dhma + nadh <-> 34dhpeg + nad
GENDO MALPYRI	Tyrosine metabolism Tyrosine metabolism	gentisate 1,2-dioxygenase maleylpyruvate isomerase	1.13.11.4 5.2.1.4	KOX_25690 KOX_25680	gensa + o2 -> malpyr malpyr -> fumpyr
ACPYRH	Tyrosine metabolism	acylpyruvate hydrolase	3.7.1.5	KOX_25685	fumpyr -> fum + pyr
	ut :	MARILLE :	1.653	KOX_26335/KOX_26340/KOX_26345/KOX_26350/ KOX_26355/KOX_26360/KOX_26365/KOX_26370/	
NADHDH2	Ubiquinone	NADH dehydrogenase	1.6.5.3	KOX_26375/KOX_26380/KOX_26385/KOX_26390/	uq + nadh -> uqh2 + nad
NAPTS	Ubiquinone Biosynthesis	naphthoate synthase	4.1.3.36	KOX_26395 KOX_26270	sbzcoa -> d2naptcoa
CHMPL	Ubiquinone Biosynthesis	Chorismate pyruvate lyase	4.1.3.40	KOX_08240	chor <-> 4hb + pyr
DMUQMT	Ubiquinone Biosynthesis	3-Dimethylubiquinonol 3- methyltransferase	2.1.1.64	KOX_26130	2omhmbl + sam -> sah + uq
HBZOCPT	Ubiquinone Biosynthesis	Hydroxybenzoate	2.5.1	KOX_08245(ubiA)	4hb + opp -> 3op4hb + ppi
		octaprenyltransferase 2-octaprenyl-6-hydroxyphenol	244222		
OCPHPM	Ubiquinone Biosynthesis	methylase 2-Octaprenyl-6-methoxy-	2.1.1.222	KOX_26130	2op6hp + sam -> 2opmp + sah
OCTMBZM	Ubiquinone Biosynthesis	benzoquinol methylase	2.1.1.163	KOX_07775(ubiE)	2ombzl + sam -> 2ommbl + sah
OMMBZH	Ubiquinone Biosynthesis	2-octaprenyl-3-methyl-6- methoxy-1,4-benzoquinol	1.14.13	KOX_14330(ubiF)	2ommbl + o2 + nadph -> 2omhmbl + nadp
OMINIDZIT	obiquitorie biosyrtulesis	hydroxylase	1.14.13	KOX_14330(dbii)	Zominor + 02 + nadpn -> Zominor + nadp
OCMPH1	Ubiquinone Biosynthesis	2-octaprenyl-6-methoxyphenol hydroxylase	1.14.13	KOX_02500	2opmp + o2 + nadph -> 2ombzl + nadp
OCMPH2	Ubiquinone Biosynthesis	2-octaprenyl-6-methoxyphenol	1.14.13	KOX_02500	2 2opmp + o2 -> 2 2ombzl
OCH PUZ		hydroxylase 2-octaprenyl-6-methoxyphenol			
ОСМРН3	Ubiquinone Biosynthesis	hydroxylase (anaerobic)	1.14.13		2opmp + 2 atp + nad -> 2ombzl + 2 adp + nadh + 2 pi
OCHBZDC	Ubiquinone Biosynthesis	Octaprenyl-hydroxybenzoate decarboxylase	4.1.1	KOX_01005/KOX_02350/KOX_02355/KOX_07815/ KOX_26545	3op4hb -> 2opp + co2
OCPPH2	Ubiquinone Biosynthesis	2-Octaprenylphenol hydroxylase		KOX_07785(ubiB)	2opp + o2 + nadph -> 2op6hp + nadp
OCPPH1	Ubiquinone Biosynthesis	2-Octaprenylphenol		KOX_07785(ubiB)	2 2opp + o2 -> 2 2op6hp
		hydroxylase 2-Octaprenylphenol			
ОСРРН3	Ubiquinone Biosynthesis	hydroxylase (anaerobic)		KOX_07785(ubiB)	2opp + 2 atp + nad -> 2op6hp + 2 adp + nadh + 2 pi
UMBM1	Ubiquinone Biosynthesis	ubiquinone/menaquinone biosynthesis methyltransferase	2.1.1.163	KOX_07775(ubiE)	2dmmq8 + sam -> mk + sah
UMBM2	Ubiquinone Biosynthesis	ubiquinone/menaquinone	2.1.1.163	KOX_07775(ubiE)	pnpq + sam -> pq + sah
SPMS3	Ubiquinone Biosynthesis	biosynthesis methyltransferase spermidine synthase	2.5.1.16	KOX 11110	sama + sprmd -> 5mta + sprm
ALHD12	Ubiquinone Biosynthesis	aldehyde dehydrogenase	1.2.1.3	-	bapa + nad -> bala + nadh
OMMBZHx	Uhiminan Pinankaia	(NAD+) 2-octaprenyl-6-methoxyphenol	11412	KOX_14330(ubiF)	2ommbl + 2 atp + nad -> 2omhmbl + 2 adp + nadh + 2 pi
ISOCHORS	Ubiquinone Biosynthesis Ubiquinone Biosynthesis	hydroxylase isochorismate synthase	5.4.4.2		chor <-> isochor
		2-succinyl-5-enolpyruvyl-6-			
SUCEPHCS	Ubiquinone Biosynthesis	hydroxy-3-cyclohexene-1- carboxylate synthase	2.2.1.9	KOX_26280	isochor + akg -> sucephc + co2
enene-		2-succinyl-6-hydroxy-2,4-	4200	KON 2027	
SHCHCS	Ubiquinone Biosynthesis	cyclohexadiene-1-carboxylate synthase	4.2.99.20	KOX_26275	sucephc -> shchc + pyr
OSUCCBS	Ubiquinone Biosynthesis	O-succinylbenzoate synthase	4.2.1.113	KOX_26265	shchc -> osuccbenz
OSUCCBCL	Ubiquinone Biosynthesis	O-succinylbenzoic acidCoA ligase	6.2.1.26	KOX_26260	atp + osuccbenz + coa -> amp + ppi + sbzcoa
D2NAPCH	Ubiquinone Biosynthesis	1,4-dihydroxy-2-naphthoyl-CoA hydrolase	3.1.2.28		d2naptcoa -> dhn + coa
DHNOPT1	Ubiquinone Biosynthesis	1,4-dihydroxy-2-naphthoate	2.5.1.74	KOX_07270	dhn + opp -> 2dmmq8 + ppi + co2
		octaprenyltransferase 1,4-dihydroxy-2-naphthoate		_	
DHNOPT2	Ubiquinone Biosynthesis	octaprenyltransferase	2.5.1 1.11.1.6		dhn + phppi -> pnpq + co2 + ppi 2 h2o2 -> 2 h2o + o2
CAT MISRXN	Unassigned unclear reaction	catalase unclear reaction	1.11.1.6		2 h2o2 -> 2 h2o + o2 g3p + pyr -> 4mhetz
ACGPR	Urea Cycle and Metabolism of amino	N-acetyl-g-glutamyl-phosphate	1.2.1.38		naglus + nadp + pi <-> acg5p + nadph
GLU5SD	groups Urea Cycle and Metabolism of amino	reductase glutamate-5-semialdehyde	1.2.1.41		glu5p + nadph -> glugsal + nadp + pi
	groups Urea Cycle and Metabolism of amino	dehydrogenase			
AGLUS	groups	N-acetylglutamate synthase	2.3.1.1	KOX_01560	accoa + glu -> naglu + coa
SPMS1	Urea Cycle and Metabolism of amino groups	spermidine synthase	2.5.1.16	KOX_11110	sama + ptrc -> 5mta + sprmd
AORNT	Urea Cycle and Metabolism of amino	acetylornithine transaminase	2.6.1.11	KOX_04525(argD)	naorn + akg <-> naglus + glu
	groups Urea Cycle and Metabolism of amino				
GLU5K	groups	glutamate 5-kinase	2.7.2.11	KOX_12060	atp + glu -> adp + glu5p
AGLUK	Urea Cycle and Metabolism of amino groups	acetylglutamate kinase	2.7.2.8	KOX_07375	naglu + atp -> acg5p + adp
ACORND	Urea Cycle and Metabolism of amino	acetylornithine deacetylase	3.5.1.16	KOX_07365/KOX_16395/KOX_19240	naorn -> ac + orn
AGMT	groups Urea Cycle and Metabolism of amino	agmatinase	3.5.3.11	KOX_00245/KOX_02630	
	groups Urea Cycle and Metabolism of amino	•			agmatine -> ptrc + urea
ARGDC	groups	arginine decarboxylase	4.1.1.19	KOX_02635	arg -> agmatine + co2
ALLPH	Urea cycle and metabolism of amino groups	allophanate hydrolase	3.5.1.54	KOX_20290	ulcar -> 2 co2 + 2 nh4
ALHD10	Urea cycle and metabolism of amino	aldehyde dehydrogenase	1213	KOX 00375	n4aab + nad -> 4aabut + nadh
	groups Urea cycle and metabolism of amino	(NAD+) aldehyde dehydrogenase		_	
ALHD11	groups	(NAD+)	1.2.1.3/1.2.1.19	KOX_00375/KOX_19750	4ab + nad -> gaba + nadh
ALHD11p	Urea cycle and metabolism of amino groups	aldehyde dehydrogenase (NAD+)	1.2.1.3	KOX_00375	4ab + nadp -> gaba + nadph
SPMS2	Urea cycle and metabolism of amino	spermidine synthase	2.5.1.16	KOX_11110	sama + ptrc -> 5mta + sprmd
AMDS3	groups Urea cycle and metabolism of amino	amidase	3.5.1.4	KOX_09850/KOX_13720/KOX_20510	quadbut -> quadbutn + nh4
	groups Valine, Leucine and Isoleucine	amidase  3-isopropylmalate/(R)-2-			
3IPPMD1	Biosynthesis	methylmalate dehydratase	4.2.1.35	KOX_10840(leuD)/KOX_10845	r2mm -> 2mm

	Valine, Leucine and Isoleucine	3 i			
3IPPMD2	Biosynthesis	3-isopropylmalate/(R)-2- methylmalate dehydratase	4.2.1.33	KOX_10840(leuD)/KOX_10845	2mm -> e3mm
IPPMD	Valine, Leucine and Isoleucine Biosynthesis	3-isopropylmalate dehydrogenase	1.1.1.85	KOX_10850	e3mm + nad -> obut + co2 + nadh
ACCOAA1	Valine, Leucine and Isoleucine	acetyl-CoA acyltransferase	2.3.1.16	KOX_26660(fadI)	coa + 2maaccoa -> ppcoa + accoa
AUUDS	degradation Valine, Leucine and Isoleucine	aldehyde dehydrogenase	1213		••
ALHD6	degradation Valine, Leucine and Isoleucine	(NAD+)		KOX_00375	mmsa + nad -> mm + nadh
MMCS	degradation	unclear reaction	unclear reaction		mm + coa -> mmcoa-R
MMCM	Valine, Leucine, and Isoleucine Degradation	Methylmalonyl-CoA mutase	5.4.99.2	KOX_02540	succoa -> mmcoa-R
IPMALD	Valine, Leucine, and Isoleucine	3-isopropylmalate	1.1.1.85	KOX_10850	3c2hmp + nad -> oicap + nadh
	Metabolism Valine, Leucine, and Isoleucine	dehydrogenase			
KARIS1	Metabolism Valine, Leucine, and Isoleucine	ketol-acid reductoisomerase	1.1.1.86	KOX_07475	dhmva + nadp <-> alac-S + nadph
KARIS2	Metabolism	ketol-acid reductoisomerase	1.1.1.86	KOX_07475	abut + nadph <-> dhmp + nadp
ILETA	Valine, Leucine, and Isoleucine Metabolism	isoleucine transaminase	2.6.1.42	KOX_07455/KOX_1652	akg + ile <-> 3mop + glu
LEUTA	Valine, Leucine, and Isoleucine	leucine transaminase	2.6.1.42	KOX_07455/KOX_1652	4mop + glu <-> akg + leu
	Metabolism Valine, Leucine, and Isoleucine			KOX 07455/KOX 1652	
VALTA	Metabolism Valine, Leucine, and Isoleucine	valine transaminase	2.6.1.42		akg + val <-> 3mob + glu
IPPMS	Metabolism	2-isopropylmalate synthase	2.3.3.13	KOX_00490/KOX_10855	3mob + accoa -> 3c3hmp + coa
ACLACS	Valine, Leucine, and Isoleucine Metabolism	acetolactate synthase	2.2.1.6	KOX_06425/KOX_06430/KOX_07445/KOX_07450( ilvM)/KOX_10865/KOX_10870(ilvH)/KOX_22370	2 pyr -> alac-S + co2
IPMALD1	Valine, Leucine, and Isoleucine	3-isopropylmalate dehydratase	42133	KOX_10840(leuD)/KOX_10845	3c2hmp <-> 2ippm
	Metabolism Valine, Leucine, and Isoleucine				
IPMALD2	Metabolism	3-isopropylmalate dehydratase	4.2.1.33	KOX_10840(leuD)/KOX_10845	2ippm <-> 3c3hmp
DHADT1	Valine, Leucine, and Isoleucine Metabolism	dihydroxy-acid dehydratase	4.2.1.9	KOX_07460	dhmva -> 3mob
ACHBUTS	Valine, Leucine, and Isoleucine Metabolism	2-aceto-2-hydroxybutanoate synthase	2.2.1.6	KOX_06425/KOX_06430/KOX_07445/KOX_07450( ilvM)/KOX_10865/KOX_10870(ilvH)/KOX_22370	obut + pyr -> abut + co2
DHADT2	Valine, Leucine, and Isoleucine	ihydroxy-acid dehydratase	4.2.1.9	KOX_07460	dhmp -> 3mop
	Metabolism	2-Oxo-4-methyl-3-			
OMCDC	Valine, Leucine, and Isoleucine Metabolism	carboxypentanoate	spontaneous		oicap -> 4mop + co2
VALDUS **	Valine, Leucine, and Isoleucine	decarboxylation valinepyruvate	26165	VOV 05550/-+4\ "/OV 25505	Small code consult.
VALPYRAT	Metabolism	aminotransferase	2.6.1.66	KOX_05660(avtA)/KOX_26405	3mob + ala <-> val + pyr
PDXSPO	Vitamine B6 metabolism	pyridoxine 5'-phosphate oxidase	1.4.3.5	KOX_22030	o2 + pdx5p -> h2o2 + pydx5p
PYAM5PO	Vitamine B6 metabolism	pyridoxamine 5'-phosphate oxidase	1.4.3.5	KOX_22030	o2 + pyam5p -> h2o2 + nh4 + pydx5p
		O-Phospho-4-hydroxy-L-			
OHPBAKGT	Vitamine B6 metabolism	threonine:2-oxoglutarate aminotransferase	2.6.1.52	KOX_15995	glu + ohpb <-> akg + pht
HTHRS	Vitamine B6 metabolism	4-Hydroxy-L-threonine synthase	4.2.3.1	KOX_10420	pht -> 4hlt + pi
DALATA	Vitamine B6 metabolism	D-alanine transaminase	2.6.1.54		dala + pydx5p -> pyam5p + pyr
E4PDH	Vitamine B6 metabolism	Erythrose 4-phosphate	1.2.1.72	KOX_02590	e4p + nad <-> er4p + nadh
PSPPR	Vitamine B6 metabolism	dehydrogenase pyridoxal-5'-phosphate	3.1.3.74		
		phosphohydrolase Pyridoxine 5'-phosphate		VOV 10700/pdva\/VOV 11005/pdva\/VOV 17445	pyam5p -> pi + pdla
PXSPS	Vitamine B6 metabolism	synthase	1.1.1.262/2.6.99.2	(pdxA)/KOX_27535	dx5p + nad + pht -> co2 + nadh + pdx5p + pi
ER4PD	Vitamine B6 metabolism	Erythronate 4-phosphate (4per) dehydrogenase	1.1.1.290	KOX_26590	er4p + nad <-> nadh + ohpb
PYR5OXM	Vitamine B6 metabolism	pyridoxamine 5'-phosphate	1.4.3.5	KOX_22030	pdla + o2 <-> pl + nh4 + h2o2
		oxidase pyridoxamine 5'-phosphate			
PYR5OXX	Vitamine B6 metabolism	oxidase	1.4.3.5	KOX_22030	pydxn + o2 <-> pl + h2o2
HTHRPD	Vitamine B6 metabolism	4-hydroxythreonine-4- phosphate dehydrogenase	1.1.1.262	KOX_10700(pdxA)/KOX_11095(pdxA)/KOX_17445 (pdxA)	pht + nad -> ao4pob + nadh
SPOTN PDLAK	Vitamine B6 metabolism Vitamine B6 metabolism	spontaneous Pyridoxamine kinase	2.7.1.35	KOX_22020/KOX_26865(pdxK)	ao4pob -> 3a2op + co2 pdla + atp -> pyam5p + adp
PLK	Vitamine B6 metabolism	Pyrodoxal kinase	2.7.1.35	KOX_22020/KOX_26865(pdxK)	pl + atp -> pydx5p + adp
PYDXNK	Vitamine B6 metabolism	Pyridoxine kinase Propane-1,3-diol facilitated	2.7.1.35	KOX_22020/KOX_26865(pdxK)	pydxn + atp -> pdx5p + adp
13PDOt	Transport, Extracellular	transport			13pdo_e <-> 13pdo
		(R,R)-Butane-2,3-diol facilitated			23bdo_e <-> 23bdo
23BDOt	Transport, Extracellular	transport			23000_E <-> 23000
23BDOt 12PDOt	•	transport S-Propane-1,2-diol facilitated			_
12PDOt	Transport, Extracellular	S-Propane-1,2-diol facilitated transport			12ppd-S_e <-> 12ppd-S
	•	S-Propane-1,2-diol facilitated transport NMN transport via NMN glycohydrolase			_
12PDOt	Transport, Extracellular	S-Propane-1,2-diol facilitated transport NMN transport via NMN			12ppd-S_e <-> 12ppd-S
12PDOt NMNt7 ACALDt GUAt1	Transport, Extracellular Transport, Extracellular Transport, Extracellular Transport, Extracellular	S-Propane-1,2-diol facilitated transport NMN transport via NMN glycohydrolase acetaldehyde reversible transport Guanine transport			12ppd-5_e <-> 12ppd-5 namn_e > nam + r5p acal_e <-> acal gn_e <-> gn
12PDOt NMNt7 ACALDt GUAt1 HYXNt XANt1	Transport, Extracellular Transport, Extracellular Transport, Extracellular Transport, Extracellular Transport, Extracellular Transport, Extracellular	S-Propane-1,2-diol facilitated transport NMN transport via NMN glycohydrolase acetaldehyde reversible transport			12ppd-S_e <-> 12ppd-S namn_e -> nam + r5p acal_e <-> acal
12PDOt NMNt7 ACALDt GUAt1 HYXNt XANt1 NACUP	Transport, Extracellular	S-Propane-1,2-diol facilitated transport NMN transport via NMN glycohydrolase acetaldehyde reversible transport Guanine transport Guanine transport Approximation for the proparation of			12ppd-S <sub>e</sub> <> 12ppd-S namn_e >> nam + r5p acal_e <> acal gn_e <> gn hynn_e <> hyn aran_e <> kan name <> hon nac_e <> nac
12PDOt NMNt7 ACALDt GUAt1 HYXNt XANt1	Transport, Extracellular Transport, Extracellular Transport, Extracellular Transport, Extracellular Transport, Extracellular Transport, Extracellular	S-Propane-1,2-diol facilitated transport transport MNN transport via NMN glycohydrolase acetaldehyde reversible transport Guanine transport Hypoxanthine transport Nicotinic acid uptake L-asparagine transport via ABC system			12ppd-S_e <> 12ppd-S namn_e >> nam + r5p acal_e <>> acal gn_e <>> gn hynn_e <>> hynn xan_e <>> xan
12PDOt NMNt7 ACALDt GUAt1 HYXNt XANt1 NACUP	Transport, Extracellular	S-Propane-1,2-diol facilitated transport Nicotinic acid uptake Leaparagine transport vandine reversible transport ABC system Leaparagine transport via ABC system Leaparagine reversible			12ppd-S <sub>e</sub> <> 12ppd-S namn_e >> nam + r5p acal_e <> acal gn_e <> gn hynn_e <> hyn aran_e <> kan name <> hon nac_e <> nac
12PDOt NIMNt7 ACALDt GUAt1 HYXNt XAN1 NACUP ASNabc	Transport, Extracellular	S-Propane-1,2-diol facilitated transport diameter transport transport transport hypoxanthine transport Nicotinic acid uptake Leaparagine transport via ABC system transport via proton symport transport via proton symport de-diaminopinielic acid ABC underdaminopinielic acid ABC mediaminopinielic acid ABC media			12ppd-S <sub>e</sub> <>> 12ppd-S namn_e >> nam + r5p acal_e <>> acal gn_e <> gn hyan_e <>> yn hyan_e <>> xan nac_e >> nac asn_e +> adp + asn + pi
12PDOt NMN17 ACALDt GUA11 HYXN1 XAN1 NACUP ASNabc ASNtr DAPabc	Transport, Extracellular	S-Propane-1,2-diol facilitated transport nambur transport via MMN glycohydrolase acetaldehyde reversible transport Guainine transport Hypoxanthine transport Nicotinic acid uptake Leaparagine transport via ABC system transport via proton symport wide transport via proton symport Mediaminopinic acid ABC transport Le-ysteine transport via ABC transport Le-ysteine transport via ABC Leysteine transport via ABC Leysteine transport via ABC			12ppd-5,e <> 12ppd-5 namn_e >> nam + r5p  acal_e <> acal gn_e <<- gn hynn_e <<- yn hynn_e <<- sn nac_e >> nan nac_e >> nac  asn_e <> ban asn_e <>> ban 26dap-M_e + adp + adp + pi
12PDOt NMN17 ACALDt GUATI HYXN1 XANTI NACUP ASNabc ASNtr DAPabc CYSabc	Transport, Extracellular	S-Propane-1,2-diol facilitated transport transport transport NMN glycohydrolase acetaldehyde reversible transport Guanine transport Hypoxanthine transport Hypoxanthine transport Nicotinic acid uptake L-asparagine transport via ABC system L-asparagine reversible transport via proton symport M-diaminiopimelic acid ABC transport via proton symport M-diaminiopimelic acid ABC transport via proton symport L-cysteine transport via ABC system			12ppd-5,e <> 12ppd-5 namn,e >> nam + r5p  acal_e <> acal gn_e <<> gn hynn,e <>> yn hynn,e <>> hyn san_e <>> xan nac_e >> nac san_e +> atp >> adp + asn + pi asn_e +> te> + te>
12PDOt NMN17 ACALDt GUA11 HYXN1 XAN1 NACUP ASNabc ASNtr DAPabc	Transport, Extracellular	S-Propane-1,2-diol facilitated transport transport transport transport via NMN glycohydrolase acetaldehyde reversible transport Hypoxanthine transport Hypoxanthine transport Nicotinic acid uptake Leaparagine transport via ABC system Leaparagine transport via proton symport Mcdiminopimelic acid ABC transport via proton symport Mcdiaminopimelic acid ABC transport via proton symport			12ppd-5,e <> 12ppd-5 namn_e >> nam + r5p  acal_e <> acal gn_e <<- gn hynn_e <<- yn hynn_e <<- sn nac_e >> nan nac_e >> nac  asn_e <> ban asn_e <>> ban 26dap-M_e + adp + adp + pi
12PDOt NMN17 ACALDt GUATI HYXN1 XANTI NACUP ASNabc ASNtr DAPabc CYSabc	Transport, Extracellular	S-Propane-1,2-diol facilitated transport transport NMN transport via NMN glycohydrolase pycohydrolase acetaledhyde reversible transport Hyposanthine transport Nicotinic aodi uptake L-asparagine transport via ABC system L-asparagine reversible transport via proton symport M-diaminopinic acid ABC transport via proton symport M-diaminopinic acid ABC system L-cysteine transport via ABC system			12ppd-5,e <> 12ppd-5 namn,e >> nam + r5p  acal_e <> acal gn_e <<> gn hynn,e <>> yn hynn,e <>> hyn san_e <>> xan nac_e >> nac san_e +> atp >> adp + asn + pi asn_e +> te> + te>
12PDOt NMN17 ACALDt GUATI HYXN1 XANTI NACUP ASNabc ASNtr DAPabc CYSabc ACtr	Transport, Extracellular	S-Propane-1,2-diol facilitated transport namport via NMN transport via NMN glycohydrolase acctated bryce reversible transport Hypoxanthine transport Nicotinic acid uptake L-saparagine transport via proton symport M-claminopiline acid ABC transport via proton symport M-claminopiline acid ABC transport via proton symport via proton symp			12ppd-S <sub>e</sub> <>> 12ppd-S namn_e >> nam + r5p acal_e <>> acal gn_e <<> gn hyn.e <>> yn hyn.e <>> hyn axn_e <>> xan nac_e >> nac asn_e + atp >> adp + asn + pi asn_e + hext <>> asn 126dap-M,e + atp >> 2Edap-M + adp + pi atp + cys_e >> adp + cys + pi ac_e + hext <>> ac
12PDOt NMN17 ACALDt GUATI HYXNI XANTI NACUP ASNabc ASNtr DAPabc CVSabc ACtr ETOHtr PYRtr O2t	Transport, Extracellular	S-Propane-1,2-diol facilitated transport via MMN transport via MMN glycohydrolase acetaledhyde reversible transport transport via Mmn transport via Mmn transport via protein acetale via			12ppd-S <sub>e</sub> <>> 12ppd-S namn_e >> nam + r5p  acal_e <>> acal gn_e <>> gn hyun_e <>> yn hyun_e <>> hyun san_e <>> san nac_e >> nac san_e <> nac asn_e + atp >> adp + asn + pi asn_e + + bet <>> asn asn_e + atp >> adp + asn + pi asn_e + bet <<> asn 26dap-M_e + atp >> 26dap-M + adp + pi atp + cys_e >> adp + cys + pi ac_e + bet <>> ac e + bet <>> ac e + bet <>> ac e + bet <>> ce et+ > eth_e + bet bet + pyr_e <>> pyr o2_e <>> o2
12PDOt NMNt7 ACALDt GUATI HYXNt XANTI NACUP ASNabc ASNtr DAPabc CYSabc ACtr ETOHtr PYRtr O2t CO2t	Transport, Extracellular	S-Propane-1,2-diol facilitated transport transport transport transport via NMN glycohydrolase acetaldehyde reversible transport Guarine transport Hypoxanthine transport Hypoxanthine transport Nicotinic acid uptake L-asparagine transport via ABC system L-asparagine reversible transport via proton symport M-diaminopimelic acid ABC transport via proton symport via ABC system acetate reversible transport via proton symport syrtvavia reversible transport via proton symport syrtvavia reversible transport via proton symport syrtvavia proton symport syrtvavia reversible transport via proton symport syrtvavia reversible transport via proton symport syrtvavia proton symport syrtvavia proton symport syrtvavia proton symport symport syrtvavia proton symport syrtvavia proton symport symport symport symport syrtvavia proton symport symport symport syrtvavia proton symport symport syrtvavia proton symport symport symport syrtvavia symport symport syrtvavia symport symport symport syrtvavia symport sy			12ppd-S <sub>e</sub> <>> 12ppd-S namn_e >> nam + rSp  acal_e <>> acal gn_e <<> gn hynn_e <<> yn hynn_e <>> hyn san_e <>> kan nac_e >> nac asn_e + atp >> adp + asn + pi  asn_e + heat <>> asn 26dap-M_e + atp >> 26dap-M + adp + pi atp + cys_e >> adp + (ys + pi ac_e + heat <>> ac eth >> eth_e + heat heat + pyr_e <>> pyr 02_e <>> ac 22_e <>> ac 22_e <>> ac 22_e <<>> co2_e <<>> co2_e <<>> co2_e <>> co2
12PDOt NMN17 ACALDT GUATI HYXNI XANTI NACUP ASNabc ASNIT DAPabc CYSabc ACtr ETOHtr PYRtr OZt COZt DHAt	Transport, Extracellular	S-Propane-1,2-diol facilitated transport transport via NMN transport via NMN glycohydrolase acetaldehyde reversible transport Guanine transport Hypoxanthine transport Hypoxanthine transport Nicotinic acid uptake L-asparagine transport via ABC system C-asparagine reversible transport via proton symport M-claminopinelic acid ABC transport L-cysteine transport via ABC system consideration of the Control of the			12ppd-5,e <> 12ppd-5  namn_e >> nam + r5p  acal_e <> acal  gn_e <<> gn hynn_e <>> yn hynn_e <>> hyn  xan_e <>> xan nac_e >> nac  asn_e + atp >> adp + asn + pi  asn_e + bext <>> asn  26dap-M_e + atp >> 26dap-M + adp + pi  atp + cys_e -> adp + cys + pi  ac_e + bext <>> ac  eth >> eth_e + bext hext + pyr_e <>> pyr  02_e <>> o2  co2_e <>> co2  ghn_e <>> ghn e <>> ghn
12PDOt NMN17 ACALDt GUA11 HYXN1 XAN1 NACUP ASNabc ASNtr DAPabc CYSabc ACtr ETOHtr PYRtr O2t CO2t DHAt NH3t	Transport, Extracellular	S-Propane-1,2-diol facilitated transport via MMN transport via MMN glycohydroise acetaledhyde reversible transport transport via Mine transport via Mine transport via Mine transport via more v			12ppd-5,e <> 12ppd-5  namn_e >> nam + r5p  acal_e <> acal  gn_e <> gn  hym.e <> hym  san_e <> san  nac_e >> nac  asn_e +> atp >> adp + asn + pi  asn_e +> ban  26dap-M_e + atp >> 26dap-M + adp + pi  atp + cys_e >> adp + cys + pi  ac_e + hext <> ac  eth -> eth_e + hext  hext + pyr_e <> pyr  o2_e <> o2  cys_e <> o2  dyn_e <> sph  nh4_e <> nb4
12PDOt NMN17 ACALDT GUATI HYXNI XANTI NACUP ASNabc ASNtr DAPabc CYSabc ACtr ETOHtr PYRtr O2t CO2t DHAt NHSt ARBtr	Transport, Extracellular	S-Propane-1,2-diol facilitated transport transport transport via MMN glycohydrolase acetaldehyde reversible transport Hypoanthine transport Alpoanthine transport Nicotinic acid uptake L-asparagine transport via ABC system Chaminopimelic acid ABC transport via proton symport M-diaminopimelic acid ABC transport via proton symport M-diaminopimelic acid ABC transport via proton symport system certain control of transport via proton symport private reversible transport via proton symport via proton symport via proton symport			12ppd-5,e <> 12ppd-5 acal_e <> acal gn_e <> gn hyan,e <> hyan san_e <> nam hyan,e <> hyan san_e <> san nac_e > nac asn_e + atp >> adp + asn + pi asn_e + bext <> asn 26dap-M_e + atp >> 26dap-M + adp + pi atp + cys_e >> adp + cys + pi ac_e + hext <> ac eth -> eth_e + hext hext + pyr_e <> pyr o2_e <> o2 co2_e <> o2 dyn_e <> ob) ghn_e <> ghn h44_e <> nb4 larabinose_e + hext -> larabinose
12PDOt NMN17 ACALDt GUA11 HYXN1 XAN1 NACUP ASNabc ASNtr DAPabc CYSabc ACtr ETOHtr PYRtr O2t CO2t DHAt NH3t	Transport, Extracellular	S-Propane-1,2-diol facilitated transport NMN transport via MMN glycohydrolase acetaledhyde reversible transport transport transport transport transport transport via protein et arrasport via protein symport et arrasport via protein symport via facilitated diffusion ammonia reversible transport via protein symport via protein			12ppd-5,e <> 12ppd-5  namn_e >> nam + r5p  acal_e <> acal  gn_e <> gn  hym.e <> hym  san_e <> san  nac_e >> nac  asn_e +> atp >> adp + asn + pi  asn_e +> ban  26dap-M_e + atp >> 26dap-M + adp + pi  atp + cys_e >> adp + cys + pi  ac_e + hext <> ac  eth -> eth_e + hext  hext + pyr_e <> pyr  o2_e <> o2  cys_e <> o2  dyn_e <> sph  nh4_e <> nb4
12PDOt NMN17 ACALDT GUATI HYXNI XANTI NACUP ASNabc ASNtr DAPabc CYSabc ACtr ETOHtr PYRtr O2t CO2t DHAt NHSt ARBtr	Transport, Extracellular	S-Propane-1,2-diol facilitated transport transport via MMN glycohydrolase acetaldehyde reversible transport Guainine transport Hypoxanthine transport Nicotinic acid uptake Leaparagine transport via proton symport Microtinic acid uptake Leaparagine reversible transport via proton symport McIaminopinelic acid ABC transport via proton symport McIaminopinelic acid ABC transport via proton symport via diffusion ammonia reversible transport via proton symport via diffusion ammonia reversible transport via proton symport Leapainose transport via ABC system Linstoline reversible transport via Linstoline reversible reversible transport via Linstoline reversible reversible reversible transport via Linstoline reversible reversibl			12ppd-S <sub>e</sub> <> 12ppd-S  namn_e >> nam + r5p  acal_e <> acal gn_e <> gn hyan_e <> hyan san_e <> nac san_e + atp >> adp + asn + pi san_e + hext <> asn 26dap-M_e + atp >> 26dap-M + adp + pi atp + cys_e >> adp + cys + pi ac_e + hext <> ac eth -> eth_e + hext hext + pyr_e <> pyr co_e <> co_e co_e <> co_e co_e <> co_e co_e <> co_e dyn_e <> sph nh4_e <> nb4 larabinose e + hext -> larabinose
12PDOt NMN17 ACALDT GUATI HYXNT XANTI NACUP ASNabc ASNtr DAPabc CYSabc ACtr ETOHTr PYRtr OZt COZt DHAt NH3t ARBtr ARBabc	Transport, Extracellular	S-Propane-1,2-diol facilitated transport transport via MMN glycohydrolase acetaldehyde reversible transport Guainine transport Hypoxanthine transport Nicotinic acid uptake Leaparagine transport via control service of the service of			12ppd-5,e <> 12ppd-5 acal_e <> acal gn_e <> gn hyan_e <> yn hyan_e <> yn hyan_e <> san ac_e >> nac asn_e +> san ac_e >> nac asn_e +> san ac_e >> nac asn_e +> san ac_e >> nac asn_e += sap >> adp + asn + pi asn_e ++ best <> asn 26dap-M_e += atp >> 26dap-M += adp += pi atp += cys_e >> adp += cys += pi ac_e += hest <>> ac eth >> eth_e += hest hest += pyr_e <>> pyr co_e <>> co_e cys_e <>> co_e gyn_e <>> gyn nh4_e <>> ph4 larabinose_e += hest >> larabinose larabinose_e += atp >> adp += larabinose += pi
12PDOt NMN17 ACALDT GUATI HYXNI XANTI NACUP ASNabc ASNitr DAPabc CYSabc ACtr ETOHIT PYRIT OZt COZt DHAT NHST ARBabc HISTr PHET	Transport, Estracellular	S-Propane-1,2-diol facilitated transport nansport variansport support of the properties of the propert			12ppd-S <sub>e</sub> <>> 12ppd-S namn_e -> nam + fSp  acal_e <>> acal gn_e <>> gn hynn_e <>> hyn xan_e <>> xan xan_e <> xan xan xan_e <> xan xan xan_e <> xan
12PDOt NMN17 ACALDT GUATI HYXNT XANTI NACUP ASNabc ASNtr DAPabc CYSabc ACtr ETOHTr PYRtr O2t CO2t DHAt NH3t ARBabc HIStr	Transport, Estracellular	S-Propane-1,2-diol facilitated transport nansport was recommended by the property of the prope			12ppd-5,e <> 12ppd-5 acal_e <> acal gn_e <> gn hyan_e <> yn hyan_e <> yn hyan_e <> kan acal_e <> acal gn_e <> yn hyan_e <> kan ac_e >> nac asn_e + bat <> asn ac_e >> nac asn_e + bat <> asn 26dap-M_e + atp >> 26dap-M + adp + pi atp + cys_e -> adp + cys + pi ac_e + best <> ac ac_e + best <> ac ac_e <> bat ac_e + best <> ac ac_e <> co_c cys_e <> co_c cys_e <> co_c gyn_e <> cys_e + best larabinose_e + best >> larabinose larabinose_e + atp >> adp + larabinose + pi hext + his_e <> his
12PDOt NMN17 ACALDT GUATI HYXNI XANTI NACUP ASNabc ASNitr DAPabc CYSabc ACtr ETOHIT PYRIT OZt COZt DHAT NHST ARBabc HISTr PHET	Transport, Estracellular	S-Propane-1,2-diol facilitated transport transport via MMN glycohydrolase acetaldehyde reversible transport Guainine transport Hypoxanthine transport Nicotinic acid uptake Leaparagine reversible transport via proton symport Microtinic acid uptake Leaparagine reversible transport via proton symport Microtinic acid uptake Leaparagine reversible transport via proton symport Microtinic acid ABC transport via proton symport certain via microtinic via Microtinic via Microtinic via Microtinic via Microtinic via			12ppd-S <sub>e</sub> <>> 12ppd-S namn_e -> nam + fSp  acal_e <>> acal gn_e <>> gn hynn_e <>> hyn xan_e <>> xan xan_e <> xan xan xan_e <> xan xan xan_e <> xan
12PDOt NMN17 ACALDT GUATI HYXNI XANTI NACUP ASNabc ASNIT DAPabc CYSabc ACIT ETOHIT PYRIT OZI COZI DHAT NH3T ARBID ARBID ARBID HISTI PHET LEUT	Transport, Estracellular	S-Propane-1,2-diol facilitated transport van Samman van Verschaften van Versch			12ppd-S <sub>e</sub> <>> 12ppd-S namn_e -> nam + fSp  acal_e <>> acal gn_e <>> gn hynn_e <>> hyn xan_e <>> xan xan_e <> xan xan xan_e <> xan xan xan_e <> xan
12PDOt NMN17 ACALDT GUATI HYXN1 XANTI NACUP ASNabc ASNIT DAPabc CYSabc ACT ETOHIT PYRT O2t CO2t DHAT NH3T ARBIT ARBIT ARBIT LEUT VALTE LLEUT VALTE LLET	Transport, Estracellular	S-Propane-1,2-diol facilitated transport van MMN transport via MMN glycohydrolase acetaledhyde reversible transport transport van transport van Miller van van de versible transport van van de versible transport van			12ppd-S <sub>e</sub> <>> 12ppd-S namn_e -> nam + fSp  acal_e <>> acal gn_e <>> gn hynn_e <>> hyn xan_e <>> han xan_e <> han xan_e <> han xan_e xan_e <> han xan_e xan_e <> han xan_e xan_e <> han xan_e xan_e < han xan_e xan_e < han xan_e xan_e < han x
12PDOt NMN17 ACALDT GUATI HYXNI XANTI NACUP ASNabc ASNIT DAPabc CYSabc ACtr ETOHIT PYRIT OZI COZI DHAT NHST ARBID ARBID HIST PHET LEUT VALIT	Transport, Estracellular	S-Propane-1,2-diol facilitated transport via ABC system  L-asparagine transport via ABC system  L-asparagine reversible transport via ABC system  L-asparagine reversible transport via ABC system  L-asparagine transport via proton symport  L-creation of transport via proton symport L-arabinose transport via proton symport L-decine reversible transport via proton symport L-leucine reversible transport via proton symport L-decine reversible transport via proton symport Sporton symport L-decine reversible transport via proton symport Sporton symport Sporton symport Sporton symport Sporton symport Sporton symport Via proton symport Via prot			12ppd-S <sub>e</sub> <>> 12ppd-S namn_e >> nam + r5p  acal_e <>> acal gn_e <>> gn hyan_e <>> yn hyan_e <>> hyan san_e <>> san nac_e >> nac san_e + atp >> adp + asn + pi  asn_e + best <>> asn asn_e + atp >> adp + asn + pi  asn_e + best <>> asn atp + best <>> adp + cys + pi ac_e + best <>> ac eth >> eth_e + best best + pyr_e <>> pyr o2_e <>> o2 co2_e <>> o2 gyn_e <>> o2 gyn_e <>> gyn_e <>> byn heat + best >> blarabinose + pi best + bis_e <>> bis best + pi => adp + larabinose + pi best + bis_e <>> bis best + pie_e <>> pie best + leu_e <>> leu best + val_e <>> val best + leu_e <>> leu best + val_e <>> val best + leu_e <>> leu best + val_e <>> val best + leu_e <>> leu best + val_e <>> val best + leu_e <>> leu best + val_e <>> val best + leu_e <>> leu best + val_e <>> val best + leu_e <>> leu best + val_e <>> val best + leu_e <>> leu best + val_e <>> val best + leu_e <>> leu best + val_e <>> val best + leu_e <>> leu best + val_e <>> val best + leu_e <>> leu best + val_e <>> val best + leu_e <>> leu best + val_e <>> val
12PDOt  NMN17  ACALDt GUATI HYXNI XANTI NACUP ASNabc ASNtr DAPabc CVSabc ACtr ETOHtr PYRtr OZt COZt DHAT NH3T ARBitr ARBabc HIStr PHEtr LEUtr VALtr ILEtr CBLlabc	Transport, Extracellular	S-Propane-1,2-diol facilitated transport nansport was recommended by the properties of the properties			12ppd-S <sub>e</sub> <>> 12ppd-S namn_e >> nam + r5p  acal_e <>> acal gn_e <<> gn hym_e <<> yn hym_e <>> yn hym_e <>> hym xan_e <>> xan nac_e >> nac  asn_e + atp >> adp + asn + pi  asn_e + heat <>> as  26dap-M_e + atp >> 26dap-M + adp + pi atp + cys_e >> adp + cys + pi ac_e + heat <>> ac  eth -> eth_e + heat  heat + pyr_e <>> pyr o2_e <>> o2 co2_e <>> o2 cyl_e <>> o2 cyl_e <>> o2 dyn_e <>> gyh hat e <>> hot larabinose_e + heat -> larabinose larabinose_e + atp >> adp + larabinose + pi hext + bre_e <>> phe hext + pte_e <>> phe hext + pte_e <>> phe hext + leu_e <>> leu hext + pte_e <>> phe hext + leu_e <>> leu hext + ral_e <>> val hext + ral_e <>> leu hext + val_e <>> val hext + ral_e <>> leu atp + cbl_e >> adp + cbl1 + pi 15dap + bext + lys_e >> 15dap_e + lys
12PDOt NMN17 ACALDt GUATI HYXNI XANTI NACUP ASNabc ASNtr DAPabc CYSabc ACtr ETOHtr PYRtr OZt COZt DHAt ARBitr ARBitr ARBitr LEUtr VALtr LIEtr CBLlabc CADVt CRN17	Transport, Extracellular	S-Propane-1,2-diol facilitated transport van MMN transport via MMN glycohydrolase acetaledhyde reversible transport transport van transport van Miller van van de versible transport van van de versible transport van			12ppd-S <sub>e</sub> <>> 12ppd-S namn_e >> nam + r5p  acal_e <>> acal gn_e <<> gn hym_e <<> yn hym_e <>> hym xan_e <>> xan nac_e >> nac asn_e + atp >> adp + asn + pi  asn_e + heat <>> asn 26dsp-M_e + atp >> 26dsp-M + adp + pi atp + cys_e -> adp + cys + pi ac_e + heat <>> ac eth -> eth_e + heat heat + pyr_e <>> pyr o2_e <>> o2_e <>> o2 cyl_e <>> o2 cyl_e <>> o2 dyn_e <>> gyh_m + adp + larabinose larabinose_e + atp >> adp + larabinose + pi heat + bre_e <>> bhe heat + pu_e <>> phe heat + pu_e <>> phe heat + ble_e <>> phe
12PDOt NMN17 ACALDt GUATI HYXNI XANTI NACUP ASNabc ASNtr DAPabc CYSabc ACtr ETOHtr PYRtr OZt COZt DHAT ARBitr ARBitr ARBitr LEUtr VALtr LILEtr CBLlabc CADVt CRN17 NAt_1	Transport, Extracellular	S-Propane-1,2-diol facilitated transport nambor transport with a contract of the contract of t			12ppd-S <sub>e</sub> <>> 12ppd-S namn_e >> nam + r5p  acal_e <>> acal gn_e <<> gn hym_e <<> yn hym_e <>> hym xan_e <>> xan nac_e >> nac asn_e + atp >> adp + asn + pi  asn_e + heat <>> as  26dap-M_e + atp >> 26dap-M + adp + pi atp + cys_e >> adp + cys + pi ac_e + heat <>> ac  eth -> eth_e + heat  heat + pyr_e <>> pyr o2_e <>> o2 co2_e <>> o2 cyl_e <>> o2 cyl_e <>> o2 dyn_e <>> ghy heat <>> his heat + pi => adp + larabinose larabinose_e + heat -> larabinose larabinose_e + atp >> adp + larabinose + pi hext + bi_e <>> his hext + pie_e <>> phe hext + leu_e <>> leu hext + leu_e <> leu hext + leu
12PDOt NMN17 ACALDt GUATI HYXNI XANTI NACUP ASNabc ASNtr DAPabc CYSabc ACtr ETOHtr PYRtr OZt COZt DHAt ARBitr ARBitr ARBitr LEUtr VALtr LIEtr CBLlabc CADVt CRN17	Transport, Extracellular	S-Propane-1,2-diol facilitated transport nambor transport with a contract of the contract of t			12ppd-S <sub>e</sub> <>> 12ppd-S namn_e >> nam + r5p  acal_e <>> acal gn_e <<> gn hym_e <<> yn hym_e <>> hym xan_e <>> xan nac_e >> nac asn_e + atp >> adp + asn + pi  asn_e + heat <>> asn 26dsp-M_e + atp >> 26dsp-M + adp + pi atp + cys_e -> adp + cys + pi ac_e + heat <>> ac eth -> eth_e + heat heat + pyr_e <>> pyr o2_e <>> o2_e <>> o2 cyl_e <>> o2 cyl_e <>> o2 dyn_e <>> gyh_m + adp + larabinose larabinose_e + atp >> adp + larabinose + pi heat + bre_e <>> bhe heat + pu_e <>> phe heat + pu_e <>> phe heat + ble_e <>> phe
12PDOt NMN17 ACALDt GUATI HYXNI XANTI NACUP ASNabc ASNtr DAPabc CYSabc ACtr ETOHtr PYRtr OZt COZt DHAT ARBitr ARBitr ARBitr LEUtr VALtr LILEtr CBLlabc CADVt CRN17 NAt_1	Transport, Extracellular	S-Propane-1,2-diol facilitated transport vanithine reversible transport via ABC system  L-asparagine transport via ABC system  L-asparagine reversible transport via ABC system  L-asparagine reversible transport via proton symport  L-opsteine transport via ABC system aceitale reversible transport via proton symport transport via proton symport L-arabinose transport via proton symport Cadquerine reversible transport via proton symport L-arabinose transport via proton symport L-arabinose transport via proton symport L-arabinose transport via proton symport con symport via proton symport v			12ppd-S <sub>e</sub> <>> 12ppd-S namn_e >> nam + r5p  acal_e <>> acal gn_e <<> gn hym_e <<> yn hym_e <>> hym xan_e <>> xan nac_e >> nac asn_e + atp >> adp + asn + pi  asn_e + heat <>> as  26dap-M_e + atp >> 26dap-M + adp + pi atp + cys_e >> adp + cys + pi ac_e + heat <>> ac  eth -> eth_e + heat  heat + pyr_e <>> pyr o2_e <>> o2 co2_e <>> o2 cyl_e <>> o2 cyl_e <>> o2 dyn_e <>> ghy heat <>> his heat + pi => adp + larabinose larabinose_e + heat -> larabinose larabinose_e + atp >> adp + larabinose + pi hext + bi_e <>> his hext + pie_e <>> phe hext + leu_e <>> leu hext + leu_e <> leu hext + leu
12PDOt NMN17 ACALDT GUATI HYXNI XANTI NACUP ASNabc ASNIT DAPabc CYSabc ACIT ETOHIT PYRIT OZI COZI DHAI ARBIT ARBIT ARBIT LEUT VALIT LEUT UALIT LET CBLIabc CADVI CRN17 NAL_1 CITISUC	Transport, Extracellular	S-Propane-1,2-diol facilitated transport nansport with a second process of the second pr			12ppd-S <sub>e</sub> <>> 12ppd-S namn_e >> nam + r5p  acal_e <>> acal gn_e <<> gn hynn_e <>> fp hynn_e <>> hyn san_e <>> san nac_e >> nac asn_e + atp >> adp + asn + pi  asn_e + heat <>> asn the >= adp + ys + pi ac_e + atp >> 26dap-M + adp + pi atp + cys_e >> adp + cys + pi ac_e + heat <>> ac eth >> eth => heat heat + pyr_e <>> pyr co_e <>> co_2 co_e <>> co_2 gyn_e <>> gyn hhd_e <>> hot larabinose_e + heat >> larabinose larabinose_e + atp >> adp + larabinose + pi heat + bis_e <>> his heat + pu_e <>> pe heat + leu_e <>> leu heat + leu_e <> leu heat + leu_e <>> leu heat + leu_e <>> leu heat + leu_e <>> leu heat + leu_e <> sic_e + leu heat + leu_e <> sic_e + leu heat + leu_e <> sic_e <-> cic_e <= cic_e + leu heat + leu_e <> sic_e <-> cic_e <= cic_e <= leu heat + leu_e <> sic_e <= cic_e <= leu heat + leu_e <> sic_e <= cic_e <= c
12PDOt NMN17 ACALDT GUATI HYXNI XANII NACUP ASNabc ASNIT DAPabc CYSabc ACIT ETOHIT PYRIT OZI COZI DHAI ARBIT ARBIT ARBIT LEUT VALIT ILET CBLIabc CADVI CRN17 NAL,1 CITSUC CSN12 ACGApts	Transport, Extracellular	S-Propane-1,2-diol facilitated transport nambor transport with a control of the c			12ppd-S <sub>e</sub> <>> 12ppd-S namn_e >> nam + r5p  acal_e <>> acal gn_e <<> gn hynn_e <>> fyn hynn_e <>> hyn san_e <>> san nac_e >> nac  asn_e + atp >> adp + asn + pi  asn_e + heat <>> asn the + atp >> 26dap-M + adp + pi atp + cys_e -> adp + cys + pi ac_e + heat <>> ac  eth -> eth_e + heat  best + pyr_e <>> pyr o2_e <>> o2 cy_e <>> o2 cyh_e <>> o2 cyh_e <>> dyh heat + bis_e <>> his  heat + pis_e <>> phe heat + larabinose + pi heat + bis_e <>> his heat + pis_e <>> phe heat + larabinose + pi heat + larabinose + pi heat + bis_e <>> his heat + pis_e <>> phe heat + larabinose + pi heat + larabinose + p
12PDOt NMN17 ACALDT GUATI HYXNI XANII NACUP ASNabc ASNIT DAPabc CYSabc ACIT ETOHIT PYRIT OZI COZI DHAI ARBIT ARBIT ARBIT LEUT VALIT LEUT VALIT LET CBLIabc CADVI CRN17 NAL_I CITISUC CSN12	Transport, Extracellular	S-Propane-1,2-diol facilitated transport nambor transport with proton symport or yrivate reversible transport with proton symport or yrivate reversible transport with proton symport with transport with proton symport with transport with with the with transport with proton symport with transport with with the with the with transport with the with the with transport with the with			12ppd-S <sub>e</sub> <>> 12ppd-S namn_e >> nam + r5p  acal_e <>> acal gn_e <<> gn hynn_e <>> fp hynn_e <>> hyn san_e <>> san nac_e >> nac  asn_e + atp >> adp + asn + pi  asn_e + heat <>> asn the >= adp + ys + pi  ac_e + atp >> 26dap-M_e + adp + pi  atp + cys_e >> adp + cys + pi  ac_e + heat <>> ac  eth >=
12PDOt NMN17 ACALDT GUATI HYXNI XANII NACUP ASNabc ASNIT DAPabc CYSabc ACIT ETOHIT PYRIT OZI COZI DHAI ARBIT ARBIT ARBIT LEUT VALIT ILET CBLIabc CADVI CRN17 NAL,1 CITSUC CSN12 ACGApts	Transport, Extracellular	S-Propane-1,2-diol facilitated transport nambor transport with proton symport or transport with transport with proton symport or with transport with proton symport Levaline reversible transport with proton symport Levaline reversible transport with proton symport with transport with transport with proton symport with transport with with the with transport with proton symport with transport with with the with transport with the with the with the with the with transport with the with			12ppd-S <sub>e</sub> <>> 12ppd-S namn_e >> nam + r5p  acal_e <>> acal gn_e <<> gn hynn_e <>> fyn hynn_e <>> hyn san_e <>> san nac_e >> nac  asn_e + atp >> adp + asn + pi  asn_e + heat <>> asn the + atp >> 26dap-M + adp + pi atp + cys_e -> adp + cys + pi ac_e + heat <>> ac  eth -> eth_e + heat  best + pyr_e <>> pyr o2_e <>> o2 cy_e <>> o2 cyh_e <>> o2 cyh_e <>> dyh heat + bis_e <>> his  heat + pis_e <>> phe heat + larabinose + pi heat + bis_e <>> his heat + pis_e <>> phe heat + larabinose + pi heat + larabinose + pi heat + bis_e <>> his heat + pis_e <>> phe heat + larabinose + pi heat + larabinose + p
NMN17  ACALDT GUATI HYXNI XANI NACUP ASNabc ASNIT DAPabc CYSabc ACIT ETOHIT PYRIT OZI COZI DHAI ARBID ARBID ARBID HIST PHET LEUT VALT ILET CBLIabc CADVI CRN17 NAL,1 CITSUC CSNL2 ACGAPIS DALATT	Transport, Extracellular	S-Propane-1,2-diol facilitated transport nambor transport with a second process of the s			12ppd-S <sub>e</sub> <>> 12ppd-S namn_e >> nam + r5p  acal_e <>> acal gn_e <<> gn hynn_e <>> fp hynn_e <>> fyn san_e <>> san nac_e >> nac  asn_e + atp >> adp + asn + pi  asn_e + heat <>> asn the >= adp + cys + pi  ac_e + atp >> 26dap-M_e + adp + pi  atp + cys_e >> adp + cys + pi  ac_e + heat <>> ac  eth >> eth => heat  heat + pyr_e <>> pyr  co_e <>> co_2 co_e <>> co_2 gyn_e <>> gyn heat <>> gyn heat <>> heat >> heat  heat + bis_e <>> heat  adp + larabinose + pi heat + his_e <>> he heat + pu_e <>> pe heat + bis_e <>> he heat + pu_e <>> pe heat + heat >> larabinose  larabinose_e + atp >> adp + larabinose  larabinose_e + atp >> adp + larabinose  larabinose_e + bet <>> larabinose_e + pi heat + his_e <>> his heat + phe_e <>> phe heat + leu_e <>> leu heat + leu_e <>> leu heat + leu_e <>> leu heat + ale_e <>> adp + chll + pi 15dap + heat + lys_e >> 15dap_e + lys cm_e + gibtin >> cm + gibtin_e heat + na <>> nu_e cit_e + succ_e ct_e + heat >> ct + succ_e ct_e + heat <>> ct + ct + succ_e ct_e + heat <>> ct + ct + succ_e ct_e + heat <>> ct + ct + succ_e ct_e + heat <>> ct + succ_e ct_e + heat <>> ct + ct + succ_e ct_e + heat <>> ct + ct + succ_e ct_e + heat <>> ct + succ_e ct_e + leat <= ct + succ_e ct_e + leat
12PDOt NMN17 ACALDT GUATI HYXNI XANII NACUP ASNabc ASNIT DAPabc CYSabc ACIT ETOHIT PYRIT OZI COZI DHAI ARBIT ARBIT ARBIT LEUT VALET LEUT VALET LEUT CELIABC CADVI CRN17 NAL, 1 CITISUC CSNL2 ACGAPIS DALATT DSERIT GLYT	Transport, Extracellular	S-Propane-1,2-diol facilitated transport name transport with transport with transport with transport with transport was transport was the transport was proton symport. L-system creates reversible transport was proton symport or transport was proton symport or transport was proton symport. A transport was transport was transport was proton symport. L-arabinose transport was proton symport. A-acetyl-D-glucosamine transport via succinate antiport was proton symport. D-serine transport via proton symport. Soldier transport via proton symport.			12ppd-S <sub>e</sub> <>> 12ppd-S namn_e >> nam + r5p  acal_e <>> acal gn_e <<> gn hynn_e <>> fyn hynn_e <>> hyn san_e <>> san nac_e >> nac  asn_e + atp >> adp + asn + pi  asn_e + heat <>> asn the + atp >> 26dap-M + adp + pi atp + cys_e -> adp + cys + pi ac_e + heat <>> ac  eth -> eth_e + heat  heat + pyr_e <>> pyr o2_e <>> o2 co2_e <>> o2 cyl_e <>> o2 cyl_e <>> o2 cyl_e <>> o4 hid_e <>> hot larabinose_e + heat >> larabinose larabinose_e + atp >> adp + larabinose larabinose_e + atp >> adp + larabinose larabinose_e + atp >> adp + larabinose + pi heat + bis_e <>> his heat + phe_e <>> phe heat + leu_e <>> leu heat + leu_e <>> leu heat + leu_e <>> co1 che + beat <>> leu heat + atp <>> co2, es <> co2 co2, es <> co3 co3, es <> co3, es <> co3 co3, es <> co4, es <> co4 larabinose_e + atp >> adp + larabinose + pi heat + his_e <>> his heat + phe_e <>> phe heat + leu_e <>> leu heat + leu_e <>> leu heat + cb1_e >> adp + cb11 + pi 15dap + heat + lys_e >> 15dap_e + lys cm_e + gibtin >> cm + gibtin_e heat + as <>> nu_e cit_e + succ_e ct_e + heat <>> ct_e + heat <>> ct naga_e + pep >> naga6p + pyr dala_e + heat <>> dala heat + dse_e <>> der gly_e + heat <>> gly e + heat <>> gly
NMN17 ACALDT GUATI HYXNI XANTI NACUP ASNabc ASNIT DAPabc CYSabc ACIT ETOHIT PYRIT OZI COZI DHAI ARBIT ARBIT ARBIT LEUT VALTT LEUT VALTT LEUT CBLIabc CADVI CRN17 NAT_1 CITISUC CSN12 ACGApts DALATT DSERTT	Transport, Extracellular	S-Propane-1,2-diol facilitated transport nambor transport with transport with transport with transport with transport with transport was the transport was proton symport exhand neversible transport was proton symport of the transport was proton symport was proton symport was the transport was proton symport was proton symport was the transport was proton symport was proton symport was the transport was proton symport to the transport was proton symport of proton symport was proton symport was proton symport was proton symport was proton symport vas proton symport v			12ppd-S <sub>e</sub> <>> 12ppd-S namn_e >> nam + r5p acal_e <>> acal gn_e <>> gn hynn_e <>> yn hynn_e <>> hyn san_e <>> san nac_e >> nac asn_e + atp >> adp + asn + pi asn_e + heat <>> asn the > adp + sp >> 26dap-M + adp + pi atp + cys_e >> adp + cys + pi ac_e + heat <>> ac eth >> eth e + eth heat + pyr_e <>> pyr co_e <>> co_2 co_e <>> co_2 gyn_e <>> gyn hhd_e <>> hot larabinose_e + heat >> larabinose larabinose_e + beat >> larabinose larabinose_e + atp >> adp + larabinose + pi heat + his_e <>> his heat + phe_e <>> phe heat + leu_e <>> leu heat + val_e <>> val heat + si_e <> si_e atp + cbll_e >> adp + cbll + pi 15dap + heat + ls_e <>> lsap + chet + na <>> na_e cit_e + succ_> cit_e + succ_e ct_e + heat >> cit + succ_e ct_e + heat >> cit + succ_e ct_e + heat >> cit + succ_e ct_e + heat <>> cit + succ_e ct_e + coc +

ASPt_2	Transport, Extracellular	Aspartate transport via proton symport (2 H)		asp_e + 2 hext -> asp
FUMt_2	Transport, Extracellular	Fumarate transport via proton symport (2 H)		fum_e + 2 hext -> fum
MALt_2	Transport, Extracellular	Malate transport via proton symport (2 H)		2 hext + mal_e -> mal
SUCCt_2	Transport, Extracellular	succinate transport via proton symport (2 H)		2 hext + succ_e -> succ
ASPt_3	Transport, Extracellular	L-asparate transport via proton		asp_e + 3 hext -> asp
MALt_3	Transport, Extracellular	symport (3 H) Malate transport via proton		3 hext + mal_e -> mal
SUCCt_3	Transport, Extracellular	symport (3 H) Succintate transport via proton		3 hext + succ_e -> succ
SUCCet	Transport, Extracellular	symport (3 H) Succinate efflux via proton		succ -> hext + succ_e
		symport Fumarate transport via proton		
FUMt_3 SUCFUMt	Transport, Extracellular Transport, Extracellular	symport (3 H) succinate:fumarate antiporter		fum_e + 3 hext -> fum fum e + succ <-> fum + succ e
GALCTNtr	Transport, Extracellular	D-galactonate transport via proton symport, reversible		dgalctn_e + hext <-> dgalctn
GALACtr	Transport, Extracellular	D-galacturonate transport via proton symport, reversible		dgalac_e + hext <-> dgalac
GLCURtr	Transport, Extracellular	D-glucuronate transport via		dgluc_e + hext <-> dgluc
OCDCAt	Transport, Extracellular	proton symport, reversible Octadecanoate transport via		hext + c180_e -> c180
HDCAt	Transport, Extracellular	proton symport Hexadecanoate transport via		hext + c160 e -> c160
TTDCAt	Transport, Extracellular	proton symport Tetradecanoate transport via		hext + c140_e -> c140
FE2abc		proton symport iron (II) transport via ABC		
FORt	Transport, Extracellular Transport, Extracellular	system formate transport via diffusion		atp + fe2_e -> adp + fe2 + pi formate e <-> formate
FUCt	Transport, Extracellular	L-fucose transport via proton symport		fuc_e + hext <-> fuc
ABUTt	Transport, Extracellular	4-aminobutyrate transport in		gaba_e + hext -> gaba
GLACt	Transport, Extracellular	via proton symport D-galactose transport in via		glac_e + hext -> glac
GLCt	Transport, Extracellular	proton symport D-glucose transport in via		glc_e + hext -> glc
GALTpts	Transport, Extracellular	proton symport Galactitol transport via PEP:Pyr 2.7.1.6	50	
		PTS 2.7.1.6 Maltose transport via PEP:Pyr 2.7.1.6		.03530/KOX_21000 galt_e + pep -> galt1p + pyr
MALTpts	Transport, Extracellular	PTS Z./.LX		mlt_e + pep -> mlt6p + pyr
TREpts	Transport, Extracellular	PTS 2.7.1.1		tre_e + pep -> tre6p + pyr
SUCpts	Transport, Extracellular	PTS 2.7.1.6 Glucose transport via PEP:Pyr	69 KOX_13365	suc_e + pep -> suc6p + pyr
GLCpts	Transport, Extracellular	PTS 2.7.13	69 KOX_26855	glc_e + pep -> g6p + pyr
NAMURpts	Transport, Extracellular	N-Acetylmuramate transport via PEP:Pyr PTS 2.7.1.6	69 KOX_06290(murP)/KOX_2685	namur_e + pep -> namur6p + pyr
GLNabc	Transport, Extracellular	L-glutamine transport via ABC system		atp + gln_e -> adp + gln + pi
GLYALDt	Transport, Extracellular	glycerol transport via channel Glyceraldehyde facilitated		gl <-> gl_e
UREAt	Transport, Extracellular	diffusion Urea transport via facilitate		t3_e <-> t3
	Transport, Extracellular	diffusion Glycerol-3-phosphate :		urea_e <-> urea
GLYC3Pt	Transport, Extracellular	phosphate antiporter L-aspartate transport via ABC		glyc3p_e + pi -> glyc3p + pi_e
ASPabc	Transport, Extracellular	system		asp_e + atp -> adp + asp + pi
GLUabc	Transport, Extracellular	L-glutamate transport via ABC system		atp + glu_e -> adp + glu + pi
ASPt	Transport, Extracellular	L-aspartate transport in via proton symport		asp_e + hext -> asp
GLUtr	Transport, Extracellular	L-glutamate transport via proton symport, reversible		glu_e + hext <-> glu
GLUt ORNabc	Transport, Extracellular Transport, Extracellular	Na+/glutamate symport ornithine transport via ABC		glu_e + na_e -> glu + na
		system L-arginine transport via ABC		atp + orn_e -> adp + orn + pi
ARGabc	Transport, Extracellular	system L-histidine transport via ABC		arg_e + atp -> adp + arg + pi
HISabc	Transport, Extracellular	system L-lysine transport via ABC		atp + his_e -> adp + his + pi
LYSabc	Transport, Extracellular	system L-idonate transport via proton		atp + lys_e -> adp + lys + pi
IDONtr	Transport, Extracellular	symport, reversible		hext + idon_e <-> idon
GLCNtr	Transport, Extracellular	D-gluconate transport via proton symport, reversible		gluc_e + hext <-> gluc
DDGLCNtr	Transport, Extracellular	2-dehydro-3-deoxy-D- gluconate transport via proton		kdg_e + hext <-> kdg
Kabc	Transport, Extracellular	symport, reversible Potassium ABC transporter		atp + k_e -> adp + k + pi
AKGt	Transport, Extracellular	2-oxoglutarate reversible transport via symport		akg_e + hext <-> akg
LCTSt	Transport, Extracellular	Lactose transport via proton symport		hext + lactose_e <-> lactose
ILEabc	Transport, Extracellular	L-isoleucine transport via ABC system		atp + ile_e -> adp + ile + pi
THRabc	Transport, Extracellular	L-threonine transport via ABC		atp + thr_e -> adp + pi + thr
ALAabc	Transport, Extracellular	system L-alanine transport via ABC		ala_e + atp -> adp + ala + pi
VALabc	Transport, Extracellular	system L-valine transport via ABC		atp + val_e -> adp + pi + val
LEUabc	Transport, Extracellular	system L-leucine transport via ABC		atp + leu_e -> adp + leu + pi
DLACt	Transport, Extracellular	system D-lactate transport via proton		hext + lac e <-> lac
GLYCLTtr		symport glycolate transport via proton		_
	Transport, Extracellular  Transport, Extracellular	symport, reversible L-lactate reversible transport		glycolate_e + hext <-> glycolate
LLACtr		via proton symport L-lysine reversible transport via		hext + llac_e <-> llac
LYStr	Transport, Extracellular	proton symport maltopentaose transport via		hext + lys_e <-> lys
MALTPTabc	Transport, Extracellular	ABC system maltose transport via ABC		atp + maltpt_e -> adp + maltpt + pi
MLTabc	Transport, Extracellular	system		atp + mlt_e -> adp + mlt + pi
MALTTTRabc	Transport, Extracellular	maltotetraose transport via ABC system		atp + mltttr_e -> adp + mltttr + pi
MALTHXabc	Transport, Extracellular	maltohexaose transport via ABC system		atp + mlthx_e -> adp + mlthx + pi
MALTTRabc	Transport, Extracellular	Maltotriose transport via ABC system		atp + mlttr_e -> adp + mlttr + pi
FRUpts2	Transport, Extracellular	Fructose transport via PEP:Pyr PTS (f6p generating)		fru_e + pep -> f6p + pyr
MANpts	Transport, Extracellular	D-mannose transport via PEP:Pyr PTS 2.7.1.0	KOX_02420/KOX_02425/KOX_ KOX_10140/KOX_10145/KOX_ 69 KOX_13540/KOX_13545/KOX_ KOX_16355/KOX_16360/KOX_	.10150/KOX_10155/ .16345/KOX_16350/ man_e + pep -> man6p + pyr
cus:		D-glucosamine transport via	KOX_23660	
GAMpts	Transport, Extracellular	PEP:Pyr PTS melibiose transport in via		gam_e + pep -> ga6p + pyr
MELIBt	Transport, Extracellular	symport		hext + meli_e -> meli
METabc	Transport, Extracellular	L-methionine transport via ABC system		atp + met_e -> adp + met + pi
METDabc	Transport, Extracellular	D-methionine transport via ABC system		atp + dmet_e -> adp + dmet + pi
GLACabc		D-galactose transport via ABC		atp + glac_e -> adp + glac + pi
	Transport, Extracellular	system		
INDOLEtr	Transport, Extracellular Transport, Extracellular	system Indole transport via proton symport, reversible		hext + indole_e <-> indole

ACNAMt	Transport, Extracellular	N-acetylneuraminate proton	naneu_e + hext -> naneu
		symport nitrate transport in via nitrite	
NO3t	Transport, Extracellular	antiport nitrite transport in via proton	no2 + no3_e -> no2_e + no3
NO2tr	Transport, Extracellular	symport, reversible	hext + no2_e <-> no2
NAt_2	Transport, Extracellular	sodium proton antiporter (H:NA is 2)	2 hext + na -> na_e
NAt_1.5	Transport, Extracellular	sodium proton antiporter (H:NA is 1.5)	3 hext + 2 na -> 2 na_e
GSNt	Transport, Extracellular	guanosine transport in via proton symport	gsn_e + hext -> gsn
DGSNt	Transport, Extracellular	deoxyguanosine transport in	dg_e + hext -> dg
		via proton symport inosine transport in via proton	
INSt	Transport, Extracellular	symport deoxyinosine transport in via	hext + ins_e -> ins
DINSt	Transport, Extracellular	proton symport	din_e + hext -> din
ADNt	Transport, Extracellular	adenosine transport in via proton symport	adn_e + hext -> adn
URIt	Transport, Extracellular	uridine transport in via proton symport	hext + uri_e -> uri
CYTDt	Transport, Extracellular	cytidine transport in via proton	cytd_e + hext -> cytd
DCYTt	Transport. Extracellular	symport deoxycytidine transport in via	dc e + hext -> dc
DURIt	Tonorest Entre-villation	proton symport deoxyuridine transport in via	_
	Transport, Extracellular	proton symport deoxyadenosine transport in via	du_e + hext -> du
DADNt	Transport, Extracellular	proton symport	da_e + hext -> da
THMDt	Transport, Extracellular	thymidine transport in via proton symport	hext + thymd_e -> thymd
PNTOt	Transport, Extracellular	Pantothenate sodium symporter	na_e + pnto_e -> na + pnto
PItr	Transport, Extracellular	phosphate reversible transport via symport	hext + pi_e <-> pi
NMNP	Transport, Extracellular	NMN permease	namn_e -> namn
PTRCabc	Transport, Extracellular	putrescine transport via ABC system	atp + ptrc_e -> adp + pi + ptrc
SPMDabc	Transport, Extracellular	spermidine transport via ABC system	atp + sprmd_e -> adp + pi + sprmd
PTRCORNt	Transport, Extracellular	putrescine/ornithine antiporter	orn + ptrc_e <-> orn_e + ptrc
PTRCtr	Transport, Extracellular	putrescine transport in via proton symport, reversible	hext + ptrc_e <-> ptrc
PROtr	Transport, Extracellular	L-proline reversible transport via proton symport	hext + pro_e <-> pro
PROabc	Transport, Extracellular	L-proline transport via ABC system	atp + pro_e -> adp + pi + pro
PIabc	Transport, Extracellular	phosphate transport via ABC	atp + pi.e -> adp + 2 pi
ACMANApts	Transport, Extracellular	system N-acetyl-D-mannosamine	nadma e + pep -> nadma6p + pyr
		transport via PTS	
MNLpts	Transport, Extracellular		mnt_e + pep -> mnt1p + pyr
FRUpts	Transport, Extracellular	D-fructose transport via PEP:Pyr 2.7.1.69 KOX_03505/KOX_06130/KOX_25810/KOX_25820	fru_e + pep -> flp + pyr
FRUabc	Transport, Extracellular	D-fructose transport via ABC system	atp + fru_e -> adp + pi + fru
PROt	Transport, Extracellular	Na+/Proline-L symporter	na_e + pro_e -> na + pro
RMNt	Transport, Extracellular	L-rhamnose transport via proton symport	hext + rmn_e -> rmn
TSULabc	Transport, Extracellular	thiosulfate transport via ABC system	atp + tsul_e -> adp + pi + tsul
SERtr	Transport, Extracellular	L-serine reversible transport via proton symport	hext + ser_e <-> ser
THMabc	Transport, Extracellular	thiamine transport via ABC	atp + thiamin e -> adp + pi + thiamin
SBTpts	Transport, Extracellular	system D-sorbitol transport via PEP:Pyr 2.7.1.69 KOX_00575/KOX_00580/KOX_00585/KOX_17460	
	•	L corbona transport via DED:Dvr	
SORBpts SERt	Transport, Extracellular	P12	pep + sorb_e -> pyr + sb1p
THRt	Transport, Extracellular Transport, Extracellular	L-serine via sodium symport L-threonine via sodium	na_e + ser_e -> na + ser na_e + thr_e -> na + thr
		symport taurine transport via ABC	
TAURabc	Transport, Extracellular	system L-threonine reversible transport	atp + taur_e -> adp + pi + taur
THRtr	Transport, Extracellular	via proton symport	hext + thr_e <-> thr
TRPtr	Transport, Extracellular	L-tryptophan reversible transport via proton symport	to the second se
			hext + trp_e <-> trp
Ktr	Transport, Extracellular	potassium reversible transport	hext + trp_e <-> trp
Ktr		potassium reversible transport via proton symport L-tyrosine reversible transport	
	Transport, Extracellular Transport, Extracellular	potassium reversible transport via proton symport L-lynosine reversible transport via proton symport sin-Glycerd 3-phosphate	hext + k_e <-> k hext + tyr_e <-> tyr
TYRtr	Transport, Extracellular Transport, Extracellular Transport, Extracellular	potassium reversible transport via proton symport L-byrosine reversible transport via proton symport	hext + k_e <-> k
TYRtr	Transport, Extracellular Transport, Extracellular	potassium reensible transport via proton sympot L-lyrosine revensible transport via proton sympot sn-Glycerol 3-phosphate transport via A&C system Mannose-6-phosphate transport via A&C system Mannose-6-phosphate transport via Ahosphate	hext + k_e <-> k hext + tyr_e <-> tyr
TYRtr GLYC3Pabc	Transport, Extracellular Transport, Extracellular Transport, Extracellular	potassium reensible transport via proton sympot L-lyrosine revensible transport via proton sympot sn-Glycerol 3-phosphate transport via A&C system Mannose-6-phosphate transport via A&C system for the sympot for the s	$\begin{array}{lll} hext + k_{,e} <-> & k \\ \\ hext + tyr_{,e} <-> & tyr \\ \\ atp + glyc3p_{,e} -> & adp + glyc3p + pi \end{array}$
TYRtr GLYC3Pabc MAN6Pt_2 G6Pt_2	Transport, Extracellular Transport, Extracellular Transport, Extracellular Transport, Extracellular Transport, Extracellular	potassium reversible transport via proton sympot L-lyrosine reversible transport via proton sympot sn-Glycerol 3-phosphate transport via A&C system Mannose-6-phosphate transport via A&C system Mannose-6-phosphate antiport Glucose-6-phosphate transport via phosphate antiport Via phosphate antiport Via phosphate antiport	hext + k,e <-> k hext + tyr_e <-> tyr atp + glyc3p_e -> adp + glyc3p + pi man6p_e + 2 pi -> man6p + 2 pi_e g6p_e + 2 pi -> g6p + 2 pi_e
TYRtr GLYC3Pabc MAN6Pt_2 G6Pt_2 FUCPt_2	Transport, Extracellular Transport, Extracellular Transport, Extracellular Transport, Extracellular Transport, Extracellular Transport, Extracellular	potassium reversible transport via proton sympot L-tyrosine reversible transport via proton sympot sn-Glyerod 3-phosphate transport via ABC system Marnose-6-p-hosphate transport via phosphate dariport Gliucose-6-phosphate transport via phosphate antiport	hext + k,e <-> k hext + byr_e <-> byr atp + glyc3p_e -> adp + glyc3p + pi man6p_e + 2 pi -> man6p + 2 pi_e g6p_e + 2 pi -> g6p + 2 pi_e fuc1p_e + 2 pi -> fuc1p + 2 pi_e
TYRtr GLYC3Pabc MAN6Pt_2 G6Pt_2	Transport, Extracellular Transport, Extracellular Transport, Extracellular Transport, Extracellular Transport, Extracellular	potassium reversible transport via proton sympot L-lyrosine reversible transport via proton sympot sn-Glycerol 3-phosphate transport via AEC system Mannoes-6-phosphate transport via phosphate antiport Gliucose-6-phosphate transport via phosphate antiport Fucose 1-phosphate transport via phosphate antiport uracil transport in via proton sympot	hext + k,e <-> k hext + tyr_e <-> tyr atp + glyc3p_e -> adp + glyc3p + pi man6p_e + 2 pi -> man6p + 2 pi_e g6p_e + 2 pi -> g6p + 2 pi_e
TYRtr GLYC3Pabc MAN6Pt_2 G6Pt_2 FUCPt_2	Transport, Extracellular Transport, Extracellular Transport, Extracellular Transport, Extracellular Transport, Extracellular Transport, Extracellular	potassium reversible transport via proton sympot L-lyrosine reversible transport via proton sympot sn-Glyceril 3-phosphate transport via AEC system Mannoes-6-phosphate transport via phosphate antiport Glucose-6-phosphate transport via phosphate transport via phosphate antiport Fucose 1-phosphate transport via phosphate antiport uracil transport in via proton symport Xanthonies transport via proton symport Xanthonies transport via proton symport	hext + k,e <-> k hext + byr_e <-> byr atp + glyc3p_e -> adp + glyc3p + pi man6p_e + 2 pi -> man6p + 2 pi_e g6p_e + 2 pi -> g6p + 2 pi_e fuc1p_e + 2 pi -> fuc1p + 2 pi_e
TYRtr GLYC3Pabc MAN6Pt_2 G6Pt_2 FUCPt_2 URAt	Transport, Extracellular	potassium reversible transport via proton sympot L-tyrosine reversible transport via proton sympot sn-Glyceril 3-phosphate transport via AEC system Mannose-6-phosphate transport via phosphate antiport Glucose-6-phosphate transport via phosphate antiport via phosphate antiport Fucose 1-phosphate transport via phosphate antiport uracil transport in via proton sympot Xanthosine transport via proton sympot vandine transport via proton sympot vandine transport via proton sympot inosine transport in via proton sympot mymot reversible	hext + k,e <-> k hext + tyr_e <-> tyr atp + glyc3p_e -> adp + glyc3p + pi man6p_e + 2 pi -> man6p + 2 pi_e g6p_e + 2 pi -> g6p + 2 pi_e fuc1p_e + 2 pi -> fuc1p + 2 pi_e hext + ura_e -> ura
TYRtr GLYC3Pabc MAN6Pt_2 G6Pt_2 FUCPt_2 URAt XTSNtr	Transport, Extracellular	potassium reversible transport via proton sympot L-lyrosine reversible transport via proton sympot sn-Glycerol 3-phosphate transport via ARC system Mannose-6-phosphate transport via ARC system Mannose-6-phosphate transport via phosphate antiport Glucose-6-phosphate transport via phosphate antiport via phosphate invisor via proton symport in sosine transport via proton symport inosine transport in via proton symport dendensie transport in via proton symport dendensie transport in via proton symport dendensie transport in via proton symport reversible adendensie transport in via	hext + k,e <-> k hext + kyr_e <-> kyr atp + glyc3p_e -> adp + glyc3p + pi man6p_e + 2 pi -> man6p + 2 pi_e g6p_e + 2 pi -> g6p + 2 pi_e fuc1p_e + 2 pi -> fuc1p + 2 pi_e hext + ura_e -> ura hext + xtsin_e <-> xtsine
TYRtr GLYC3Pabc MAN6Pt_2 G6Pt_2 FUCPt_2 URAt XTSNtr INStr	Transport, Extracellular	potassium reversible transport via proton sympot L-lyrosine reversible transport via proton sympot sn-Glycerol 3-phosphate transport via ARC system Mannose-6-phosphate transport via ARC system Mannose-6-phosphate transport via phosphate antiport Glucose-6-phosphate transport via phosphate antiport via phosphate in via proton symport symport discriment via proton symport denoise transport via proton symport denoise transport in via proton symport, reversible adenoise transport in via proton symport, reversible of adenoise transport in via proton symport, reversible of colories of the proton symport, reversible of colories of the proton symport in via proton	hext + k,e <-> k hext + kyr_e <-> kyr atp + glyc3p_e >> adp + glyc3p + pi man6p_e + 2 pi -> man6p + 2 pi_e g6p_e + 2 pi -> g6p + 2 pi_e fuc1p_e + 2 pi -> fuc1p + 2 pi_e hext + ura_e -> ura hext + xtsine_e <-> xtsine hext + ins_e <-> ins
TYRtr GLYC3Pabc MAN6Pt_2 G6Pt_2 FUCPt_2 URAt XTSNtr INStr ADNtr	Transport, Extracellular	potassium reversible transport via proton sympot L-lyrosine reversible transport via proton sympot sn-Glycerol 3-phosphate transport via ARC system Mannose-6-phosphate transport via ARC system Mannose-6-phosphate transport via phosphate antiport Glucose-6-phosphate transport via phosphate antiport via phosphate in via proton symport symport dender in via proton symport dendersible adenosine transport in via proton symport cytidine transport in via proton symport, reversible adenosine transport in via proton symport, reversible cytidine transport in via	hext + k,e <-> k hext + kyr_e <-> kyr atp + glyc3p_e >> adp + glyc3p + pi man6p_e + 2 pi -> man6p + 2 pi_e g6p_e + 2 pi -> g6p + 2 pi_e fuc1p_e + 2 pi -> fuc1p + 2 pi_e hext + ura_e >> ura hext + xtsine_e <-> xtsine hext + ins_e <-> ins adn_e + hext <-> adn cytd_e + hext <-> cytd
TYRIT GLYC3Pabc MAN6Pt_2 G6Pt_2 FUCPt_2 URAt XTSNitr INStr ADNtr CYTDtr THMDtr	Transport, Extracellular	potassium reversible transport via proton sympotar L-tyrosine reversible transport via proton sympotar sn-Glycerol 3-phosphate transport via AGC system Mannose-6-phosphate transport via Abnosphate antiport Glucose-6-phosphate transport via phosphate antiport Glucose-6-phosphate transport via phosphate antiport Fucose 1-phosphate transport via phosphate antiport via phosphate antiport Surgent via proton sympot varsible antiport Vanthosine transport via proton sympot sympot reversible adenosine transport in via proton sympot; reversible adenosine transport in via proton sympot; reversible cytidine transport in via proton sympot; reversible cytidine transport in via proton sympot; reversible	hext + k,e <-> k hext + kyr_e <-> kyr atp + glyc3p_e -> adp + glyc3p + pi man6p_e + 2 pi -> man6p + 2 pi_e g6p_e + 2 pi -> g6p + 2 pi_e fuc1p_e + 2 pi -> fuc1p + 2 pi_e hext + ura_e -> ura hext + xtsine_e <-> xtsine hext + ins_e <-> ins adn_e + hext <-> adn cytd_e + hext <-> cytd hext + thymd_e <-> thymd hext + thymd_e <-> thymd hext + thymd_e <-> thymd
TYRIT GLYC3Pabc  MAN6Pt_2 G6Pt_2 FUCPt_2 URAt XTSNitr INStr ADNitr CYTDir THMDtr URItr	Transport, Extracellular	potassium reversible transport via proton sympot  L-lyvosine reversible transport  via proton sympot  sn-Glycerol 3-phosphate  transport via AEC system  Mannose-6-phosphate  transport via Phosphate  transport via Phosphate  antiport  Glucose-6-phosphate transport  via phosphate antiport  Fucuse 1-phosphate transport  via phosphate antiport  via phosphate transport  via phosphate proton  symport  Xanthosine transport via proton  sympot  sympot reversible  adenosine transport in via proton  sympot, reversible  opticial transport in via  proton symport, reversible  thymidine transport in via  proton symport, reversible  thymidine transport in via  proton symport, reversible  undine transport in via  proton symport, reversible	hext + k,e <-> k hext + kyr_e <-> kyr atp + glyc3p_e >> adp + glyc3p + pi man6p_e + 2 pi -> man6p + 2 pi_e g6p_e + 2 pi -> g6p + 2 pi_e fuc1p_e + 2 pi -> fuc1p + 2 pi_e hext + ura_e -> ura hext + xtsine_e <-> xtsine hext + ins_e <-> ins adn_e + hext <-> adn cyrd_e + hext <-> cytd hext + thymd_e <-> thymd hext + thymd_e <-> thymd hext + uri_e <-> thymd hext + thymd_e <-> thymd hext + uri_e <-> uri
TYRIT GLYC3Pabc MAN6Pt_2 G6Pt_2 FUCPt_2 URAt XTSNitr INStr ADNtr CYTDtr THMDtr	Transport, Extracellular	potassium reversible transport via proton sympot L-lyvosine reversible transport via proton sympot sn-Glycerol 3-phosphate transport via proton sympot sn-Glycerol 3-phosphate transport via phosphate transport via phosphate transport via phosphate antiport Glucose-6-phosphate transport via protosphate antiport via phosphate antiport Locase-1-phosphate transport via proton-sympot via phosphate antiport Viandinie transport via proton sympot sympot reversible adenosine transport in via proton sympot reversible adenosine transport in via proton sympot, reversible oylidine transport in via proton sympot, reversible thymidine transport in via proton sympot, reversible thymidine transport in via proton sympot, reversible undine transport in via proton sympot, reversible bymoton sympot, reversible	hext + k,e <-> k hext + kyr_e <-> kyr atp + glyc3p_e -> adp + glyc3p + pi man6p_e + 2 pi -> man6p + 2 pi_e g6p_e + 2 pi -> g6p + 2 pi_e fuc1p_e + 2 pi -> fuc1p + 2 pi_e hext + ura_e -> ura hext + xtsine_e <-> xtsine hext + ins_e <-> ins adn_e + hext <-> adn cytd_e + hext <-> cytd hext + thymd_e <-> thymd hext + thymd_e <-> thymd hext + thymd_e <-> thymd
TYRIT GLYC3Pabc  MAN6Pt_2 G6Pt_2 FUCPt_2 URAt XTSNitr INStr ADNitr CYTDir THMDtr URItr	Transport, Extracellular	potassium reversible transport via proton sympot L-lyrosine reversible transport via proton sympot sn-Glycerol 3-phosphate transport via proton sympot sn-Glycerol 3-phosphate transport via phosphate antiport Glucose 6-phosphate transport via phosphate antiport Glucose 6-phosphate transport via phosphate antiport via phosphate antiport succed 1-phosphate transport via proton sympot via phosphate antiport Xanthosine transport via proton symport sympot reversible adenosine transport in via proton symport, reversible opticial transport in via proton symport, reversible thymidine transport in via proton symport, reversible thymidine transport in via proton symport, reversible thymidine transport in via proton symport, reversible undine transport in via proton symport, reversible thymidine transport in via proton symport, reversible by somport reversible symport reversible by somport reversible	hext + k,e <-> k hext + kyr_e <-> kyr atp + glyc3p_e >> adp + glyc3p + pi man6p_e + 2 pi -> man6p + 2 pi_e g6p_e + 2 pi -> g6p + 2 pi_e fuc1p_e + 2 pi -> fuc1p + 2 pi_e hext + ura_e -> ura hext + xtsine_e <-> xtsine hext + ins_e <-> ins adn_e + hext <-> adn cyrd_e + hext <-> cytd hext + thymd_e <-> thymd hext + thymd_e <-> thymd hext + uri_e <-> thymd hext + thymd_e <-> thymd hext + uri_e <-> uri
TYRIT GLYC3Pabc MAN6Pt_2 G6Pt_2 FUCPt_2 URAt XTSNitr INStr ADNitr CYTDir THMDtr URitr XYLt	Transport, Extracellular	potassium reversible transport via proton symport L-lyrosine reversible transport via proton sympot sn-Gyleroil 3-phosphate transport via McK System Mannose-6-phosphate transport via Morbashate antiport Glucose-6-phosphate transport via phosphate antiport via phosphate transport via proton symport symport description of the symport via phosphate proton symport via phosphate proton symport symport description of the symport symport description of the symport symport reversible adenosine transport in via proton symport, reversible unified transport in via proton symport, reversible unified transport in via proton symport, reversible symport, reversible symport, reversible symport symp	hext + k,e <-> k hext + kyr_e <-> kyr atp + glyc3p_e >> adp + glyc3p + pi man6p_e + 2 pi -> man6p + 2 pi_e g6p_e + 2 pi -> g6p + 2 pi_e fuc1p_e + 2 pi -> fuc1p + 2 pi_e hext + ura_e -> ura hext + xtsine_e <-> xtsine hext + ins_e <-> ins adn_e + hext <-> adn cyrd_e + hext <-> cytd hext + thymd_e <-> thymd hext + thymd_e <-> thymd hext + uri_e <-> uri hext + uri_e <-> uri hext + uri_e <-> uri hext + thymd_e <-> thymd hext + uri_e <-> uri hext + uri_e <-> uri
TYRIT GLYC3Pabc  MAN6Pt_2 G6Pt_2 FUCPt_2 URAt XTSNitr INStr ADNitr CYTDir THMDtr URitr XYL1 XYLabc	Transport, Extracellular	potassium reversible transport via proton symport L-lyrosine reversible transport via proton symport sn-Gyleroll 3-phosphate transport via proton symport sn-Gyleroll 3-phosphate transport via phosphate transport via phosphate antiport Glucose-6-phosphate transport via phosphate antiport via phosphate proton symport symport symport symport expersible adenosine transport in via proton symport, reversible syndomic proton symport, reversible cytidine transport in via proton symport, reversible typridine transport in via proton symport, reversible unifine transport in via proton symport, reversible unifine transport in via proton symport, reversible D-sylose transport in via proton symport, reversible D-sylose transport via proton symport D-sylose transport via proton symport, reversible definite transport via proton symport, reversible adenine transport via proton symport, reversible adenine transport via proton	hext + k,e <-> k hext + kyr_e <-> kyr atp + glyc3p_e -> adp + glyc3p + pi man6p_e + 2 pi -> man6p + 2 pi_e g6p_e + 2 pi -> g6p + 2 pi_e fuc1p_e + 2 pi -> fuc1p + 2 pi_e hext + ura_e -> ura hext + xtsine_e <-> xtsine hext + ins_e <-> ins adn_e + hext <-> adn cytd_e + hext <-> cytd hext + tynd_e <-> thynd hext + tynd_e <-> thynd hext + tynd_e <-> thynd hext + uri_e <-> uri hext + tynd_e <-> thynd hext + uri_e <-> uri hext + xyl_e -> xyl atp + xyl_e -> xyl atp + xyl_e -> adp + xyl + pi
TYRIT GLYC3Pabc  MAN6Pt_2 G6Pt_2 FUCPt_2 URAt XTSNitr INStr ADNtr CYTDir THMDtr URitr XYL1 XYLabc CHLtr ADEtr	Transport, Extracellular	potassium reversible transport via proton symport L-lyrosine reversible transport via proton symport sn-Gyleroll 3-phosphate transport via ABC system Mannose-6-phosphate transport via phosphate antiport Glucose-6-phosphate transport via phosphate antiport via phosphate transport via proton symport via phosphate antiport via phosphate antiport via phosphate antiport via phosphate antiport via phosphate proton symport symport expensible adenosine transport via proton symport, reversible adenosine transport in via proton symport, reversible yorkidine transport in via proton symport, reversible dyndine transport in via proton symport, reversible vidine transport in via proton symport, reversible unidine transport in via proton symport, reversible bylose transport in via proton symport, reversible unidine transport in via proton symport, reversible bylose transport via ABC system choline transport via proton symport, reversible adenine transport via proton symport, reversible adenine transport via proton symport, reversible adenine transport via proton symport, reversible bylose transport via proton	hext + k,e <-> k hext + kyr_e <-> kyr atp + glyc3p_e >> adp + glyc3p + pi man6p_e + 2 pi -> man6p + 2 pi_e g6p_e + 2 pi -> g6p + 2 pi_e fuc1p_e + 2 pi -> fuc1p + 2 pi_e hext + ura_e >> ura hext + xtsin_e <-> xtsine hext + int_e <-> ins adn_e + hext <-> adn cyrd_e + hext <-> cyrtd hext + tyrmd_e <-> thymd hext + tyrl_e <-> uri hext + xyl_e -> xyl atp + xyl_e >> adp + xyl + pi cholin_e + hext <-> choline ad_e + hext <-> ad
TYRIT GLYC3Pabc  MANSPt_2 G6Pt_2 FUCPt_2 URAt XTSNIT INSTT ADNIT CYTDIT THMDIT URITT XYLL XYLabc CHLIT ADEIT RIBabc CRNabc	Transport, Extracellular	potassium reversible transport via proton sympot  L-lyrosine reversible transport via proton sympot  sn-Glycerol 3-phosphate  transport via A&C system  Mannose-6-phosphate transport via proton sympot  (ilicusos-6-phosphate transport via phosphate antiport  Glucose-6-phosphate transport via phosphate antiport  via phosphate via proton  symport  symport  symport reversible  adenistic transport in via proton  symport, reversible  thymidine transport in via  proton symport, reversible  thymidine transport in via  proton symport, reversible  thymidine transport in via  proton symport, reversible  thymidine transport in via  proton symport, reversible  D-sylose transport in via  proton  symport  sympote  symport  symport  symport  symport  symport  sympote	hext + k,e <-> k hext + kyr_e <-> kyr atp + glyc3p_e >> adp + glyc3p + pi man6p_e + 2 pi -> man6p + 2 pi_e g6p_e + 2 pi -> g6p + 2 pi_e fuc1p_e + 2 pi -> fuc1p + 2 pi_e hext + ura_e >> ura hext + xtsine_e <-> xtsine hext + ine_e <-> ins adn_e + hext <-> adn cyrd_e + hext <-> cytd hext + thymd_e <-> thymd hext + thymd_e <-> thymd hext + thymd_e <-> thymd hext + uri_e <-> uri hext + xyl_e -> xyl atp + xyl_e >> adp + xyl + pi choline_e + hext <-> choline
TYRIT GLYC3Pabc MANGPt_2 GGPt_2 FUCPt_2 URAt XTSNitr INStr ADNitr CYTDir THMDir URitr XYLt XYLabc CHLtr ADEtr RiBabc	Transport, Extracellular	potassium reversible transport via proton symport L-lyrosine reversible transport via proton symport sn-Gyleroll 3-phosphate transport via ABC system Mannose-6-phosphate transport via phosphate antiport Glucose-6-phosphate transport via phosphate antiport via phosphate transport via proton symport via phosphate antiport via phosphate antiport via phosphate antiport via phosphate antiport via phosphate proton symport symport expensible adenosine transport via proton symport, reversible adenosine transport in via proton symport, reversible yorkidine transport in via proton symport, reversible dyndine transport in via proton symport, reversible vidine transport in via proton symport, reversible unidine transport in via proton symport, reversible bylose transport in via proton symport, reversible unidine transport in via proton symport, reversible bylose transport via ABC system choline transport via proton symport, reversible adenine transport via proton symport, reversible adenine transport via proton symport, reversible adenine transport via proton symport, reversible bylose transport via proton	hext + k,e <-> k hext + kyr_e <-> kyr atp + glyc3p_e -> adp + glyc3p + pi man6p_e + 2 pi -> man6p + 2 pi_e g6p_e + 2 pi -> g6p + 2 pi_e fuc1p_e + 2 pi -> fuc1p + 2 pi_e hext + ura_e -> ura hext + xtsine_e <-> xtsine hext + ins_e <-> ins adn_e + hext <-> ord hext + thymd_e <-> thymd hext + thymd_e <-> thymd hext + thymd_e <-> thymd hext + uri_e <-> uri hext + xyl_e -> xyl atp + xyl_e -> xyl atp + xyl_e -> xyl atp + xyl_e -> adp + pi + pi choline_e + hext <-> ad atp + rib_e -> adp + pi + rib atp + rrn_e <-> adp + pi + rib atp + rrn_e <-> adp + cm + pi atp + mobd_e <-> adp + pi + mobd
TYRIT GLYC3Pabc MANGPt_2 GGPt_2 FUCPt_2 URAt XTSNitr INSIT ADNItr CYTDir THMDtr URitr XYLt XYLabc CHLtr ADEtr RIBabc CRNabc MOBDabc ASO311 MG2t	Transport, Extracellular	potassium reversible transport via proton symport L-lyrosine reversible transport via proton symport sn-Gyleroll 3-phosphate transport via proton symport sn-Gyleroll 3-phosphate transport via phosphate transport via phosphate antiport Glucose-6-phosphate transport via phosphate antiport via phosphate artiport via phosphate artiport via phosphate artiport via phosphate artiport via phosphate antiport via proton symport symport exersible adenosine transport in via proton symport, reversible vicilitie transport in via proton symport, reversible vicilitie transport in via proton symport, reversible unidine transport in via proton symport, reversible vicilitie transport in via proton symport, reversible vicilitie transport in via proton symport, reversible vicilitie transport via proton symport, reversible adenine transport via proton symport, reversible adenine transport via proton symport, reversible of the transport via proton symport reversible of the transport via proton symport reversib	hext + k,e <-> k hext + kyr_e <-> kyr atp + glyc3p_e -> adp + glyc3p + pi man6p_e + 2 pi -> man6p + 2 pi_e g6p_e + 2 pi -> g6p + 2 pi_e fuc1p_e + 2 pi -> fuc1p + 2 pi_e hext + ura_e -> ura hext + xtsine_e <-> xtsine hext + ira_e <-> iris adn_e + hext <-> adn cyrd_e + hext <-> cytd hext + tymd_e <-> tymd hext + tymd_e +> tymd hext + tymd_e <-> tymd hext + tymd_e -> di hext + tymd_e -> tymd hext + tymd_e -> xyl atp + xyl_e -> xyl atp + xyl_e -> xyl atp + xyl_e -> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + mobd aso3 <-> aso3_e mg2_e <-> mg2 mg2_e <-> mg2 mg2_e <-> mg2
TYRIT GLYC3Pabc MANGPt_2 GGPt_2 FUCPt_2 URAt XTSNitr INSIT ADNItr CYTDir THMDtr URitr XYLt XYLabc CHLtr ADEtr RIBabc CRNabc MOBDabc ASO311 MG2t COBT ASPALAt	Transport, Extracellular	potassium reversible transport via proton symport L-lyrosine reversible transport via proton symport sn-Gyleroll 3-phosphate transport via proton symport sn-Gyleroll 3-phosphate transport via phosphate transport via phosphate antiport Glucose-6-phosphate transport via phosphate antiport via phosphate artiport via phosphate artiport via phosphate artiport via phosphate artiport via phosphate antiport via proton symport symport exersible adenosine transport in via proton symport, reversible vicilitie transport in via proton symport, reversible vicilitie transport in via proton symport, reversible unidine transport in via proton symport, reversible vicilitie transport in via proton symport, reversible vicilitie transport in via proton symport, reversible vicilitie transport via proton symport, reversible adenine transport via proton symport, reversible adenine transport via proton symport, reversible of the transport via proton symport reversible of the transport via proton symport reversib	hext + k,e <-> k hext + kyr_e <-> kyr atp + glyc3p_e -> adp + glyc3p + pi man6p_e + 2 pi -> man6p + 2 pi_e g6p_e + 2 pi -> g6p + 2 pi_e fuc1p_e + 2 pi -> fuc1p + 2 pi_e hext + ura_e -> ura hext + xtsine_e <-> xtsine hext + ira_e <-> iris adn_e + hext <-> ord hext + tyme_e <-> tytd hext + tyme_e <-> tyme hext + tyme_e <-> tyme hext + tyme_e <-> tyme hext + tyme_e <-> wi hext + tyme_e <-> tyme hext + tyme_e <-> tyme hext + tyl_e -> wi hext + tyl_e -> wi hext + wi_e <-> choline ad_e + hext <-> choline ad_e + hext <-> dap + pi + rib atp + rib_e -> adp + pi + rib atp + rib_e -> adp + pi + rib atp + rib_e -> adp + pi + rib atp + rib_e -> adp + pi + rib atp + mobd_e -<-> adp - pi + rib atp + rib_e -> adp - pi + rib atp + rib_e -> adp - pi + rib atp + rib_e -> adp - rid + pi + rib atp + rid -> cobalt2_e -> mg2_e -> mg2
TYRIT GLYC3Pabc  MAN6Pt_2 G6Pt_2 FUCPt_2 URAt XTSNtr INStr ADNtr CYTDtr THMDtr URItr XVLt XVLabc CHLtr ADEtr RiBabc CRNabc MO8Dabc ASO3t1 MGQt COBT ASPALAt ASO3t2	Transport, Estracellular	potassium reversible transport via proton symport L-lyrosine reversible transport via proton symport sn-Gyleroll 3-phosphate transport via proton symport sn-Gyleroll 3-phosphate transport via phosphate transport via phosphate antiport Glucose-6-phosphate transport via phosphate antiport via phosphate artiport via phosphate artiport via phosphate artiport via phosphate artiport via phosphate antiport via proton symport symport exersible adenosine transport in via proton symport, reversible vicilitie transport in via proton symport, reversible vicilitie transport in via proton symport, reversible unidine transport in via proton symport, reversible vicilitie transport in via proton symport, reversible vicilitie transport in via proton symport, reversible vicilitie transport via proton symport, reversible adenine transport via proton symport, reversible adenine transport via proton symport, reversible of the transport via proton symport reversible of the transport via proton symport reversib	hext + k,e <-> k hext + kye,e <-> kyr atp + glyc3p,e >> adp + glyc3p + pi man6p_e + 2 pi -> man6p + 2 pi_e g6p_e + 2 pi -> g6p + 2 pi_e fuc1p_e + 2 pi -> fuc1p + 2 pi_e hext + ura_e -> ura hext + xtsine_e <-> xtsine hext + ins_e <-> ins adn_e + hext <-> odd hext + tymd_e <-> tydd hext + tymd_e <-> tymd hext + tymd_e <-> tydd hext + tymd_e <-> tyde hext + tymd_e <-> tymde hext + tymd_e <-
TYRIT GLYC3Pabc  MAN6Pt_2 G6Pt_2 FUCPt_2 URAt XTSNtr INStr ADNtr CYTDtr THMDtr URItr XVLt XVLabc CHLtr ADEtr RiBabc CRNabc MO8Dabc ASO311 MGQt COBT ASPALAt ASPALAt ASPALAt NA112 NA11	Transport, Estracellular	potassium reversible transport via proton symport L-lyrosine reversible transport via proton symport sn-Gyleroll 3-phosphate transport via proton symport sn-Gyleroll 3-phosphate transport via phosphate transport via phosphate antiport Glucose-6-phosphate transport via phosphate antiport via phosphate artiport via phosphate artiport via phosphate artiport via phosphate artiport via phosphate antiport via proton symport symport exersible adenosine transport in via proton symport, reversible vicilitie transport in via proton symport, reversible vicilitie transport in via proton symport, reversible unidine transport in via proton symport, reversible vicilitie transport in via proton symport, reversible vicilitie transport in via proton symport, reversible vicilitie transport via proton symport, reversible adenine transport via proton symport, reversible adenine transport via proton symport, reversible of the transport via proton symport reversible of the transport via proton symport reversib	hext + k,e <-> k hext + ky_e <-> k hext + ty_e <-> tyr atp + glyc3p_e -> adp + glyc3p + pi man6p_e + 2 pi -> man6p + 2 pi_e g6p_e + 2 pi -> g6p + 2 pi_e fuc1p_e + 2 pi -> fuc1p + 2 pi_e hext + ura_e -> ura hext + xtsine_e <-> xtsine hext + irs_e <-> irs adn_e + hext <-> adn cytd_e + hext <-> cytd hext + tyymd_e <-> tyymd hext + tyymd_e <-> tyymd hext + tyymd_e <-> typd atp + xyl_e -> xyl atp + xyl_e -> xyl atp + xyl_e -> xdp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi + rib atp + crn_e <-> adp + pi
TYRIT GLYC3Pabc  MAN6Pt_2 G6Pt_2 FUCPt_2 URAt XTSNtr INStr ADNtr CYTDtr THMDtr URItr XYLt XYLabc CHLtr ADEtr RIBabc CRNabc MO8Dabc ASO311 MGQ1 COBIT ASPALAt ASO312 NA1t NA1t2 SUCCt	Transport, Extracellular	potassium reversible transport via proton symport L-lyrosine reversible transport via proton symport sn-Gyleroll 3-phosphate transport via proton symport sn-Gyleroll 3-phosphate transport via phosphate transport via phosphate antiport Glucose-6-phosphate transport via phosphate antiport via phosphate artiport via phosphate artiport via phosphate artiport via phosphate artiport via phosphate antiport via proton symport symport exersible adenosine transport in via proton symport, reversible vicilitie transport in via proton symport, reversible vicilitie transport in via proton symport, reversible unidine transport in via proton symport, reversible vicilitie transport in via proton symport, reversible vicilitie transport in via proton symport, reversible vicilitie transport via proton symport, reversible adenine transport via proton symport, reversible adenine transport via proton symport, reversible of the transport via proton symport reversible of the transport via proton symport reversib	hext + k,e <-> k hext + kye,e <-> kyr atp + glyc3p,e >> adp + glyc3p + pi man6p,e + 2 pi -> man6p + 2 pi_e g6p,e + 2 pi -> g6p + 2 pi_e fuc1p,e + 2 pi -> fuc1p + 2 pi_e hext + ura_e -> ura hext + xtsine_e <-> xtsine hext + irs_e <-> irs adn_e + hext <-> adn cytd_e + hext <-> cytd hext + tymd_e <-> tymd hext + uri_e <-> uri hext + xyl_e -> xgl atp + xyl_e >> xgl hext -> adp + pi + rib atp + rib_e -> adp + pi + rib atp + cm_e <-> adp + pi + rib atp + cm_e <-> adp + pi + rib atp + cm_e <-> adp + pi + rib atp + cm_e <-> adp + pi + rib atp + cm_e <-> adp + pi + rib atp + cm_e <-> adp + pi + rib atp + cm_e <-> adp + pi + rib atp + cm_e <-> adp + pi + rib atp + cm_e <-> adp + pi + rib atp + cm_e <-> adp + pi + rib atp + cm_e <-> adp + pi + rib atp + cm_e <-> adp + pi + rib atp + cm_e <-> adp + pi + rib atp + cm_e <-> adp + pi + rib atp + cm_e <-> adp + pi + rib atp + cm_e <-> adp + pi + rib atp + cm_e <-> adp + pi + rib atp + cm_e <-> adp + pi + rib atp + cm_e <-> colabil <-> col
TYRIT GLYC3Pabc  MAN6Pt_2 G6Pt_2 FUCPt_2 URAt XTSNitr INSIT ADNItr CYTDir THMDir URitr XYLt XYLabc CHLIT ADEtr RIBabc CRNabc MOBDabc ASO311 MG2t COBT ASPALAt ASO312 NA112 SUCCt	Transport, Extracellular	potassium reversible transport via proton symport L-lyrosine reversible transport via proton symport sn-Gyleroll 3-phosphate transport via proton symport sn-Gyleroll 3-phosphate transport via phosphate transport via phosphate antiport Glucose-6-phosphate transport via phosphate antiport via phosphate artiport via phosphate artiport via phosphate artiport via phosphate artiport via phosphate antiport via proton symport symport exersible adenosine transport in via proton symport, reversible vicilitie transport in via proton symport, reversible vicilitie transport in via proton symport, reversible unidine transport in via proton symport, reversible vicilitie transport in via proton symport, reversible vicilitie transport in via proton symport, reversible vicilitie transport via proton symport, reversible adenine transport via proton symport, reversible adenine transport via proton symport, reversible of the transport via proton symport reversible of the transport via proton symport reversib	hext + k,e <>> k hext + kyr_e <>> kyr atp + glyc3p_e >> adp + glyc3p + pi man6p_e + 2 pi -> man6p + 2 pi_e g6p_e + 2 pi -> g6p + 2 pi_e fuc1p_e + 2 pi -> fuc1p + 2 pi_e hext + ura_e -> ura hext + xtsine_e <>> xtsine hext + ins_e <>> ins adn_e + hext <>> adn cyrd_e + hext <>> cytd hext + tymd_e <> tymd hext + tymd_e >> uri hext + tymd_e <>> tymd hext + tymd_e <>> tymd hext + tymd hext + tymd_e <>> tymd hext + tymd hext + tymd,e <>> tymd hext + tymd hext + uri_e <>> uri hext + xyl_e -> xyl atp + xyl_e -> xyl atp + xyl_e -> adp + xyl + pi choline_e + hext <>> choline ad_e + hext <>> ado + pi + rib atp + crn_e <>> adp + pi + rib atp + crn_e <>> adp + pi + rib atp + crn_e <>> adp - pi + rib atp + crn_e <>> adp - pi + rib atp + crn_e <>> adp - pi + rib atp + crn_e <>> adp - pi + rib atp + crn_e <>> adp - pi + rib atp + crn_e <>> adp - pi + rib atp + crn_e <>> adp - pi + rib atp + crn_e <>> adp - pi + rib atp + crn_e <>> adp - rid + ri
GLYC3Pabc  MANGPt_2  GGPt_2  FUCPt_2  URAt  XTSNitr  INStr  ADNitr  CYTDir  THMDir  URitr  XYLt  XYLabc  CHLtr  ADEtr  RiBabc  CRNabc  MOBDabc  ASO311  MG2t  COBT  ASPALAt  ASO312  NA112  SUCCt  SUC	Transport, Extracellular Transport, Extracellu	potassium reversible transport via proton symport L-lyrosine reversible transport via proton symport sn-Gyleroll 3-phosphate transport via proton symport sn-Gyleroll 3-phosphate transport via phosphate transport via phosphate antiport Glucose-6-phosphate transport via phosphate antiport via phosphate artiport via phosphate artiport via phosphate artiport via phosphate artiport via phosphate antiport via proton symport symport exersible adenosine transport in via proton symport, reversible vicilitie transport in via proton symport, reversible vicilitie transport in via proton symport, reversible unidine transport in via proton symport, reversible vicilitie transport in via proton symport, reversible vicilitie transport in via proton symport, reversible vicilitie transport via proton symport, reversible adenine transport via proton symport, reversible adenine transport via proton symport, reversible of the transport via proton symport reversible of the transport via proton symport reversib	hext + k,e <>> k hext + kyr_e <>> ky atp + glyc3p_e >> adp + glyc3p + pi man6p_e + 2 pi -> man6p + 2 pi_e g6p_e + 2 pi -> g6p + 2 pi_e fuc1p_e + 2 pi -> fuc1p + 2 pi_e hext + ura_e -> ura hext + xtsine_e <>> xtsine hext + ira_e <>> iris adn_e + hext <>> adn cyrd_e + hext <>> ord hext + tymd_e <> bit in the tymd_e <>> tymd hext + tymd_e >> adp + pi + pi choline_e + hext <>> choline ad_e + hext <>> ado + pi + rib atp + rrn_e <-> adp + crn + pi atp + mobd_e <-> adp + pi + mobd aso3 <-> aso3_e mg2_e <-> mg2 cobalt2 <-> cobalt2_e aso3 -> aso3_e mg2_e <-> mg2 e cobalt2 <-> aso + bext as + hext <>> na_e succ_e + hext <>> succ succ_e + hext <>> succ_e + hext <>> succ succ_e + hext <>> succ_e + hext <>> succ succ_e + hext <>> succ_e + hext <>> succ_e + hext <>> succ_e + hext <>> succ_e + hext <-> succ_e + hext <<-> succ_e + hext <>> succ_e + hext <> succ_e + hext <-
GLYC3Pabc  MANGPt_2  GGPt_2  FUCPt_2  URAt  XTSNitr  INStr  ADNitr  CYTDir  THMDir  URitr  XYLt  XYLabc  CHLtr  ADEtr  RiBabc  CRNabc  MOBDabc  ASO311  MG2t  COBIT  ASPALAt  ASO322  NA112  SUCCT  SU	Transport, Extracellular Transport, Extracellu	potassium reversible transport via proton symport L-lyrosine reversible transport via proton symport sn-Gyleroll 3-phosphate transport via proton symport sn-Gyleroll 3-phosphate transport via phosphate transport via phosphate antiport Glucose-6-phosphate transport via phosphate antiport via phosphate artiport via phosphate artiport via phosphate artiport via phosphate artiport via phosphate antiport via proton symport symport exersible adenosine transport in via proton symport, reversible vicilitie transport in via proton symport, reversible vicilitie transport in via proton symport, reversible unidine transport in via proton symport, reversible vicilitie transport in via proton symport, reversible vicilitie transport in via proton symport, reversible vicilitie transport via proton symport, reversible adenine transport via proton symport, reversible adenine transport via proton symport, reversible of the transport via proton symport reversible of the transport via proton symport reversib	hext + k,e <>> k hext + kyr_e <>> ky atp + glyc3p_e >> adp + glyc3p + pi man6p_e + 2 pi >> man6p + 2 pi_e g6p_e + 2 pi >> g6p + 2 pi_e fuc1p_e + 2 pi >> fuc1p + 2 pi_e hext + ura_e >> ura hext + xtsin_e <<>> xtsine hext + irs_e <<>> irs adn_e + hext <<>> adn cyrd_e + hext <<>> cytd hext + tymd_e <>> try man6p_e + hext <>> irs adn_e + hext <>> adn cyrd_e + hext <>> ord hext + tymd_e <>> try man6p_e + hext <>> cytd hext + tymd_e <>> try man6p_e + hext <>> cytd hext + tymd_e <>> win hext + tymd_e <>> try man6p_e + hext <>> choline ad_e + hext <>> doline ad_e + hext <>> adp + pi + rib atp + rrb_e <>> adp + pi + rib atp + rrb_e <>> adp + pi + rib atp + rrb_e <>> adp + pi + rib atp + rrb_e <>> adp + pi + rib atp + rrb_e <>> adp + pi + rib atp + rrb_e <>> adp + pi + rib atp + rrb_e <>> adp + pi + rib atp + rrb_e <>> adp + pi + rib atp + rrb_e <>> adp + pi + rib atp + rrb_e <>> adp + pi + rib atp + rrb_e <>> rr
GLYC3Pabc  MANGPt_2  GGPt_2  FUCPt_2  URAt  XTSNitr  INStr  ADNItr  CYTDir  THMDir  URitr  XYLt  XYLabc  CHLtr  ADEtr  RiBabc  CRNabc  MOBDabc  ASO311  MG2t  COBIT  ASPALAt  ASO322  NA112  SUCCT  SU	Transport, Extracellular Transport, Extracellu	potassium reversible transport via proton symport L-lyrosine reversible transport via proton symport sn-Gyleroll 3-phosphate transport via proton symport sn-Gyleroll 3-phosphate transport via phosphate transport via phosphate antiport Glucose-6-phosphate transport via phosphate antiport via phosphate artiport via phosphate artiport via phosphate artiport via phosphate artiport via phosphate antiport via proton symport symport exersible adenosine transport in via proton symport, reversible vicilitie transport in via proton symport, reversible vicilitie transport in via proton symport, reversible unidine transport in via proton symport, reversible vicilitie transport in via proton symport, reversible vicilitie transport in via proton symport, reversible vicilitie transport via proton symport, reversible adenine transport via proton symport, reversible adenine transport via proton symport, reversible of the transport via proton symport reversible of the transport via proton symport reversib	hext + k,e <>> k hext + kyr_e <>> ky atp + glyc3p_e >> adp + glyc3p + pi man6p_e + 2 pi -> man6p + 2 pi_e g6p_e + 2 pi -> g6p + 2 pi_e fuc1p_e + 2 pi -> fuc1p + 2 pi_e hext + ura_e -> ura hext + xtsine_e <>> xtsine hext + ira_e <>> iris adn_e + hext <>> adn cyrd_e + hext <>> oytd hext + tymd_e <>> tymd hext + tymd_e >> adp + pi + rib atp + rib_e -> adp + pi + ri
GLYC3Pabc  MAN6Pt_2  G6Pt_2  FUCPt_2  URAt  XTSNtr  INStr  ADNtr  CYTDtr  THMDtr  URitr  XYLt  XYLabc  CHLtr  ADEtr  RiBabc  CRNabc  MGBDabc  ASO3H1  MG2t  COBIT  ASPALAt  ASO312  NA1t  NA1t  NA1t  SUCCt  SUCCt  SUCCt  SUCCt  SUCCt  FYST  CHB2t  PPAt  CHB1  CHLYSC  CHLT  AFRED  AFR	Transport, Extracellular Transport, Extracellu	potassium reversible transport via proton symport L-lyrosine reversible transport via proton symport sn-Gyleroll 3-phosphate transport via proton symport sn-Gyleroll 3-phosphate transport via phosphate transport via phosphate antiport Glucose-6-phosphate transport via phosphate antiport via phosphate artiport via phosphate artiport via phosphate artiport via phosphate artiport via phosphate antiport via proton symport symport exersible adenosine transport in via proton symport, reversible vicilitie transport in via proton symport, reversible vicilitie transport in via proton symport, reversible unidine transport in via proton symport, reversible vicilitie transport in via proton symport, reversible vicilitie transport in via proton symport, reversible vicilitie transport via proton symport, reversible adenine transport via proton symport, reversible adenine transport via proton symport, reversible of the transport via proton symport reversible of the transport via proton symport reversib	hext + k,e <-> k hext + kyr_e <-> kyr atp + glyc3p_e -> adp + glyc3p + pi man6p_e + 2 pi -> man6p + 2 pi_e g6p_e + 2 pi -> g6p + 2 pi_e fuc1p_e + 2 pi -> fuc1p + 2 pi_e hext + ura_e -> ura hext + xtsine_e <-> xtsine hext + ins_e <-> ins adn_e + hext <-> adn cytd_e + hext <-> oytd hext + tymd_e <-> tymd hext + t
GLYC3Pabc  MAN6Pt_2  G6Pt_2  FUCPt_2  URAt  XTSNtr  INStr  ADNtr  CYTDtr  THMDtr  URitr  XYLt  XYLabc  CHLtr  ADEtr  RiBabc  CRNabc  MoBoabc  ASO3L1  MGQT  COBT  ASPALAt  ASO3L2  NAL1  SUCCt  SUCCt  SUCCt  SUCCt  SUCCt  FYS  CHB  CRNabc  MoBoabc  ASO3L1  MGQT  COBT  ASPALAt  ASO3L2  NAL1  SUCCt  SUC	Transport, Extracellular Transport, Extracellu	potassium reversible transport via proton symport L-lyrosine reversible transport via proton symport sn-Gyleroll 3-phosphate transport via ABC system Mannose-6-phosphate transport via phosphate antiport Glucose-6-phosphate transport via phosphate antiport via phosphate transport via proton symport via phosphate antiport via phosphate antiport via phosphate antiport via phosphate antiport via phosphate proton symport symport symport via proton symport symport reversible adenosine transport in via proton symport, reversible syndomic proton symport, reversible cytidine transport in via proton symport, reversible syndomic proton symport, reversible vidine transport in via proton symport, reversible syndomic proton symport, reversible unidine transport in via proton symport, reversible bydise transport in via proton symport, reversible syndomic proton symport, reversible syndomic proton symport, reversible syndomic proton symport, reversible adenine transport via proton symport, reversible adenine transport via proton symport, reversible syndomic proton symport (reversible)	hext + k,e <-> k hext + kyr_e <-> kyr atp + glyc3p_e -> adp + glyc3p + pi man6p_e + 2 pi -> man6p + 2 pi_e g6p_e + 2 pi -> g6p + 2 pi_e fuc1p_e + 2 pi -> fuc1p + 2 pi_e hext + ura_e -> ura hext + xtsine_e <-> xtsine hext + ins_e <-> ins adn_e + hext <-> adn cytd_e + hext <-> otd hext + tymd_e <-> tymd hext + tym
TYRIT GLYC3Pabc  MANGPt_2 G6Pt_2 FUCPt_2 URAt  XTSNitr INSIT ADNItr CYTDir THMDir URitr XYLt XYLabc CHLIT ADEtr RIBabc CRNabc MOBDabc ASO311 MG2t COBT MG2t COBT ASPALAt ASO312 NA112 SUCCT SUCCT SUCCT SUCCT SUCCT SUCCT SUCT CITt 4HB2t PPA1 CIBIT G6RN 2PG1 2PG1 2PG1 2PG1 2PG1 2PG1	Transport, Extracellular Transport, Extracellu	potassium reversible transport via proton symport L-lyrosine reversible transport via proton symport sn-Gyleroll 3-phosphate transport via ABC system Mannose-6-phosphate transport via phosphate antiport Glucose-6-phosphate transport via phosphate antiport via phosphate transport via proton symport via phosphate antiport via phosphate antiport via phosphate antiport via phosphate antiport via phosphate proton symport symport symport via proton symport symport reversible adenosine transport in via proton symport, reversible syndomic proton symport, reversible cytidine transport in via proton symport, reversible syndomic proton symport, reversible vidine transport in via proton symport, reversible syndomic proton symport, reversible unidine transport in via proton symport, reversible bydise transport in via proton symport, reversible syndomic proton symport, reversible syndomic proton symport, reversible syndomic proton symport, reversible adenine transport via proton symport, reversible adenine transport via proton symport, reversible syndomic proton symport (reversible)	hext + k,e <>> k hext + kyr_e <>> ky atp + glyc3p_e >> adp + glyc3p + pi amn6p_e + 2 pi >> man6p + 2 pi_e g6p_e + 2 pi >> g6p + 2 pi_e fuc1p_e + 2 pi >> fuc1p + 2 pi_e hext + ura_e >> ura hext + xtsin_e <<>> xtsine hext + ira_e <>> ira hext + xtsin_e <<>> ira hext + wine <=<> vid hext + ira_e <>> ira hext -> ira hext -> ira_e ira hext -> ir

ICITt		Transport, Extracellular				icit_e + hext <-> icit
ADIPt		Transport, Extracellular				adip_e + hext <-> adip
PACt		Transport, Extracellular				pac_e + hext <-> pac
CCMU	ICt	Transport, Extracellular				ccmuc_e + hext <-> ccmuc
MCLAG	CTt	Transport, Extracellular				mclact_e + hext <-> mclact
KNTt		Transport, Extracellular				knt e + hext <-> knt
ANt		Transport, Extracellular				an_e + hext <-> an
ACON	ICt	Transport, Extracellular				acon-C e + hext -> acon-C
UROCA	ANt	Transport, Extracellular				urocan e + hext <-> urocan
2HBAt		Transport, Extracellular				2hba_e + hext -> 2hba
4HBTt		Transport, Extracellular				4hbt e + hext -> 4hbt
4HPHE	EACt	Transport, Extracellular				4hpheac e + hext -> 4hpheac
4HPHE	EAO	Transport, Extracellular				4hpheac + o2 + nadh -> homogen + nad
OBUTt	t	Transport, Extracellular				obut e + hext -> obut
R3HBN		Transport. Extracellular				r3hbn e + hext -> r3hbn
4FLRB2		Transport, Extracellular				4firbz e + hext -> 4firbz
ACETO		Transport, Extracellular				acetoin -> acetoin e
SPOXE		Unassigned	superoxide dismutase	1.15.1.1	KOX 07230/KOX 22075/KOX 22125	2 h + o2 -> h2o2
			trans-aconitate 2-			
TACON	NMT	Unassigned	methyltransferase	2.1.1.144	KOX_21215	acon-T + sam -> e3mcpen + sah
			Bicarbonate (HCO <sub>3</sub> )			
HCO3E	ER	Unassigned	equilibration reaction			co2 <-> hco3
			equilibration reaction		KOX 06970/KOX 06975/KOX 06990/KOX 08925	
					ulaA)/KOX 08930/KOX 08935/KOX 11160/KOX	· ·
ASCBp	ate	Transport, Inner Membrane	L-ascorbate transport via	2.7.1.69	15955/KOX 15960/KOX 20835(ulaA)/KOX 20840	Larch out non a archén a nur
Азсыр	J15	rransport, filler Membrane	PEP:Pyr PTS (periplasm)	2.7.1.03	/KOX 20845/KOX 26455(ulaA)/KOX 26460/KOX	
					26465	•
IMLTA	D	Transport, Outer Membrane	ATPase (isomaltose)	3.6.1	20403	atp + imal e -> imal + pi + adp
Mainte		transport, Outer Membrane	ATPase (Isomalitose)	5.0.1		atp -> adp + pi
IVIdilite	enance	Lipopolysaccharide Biosynthesis /				0.14 lipa + 0.42 adphep + 0.28 udpq + 0.28 cdpetn + 0.42 ckdo -> 0.42 adp + 0.28 udp + 0.42 cmp + 0.28
LPS		Recycling	Lipopolysaccharide biosynthesi	is		cdp + LPS
		Recycling				
						1.133 ala + 0.493 arg + 0.41 asn + 0.41 asp + 0.096 cys + 0.499 gln + 0.499 glu + 1.041 gly + 0.19 his +
Proteir	n					0.436 ile + 0.768 leu + 0.448 lys + 0.238 met + 0.289 phe + 0.42 pro + 0.534 ser + 0.583 thr + 0.014 trp +
						0.259 tyr + 0.666 val + 40 atp -> 40 adp + PROTEIN
					KOX_06570/KOX_06860/KOX_09330/KOX_10260,	
DNA				2.7.7.7		(0.711 datp + 0.907 dctp + 0.711 dttp + 0.907 dgtp + 4.4 atp -> 4.4 adp + 4.4 pi + DNA
					holA)/KOX_17320/KOX_23820	
RNA				2.7.7.6	KOX_04250/KOX_06005(rpoZ)/KOX_07910(rpoB)	0.648 atp + 0.737 qtp + 0.98 ctp + 0.762 utp -> 1.25 adp + 1.25 pi + RNA
					KOX_07915	
	holipid					1.186 pe + 0.062 pg + 0.027 ps + 0.077 pa + 0.048 clpn -> PHOSPHOLIPID
	tors and vitamins					0.656 pydxn + 0.145 coa + 0.141 fad + 0.243 fmn + 0.14 uq + 0.167 nad + 0.149 nadp + 0.249 thf + 0.418
(CAV)						thiamin -> CAV
Carbol	hydrate (CARBO)					4.244 udpnag + 0.849 udgal -> 5.093 udp + CARBO
Biomas	ISS					0.521 PROTEIN + 0.023 DNA + 0.131 RNA + 0.035 PEPTIDO + 0.153 CARBO + 0.03 CAV + 0.034 LPS + 0.073
						PHOSPHOLIPID + 71.7 atp -> BIOMASS + 71.7 adp + 71.7 pi