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

<u>Compartment Abbreviations</u>

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Abbreviation	Reaction Name	Reaction	E.C. #	Pathway	Gene association
LCADi	lactaldehyde dehydrogenase	[c] : h2o + lald-L + nad --> (2) h + lac-L + nadh	1.2.1.21	Pyruvate Metabolism	(216.1 or 8854.1 or 8854.2 or 8854.3 or 220.1 or 218.1 or 224.1 or 221.1 or 222.1 or 501.1 or 223.1)
LCADi_D	lactaldehyde dehydrogenase	[c] : h2o + lald-D + nad --> (2) h + lac-D + nadh	1.2.1.21	Pyruvate Metabolism	(216.1 or 8854.1 or 8854.2 or 8854.3 or 220.1 or 218.1 or 224.1 or 221.1 or 222.1 or 501.1 or 223.1)
LCADi_Dm	lactaldehyde dehydrogenase, mitochondrial	[m] : h2o + lald-D + nad --> (2) h + lac-D + nadh	1.2.1.21	Pyruvate Metabolism	(5832.1 or 219.1 or 217.1 or 8659.1 or 8659.2 or 7915.1 or 7915.2 or 4329.1)
LCADim	lactaldehyde dehydrogenase, mitochondrial	[m] : h2o + lald-L + nad --> (2) h + lac-L + nadh	1.2.1.21	Pyruvate Metabolism	(5832.1 or 219.1 or 217.1 or 8659.1 or 8659.2 or 7915.1 or 7915.2 or 4329.1)
LCAT1e	Lecithin-cholesterol acyltransferase	[e] : chsterol + pchol_hs --> lpchol_hs + xolest2_hs	2.3.1.43	Fatty Acid Metabolism	3931.1
LCTStg	lactose transport from Golgi to extracellular (via vesicle)	lcts[g] --> lcts[e]		Transport, Extracellular	
LCTStl	lactose transport from cytosol to lysosome (via autophagocytosis)	lcts[c] --> lcts[l]		Transport, Lysosomal	
LCYSTAT	L-Cysteate:2-oxoglutarate aminotransferase	[c] : Lcyst + akg <==> 3spyr + glu-L		Cysteine Metabolism	2805.1
LCYSTATm	L-Cysteate:2-oxoglutarate aminotransferase, mitochondrial	[m] : Lcyst + akg <==> 3spyr + glu-L		Cysteine Metabolism	2806.1
LCYSTCBOXL	3-Sulfoalanine carboxy-lyase	[c] : Lcyst + h --> co2 + taur	4.1.1.15	Taurine and hypotaurine metabolism	(2571.1 or 2571.2 or 2572.1 or 51380.1)
LDH_D	D-lactate dehydrogenase	[c] : lac-D + nad <==> h + nadh + pyr	1.1.1.28	Pyruvate Metabolism	(197257.1 or 197257.2)
LDH_L	L-lactate dehydrogenase	[c] : lac-L + nad <==> h + nadh + pyr	1.1.1.27	Glycolysis/Gluconeogenesis	(3939.1 or 3945.1 or 3948.1 or 3948.2 or 92483.1 or 160287.1 or 55293.1 or (3945.1 and 3939.1))
LDH_Lm	L-lactate dehydrogenase	[m] : lac-L + nad <==> h + nadh + pyr	1.1.1.27	Pyruvate Metabolism	3939.1
LEUKTRA4tr	leukotriene intracellular transport	leuktrA4[c] <==> leuktrA4[r]		Transport, Endoplasmic Reticular	
LEUKTRB4tr	leukotriene intracellular transport	leuktrB4[c] <==> leuktrB4[r]		Transport, Endoplasmic Reticular	
LEUKTRC4t	leukotriene C4 transport via bicarbonate countertransport	hco3[c] + leuktrC4[e] <==> hco3[e] + leuktrC4[c]		Transport, Extracellular	(10599.1 or 28234.1)
LEUKTRD4tr	leukotriene intracellular transport	leuktrD4[c] <==> leuktrD4[r]		Transport, Endoplasmic Reticular	
LEUt4	L-leucine transport in via sodium symport	leu-L[e] + na1[e] --> leu-L[c] + na1[c]		Transport, Extracellular	(11254.1 or 6520.1 or 55089.1 or 81539.1 or 6541.1 or 6542.1 or 84889.1)
LEUt5m	leucine mitochondrial transport	leu-L[c] <==> leu-L[m]		Transport, Mitochondrial	
LEUTA	leucine transaminase	[c] : akg + leu-L <==> 4mop + glu-L	2.6.1.6	Valine, Leucine, and Isoleucine Metabolism	586.1
LEUTAm	leucine transaminase, mitochondrial	[m] : akg + leu-L <==> 4mop + glu-L	2.6.1.6	Valine, Leucine, and Isoleucine Metabolism	587.1
LEUtec	L-leucine transport via diffusion (extracellular to cytosol)	leu-L[e] <==> leu-L[c]		Transport, Extracellular	(8501.1 or 124935.1)
LFORKYNHYD	L-Formylkynurenine hydrolase	[c] : Lfmkynr + h2o --> ala-L + h + nformanth	3.7.1.3	Tryptophan metabolism	8942.1
LGNCCOAtx	fatty acid intracellular transport	lgnccoa[c] <==> lgnccoa[x]		Transport, Peroxisomal	
LGNCCPT1	carnitine O-palmitoyltransferase	[c] : crn + lgnccoa --> coa + lgnccrn	2.3.1.21	Carnitine shuttle	(1375.4 or 1374.1 or 126129.1 or 1375.3 or 1375.2 or 1375.1)
LGNCCPT2	transport into the mitochondria (carnitine)	[m] : coa + lgnccrn --> crn + lgnccoa		Carnitine shuttle	1376.1
LGNCCRNt	transport into the mitochondria (carnitine)	lgnccrn[c] --> lgnccrn[m]		Carnitine shuttle	788.1
LGNCt	fatty acid transport via diffusion	lgnc[e] <==> lgnc[c]		Transport, Extracellular	
LGTHL	lactoylglutathione lyase	[c] : gthrd + mthgxl --> lgt-S	4.4.1.5	Pyruvate Metabolism	2739.1
LIMNENte	xenobiotic transport	limnen[e] <==> limnen[c]		Transport, Extracellular	
LINKDEG1ly	degradation of proteoglycan linkage region, lysosoma	[l] : (3) h2o + hs_deg25 --> (2) gal + glcur + xyl-D		Heparan sulfate degradation	
LINKDEG2ly	degradation of proteoglycan linkage region, lysosoma	[l] : cs_a_deg5 + (4) h2o --> (2) gal + glcur + h + so4 + xyl-D		Chondroitin sulfate degradation	
LINKDEG3ly	degradation of proteoglycan linkage region, lysosoma	[l] : cs_c_deg5 + (4) h2o --> (2) gal + glcur + h + so4 + xyl-D		Chondroitin sulfate degradation	
LINKDEG4ly	degradation of proteoglycan linkage region, lysosoma	[l] : cs_e_deg7 + (5) h2o --> (2) gal + glcur + (2) h + (2) so4 + xyl-D		Chondroitin sulfate degradation	
LIPOti	Lipoate transport via sodium symport	atp[c] + h2o[c] + lipoate[e] + (2) na1[e] --> adp[c] + h[c] + lipoate[c] + (2) na1[c] + pi[c]		Transport, Extracellular	8884.1
L-LACDcm	L-Lactate dehydrogenase, cytosolic/mitochondrial	(2) ficytC[m] + lac-L[c] --> (2) focytC[m] + (2) h[c] + pyr[c]	1.1.2.3	Pyruvate Metabolism	124637.1
L-LACt2r	L-lactate reversible transport via proton symport	h[e] + lac-L[e] <==> h[c] + lac-L[c]		Transport, Extracellular	(6566.1 or 9194.1 or 23539.1 or 9123.1)
L-LACt4r	L-lactate reversible transport via sodium symport	lac-L[e] + na1[e] <==> lac-L[c] + na1[c]		Transport, Extracellular	
L-LACtcm	L-lactate transport via diffusion (cytosol to mitochondria)	lac-L[c] --> lac-L[m]		Transport, Mitochondrial	366.1
L-LACtm	L-lactate transport, mitochondrial	h[c] + lac-L[c] <==> h[m] + lac-L[m]		Transport, Mitochondrial	6566.1
LNELDCCPT1	carnitine O-palmitoyltransferase	[c] : crn + lneldccoa --> coa + lneldccrn	2.3.1.21	Carnitine shuttle	(1375.4 or 1374.1 or 126129.1 or 1375.3 or 1375.2 or 1375.1)
LNELDCCPT2	carnitine transferase	[m] : coa + lneldccrn --> crn + lneldccoa		Carnitine shuttle	1376.1
LNELDCCRNt	transport into the mitochondria (carnitine)	lneldccrn[c] --> lneldccrn[m]		Carnitine shuttle	788.1
LNELDCt	fatty acid transport via diffusion	lneldc[e] <==> lneldc[c]		Transport, Extracellular	
LNLCCPT1	carnitine O-palmitoyltransferase	[c] : crn + lnlccoa --> coa + lnlccrn	2.3.1.21	Carnitine shuttle	(1375.4 or 1374.1 or 126129.1 or 1375.3 or 1375.2 or 1375.1)
LNLCCPT2	carnitine transferase	[m] : coa + lnlccrn --> crn + lnlccoa		Carnitine shuttle	1376.1
LNLCCRNt	transport into the mitochondria (carnitine)	lnlccrn[c] --> lnlccrn[m]		Carnitine shuttle	788.1
LNLCt	Linoleic acid (n-C18:2) transport in via diffusion	lnlc[e] <==> lnlc[c]		Transport, Extracellular	
LNLNCACPT1	carnitine O-palmitoyltransferase	[c] : crn + lnlncacoa --> coa + lnlncacrn	2.3.1.21	Carnitine shuttle	(1375.4 or 1374.1 or 126129.1 or 1375.3 or 1375.2 or 1375.1)
LNLNCACPT2	carnitine transferase	[m] : coa + lnlncacrn --> crn + lnlncacoa		Carnitine shuttle	1376.1

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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