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Systems-level characterization of a host-microbe metabolic symbiosis in the mammalian gut

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Supplemental results

Curation of an automated draft reconstruction for Bacteroides thetaiotaomicron

We automatically generated a partially curated draft reconstruction using Model Seed[1]. We then manually inspected, curated, and validated the content of the draft reconstruction based on a protocol for curation of automated models[1] and established methods in metabolic network reconstruction[2] (Figure S1). Primary and review literature and databases (Table S13) were used to obtain *B. thetaiotaomicron*-specific information for gene annotation, biochemical pathway utilization, cofactor and electron carrier usage, and other physiological and phenotypical properties.

The draft reconstruction for *B. thetaiotaomicron*, deemed *BΘ_Seed_v1*, contained 777 genes, 944 metabolites, and 989 reactions, of which 429 could not carry any flux (i.e., blocked reactions). Careful inspection of pathways, cofactor and electron carrier utilization, and reaction directionality led to rejection of 87 reactions (8,8%) and a change in directionality for 230 reactions (23%). One reaction, formate tetrahydrofolate ligase (FTHFL), was made irreversible to prevent biologically infeasible ATP production. Gene-protein-reaction associations (GPRs) define the gene(s) whose product(s) catalyzes a reaction(s) through Boolean rules ('AND', 'OR'). Ten GPRs were changed manually based on online genome databases. A total of 108 genes (14%) were removed, most of which were involved in transcription and translation processes, which are generally considered to be outside the scope of metabolic reconstructions[2].

Curation of the biomass reaction

A biomass reaction contains the fractional contribution of all known metabolic precursors required to synthesize a new cell. The biomass reaction in *BΘ_Seed_v1* included 76 default components[1]. Apo-ACP was removed since no other model in the BIGG database[3] includes this compound in the biomass reaction. Sulfate was removed as it does not serve as sulfur source for *B. thetaiotaomicron*[4]. Sulfide is used to synthesize cysteine, which is captured by the biomass reaction. Biotin was also added as a universally required cofactor. The essential cofactors Vitamin B12 (cob(I)alamin) and protoheme were added[4]. Sodium was added [5]. The components names biomass, DNA replication, RNA transcription, and protein biosynthesis were removed from the curated biomass reaction.

Curation of electron transport chain reactions

Electron transport chain reactions in *BΘ_Seed_v1* were curated based on literature. *B. thetaiotaomicron* possesses an anaerobic electron transport chain with fumarate as the terminal electron acceptor, which is reduced to succinate. NADH serves as electron donor[6], but not NADPH[7]. This electron transport system provides additional ATP. It is catalyzed by a succinate: quinone oxidoreductase (EC 1.3.99.1, BiGG ID: FRD2, SUCDi) that functions both as fumarate reductase and succinate dehydrogenase. If fumarate reductase is not functional due to lack of heme, or if the SQR operon is knocked out, growth yield decreases two- to threefold[8, 9]. Apart from NADH, hydrogen can also serve as electron donor for fumarate reduction via a fumarate-dependent hydrogenase. The flow of electrons from hydrogen to NAD^+ is mediated by ferredoxin[7, 9]. Apart from fumarate, oxygen also serves as terminal electron acceptor. This is mediated by cytochrome bd oxidase. Fumarate reductase and cytochrome oxidase have redundant roles in metabolism[10]. Ubiquinone was not found in *B. thetaiotaomicron*[11]. However, a NADH: ubiquinone oxidoreductase is annotated in its genome. *B. thetaiotaomicron* possesses a pyruvate: quinone oxidoreductase (EC 1.2.2.2, BiGG ID: POX, BT_1820, BT_1822), which does not accept menaquinone (KEGG Enzyme[12]). Taken together, this evidence suggests involvement of fumarate, ferredoxin,

hydrogen, NADH, oxygen and menaquinone, but not NADPH, in the electron transport chain of *B. thetaiotaomicron*. It is unclear whether *B. thetaiotaomicron* utilizes ubiquinone. Since evidence from literature is unclear, it was assumed that both menaquinone and ubiquinone are used as cofactors. Therefore, menaquinone-utilizing reactions were added where appropriate.

Carbohydrate metabolism

The following central metabolic pathways of *B. thetaiotaomicron* were all accounted for in *BΘ_Seed_v1*: i) carbohydrates metabolism via Embden-Meyerhof[13] and pentose phosphate pathway[14], ii) acetate fermentation and the succinate-propionate pathways[13], and iii) the oxidative branch of the citric acid cycle[15].

Amino acid metabolism

B. thetaiomicron is able to synthesize all amino acids *de novo*[4]. *BΘ_Seed_v1* could not synthesize arginine, since the wrong reaction was associated with N-acetyl-L-ornithine transcarbamylase (BT_3717). The reaction catalyzed by this enzyme is different in *Bacteroides* species, as it catalyzes the carbamylation of N-succinyl-L-ornithine to N-succinyl-L-citrulline[16], is converted to citrulline, a precursor of arginine. It is not known how N-succinyl-L-ornithine is formed. Thus, a hypothetical synthesis reaction (BiGG ID: HYPSUCORNS) was included for this metabolite, assuming that N-succinyl-L-ornithine is synthesized from succinate and ornithine. Formation of citrulline from N-succinyl-L-citrulline was assumed to occur spontaneously, as proposed by KEGG Pathway[17]. Adding these reactions allowed the model to synthesize arginine. Furthermore, *BΘ_Seed_v1* lacked an associated gene for homoserine kinase (EC 2.7.1.39, BiGG ID: HSK). We assigned gene BT_2402 to this reaction, as the associated protein has 90- 99% sequence identity with several *Bacteroides ssp*. homoserine kinases (determined using blastp). An additional pathway for isoleucine biosynthesis via citramalate, which is mainly found in archaea, is annotated in the *B. thetaiotaomicron* genome. This pathway was added to the reconstruction. It is unclear whether urea excretion occurs in *B. thetaiotaomicron*. Most urea cycle enzymes, namely argininosuccinate synthase (EC 6.3.4.5), argininosuccinate lyase (EC 4.3.2.1), and a putative arginase (EC 3.5.3.1) are annotated in the *B. thetaiotaomicron* genome. A transport reaction for urea was included in *BΘ_Seed_v1*. In the absence of contrary information, the reaction was left in the reconstruction.

B. thetaiotaomicron's proteolytic activity is weak, but detectable[18], and several di-and tripeptide transporters and aminopeptidases are annotated in its genome. Dipeptide degradation was already accounted for in *BΘ_Seed_v1* but the corresponding transporters were added. We included a dipeptidyl peptidase specific for arginylarginine and phenylalanylarginine[19].

Fatty acid metabolism

B. thetaiotaomicron is well established to synthesize anteiso- and iso-methyl-branched chain fatty acids[11, 20, 21]. Biosynthesis pathways for most these fatty acids were already included in *BΘ_Seed_v1* but the biomass reaction was incomplete. We modified the biomass function accordingly. The enzymes glycerol-3-phosphate acyltransferase (EC 2.3.1.15, BiGG ID: G3PAT) and glycerol kinase (EC 2.7.1.30, BiGG ID: GLYKr), which were added by Model Seed during the auto-completion step, are not annotated in the *B. thetaiotaomicron* genome, but are required in the reconstruction for fatty acid biosynthesis to be functional. It is not known, which enzymes perform these steps *in vivo*.

Biosynthesis of cofactors and prosthetic groups

B. thetaiotaomicron is able to synthesized all required cofactors *de novo*[4], except heme and cobalamin (Vitamin B12). *BΘ_Seed_v1* could not synthesize *de novo* pantothenate, folate,

thiamin, and biotin. For pantothenate biosynthesis, we added the annotated pantothenate synthetase (EC 6.3.2.1, BiGG ID: PANTS, BT_4308). For completion of the folate biosynthesis, we added the folate reductase (EC 1.5.1.3, BiGG ID: FOLR,BT_0106 or BT_2048).. We assumed that BT_3017, an acid phosphatase with wide specificity, catalyzed the reaction of the thiamin diphosphatase (EC 3.1.3.2, BiGG ID: THMDP). We also added a demand reaction for (4-hydroxybenzyl alcohol, BiGG ID: 4hba), whose metabolic fate is unknown. These two additions completed the thiamine synthesis. The complete biotin biosynthesis pathway was recently discovered in *E. coli*[22]. We assumed the same pathway to occur in *B. thetaiotaomicron*. *BΘ_Seed_v1* accounted for menaquinone-(MK-) 8, but we also included biosynthesis pathways for MK-7, MK-9, MK-10 and MK-11, as these isoprenes were found in *B. thetaiotaomicron*[11]. Menaquinone (vitamin K_2) synthesized by the microbiota, particularly *Bacteroides*, also partially contribute to human vitamin K homeostasis[23]. Therefore, we included transport and exchange reactions for menaquinone 7-11.

Validation of the metabolic reconstruction of *B. thetaiotaomicron*

The resulting updated draft reconstruction was deemed *BΘ_Seed_v2*. By comparing its *in silico* phenotypic capabilities with published data, we further refined and ultimately validated its content. *B. thetaiotaomicron* can grow anaerobically on glucose minimal medium[4], consisting of glucose, minerals, CO_2, NH_4, heme, cobalamin (Vitamin B12), and either sulfide or L-cysteine.

BΘ_Seed_v2 was incapable of growing without oxygen. *B. thetaiotaomicron* does not require oxygen for growth and colonies stop growing when exposed to oxygen due to enzyme damage in central metabolism[6]. We evaluated *BΘ_Seed_v2's* oxygen usage using flux variability analysis, FVA[24, 25]. Oxygen was consumed by the reaction catalyzed by L-aspartate oxidase (EC 1.4.3.16, BT_3184), but this enzyme is also able to use fumarate for the cofactor reoxidation[12]. We added the fumarate-dependent reaction (BiGG ID: ASPO5), which enabled the model to grow anaerobically. *Bacteroides* species have been found to benefit from nanomolecular concentrations of oxygen due to cytochrome oxidase bd acitivity[10]. This reaction was accounted for in *BΘ_Seed_v2* (BiGG ID: CYTBD, EC 1.10.3.10; BT_3053, BT_1209, and BT_1210). Consistently, the model grew faster in presence of oxygen (Table S3a). Since the employed constraint-based modeling approach does not permit simulating enzyme inhibition or DNA damage due to oxygen exposure, we assumed strictly anaerobic conditions for all following simulations.

The model could not grow on cysteine as sole sulfur source. *In vivo*, cysteine can replace sulfide as sulfur source[4]. Sulfide is required for synthesis of methionine, S-adenosyl-L-methionine, and biotin. We added the cysteine desulfhydrolase activity (BiGG ID: CYSDS), which is catalyzed by cystathionine beta-lyase (EC 4.4.1.8, BT_2387 and BT_1923). *BΘ_Seed_v2* required N-acetyl-D-glucosamine. This metabolite has been reported to serve as sole carbon source[26], but to be not required for growth *in vivo*. The N-acetyl-D-glucosamine synthesis from glucose requires either glucosamine-6-phosphate-acetyltransferase (EC 2.3.1.4) or glucosamine-1-phosphate-acetyltransferase (EC 2.3.1.157), but no gene could be found in *B. thetaiotaomicron*'s genome. We assumedthe presence of the glucosamine-1-phosphate-acetyltransferase activity (BiGG ID: G1PACT).

These additions enabled *BΘ_Seed_v2* to grow on anaerobic glucose minimal medium (Table S3a).

Addition of species-specific pathways

As one would expect, organism-specific pathways were generally poorly represented in the draft reconstruction and thus were added manually based on thorough literature review.

Polysaccharide utilization

B. thetaiotaomicron's versatile carbohydrate utilization capacity was not well captured in *BΘ_Seed_2*. N-acetyl-D-galactosamine serves as sole carbon source *in vivo*[27], but the corresponding pathway is not annotated in *B. thetaiotaomicron's* genome. We assumed the presence of *E. coli's* pathway[28] and the gaps in N-acetyl-D-galactosamine metabolism were putatively filled by adding the reactions of N-acetyl-D-galactosamine kinase (BiGG ID: ACGALK3), N-acetyl-D-galactosamine 6-phosphate amidohydrolase (EC 3.5.1.2, BiGG ID: AGDC2), Galactosamine-6-phosphate isomerase/ deamidase (BiGG ID: GALAM6PDA), and Tagatose-bisphosphate aldolase (EC 4.1.2.4, BiGG ID: TGBPA). A transport reaction for N-acetyl-D-galactosamine was also included.

Starch utilization is a well studied example of *B. thetaiotaomicron*'s polysaccharide degradation systems[29]. It involves the gene cluster of the starch utilization system (Sus), which consists of the outer-membrane proteins (SusC and SusD) that bind starch to the cell surface) and two starch-degrading α-amylases (SusA and SusG). The appropriate reactions and GPR associations were added. The starch and pullulan molecules defined to consist of 1200 monosaccharide units. The amylose molecule consists of 300 monosacharide units.

B. thetaiotaomicron utilizes a number of plant-derived polysaccharides including pectin, arabinan, and rhamnogalacturonan, as well as yeast-derived α-mannan. Specific polysaccharide utilization loci (PULs) are upregulated during growth on these complex carbohydrates[30]. 61% of *B. thetaiotaomicron* glycosidases are predicted to be located in the extracellular space or in the periplasm[31]. *B. thetaiotaomicron* may also require susC/susD homologs. We added the corresponding reactions and GPR associations based on transcriptomic data[30].

Degradation reactions of host-derived glycans were based on the glycans included in the human metabolic reconstruction Recon1[32]. Additionally, we accounted for human milk oligosaccharides (HMO). Chondroitin sulfate degradation is carried out by a PUL (BT_3324 – BT_3350)[33], resulting in monosulfated disaccharides[34]. A susC and a susD homolog are needed for chondroitin sulfate utilization[33]. Further degradation involves sulfatases, which require sulfatase-maturing enzyme (SME) for functionality[35], and at least two periplasmatic chondroitinases, which breaks down the desulfated disaccharides[33]. Hyaluronan degradation is also carried out by PUL (BT_3324 – BT_3350)[33] and may occur in a similar way. The first step in heparin degradation is carried out by heparin lyase I, which cleaves the glycosidic linkage to the nonreducing end of iduronate[36]. Further degradation may involve glucuronidase and alpha-N-acetylglucosaminidase. *B. thetaiotaomicron* utilizes host-derived mucin-type O-glycans, and a number of PULs, and susC/ susD homologs, are upregulated during utilization of these glycans[33]. HMO degradation pathways were constructed based on structural information for these oligosaccharides[37, 38]. *B. thetaiotaomicron* employs similar mechanisms as for mucus utilization to degrade HMOs, and several PULs, and susC/susD homologs, are upregulated during growth on HMOs[39].

All carbohydrates that can serve as sole carbon sources are listed in Table S1.

Production of known secretion products

The major fermentation products of *B. thetaiotaomicron* are acetate, propionate, succinate, CO_2, and H_2[40, 41]. Minor secretion products include lactate, isovalerate, and isobutyrate[40]. Moreover, when L-fucose or L-rhamnose is fermented, 1,2-propanediol is formed[42, 43]. Isobutyrate and isovalerate are formed by the gut microbiota by an unknown degradation of valine and leucine, respectively[44]. A minor product of microbial protein degradation in the gut is isocaproate, which is formed by reduction of leucine[45]. It is not known if *B. thetaiotaomicron* produces isocaproate, but its inclusion was required for the putative leucine degradation pathway.

Phenylacetate is an end product of aromatic amino acid degradation in *B. thetaiotaomicron*[46]. The reversible reaction of the annotated phenylacetate-CoA ligase was added to *BΘ_Seed_2* as well as a phenylpyruvate-dependent reaction of indolepyruvate ferredoxin oxidoreductase (EC 1.2.7.8, BiGG ID: IOR2, BT_0429 and BT_0430). Phenylpyruvate formation via phenylalanine transaminase (EC 2.6.1.58, PHETA1, BT_0202 or BT_3935) was already included in *BΘ_Seed_2*.
Transport reactions were added for known secretion products metabolites (Table S2). The gene for succinate transport (BT_2756) was included.

Bile acid metabolism
The human gut microbiota is well known to carry out chemical modifications of host-produced bile acids in the large intestine[47]. Different bile acid biotransformations are performed by different species. *B. thetaiotaomicron* possesses a bile acid hydrolase (BT_1259 or BT_2086), which degrades choloylglycine and choloyltaurine[48], and a NAD-dependent 7α-hydroxysteroid dehydrogenase (BT_1911) [47], which converts cholate to alpha,12alpha-Dihydroxy-7-oxo-5beta-cholanate.

Lipopolysaccharide (LPS), capsular polysaccharide (CPS), and sphingolipid biosynthesis
The LPS synthesis pathway was incomplete in *BΘ_Seed_2* due to unknown genes. *B. thetaiotaomicron* synthesizes a LPS with similar structure to the LPS of the periodontal pathogen *Porphyromonas gingivalis*[49]. A metabolic reconstruction of *P. gingivalis* has been published[50], whose LPS synthesis pathway was based on a metabolic reconstruction of *Helicobacter pylori*, iIT341[51]. Therefore, the LPS synthesis pathway of *B. thetaiotaomicron* was also partly based on *H. pylori* iIT341 but the reactions were modified to reflect structural properties of *B. thetaiotaomicron*'s LPS[49, 52]. CPS synthesis is mediated by eight CPS loci in the genome[53]. The exact structure of *B. thetaiotaomicron*'s CPS is unknown, however, it is thought to contain 2-aminoethylphosphonate[54], CMP-2-Keto-3-deoxy-D-glycero-D-galacto-nononic acid (CMP-KDN)[55], and GDP-fucose[56]. *B. fragilis* and *B. thetaiotaomicron* can harvest L-fucose from host glycoproteins and incorporate it into their own surface CPSs through a mammalian-like pathway[56]. We included the reaction of the fucose-1-phosphate guanylyltransferase (EC 2.7.7.30, BiGG ID F1PGT, BT_2128). We assumed a stoichiometric coefficient of one for each metabolite. An unusual trait of *B. thetaiotaomicron* is its ability to synthesize sphingolipids. The main sphingolipid types in *B. thetaiotaomicron* are ceramide-1-phosphoethanolamine and sphingomyelin[57-59]. Information on sphingolipid biosynthesis pathways in *Bacteroides* is sparse. A putative homolog of human serine C-palmitoyltransferase (EC 2.3.1.50) was identified in *B. thetaiotaomicron* (BT_0870); however, no homologs of human 3-dehydrosphinganine reductase and ceramide synthase could be found[60]. Thus, sphingolipid synthesis may occur by a different mechanism in *Bacteroides* species from the one currently known. In the absence of other information, reactions involved in sphingolipid synthesis were taken from the human metabolic reconstruction[32] and modified based on available structural data. Species-specific lipids were then added to the biomass reaction.

In silico gene essentiality analysis
In silico single gene essentiality analysis was carried out using the COBRA Toolbox[61]. Three *in silico* growth conditions were considered: glucose minimal medium, tryptone-yeast extract-glucose medium, and rich medium. For the simulation of rich medium, uptake of every nutrient was allowed in unlimited amounts (i.e., the lower bounds on all exchange reactions were set to -1000 mmol $g_{Dw}^{-1}.hr^{-1}$ and the upper bounds to 1000 mmol $g_{Dw}^{-1}.hr^{-1}$). For simulation of tryptone-yeast extract-glucose medium, yeast extract was assumed to consist of all metabolites included in the yeast reconstruction iMM904[62] that could also be transported

by iAH991. Furthermore, yeast α-mannan (Metabolite ID: amannan140) was included. Tryptone was assumed to include all 20 amino acids. Simulation conditions and constraints are listed in Table S8.
In glucose minimal medium, 204/991 (20,6%) of the genes were essential, most of which belonged to the subsystems associated with *de novo* synthesis of biomass precursors (Figure S6). Carbohydrate metabolism makes up only 3% of essential genes. No genes in central metabolism (fermentation pathways and electron transport chain) and citric acid cycle were found to be essential *in silico* (Figure S6), highlighting the redundant nature of *B. thetaiotaomicron*'s energy and carbohydrate metabolic network. In rich medium, only 61/991 (6,2%) of the metabolic genes were essential.
To assess how well iAH991 can predict single gene essentiality for growth, we compared our predictions with experimental data reported in literature. We predicted correctly 11 out of 12 reported knockout growth phenotypes of *B. thetaiotaomicron*, or the closely related species *Bacteroides fragilis* (Table S14). iAH991 failed to predict growth on L-rhamnose as sole carbon source of the lactaldehyde reductase knockout (BT_3767).
We also compared the gene essentiality reported in an *in vitro* transposon mutant study covering 78% of open reading frames in the *B. thetaiotaomicron* genome[63]. 75,1% (744/991) of the genes in iAH991 were captured in the transposon study, corresponding to 95 in vitro candidate essential (probability > 90%) and 649 unessential genes. We computed the *in silico* gene in anaerobic conditions on tryptone-yeast extract-glucose (TYG) medium. 93 of the 116 *in silico* essential and 651of the 875 non-essential genes were captured by the transposon library. Overall, the model predicted correctly the essentiality for 44 genes and the non-essentiality for 600 genes. 49 predictions were false-positives, while 51 predictions were false-negatives. The model predicts thus gene essentiality with an accuracy of 86,6%.

Rational and implementation of coupling constraints in the integrated model

Using the integrated model setup (Figure 1a), we realized that unless additional constraints were implemented, we computed biologically implausible solutions, in which microbial or host reactions were active even though microbe, or the host, did not generate ATP or produce biomass. Also, if a reaction has a higher flux, than the ATP or biomass production should be higher, as more of the enzyme is required. Since most enzymes do not operate at saturation level[64], our implementation of the reaction coupling sets bounds on the reaction ratio between each network reaction and the biomass reaction rather than to fix the ratio to a particular value (Figure S2). These constraints rendered the model's more realistic (Figure S3).

We performed a sensitivity analysis to investigate the effect of coupling coefficient c on the model's predictive potential. For the uncoupled model, a negatively linear relationship between the maximal possible growth rate of iSS1393 and of iAH991 was computed (Figure S3a), which corresponds to a competitive interaction. This is due to the fact that at maximal growth rate of the mouse model it profits by the presence of the *B. thetaiotaomicron* metabolic network, which is not utilized for *B. thetaiotaomicron* growth. With the coupling constraints in place, the mouse can still benefit from *B. thetaiotaomicron*'s metabolic network but now *B. thetaiotaomicron* has to grow to some extend to be able to provide metabolites to the mouse. Mutualism and competition, depending on the growth rate of both organisms, is captured by the integrated, coupled model. Increasing c causes an extension of the feasible solution space (Figure S4), and the relationship between the two biomass reactions becomes more linear. We employed c=400 for all simulations in this work.

Supplemental figures

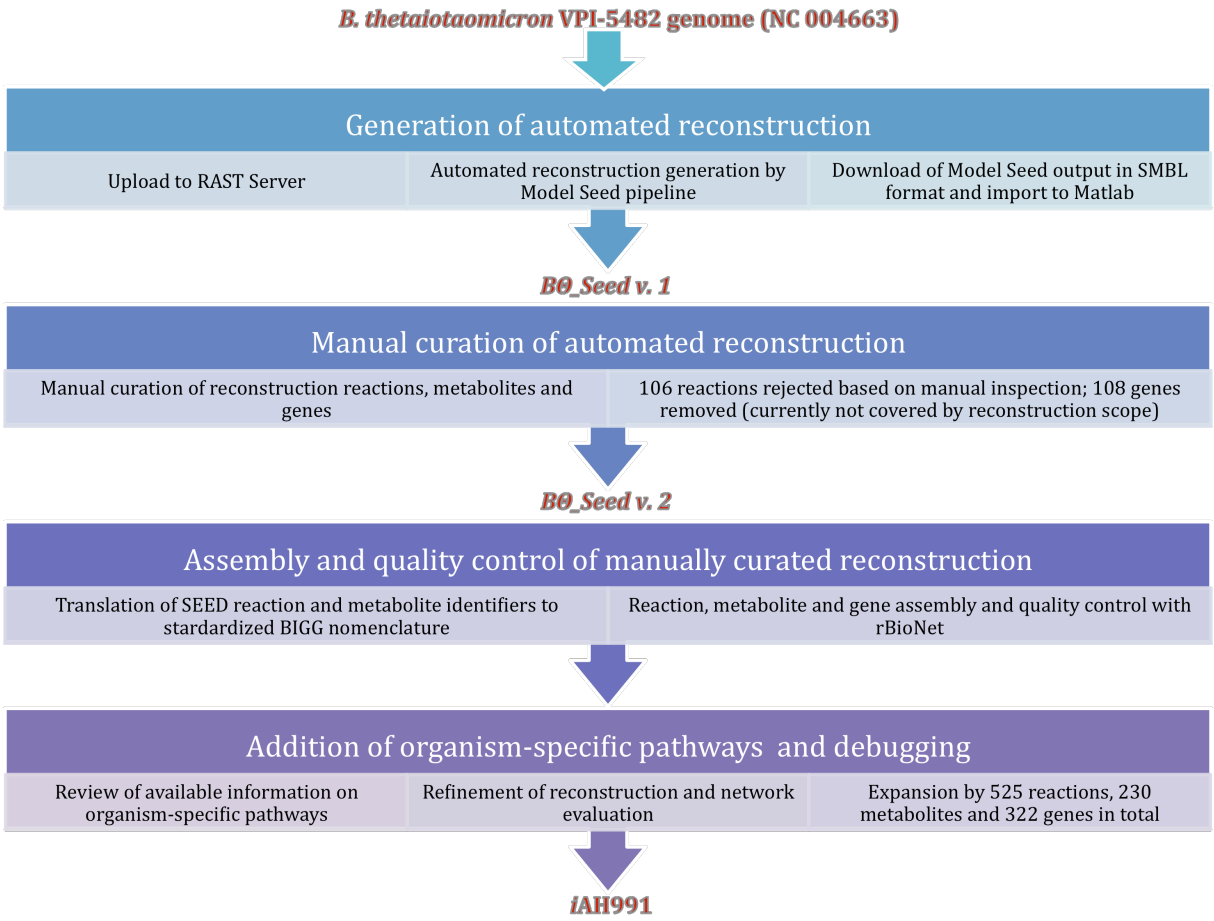

Figure S1: Pipeline employed to build a high-quality metabolic reconstruction of *B. thetaiotaomicron* based on an automated draft reconstruction. Shown is the reconstruction process starting from upload of the *B. thetaiotaomicron* VPI-5482 genome to the RAST server[65]. The automated draft reconstruction generated by Model Seed[1] was then subjected to several manual curation and expansion steps and underwent quality control in a reconstruction environment tool, rBioNet[66].

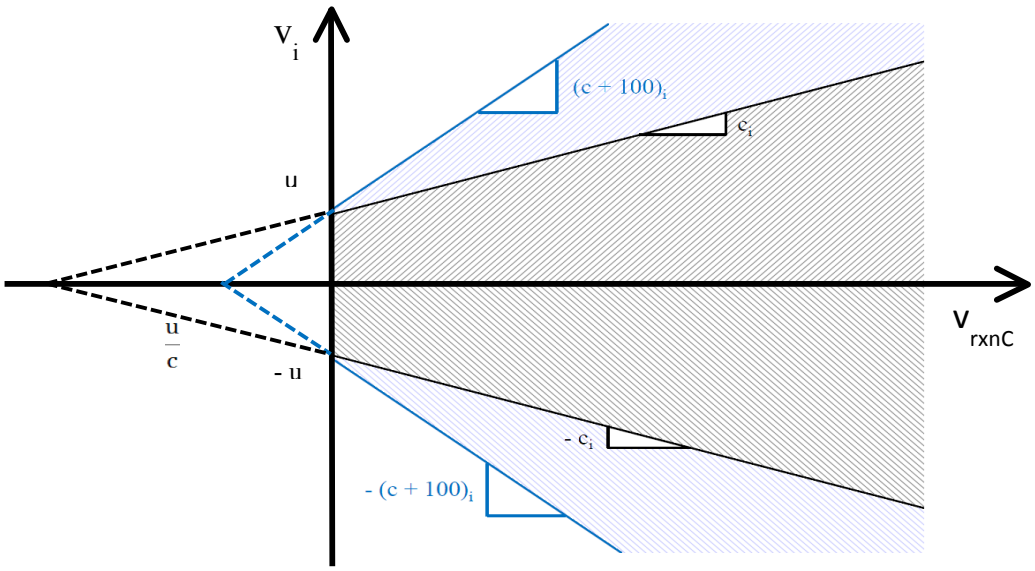

Figure S2: Schematic representation of the relationship between the fluxes v_i of coupled reactions, the flux v_{rxnC} of the specified reaction to which fluxes are coupled, the threshold u and the coupling factor c. The feasible solution space if the coupling factor c is implemented is indicated by grey diagonal lines. The expansion of the solution space if the value of c is raised by 100 is indicated by blue diagonal lines. The value for the threshold u is constant in our study.

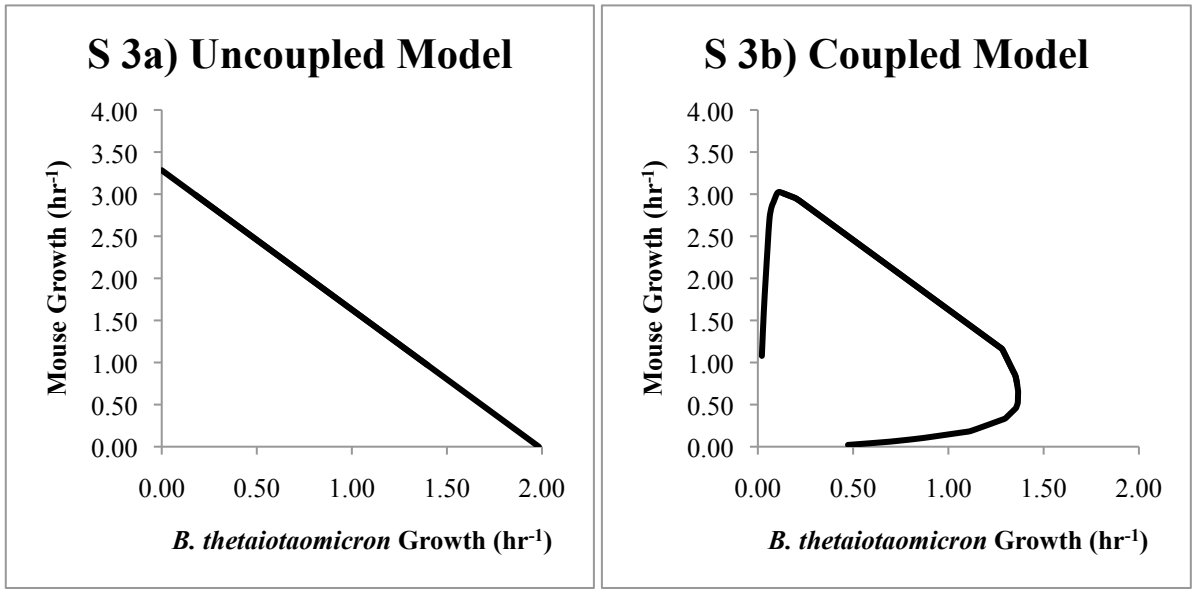

Figure S3: Pareto optimality analysis of the joint model on Western diet before implementing coupling constraints (a) and with coupling constraints (c = 400, u = 0.01 mmol/g_{DW}/hr) in place (b).

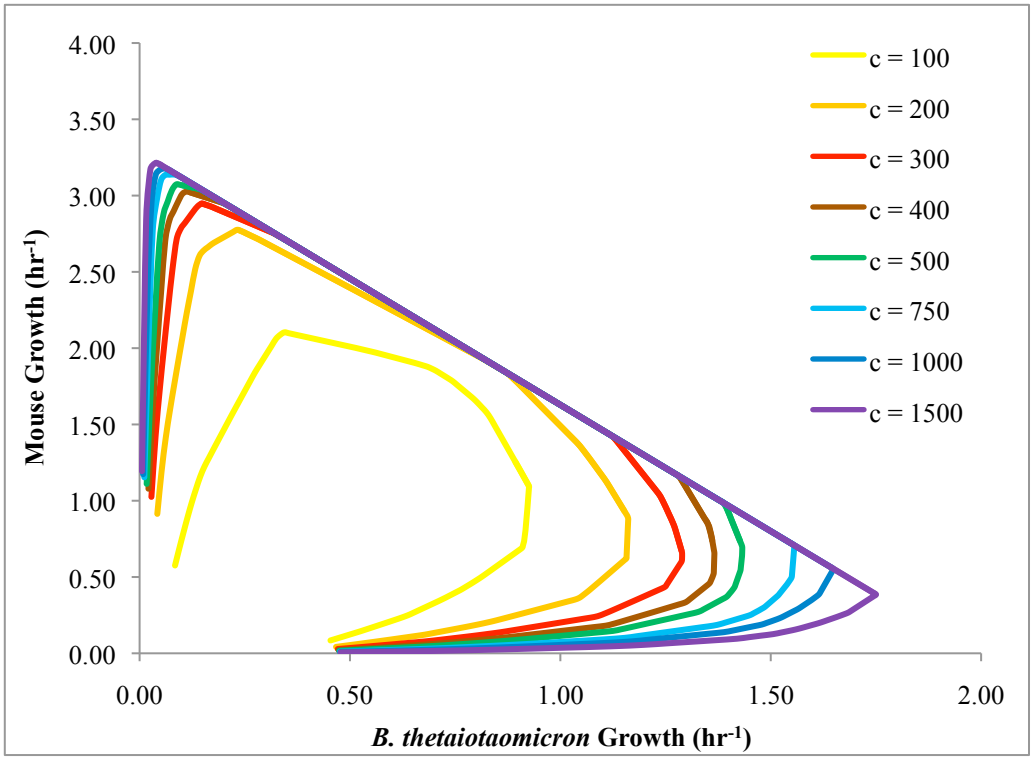

Figure S4: Sensitivity analysis of coupling factor c. The effect of varying c between 100 and 1500 is shown. The analysis was performed for the joint model while simulating growth on Western Diet and setting the threshold u to 0.01 mmol/g_{DW}/hr.

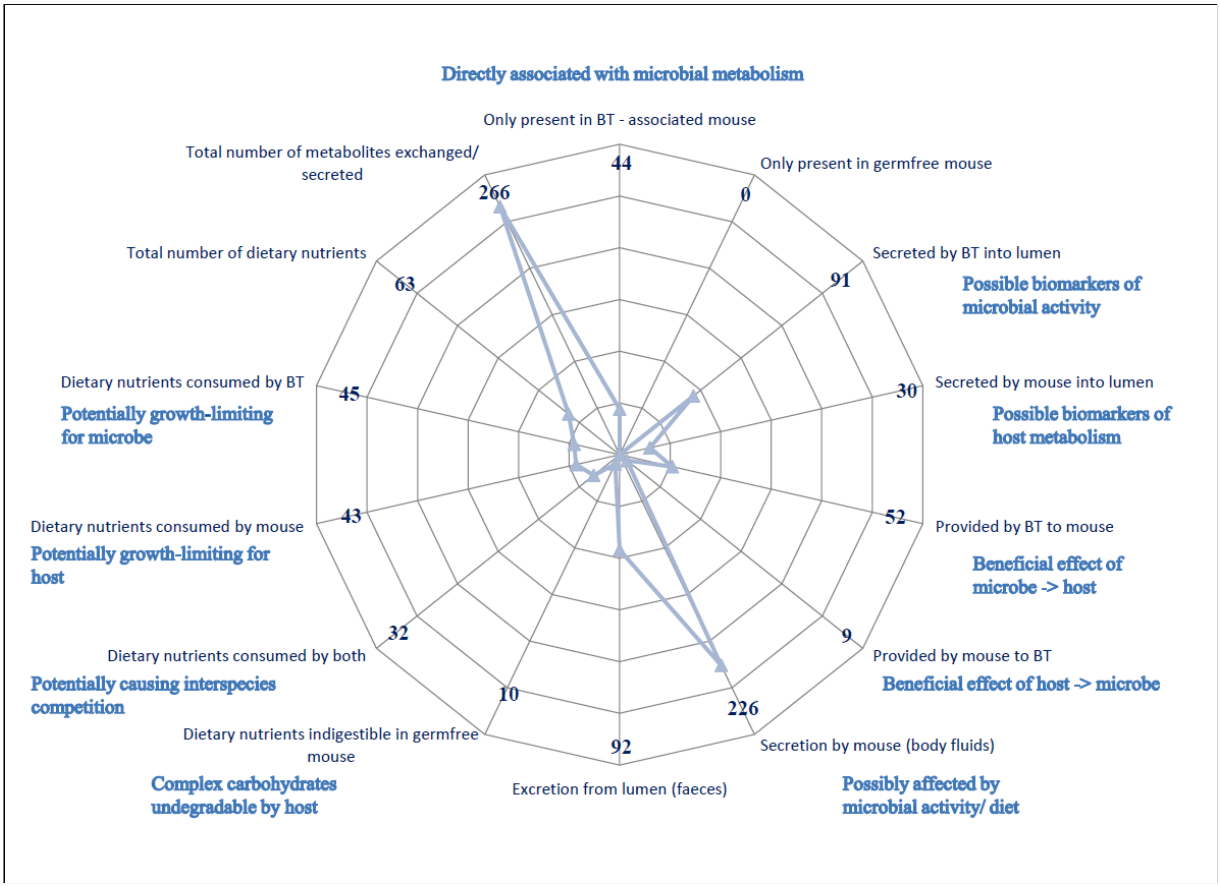

Figure S5: Predicting the metabolome. Metabolites exchanged in the joint *B. thetaiotaomicron* – mouse model classified by metabolic fate.

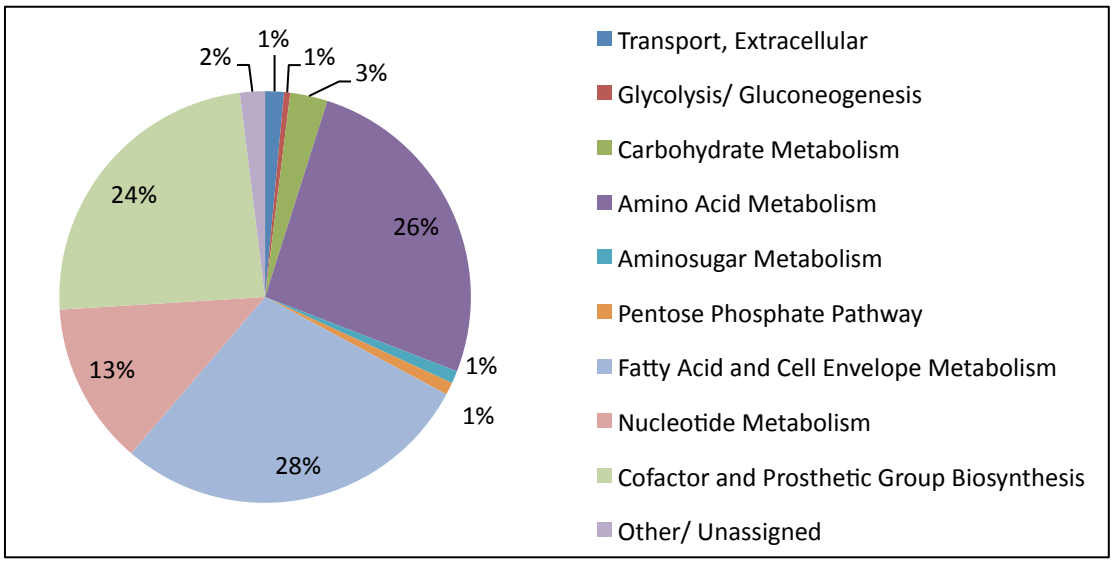

Figure S6: Subsystem participation of iAH991 genes predicted to be essential on glucose minimal medium.

Supplemental tables

Table S1: List of carbohydrates that can serve as sole carbon sources for iAH991, and supporting references.

Carbohydrate	BIGG ID:	*BΘ_Seed_v1*	iAH991	Reference
Monosaccharides				
D-glucose	glc-D	no	yes	[4]
D-mannose	man	no	yes	[67]
D-galactose	gal	no	yes	[67, 68]
D-fructose	fru	no	yes	[69]
D-xylose	xyl-D	no	yes	[67]
L-arabinose	ara-L	yes	yes	[67, 68]
N-acetylglucosamine	acgam	no	yes	[26]
N-acetylgalactosamine	acgal	no	yes	[27]
D-glucuronate	glcur	no	yes	[70]
D-galacturonate	galur	no	yes	[70]
D-glucosamine	gam	no	yes	[70]
L-fucose	fuc-L	no	yes	[70, 71]
L-rhamnose	rmn	no	yes	[42]
D-ribose	rib-D	no	yes	[30]
Di-and oligosaccharides				
Trehalose	tre	no	yes	[40, 72]
Raffinose	raffin	no	yes	[40]
Melibiose	melib	no	yes	[73]
Maltose	malt	no	yes	[73]
Maltotriose	malttr	no	yes	[74]
Maltotetraose	maltttr	no	yes	[74]
Maltopentose	maltpt	no	yes	[74]
Maltohexose	malthx	no	yes	[74]
Maltoheptaose	malthp	no	yes	[74]
Sucrose	sucr	no	yes	[69]
Kestose	kesto	no	yes	[69]
Kestotetraose	kestottr	no	yes	[69]
Kestopentaose	kestopt	no	yes	[69]
Levanbiose	levanb	no	yes	[69]
Levantriose	levanttr	no	yes	[69]
Levantetraose	levantttr	no	yes	[69]
Lactose	lcts	no	yes	[40]
Oligofructose	oligofru4	no	yes	[75]
Human milk oligosaccharides (HMO)	2fuclac, 3fuclac, lacdfucttr, lacndfuchx, lacnfucpt, lacnttr, neulacnttr, fucneulacnhx	no	yes	[39]

Stachyose	stys	no	yes	[76]
Mannobiose	manb	no	yes	[77]
Mannotriose	mantr	no	yes	[77]
Mannotetraose	manttr	no	yes	[77]
Mannopentaose	manpt	no	yes	[77]
Chitobiose	chtbs	no	yes	KEGG Pathway
Polysaccharides				
Amylose	amylose300	no	yes	[70]
Starch (insoluble)	starch1200	no	yes	[70]
Starch (human enzyme-accessible form)	strch1, strch2	no	yes	[70]
Pullulan	pullulan1200	no	yes	[73]
Dextran	dextran40	no	yes	[70]
Pectin	pect	no	yes	[70]
Larch arabinogalactan	arabinogal	no	yes	[70]
Laminarin	lmn30	no	yes	[70, 78]
Inulin	inulin	no	yes	[30]
Levan	levan1000	no	yes	[69]
Glycogen	glycogen1500	no	yes	[72]
Chondroitin sulfate A	cspg_a	no	yes	[70, 79]
Chondroitin sulfate B	cspg_b	no	yes	[70, 79]
Chondroitin sulfate C	cspg_c	no	yes	[70, 79]
Heparan sulfate	hspg	no	yes	[33, 70]
Hyaluronan	ha	no	yes	[33, 70]
PA6 (a N-glycan containing L-fucose)	s2l2fn2m2masn	no	yes	[71]
Mucin-type O-glycans	f1a, core4, core5, core7, core7, gncore1, gncore2, sTn_antigen, dsT_antigen	no	yes	[33, 70]
alpha-mannan (yeast)	amannan140	no	yes	[30]
Homogalacturonan	homogal	no	yes	[30]
Rhamnogalactorunan I	rhamnogalurI	no	yes	[30]
Rhamnogalacturonan II	rhamnogalurII	no	yes	[30]
Arabinan	arabinan101	no	yes	[30]
Pectic galactan	pecticgal	no	yes	[30]

Table S2: List of known secretion products captured by iAH991, and supporting references.

a - KEGG Pathway, b - NCBI Entrez Gene.

Secretion Product	BiGG Identifier	*BΘ_Seed_v1*	iAH991	Ref.	Comments
Acetate	ac	no	yes	[72]	
Propionate	ppa	no	yes	[72]	
Succinate	succ	no	yes	[72]	
CO_2	co2	yes	yes	[41]	
H_2	h2	no	yes	[41]	
D-lactate	lac-D	no	yes	[72]	Not determined in literature if *B. thetaiotaomicron* secretes L-lactate or D-lactate, or both.
L-lactate	lac-L	no	yes	[72]	Not determined in literature if *B. thetaiotaomicron* secretes L-lactate or D-lactate, or both.
Isovalerate	isoval	no	yes	[72]	
Isobutyrate	isobut	no	yes	[72]	
Isocaproate	isocapr	no	yes	[45]	Secreted by gut microbiota; not known if *B. thetaiotaomicron* in particular produces this metabolite. Needed for leucine degradation pathway to be mass and charge balanced.
Phenylacetate	pac	no	yes	[46]	
Pyruvate	pyr	no	yes	[6]	
Acetol	acetol	no	yes	[6]	
Methylglyoxal	mthgxl	no	yes	[6]	
Formate	for	no	yes	[78]	
Ethanol	etoh	no	yes	[80]	
Putrescine	ptrc	no	yes	[81]	
Spermidine	spmd	no	yes	[81]	
(R)-1,2-propanediol	12ppd-R	no	yes	[42], a	*B. thetaiotaomicron* possesses at least one additional route for 1,2-propanediol production apart from lactaldehyde reductase. It is assumed that 1,2-propanediol formation occurs via methylglyoxal and acetol.
(S)-1,2-propanediol	12ppd-S	no	yes	[42, 43]	Only produced during growth on L-rhamnose or L-fucose.
Menaquinones	mqn7, mqn8, mqn9, mqn10, mqn11	no	yes	[23, 82]	

1,2-Ethanediol	12ethd	no	yes	a	Production of this metabolite is predicted by KEGG Pathway[17]. Last checked on 28.10.11.
Urea	urea	no	yes	b	No biochemical evidence for urea excretion is available, but urea cycle is annotated in *B. thetaiotaomicron* genome.
Methanol	meoh	no	yes	[22]	Only produced from one reaction in the biotin biosynthesis pathway. Assumed to be excreted since no further metabolic fate of methanol is known.

Table S3: Growth rates and secretion product amounts produced by iAH991 on several carbon sources, and comparison with available experimental data.

a) Growth rates. [a] Type of mucin O-glycan is not specified in experimental data. [b] Type of chondroitin sulfate is not specified in experimental data. [c] Previous studies report that *B. thetaiotaomicron* grows on laminarin (see Table S1). Simulation conditions are reported in Table S8.

Carbon Source (uptate rate scaled to 10 mmol.g_{Dw}^{-1}.hr^{-1} 6arbon units)	**Growth rate *in silico* (hr^{-1})**	**Growth rate *in vivo* (hr^{-1})**	**Growth rate *in vivo* (ΔA_{600}/h)[30]**	
Arabinose	0.23	0.10[67]	0.031	Monosaccharides
Fructose	0.24	0.39[69]	0.073	
Fucose	0.0012		0.024	
Galactose	0.24	0.38[67]	0.038	
Galacturonate	0.14		0.021	
Glucosamine	0.24		0.008	
Glucose	0.24	0.42[67]	0.067	
Glucose + 1 mmol.g_{Dw}^{-1}.hr^{-1} oxygen	0.27			
Glucuronate	0.14		0.024	
Mannose	0.16		0.103	
N-acetylgalactosamine	0.17		0.007	
N-acetylglucosamine	0.18		0.066	
N-acetylneuraminate	0		0	
Rhamnose	0.0012		0.033	
Ribose	0.23		0.040	
Xylose	0.23	0.16[67]	0.049	
Arabinan	0.23		0.037	Pectins
Arabinogalactan	0.23		0.045	
Homogalacturonan	0.12		0.066	
Pectic galactan	0.22		0.093	
Rhamnogalacturonan I	0.13		0.027	
Rhamnogalacturonan II	0.08		0.033	
Amylopectin	0.25		0.075/ 0.0056	Starch. fructan and α-glucans
Pullulan	0.25		0.063	
Dextran	0.26		0.108	
Inulin	0.24		0.005	
Levan	0.24		0.036	
F1alpha (Gal-beta-1,4-GlcNAc-beta-1,6-GalNAc-alpha-1-O-Ser/Thr)	0.15		0.015[a]	Mucin-type O-glycans
Core 4 ([GlcNAc-beta-1,6-], [GlcNAc-beta-1,3] GalNAc-alpha-1-O-Ser/Thr)	0.12		0.015[a]	
Core 5 (GalNAc-alpha-1,3-GalNAc-alpha-1-O-Ser/Thr)	0.11		0.015[a]	
Core 7 (GalNAc-alpha-1,6-GalNAc-alpha-1-O-Ser/Thr)	0.11		0.015[a]	
Core 8 (Gal-alpha-1,3-GalNAc-alpha-	0.17		0.015[a]	

1-O-Ser/Thr)				
GlcNAc-alpha-1,4-Core 1 (GlcNAc-alpha-1,4-Gal-beta-1,3-GalNAc-alpha-1-O-Ser/Thr)	0.15		0.015[a]	
GlcNAc-alpha-1,4-Core 2 ([GlcNAc-beta-1,6-], [GlcNAc-alpha-1,4-Gal-beta-1,3-]GalNAc-alpha-1-O-Ser/Thr)	0.14		0.015[a]	
Sialyl-Tn antigen (NeuAc-alpha-2,6-GalNAc-alpha-1-O-Ser/Thr)	0		0.015[a]	
Disialyl-T antigen ([NeuAc-alpha-2,6-], [NeuAc-alpha-2,3-Gal-beta-1,3-] GalNAc-alpha-1-O-Ser/Thr)	0.01		0.015[a]	
α-mannan	0.16		0.035	Host-derived glycans
Chondroitin sulfate A	0.05		0.065[b]	
Chondroitin sulfate B	0.02		0.065[b]	
Chondroitin sulfate	0.05		0.065[b]	
Hyaluronan	0.13		0.125	
Heparin	0.11		0.025	
Glycogen	0.25		0.050	
Laminarin[c]	0.23		0	Other
Cellobiose	0		0	

b) Secretion product flux rates. *In silico* secretion production rates are given in mmol.g_{Dw}^{-1}.hr^{-1}. Negative fluxes equal uptake. n.r. = not reported.

Carbon Source (*in silico* uptake rate 10 mmol.g_{Dw}^{-1}.hr^{-1})	**Acetate**	**Propionate**	**Succinate**	**CO_2**	**Hydrogen**
Glucose					
in silico	5.56	0 to 8.95	0 to 8.95	-1.53 to 7.41	2.10
in vivo[26]	4.2 mM	0.8 mM	4.8 mM	n.r.	n.r.
N-acetylglucosamine					
in silico	8.10 to 12.63	0 to 14.56	0 to 14.56	-5.82 to 8.75	< 0.001
in vivo[26]	12.6 mM	0.2 mM	3.6 mM	n.r.	n.r.
Glucuronate					
in silico	7.72 to 8.16	0 to 7.66	0 to 7.66	7.60 to 14.66	< 0.001
in vivo[26]	8.6 mM	0.7 mM	0.2 mM	n.r.	n.r.
Fructose					
in silico	5.56	0 to 8.95	0 to 8.95	-1.53 to 7.41	2.10
in vivo[75]	3.4 g/l	0 g/l	8.4 g/l	n.r.	n.r.

Table S6: Inborn errors of metabolism (IEMs) predicted to be lethal *in silico* on a Western Diet for the germfree mouse model.

Disease	NCBI Gene ID		Lethality *in silico*	Lethality *in vivo*	Ref.
	Mouse	Human			
AICA-ribosiduria	108147	471	Germfree mouse: lethal *BΘ* -associated mouse: nonlethal	Human: not lethal Mouse: not known	OMIM: 608688, [83]
Conradi-Hunermann syndrome	13595	10682	Lethal in *BΘ* - associated mouse and germfree mouse	Human: not lethal Mouse: lethal in homozygous males (X-linked gene)	OMIM: 302960, [84, 85]
D-bifunctional protein deficiency (DBPD)	15488	3295	Lethal in *BΘ* - associated mouse and germfree mouse	Human: lethal Mouse: pre-/ peri-/ postlethal	OMIM: 261515, [86]
Desmosterolosis	74754	1718	Lethal in *BΘ* - associated mouse and germfree mouse	Human: Usually lethal with occasional mild cases Mouse: lethal	OMIM: 602398, [87, 88]
Dihydrofolate reductase deficiency	13361	1719	Lethal in *BΘ* - associated mouse and germfree mouse	Human: Usually lethal with occasional mild cases Mouse: lethal	OMIM: 126060, [89, 90]
Lathosterolosis	235293	6309	Lethal in *BΘ* - associated mouse and germfree mouse	Human: not lethal Mouse lethal	OMIM: 607330, [91, 92]
Mevalonic aciduria	17855	4598	Lethal in *BΘ* - associated mouse and germfree mouse	Human: not lethal Mouse: not known	OMIM: 251170, [93]
Orotic aciduria	22247	7372	Germfree mouse: lethal *BΘ* -associated mouse: nonlethal	Human: not lethal Mouse: not known	OMIM: 258900, [94]
Ribose 5-phosphate isomerase deficiency	19895	22934	Germfree mouse: lethal *BΘ* -associated mouse: nonlethal	Human: not lethal Mouse: not known	OMIM: 608611, [95]
Smith-Lemli-Opitz syndrome	13360	1717	Lethal in *BΘ* - associated mouse and germfree mouse	Human : not lethal Mouse: lethal	OMIM: 270400, [96]

Table S13: Databases used to generate a knowledge base of *B. thetaiotaomicron.*

Name	**Link**
NCBI Entrez Gene	http://www.ncbi.nlm.nih.gov/gene
The SEED	http://theseed.uchicago.edu/FIG/
The SEED Viewer	http://seed-viewer.theseed.org/
KEGG	http://www.genome.jp/kegg/
UniProt	http://www.uniprot.org/
TransportDB	http://www.membranetransport.org/
BIGG Database	http://bigg.ucsd.edu/

Table S14: Knockout strains of *B. thetaiotaomicron* reported in literature, and comparison with predictions by iAH991.

Deleted gene	Growth conditions	Growth *in vivo*	Growth *in silico*	Ref.
BT_3763 - BT_3767	L-rhamnose as sole carbon source	no	no	[42]
BT_3763 - BT_3767	Glucose minimal medium	yes	yes	[42]
BT_3767	L-rhamnose as sole carbon source	yes, reduced levels of 1,2-propanediol formed	no	[42]
BT_3717	Glucose minimal medium	no	no	[161]
BT_3717	Glucose minimal medium with L-arginine supply	yes	yes	[161]
SusC (BT_3702) or SusD (BT_3701) or SusG (BT_3698)	Maltose or maltotriose as sole carbon source	yes	yes	[29, 97]
SusC (BT_3702) or SusD (BT_3701) or SusG (BT_3698)	Starch as sole carbon source	no	no	[29, 97]
SusG (BT_3698)	Maltoheptaose as sole carbon source	yes	yes	[29]
SusC (BT_3702) or SusD (BT_3701)	Maltoheptaose as sole carbon source	no	no	[29, 97]
BT_1663 or BT_4689	Pullulan as sole carbon source	yes	yes	[98]
BT_0238	Chondroitin sulfate A, B or C as sole carbon source	no	no	[35]
BT_0238	Glucose minimal medium	yes	yes	[35]
csuF (BT_3332)	Chondroitin sulfate A, B or C as sole carbon source	no	no	[99]
csuF (BT_3332)	Sulfated disaccharides as sole carbon source	yes	yes	[99]
BT_2970	Glucose minimal medium	yes	yes	[100]
BT_1760	Levan as sole carbon source	no	no	[69]
BT_1760	Glucose, fructose, sucrose or oligofructose as sole carbon source	yes	yes	[69]

[1] determined for *B. fragilis*

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Table S4: Quantitative comparison of metabolite exchange between $B\Theta$ and mouse with fluxes in germfree mouse model on three simulated diets.

Total metabolites that displayed changes above cutoff when comparing *B. thetaiotaomicron* -associated mouse with germfree mouse on at least one diet.

Only exchange reactions with a flux > 0,01 (absolute value) mmol g DW hr-1 * hr-1 and a difference of at least 10% between germfree and BΘ -associated mouse model were included in the analysis.

HP = high-protein diet; HF = high-fat diet; W = Western diet. Blue = higher flux in $B\Theta$-associated mouse. Red = higher flux in germfree mouse. Green = flux above cutoff in $B\Theta$-associated mouse only.

Name	Type	BIGG ID	*B. thetaiotaomicron* to lumen			Mouse to lumen			Mouse to outlet ("body fluids")			Lumen to outlet ("faeces")		
			HP	HF	W	HP	HF	W	HP	HF	W	HP	HF	W
1,2-Ethanediol	Microbial co-metabolites	12ethd												
(R)-Propane-1,2-diol	Microbial co-metabolites	12ppd-R												
(S)-Propane-1,2-diol	Microbial co-metabolites	12ppd-S												
1 acyl phosphoglycerol	Phospholipid metabolism	1glyc_hs												
1-Methylnicotinamide	Vitamins and cofactors	1mncam												
24R,25-Dihydroxyvitamin D3	Vitamins and cofactors	2425dhvitd3												
25-Hydroxyvitamin D3	Vitamins and cofactors	25hvitd3												
2-Methylcitrate	Other	2mcit												
3',5'-Cyclic GMP	Hormones, neurotransmitters and signalling molecules	35cgmp												
L-3-Amino-isobutanoate	Amino acid metabolism	3aib												
D-3-Amino-isobutanoate	Amino acid metabolism	3aib-D												
3-Methylimidazoleacetic acid	Amino acid metabolism	3mlda												
4-Aminobutanoate	Hormones, neurotransmitters and signalling molecules	4abut												
4-Hydroxyphenylacetate	Amino acid metabolism	4hphac												
4-Methylpentanal	Other	4mptnl												
5alpha-Dihydrotestosterone	Hormones, neurotransmitters and signalling molecules	5adtststerone												
5alpha-Dihydrotestosterone glucuronide	Hormones, neurotransmitters and signalling molecules	5adtststeroneglc												
5alpha-Dihydrotestosterone sulfate	Hormones, neurotransmitters and signalling molecules	5adtststerones												
5-Hydroxy-L-tryptophan	Amino acid metabolism	5htrp												
5-Methyltetrahydrofolate	Vitamins and cofactors	5mthf												
6 beta hydroxy testosterone	Hormones, neurotransmitters and signalling molecules	6htststerone												
L-Arabinitol	Monosaccharides	abt												
Acetate	Short chain fatty acids	ac												
Acetoacetate	Small molecules and ions	acac												
Acetaldehyde	Small molecules and ions	acald												
Acetol	Microbial co-metabolites	acetol												
Acetone	Small molecules and ions	acetone												
N-Acetyl-D-galactosamine	Monosaccharides	acgal												
N-Acetyl-D-glucosamine	Monosaccharides	acgam												
Acetylcholine	Hormones, neurotransmitters and signalling molecules	ach												
sialyl (1,3) sialyl (2,6) galactosylgloboside	Glycolipid and sphingolipid metabolism	acn13acngalgbside_hs												
sialyl (2,3) sialyl (2,6) galactosylgloboside	Glycolipid and sphingolipid metabolism	acn23acngalgbside_hs												
3',8'-LD1	Glycolipid and sphingolipid metabolism	acnacngal14acglcgalgluside_hs												
Disialyl galactosylgloboside	Glycolipid and sphingolipid metabolism	acnacngalgbside_hs												
N-acetylneuraminate	Monosaccharides	acnam												
VI3NeuAc-nLc6Cer	Glycolipid and sphingolipid metabolism	acngalacglcgal14acglcgalgluside_hs												
Adenine	Purine and pyrimidine metabolism	ade												
Adenosine	Purine and pyrimidine metabolism	adn												
adrenic acid	Fatty acids	adrn												
Adrenaline	Hormones, neurotransmitters and signalling molecules	adrnl												
2-Oxoglutarate	Energy metabolites	akg												
B-alanine	Amino acids	ala-B												
D-alanine	Amino acids	ala-D												
L-alanine	Amino acids	ala-L												
Aldosterone	Hormones, neurotransmitters and signalling molecules	aldstrn												
Androsterone	Hormones, neurotransmitters and signalling molecules	andrstrn												
20alpha-Hydroxyprogesterone	Hormones, neurotransmitters and signalling molecules	aprgstrn												
L-arabinose	Pentoses	arab-L												
Arachidic acid	Fatty acids	arach												
arachidonic acid	Fatty acids	arachd												
Arginylarginine	Dipeptides	argarg												
L-arginine	Amino acids	arg-L												
L-asparagine	Amino acids	asn-L												
L-aspartate	Amino acids	asp-L												
(R)-3-Hydroxybutanoate	Energy metabolites	bhb												
Bilirubin	Vitamins and cofactors	bilirub												
cAMP	Hormones, neurotransmitters and signalling molecules	camp												
L-Carnosine	Dipeptides	carn												
Cys-Gly	Dipeptides	cgly												
Choline	Osmoprotectants	chol												
Cholesterol	Cholesterol metabolism	chsterol												
Citrate	Energy metabolites	cit												
Clupanodonic acid	Fatty acids	CLPND												
Carbon monooxide	Gases	co												
Carbon dioxide	Gases	co2												
Creatine	Energy metabolites	creat												
Ceramide 1-phosphate	Hormones, neurotransmitters and signalling molecules	crmp_hs												
Cortisol	Hormones, neurotransmitters and signalling molecules	crtsl												
Corticosterone	Hormones, neurotransmitters and signalling molecules	crtstrn												
Cervonic acid, C22:6 n-3	Fatty acids	crvnc												
L-cysteine	Amino acids	cys-L												
Cytidine	Purine and pyrimidine metabolism	cytd												
Deoxyadenosine	Purine and pyrimidine metabolism	dad-2												
Diacylglycerol	Hormones, neurotransmitters and signalling molecules	dag_hs												
Docosa-4,7,10,13,16-pentaenoic acid (n-6)	Fatty acids	dcsptn1												
Deoxycytidine	Purine and pyrimidine metabolism	dcyt												
Chenodeoxyglycocholate	Bile acid metabolism	dgchol												
Deoxyguanosine	Purine and pyrimidine metabolism	dgsn												
Deoxyinosine	Purine and pyrimidine metabolism	din												
Dihomo-gamma-linolenic acid (n-6)	Fatty acids	dlnlcg												
Dopamine	Hormones, neurotransmitters and signalling molecules	dopa												
Deoxyribose	Monosaccharides	drib												
Disialyl-T antigen	O-glycans	dsT_antigen												
4-Deoxy-L-threo-5-hexosulose uronate	Polysaccharide digestion	dt5hsu												
Deoxyuridine	Purine and pyrimidine metabolism	duri												
Eicosatetraenoic acid	Fatty acids	eicostet												
Elaidic acid	Fatty acids	elaid												
Estradiol	Hormones, neurotransmitters and signalling molecules	estradiol												
Ethanolamine	Energy metabolites	etha												
Ethanol	Energy metabolites	etoh												
Folate	Vitamins and cofactors	fol												
Formate	Energy metabolites	for												
D-Fructose	Monosaccharides	fru												
III3Fuc-nLc6Cer	Glycolipid and sphingolipid metabolism	fuc13galacglcgal14acglcgalgluside_hs												
IV3-a-NeuAc,III3-a-Fuc-nLc4Cer	Glycolipid and sphingolipid metabolism	fucacngal14acglcgalgluside_hs												
Ley glycolipid	Glycolipid and sphingolipid metabolism	fucfuc12gal14acglcgalgluside_hs												
V3Fuc,III3Fuc-nLc6Cer	Glycolipid and sphingolipid metabolism	fucfuc132galacglcgal14acglcgalgluside_hs												
(Gal)4 (Glc)1 (GlcNAc)3 (LFuc)3 (Cer)1	Glycolipid and sphingolipid metabolism	fucfucfucgalacglc13galacglcgal14acglcgalgluside_hs												
(Gal)3 (Glc)1 (GlcNAc)2 (LFuc)3 (Cer)1	Glycolipid and sphingolipid metabolism	fucfucfucgalacglcgal14acglcgalgluside_hs												
Lacto-N-fucopentaosyl III ceramide	Glycolipid and sphingolipid metabolism	fucgal14acglcgalgluside_hs												
Fucosyl galactosylgloboside	Glycolipid and sphingolipid metabolism	fucgalgbside_hs												
L-fucose	Monosaccharides	fuc-L												
Fumarate	Energy metabolites	fum												
D-Galactose	Monosaccharides	gal												
Gal-GlcNAc-Gal globoside	Glycolipid and sphingolipid metabolism	galacglcgalgbside_hs												
Gal-Gal-Gal-Gal-Gal-Glc-Cer	Glycolipid and sphingolipid metabolism	galgalgalthcrm_hs												
D-galacturonate	Monosaccharides	galur												
globoside	Glycolipid and sphingolipid metabolism	gbside_hs												
Glycocholate	Bile acid metabolism	gchola												
GD1beta	Glycolipid and sphingolipid metabolism	gd1b2_hs												
GD1c	Glycolipid and sphingolipid metabolism	gd1c_hs												
Glycochenodeoxycholate	Bile acid metabolism	gdchola												
D-glucose	Monosaccharides	glc-D												
D-glucuronate	Monosaccharides	glcur												
D-glutamine	Amino acids	gln-L												
5-L-Glutamyl-L-alanine	Amino acid metabolism	gluala												
Glycine	Amino acids	gly												
Glycine betaine	Osmoprotectants	glyb												
Glycerol	Energy metabolites	glyc												
(S)-Glycerate	Other	glyc-S												
Glycylglycine	Dipeptides	glygly												
Glycylsarcosine	Dipeptides	glysar												
GlcNAc-alpha-1,4-Core 1	O-glycans	gncore1												
GP1c	Glycolipid and sphingolipid metabolism	gp1c_hs												
GP1c alpha	Glycolipid and sphingolipid metabolism	gp1calpha_hs												
GQ1b	Glycolipid and sphingolipid metabolism	gq1b_hs												
GQ1balpha	Glycolipid and sphingolipid metabolism	gq1balpha_hs												
Guanosine	Purine and pyrimidine metabolism	gsn												
GT1a	Glycolipid and sphingolipid metabolism	gt1a_hs												
Guanine	Purine and pyrimidine metabolism	gua												
Proton	Small molecules and ions	h												
Hydrogen	Gases	h2												
Water	Small molecules and ions	h2o												
Hydrogen peroxide	Small molecules and ions	h2o2												
Hyaluronan	Polysaccharides	ha												
Hyaluronan degradation product	Polysaccharide digestion	ha_deg1												
Hyaluronan biosynthesis, precursor 1	Polysaccharide digestion	ha_pre1												
Bicarbonate	Small molecules and ions	hco3												
Hexadecanoate (n-C16:0)	Fatty acids	hdca												
Hexadecenoate (n-C16:1)	Fatty acids	hdcea												
4,17 dihydroxy estradiol	Hormones, neurotransmitters and signalling molecules	hestratriol												
L-histidine	Amino acids	his-L												
Histamine	Hormones, neurotransmitters and signalling molecules	hista												
Hypoxanthine	Purine and pyrimidine metabolism	hxan												
L-isoleucine	Amino acids	ile-L												
myo-Inositol	Monosaccharides	inost												
Inosine	Purine and pyrimidine metabolism	ins												
Isobutyrate	Energy metabolites	isobut												
Isocaproate	Energy metabolites	isocapr												
Isovalerate	Energy metabolites	isoval												
D-lactate	Energy metabolites	lac-D												
L-lactate	Energy metabolites	lac-L												
Lactose	Disaccharides	lcts												
Leukotriene A4	Hormones, neurotransmitters and signalling molecules	leuktrA4												
Leukotriene B4	Hormones, neurotransmitters and signalling molecules	leuktrB4												
Leukotriene D4	Hormones, neurotransmitters and signalling molecules	leuktrD4												
leukotriene E4	Hormones, neurotransmitters and signalling molecules	leuktrE4												
leukotriene F4	Hormones, neurotransmitters and signalling molecules	leuktrF4												
L-leucine	Amino acids	leu-L												
Levanbiose	Polysaccharide digestion	levanb												
Levantriose	Polysaccharide digestion	levantr												
Levantetraose	Polysaccharide digestion	levanttr												
Laminaribiose	Polysaccharide digestion	lmn2												
linoelaidic acid (all trans C18:2)	Fatty acids	lneldc												
linoleic acid (all cis C18:2) n-6	Fatty acids	lnlc												
alpha-Linolenic acid, C18:3, n-3	Fatty acids	lnlnca												
gamma-linolenic acid	Fatty acids	lnlncg												
lysophosphatidylcholine	Phospholipid metabolism	lpchol_hs												
L-lysine	Amino acids	lys-L												
monoacylglycerol 2	Phospholipid metabolism	mag_hs												
Maltose	Disaccharides	malt												
Maltotriose	Polysaccharide digestion	malttr												
D-mannose	Monosaccharides	man												
Mannobiose (beta-1,4)	Polysaccharide digestion	manb												
mannotriose (beta-1,4)	Polysaccharide digestion	mantr												
mannotetraose	Polysaccharide digestion	manttr												
Methanol	Small molecules and ions	meoh												
Metanephrine	Hormones, neurotransmitters and signalling molecules	mepi												
L-methionine	Amino acids	met-L												
Methylglyoxal	Amino acid metabolism	mthgxl												
Niacin	Vitamins and cofactors	nac												
Nicotinamide	Vitamins and cofactors	ncam												
Ammonium	Small molecules and ions	nh4												
Nicotinamide mononucleotide	Vitamins and cofactors	nmn												
Nitric oxide	Small molecules and ions	no												
Norepinephrine	Hormones, neurotransmitters and signalling molecules	nrpphr												
Superoxide anion	Small molecules and ions	o2s												
9-O-Acetylated GD3	Glycolipid and sphingolipid metabolism	oagd3_hs												
9-O-Acetylated GT3	Glycolipid and sphingolipid metabolism	oagt3_hs												
octadecanoate (n-C18:0)	Fatty acids	ocdca												
octadecenoate (n-C18:1)	Fatty acids	ocdcea												
octanoate (n-C8:0)	Fatty acids	octa												
Hydroxide ion	Small molecules and ions	oh1												
Ornithine	Amino acids	orn												
Oxalate	Other	oxa												
Phenylacetate	Microbial co-metabolites	pac												
Phosphatidylcholine	Phospholipid metabolism	pchol_hs												
phosphatidylethanolamine	Phospholipid metabolism	pe_hs												
phosphatidylglycerol	Phospholipid metabolism	pglyc_hs												
alpha-N-Phenylacetyl-L-glutamine	Amino acid metabolism	pheacgln												
Phenylalanylarginine	Dipeptides	phearg												
L-phenylalanine	Amino acids	phe-L												
Panthothenate	Vitamins and cofactors	pnto-R												
Propionate	Short chain fatty acids	ppa												
Progesterone	Hormones, neurotransmitters and signalling molecules	prgstrn												
L-proline	Amino acids	pro-L												
Prostaglandin D2	Hormones, neurotransmitters and signalling molecules	prostgd2												
phosphatidylserine	Phospholipid metabolism	ps_hs												
Putrescine	Microbial co-metabolites	ptrc												
Pyruvate	Energy metabolites	pyr												
D-ribose	Monosaccharides	rib-D												
Riboflavin	Vitamins and cofactors	ribflv												
R total	Phospholipid metabolism	Rtotal												
R total 2 position	Phospholipid metabolism	Rtotal2												
R total 3 position	Phospholipid metabolism	Rtotal3												
PA6	N-glycans	s2l2fn2m2masn												
de-Fuc form of PA6 (w/o peptide linkage)	N-glycans	s2l2n2m2m												
de-Fuc form of PA6	N-glycans	s2l2n2m2masn												
D-sorbitol	Monosaccharides	sbt-D												
Protein-linked serine or threonine residue (O-glycosylation site)	Polysaccharide digestion	Ser_Thr												
L-serine	Amino acids	ser-L												
L-sulfolactate	Amino acid metabolism	sl-L												
Sulfate	Small molecules and ions	so4												
sphingosylphosphorylcholine	Glycolipid and sphingolipid metabolism	spc_hs												
Sphinganine 1-phosphate	Glycolipid and sphingolipid metabolism	sph1p												
Sphingosine 1-phosphate	Hormones, neurotransmitters and signalling molecules	sphs1p												
Spermidine	Microbial co-metabolites	spmd												
Serotonin	Hormones, neurotransmitters and signalling molecules	srtn												
stearidonic acid C18:4, n-3	Fatty acids	strdnc												
Succinate	Energy metabolites	succ												
T antigen (core 1)	O-glycans	T_antigen												
triacylglycerol	Phospholipid metabolism	tag_hs												
Taurine	Osmoprotectants	taur												
Taurocholate	Bile acid metabolism	tchola												
Taurochenodeoxycholate	Bile acid metabolism	tdchola												
5,6,7,8-Tetrahydrofolate	Vitamins and cofactors	thf												
Thiamin	Vitamins and cofactors	thm												
Thiamin monophosphate	Vitamins and cofactors	thmmp												
Thiamin triphosphate	Vitamins and cofactors	thmtp												
L-threonine	Amino acids	thr-L												
Thymine	Purine and pyrimidine metabolism	thym												
timnodonic acid C20:5, n-3	Fatty acids	tmndnc												
Tn antigen	O-glycans	Tn_antigen												
L-tryptophan	Amino acids	trp-L												
Testosterone	Hormones, neurotransmitters and signalling molecules	tststerone												
testosterone sulfate	Hormones, neurotransmitters and signalling molecules	tststerones												
Thromboxane A2	Hormones, neurotransmitters and signalling molecules	txa2												
L-tyrosine	Amino acids	tyr-L												
4-(4-Deoxy-alpha-D-gluc-4-enuronosyl)-D-galacturonate	Polysaccharide digestion	unsdigalur												
Uracil	Purine and pyrimidine metabolism	ura												
Urate	Purine and pyrimidine metabolism	urate												
Urea	Small molecules and ions	urea												
Uridine	Purine and pyrimidine metabolism	uri												
vaccenic acid	Fatty acids	vacc												
L-valine	Amino acids	val-L												
Vitamin D3	Vitamins and cofactors	vitd3												
omega hydroxy hexadecanoate (n-C16:0)	Fatty acids	whhdca												
omega hydroxy tetradecanoate (n-C14:0)	Fatty acids	whttdca												
Xanthine	Purine and pyrimidine metabolism	xan												
cholesterol ester	Cholesterol metabolism	xolest_hs												
cholesterol ester (from FULLR2)	Cholesterol metabolism	xolest2_hs												
7-alpha,24(S)-Dihydroxycholesterol	Cholesterol metabolism	xoltri24												
7-alpha,25-Dihydroxycholesterol	Cholesterol metabolism	xoltri25												
7-alpha,27-Dihydroxycholesterol	Cholesterol metabolism	xoltri27												
D-xylose	Monosaccharides	xyl-D												
Xylitol	Monosaccharides	xylt												

Table S5: Joint model analysis of flux differences between competition and non-competition phases on three diets.

Cutoff: at least twofold change in flux or flux is enabled vs zero flux, at least 0,01 flux in at least one condition and for both species (absolute value, rounded)

Essential for mouse
Production
Consumption

High-protein diet

B. thetaiotaomicron to lumen

Name	Type	BIGG ID	Exchange reaction	Flux when mouse growth is optimal		Flux in the middle of the competition plateau		Flux when BT growth is optimal	
				minFlux	maxFlux	minFlux	maxFlux	minFlux	maxFlux
L-alanine	Amino acids	ala-L	IEX_BTala-L[u]tr	-1,50	5,62	-1,50	169,82	-1,50	0,63
L-arginine	Amino acids	arg-L	IEX_BTarg-L[u]tr	-0,75	0,00	-0,75	0,00	-0,75	-0,36
L-asparagine	Amino acids	asn-L	IEX_BTasn-L[u]tr	-1,13	-0,63	-1,13	5,72	-1,13	-0,75
L-Aspartate	Amino acids	asp-L	IEX_BTasp-L[u]tr	-1,13	-0,63	-1,13	5,72	-1,13	-0,72
L-cysteine	Amino acids	cys-L	IEX_BTcys-L[u]tr	0,34	0,99	0,77	0,93	0,14	0,86
L-glutamine	Amino acids	gln-L	IEX_BTgln-L[u]tr	-0,90	1,31	-0,90	78,91	-0,90	-0,55
L-glutamate	Amino acids	glu-L	IEX_BTglu-L[u]tr	-0,90	0,00	-0,16	0,00	-0,90	-0,42
Glycine	Amino acids	gly	IEX_BTgly[u]tr	-2,14	0,04	-2,25	23,80	-2,25	-1,00
L-histidine	Amino acids	his-L	IEX_BThis-L[u]tr	-0,32	0,03	-0,47	15,11	-0,69	-0,50
L-isoleucine	Amino acids	ile-L	IEX_BTile-L[u]tr	0,23	0,32	-0,11	-0,03	-0,59	-0,49
L-leucine	Amino acids	leu-L	IEX_BTleu-L[u]tr	0,96	1,05	0,36	0,52	-0,52	-0,45
L-lysine	Amino acids	lys-L	IEX_BTlys-L[u]tr	0,98	1,04	0,37	0,53	-0,46	-0,40
L-methionine	Amino acids	met-L	IEX_BTmet-L[u]tr	-0,01	0,01	-0,12	-0,10	-0,22	-0,20
L-phenylalanine	Amino acids	phe-L	IEX_BTphe-L[u]tr	0,17	0,25	-0,06	-0,04	-0,27	-0,23
Ammonium	Small molecules and ions	nh4	IEX_BTnh4[u]tr	-2,96	1,16	-100,00	41,69	5,11	8,85
Phosphate	Small molecules and ions	pi	IEX_BTpi[u]tr	-0,10	-0,09	-1,27	-1,26	-2,43	-2,42
L-proline	Amino acids	pro-L	IEX_BTpro-L[u]tr	-0,90	1,12	-0,90	84,95	-0,90	-0,13
L-serine	Amino acids	ser-L	IEX_BTser-L[u]tr	-1,50	0,43	-1,50	128,53	-1,50	-0,47
L-Threonine	Amino acids	thr-L	IEX_BTthr-L[u]tr	0,05	0,07	-0,37	-0,35	-0,97	-0,94
L-tryptophan	Amino acids	trp-L	IEX_BTtrp-L[u]tr	0,00	0,02	-0,04	-0,02	-0,08	-0,06
L-tyrosine	Amino acids	tyr-L	IEX_BTtyr-L[u]tr	-0,01	0,09	-0,10	-0,06	-0,19	-0,16
L-valine	Amino acids	val-L	IEX_BTval-L[u]tr	0,36	0,47	-0,08	0,00	-0,73	-0,59

Lumen to mouse

Exchange reaction	Flux when mouse growth is optimal		Flux in the middle of the competition plateau		Flux when BT growth is optimal	
	minFlux	maxFlux	minFlux	maxFlux	minFlux	maxFlux
IEX_MMala-L[u]tr	-7,12	0,00	-171,32	0,00	-2,13	0,00
IEX_MMarg-L[u]tr	-0,75	0,00	-0,75	0,00	-0,39	0,00
IEX_MMasn-L[u]tr	-0,49	0,00	-6,84	0,00	-0,38	0,00
IEX_MMasp-L[u]tr	-0,49	0,00	-6,84	0,00	-0,41	0,00
IEX_MMcys-L[u]tr	-2,49	-1,84	-2,43	-2,27	-2,36	-1,64
IEX_MMgln-L[u]tr	-2,21	0,00	-79,81	0,00	-0,35	0,00
IEX_MMglu-L[u]tr	-0,90	0,00	-0,90	-0,24	-0,48	0,00
IEX_MMgly[u]tr	-2,29	-0,11	-26,05	0,00	-1,25	0,00
IEX_MMhis-L[u]tr	-0,78	-0,43	-15,86	-0,28	-0,25	-0,06
IEX_MMile-L[u]tr	-1,07	-0,98	-0,72	-0,64	-0,26	-0,14
IEX_MMleu-L[u]tr	-1,80	-1,71	-1,27	-1,11	-0,30	-0,23
IEX_MMlys-L[u]tr	-1,79	-1,73	-1,28	-1,12	-0,35	-0,27
IEX_MMmet-L[u]tr	-0,91	-0,42	-0,80	-0,27	-0,70	-0,06
IEX_MMnh4[u]tr	-101,16	-2,34	-141,69	0,00	-108,85	0,00
IEX_MMphe-L[u]tr	-0,74	-0,66	-0,46	-0,43	-0,27	-0,24
IEX_MMpi[u]tr	-99,91	-1,08	-98,74	-0,70	-97,58	-0,14
IEX_MMpro-L[u]tr	-2,02	0,00	-85,85	0,00	-0,77	0,00
IEX_MMser-L[u]tr	-1,93	0,00	-130,03	0,00	-1,03	0,00
IEX_MMthr-L[u]tr	-1,20	-1,17	-0,78	-0,76	-0,18	-0,15
IEX_MMtrp-L[u]tr	-0,42	-0,39	-0,39	-0,36	-0,35	-0,31
IEX_MMtyr-L[u]tr	-0,59	-0,48	-0,44	-0,39	-0,33	-0,29
IEX_MMval-L[u]tr	-1,37	-1,26	-0,90	-0,82	-0,31	-0,17

High-fat diet

B. thetaiotaomicron to lumen

Name	Type	BIGG ID	Exchange reaction	Flux when mouse growth is optimal		Flux in the middle of the competition plateau		Flux when BT growth is optimal	
				minFlux	maxFlux	minFlux	maxFlux	minFlux	maxFlux
L-alanine	Amino acids	ala-L	IEX_BTala-L[u]tr	-0,40	46,67	-0,40	164,02	-0,40	6,58
L-arginine	Amino acids	arg-L	IEX_BTarg-L[u]tr	-0,20	0,00	-0,20	-0,12	-0,20	-0,15
L-asparagine	Amino acids	asn-L	IEX_BTasn-L[u]tr	-0,30	-0,16	-0,30	-0,22	-0,30	-0,02
L-Aspartate	Amino acids	asp-L	IEX_BTasp-L[u]tr	-0,30	-0,18	-0,30	-0,22	-0,30	0,34
L-cysteine	Amino acids	cys-L	IEX_BTcys-L[u]tr	0,00	0,79	-0,12	0,76	-0,30	0,16
D-Fructose	Monosaccharides	fru	IEX_BTfru[u]tr	-0,10	0,69	-0,10	0,69	-0,10	0,15
D-Glucose	Monosaccharides	glc-D	IEX_BTglc-D[u]tr	-0,10	0,69	-0,10	0,69	-0,10	0,15
L-glutamine	Amino acids	gln-L	IEX_BTgln-L[u]tr	-0,24	0,48	-0,24	42,41	-0,24	0,16
L-glutamate	Amino acids	glu-L	IEX_BTglu-L[u]tr	-0,19	0,00	-0,06	0,00	-0,24	0,00
Glycine	Amino acids	gly	IEX_BTgly[u]tr	-0,14	0,55	-0,28	8,91	-0,60	0,03
L-histidine	Amino acids	his-L	IEX_BThis-L[u]tr	0,21	0,79	0,09	9,05	-0,09	-0,05
L-isoleucine	Amino acids	ile-L	IEX_BTile-L[u]tr	0,73	0,79	0,45	0,53	0,05	0,21
L-leucine	Amino acids	leu-L	IEX_BTleu-L[u]tr	1,42	1,48	0,93	11,93	0,23	0,34
L-lysine	Amino acids	lys-L	IEX_BTlys-L[u]tr	1,43	1,47	0,94	0,98	0,23	0,31
L-methionine	Amino acids	met-L	IEX_BTmet-L[u]tr	0,16	0,18	0,04	0,05	-0,13	-0,11
Ammonium	Small molecules and ions	nh4	IEX_BTnh4[u]tr	-28,12	-23,23	-100,00	-14,71	12,43	15,86
L-phenylalanine	Amino acids	phe-L	IEX_BTphe-L[u]tr	0,50	0,95	0,31	0,69	0,03	0,17
Phosphate	Small molecules and ions	pi	IEX_BTpi[u]tr	-0,40	-0,39	-1,37	-1,36	-2,35	-2,33
L-proline	Amino acids	pro-L	IEX_BTpro-L[u]tr	-0,24	0,20	-0,24	67,31	-0,24	-0,01
L-serine	Amino acids	ser-L	IEX_BTser-L[u]tr	-0,40	1,04	-0,40	82,90	-0,40	-0,11
L-Threonine	Amino acids	thr-L	IEX_BTthr-L[u]tr	0,81	0,83	0,47	0,49	-0,01	0,02
L-tryptophan	Amino acids	trp-L	IEX_BTtrp-L[u]tr	0,02	0,05	-0,02	0,01	-0,07	-0,05
L-tyrosine	Amino acids	tyr-L	IEX_BTtyr-L[u]tr	-0,04	0,43	-0,11	0,27	-0,13	0,03
L-valine	Amino acids	val-L	IEX_BTval-L[u]tr	0,95	1,00	0,59	0,63	0,08	0,33

Lumen to mouse

Exchange reaction	Flux when mouse growth is optimal		Flux in the middle of the competition plateau		Flux when BT growth is optimal	
	minFlux	maxFlux	minFlux	maxFlux	minFlux	maxFlux
IEX_MMala-L[u]tr	-47,07	0,00	-164,42	0,00	-6,98	0,00
IEX_MMarg-L[u]tr	-0,20	0,00	-0,08	0,00	-0,05	0,00
IEX_MMasn-L[u]tr	-0,14	0,00	-0,08	0,00	-0,28	0,00
IEX_MMasp-L[u]tr	-0,12	0,00	-0,08	0,00	-0,64	0,00
IEX_MMcys-L[u]tr	-1,19	-0,46	-1,16	-0,28	-0,56	-0,18
IEX_MMfru[u]tr	-0,79	0,00	-0,79	0,00	-0,25	0,00
IEX_MMglc-D[u]tr	-0,79	0,00	-0,79	0,00	-0,25	0,00
IEX_MMgln-L[u]tr	-0,72	0,00	-42,63	0,00	-0,40	0,00
IEX_MMglu-L[u]tr	-0,24	-0,05	-0,24	-0,16	-0,24	0,00
IEX_MMgly[u]tr	-1,15	-0,46	-9,51	-0,32	-0,63	0,00
IEX_MMhis-L[u]tr	-0,99	-0,41	-9,25	-0,29	-0,15	-0,11
IEX_MMile-L[u]tr	-0,99	-0,93	-0,73	-0,65	-0,41	-0,25
IEX_MMleu-L[u]tr	-1,68	-1,62	-12,13	-1,13	-0,54	-0,43
IEX_MMlys-L[u]tr	-1,67	-1,63	-1,18	-1,14	-0,51	-0,43
IEX_MMmet-L[u]tr	-0,42	-0,40	-0,29	-0,28	-0,13	-0,11
IEX_MMnh4[u]tr	-76,77	0,00	-85,29	0,00	-115,86	-27,33
IEX_MMphe-L[u]tr	-1,09	-0,63	-0,82	-0,44	-0,31	-0,17
IEX_MMpi[u]tr	-99,61	-1,02	-98,64	-0,71	-97,67	-0,27
IEX_MMpro-L[u]tr	-0,44	0,00	-67,55	0,00	-0,23	0,00
IEX_MMser-L[u]tr	-1,44	0,00	-83,30	0,00	-0,29	0,00
IEX_MMthr-L[u]tr	-1,13	-1,11	-0,79	-0,77	-0,32	-0,29
IEX_MMtrp-L[u]tr	-0,16	-0,13	-0,11	-0,09	-0,05	-0,03
IEX_MMtyr-L[u]tr	-0,56	-0,09	-0,40	-0,02	-0,17	0,00
IEX_MMval-L[u]tr	-1,24	-1,19	-0,87	-0,83	-0,57	-0,32

Western diet

B. thetaiotaomicron to lumen

Name	Type	BIGG ID	Exchange reaction	Flux when mouse growth		Flux in the middle of the		Flux when BT growth is	
				minFlux	maxFlux	minFlux	maxFlux	minFlux	maxFlux
L-alanine	Amino acids	ala-L	IEX_BTala-L[u]tr	-0,30	13,29	-0,30	159,56	-0,30	3,72
L-arginine	Amino acids	arg-L	IEX_BTarg-L[u]tr	-0,15	0,00	-0,15	0,00	-0,15	-0,08
L-asparagine	Amino acids	asn-L	IEX_BTasn-L[u]tr	-0,23	0,12	-0,23	4,14	-0,23	0,05
L-Aspartate	Amino acids	asp-L	IEX_BTasp-L[u]tr	-0,23	0,28	-0,23	4,14	-0,23	0,34
L-cysteine	Amino acids	cys-L	IEX_BTcys-L[u]tr	0,21	0,72	0,53	0,70	-0,26	0,70
D-Fructose	Monosaccharides	fru	IEX_BTfru[u]tr	-1,00	6,95	-1,00	6,95	-1,00	-0,20
D-Glucose	Monosaccharides	glc-D	IEX_BTglc-D[u]tr	-1,00	6,95	-1,00	6,95	-1,00	-0,20
L-glutamine	Amino acids	gln-L	IEX_BTgln-L[u]tr	-0,18	2,50	-0,18	77,09	-0,18	0,29
Glycine	Amino acids	gly	IEX_BTgly[u]tr	-0,45	0,74	-0,45	20,35	-0,45	0,19
L-histidine	Amino acids	his-L	IEX_BThis-L[u]tr	0,28	0,35	0,13	14,19	-0,09	-0,05
L-isoleucine	Amino acids	ile-L	IEX_BTile-L[u]tr	0,84	0,92	0,49	0,57	-0,02	0,09
L-leucine	Amino acids	leu-L	IEX_BTleu-L[u]tr	1,57	1,66	0,96	1,13	0,07	0,15
L-lysine	Amino acids	lys-L	IEX_BTlys-L[u]tr	1,58	1,64	0,97	1,14	0,07	0,14
Maltose	Di- and polysaccharides	malt	IEX_BTmalt[u]tr	-0,50	0,00	-0,50	0,75	-0,50	-0,26
L-methionine	Amino acids	met-L	IEX_BTmet-L[u]tr	0,24	0,26	0,09	0,11	-0,13	-0,10
Ammonium	Small molecules and ions	nh4	IEX_BTnh4[u]tr	-18,87	-15,09	-100,00	33,02	-9,81	-6,85
L-phenylalanine	Amino acids	phe-L	IEX_BTphe-L[u]tr	0,57	0,70	0,33	0,42	-0,01	0,07
Phosphate	Small molecules and ions	pi	IEX_BTpi[u]tr	-0,26	-0,25	-1,41	-1,40	-2,56	-2,55
L-proline	Amino acids	pro-L	IEX_BTpro-L[u]tr	-0,18	0,78	-0,18	80,20	-0,18	0,16
L-serine	Amino acids	ser-L	IEX_BTser-L[u]tr	-0,30	0,46	-0,30	114,66	-0,30	0,27
Sucrose	Di- and polysaccharides	sucr	IEX_BTsucr[u]tr	-0,50	0,00	-0,50	0,00	-0,50	-0,26
L-Threonine	Amino acids	thr-L	IEX_BTthr-L[u]tr	0,95	0,98	0,54	0,56	-0,07	-0,05
L-tryptophan	Amino acids	trp-L	IEX_BTtrp-L[u]tr	0,05	0,08	0,01	0,03	-0,06	-0,04
L-tyrosine	Amino acids	tyr-L	IEX_BTtyr-L[u]tr	0,32	0,49	0,18	0,30	-0,10	0,00
L-valine	Amino acids	val-L	IEX_BTval-L[u]tr	1,09	1,19	0,64	0,72	-0,02	0,16

Lumen to mouse

Exchange reaction	Flux when mouse growth		Flux in the middle of the		Flux when BT growth is	
	minFlux	maxFlux	minFlux	maxFlux	minFlux	maxFlux
IEX_MMala-L[u]tr	-13,59	0,00	-159,86	0,00	-4,02	0,00
IEX_MMarg-L[u]tr	-0,15	0,00	-0,15	0,00	-0,07	0,00
IEX_MMasn-L[u]tr	-0,35	0,00	-4,36	0,00	-0,28	0,00
IEX_MMasp-L[u]tr	-0,50	0,00	-4,36	0,00	-0,57	0,00
IEX_MMcys-L[u]tr	-1,02	-0,51	-1,00	-0,83	-1,00	-0,04
IEX_MMfru[u]tr	-7,95	0,00	-7,95	0,00	-0,80	0,00
IEX_MMglc-D[u]tr	-7,95	0,00	-7,95	0,00	-0,80	0,00
IEX_MMgln-L[u]tr	-2,68	0,00	-77,27	0,00	-0,47	0,00
IEX_MMgly[u]tr	-1,19	0,00	-20,80	0,00	-0,64	0,00
IEX_MMhis-L[u]tr	-0,50	-0,43	-14,34	-0,28	-0,10	-0,06
IEX_MMile-L[u]tr	-1,07	-0,99	-0,72	-0,64	-0,24	-0,15
IEX_MMleu-L[u]tr	-1,81	-1,72	-1,28	-1,11	-0,30	-0,22
IEX_MMlys-L[u]tr	-1,79	-1,73	-1,29	-1,12	-0,29	-0,22
IEX_MMmalt[u]tr	-0,50	0,00	-1,25	0,00	-0,24	0,00
IEX_MMmet-L[u]tr	-0,44	-0,42	-0,29	-0,27	-0,08	-0,05
IEX_MMnh4[u]tr	-84,91	-8,01	-133,02	0,00	-93,15	-4,40
IEX_MMphe-L[u]tr	-0,80	-0,67	-0,52	-0,43	-0,17	-0,09
IEX_MMpi[u]tr	-99,75	-1,08	-98,60	-0,70	-97,45	-0,14
IEX_MMpro-L[u]tr	-0,96	0,00	-80,38	0,00	-0,24	0,00
IEX_MMser-L[u]tr	-0,76	0,00	-114,96	0,00	-0,57	0,00
IEX_MMsucr[u]tr	-0,50	0,00	-0,50	0,00	-0,24	0,00
IEX_MMthr-L[u]tr	-1,20	-1,17	-0,78	-0,76	-0,18	-0,15
IEX_MMtrp-L[u]tr	-0,16	-0,13	-0,11	-0,09	-0,04	-0,02
IEX_MMtyr-L[u]tr	-0,59	-0,42	-0,40	-0,28	-0,10	0,00
IEX_MMval-L[u]tr	-1,37	-1,27	-0,90	-0,82	-0,34	-0,19

Table S8: Growth conditions for model behavior and growth capacity tests of iAH991.

Uptake of metabolites at a certain rate is allowed by constraining the lower bound of the respective exchange reaction to the corresponding negative value. For nutrients which are not provided in the simulated medium, the lower bund of exchange reactions is constrained to zero.

a) Essential minerals and cofactors required by iAH991

Nutrients provided in every test	BIGG ID	Uptake Rate [mmol.g_{DW}^{-1}.hr^{-1}]
Calcium	ca2	10
Cob(I)alamin	cbl1	10
$Co2^+$	cobalt2	10
$Fe2^+$	fe2	10
$Fe3^+$	fe3	10
Hydrogen sulfide	h2s	10
Potassium	k	10
Magnesium	mg2	10
$Mn2^+$	mn2	10
Sodium	na1	10
Protoheme	pheme	10
Hydrogenphosphate	pi	10
Zinc	zn2	10
Ammonium	nh4	100
CO_2	co2	100
H_2O	h2o	100

b) Uptake rates for calculations of iAH991 growth on different sole carbon sources (for Table S3)

Carbon sources	BIGG ID	Uptake Rate [mmol.g_{Dw}^{-1}.hr^{-1}]
N-Acetyl-D-galactosamine	acgal	10
N-Acetyl-D-glucosamine	acgam	10
N-acetylneuraminate	acnam	10
Alpha-mannan (yeast)	amannan140	0,07143
Arabinan	arabinan101	0,1179
Arabinogalactan	arabinogal	0,0155
L-Arabinose	arab-L	12
Cellobiose	cellb	5
Core 4 (mucin O-glycan)	core4	2,5
Core 5 (mucin O-glycan)	core5	3,75
Core 7 (mucin O-glycan)	core7	3,75
Core 8 (mucin O-glycan)	core8	4,2857
Chondroitin sulfate A (GalNAc4S-GlcA) proteoglycan	cspg_a	1,33
Chondroitin sulfate B / dermatan sulfate (IdoA2S-GalNAc4S) proteoglycan	cspg_b	1,33
Chondroitin sulfate C (GalNAc6S-GlcA) proteoglycan	cspg_c	1,33
Dextran 40, 1,6-alpha-D-Glucan	dextran40	0,125
Disialyl-T antigen (mucin O-glycan)	dsT_antigen	1,6667
F1alpha (mucin O-glycan)	f1a	2,7273
D-Fructose	fru	10
L-Fucose	fuc-L	10
D-Galactose	gal	10
D-Galacturonate	galur	10
D-Glucosamine	gam	10
D-Glucose	glc-D	10
D-Glucuronate	glcur	10
glycogen (n=1500 repeat units) (glc alpha 1,4/6 glc)	glycogen1500	0,0067
GlcNAc-alpha-1,4-Core 1 (mucin O-glycan)	gncore1	2,7273
GlcNAc-alpha-1,4-Core 2 (mucin O-glycan)	gncore2	2,7273
Hyaluronan	ha	2,12
Homogalacturonan	homogal	0,09091
Heparin sulfate proteoglycan	hspg	0,76
Inulin	inulin	0,33333
Levan, 1000 fructose units	levan1000	0,01
Laminarin (n=30 repeat units, beta -1,3 glc)	lmn30	0,33
D-Mannose	man	10
Pectic galactan	pecticgal	0,1005
Pullulan (n=1200 repeat units, alpha-1,4 and alpha-1,6 bounds)	pullulan1200	0,00833
Rhamnogalacturonan I	rhamnogalurI	0,010274
Rhamnogalacturonan II	rhamnogalurII	0,18927
D-ribose	rib-D	12
L-Rhamnose	rmn	12
Starch n=1200 repeat units (300 repeat units amylose, 900 repeat units amylopectin, corresponds to potatoe starch)	starch1200	0,00833
Sialyl-Tn antigen (mucin O-glycan)	sTn_antigen	3,1579
Starch, structure 1 (1,6-?[1,4-Glc], 4[1,4-Glc]	strch1	0,91
D-Xylose	xyl-D	12

c) Simulation constraints for gene essentiality analysis of iAH991 corresponding to glucose minimal medium [1].

Uptake of metabolites at a certain rate is allowed by constraining the lower bound of the respective exchange reaction to the corresponding negative value. For nutrients which are not provided in the simulated medium, the lower bund of exchange reactions is constrained to zero.

Nutrient	BIGG ID	Uptake Rate [mmol.g_{dw}^{-1}.hr^{-1}]
Calcium	ca2	10
Cob(I)alamin	cbl1	10
Co^{2+}	cobalt2	10
Fe^{2+}	fe2	10
Fe^{3+}	fe3	10
Hydrogen sulfide	h2s	10
Potassium	k	10
Magnesium	mg2	10
$Mn2^{+}$	mn2	10
Sodium	na1	10
Protoheme	pheme	10
Hydrogenphosphate	pi	10
Zinc	zn2	10
Ammonium	nh4	100
CO_2	co2	100
H_2O	h2o	100
D-Glucose	glc-D	10

[1] Varel, V. H. and M. P. Bryant (1974). Nutritional features of Bacteroides fragilis subsp. fragilis. Appl Microbiol 28(2): 251-257.

d) Simulation constraints for gene essentiality analysis of iAH991 corresponding to anaerobic tryptone-yeast extract-glucose medium.

Uptake of metabolites at a certain rate is allowed by constraining the lower bound of the respective exchange reaction to the corresponding negative value. For nutrients which are not provided in the simulated medium, the lower bund of exchange reactions is constrained to zero.

Yeast extract equals to metabolite included in the yeast metabolic reconstruction iMM904 [2] (excluding carbohydrates) that can be transported by iAH991, and tryptone equals all amino acids. Also includes glucose and required cofactors, as well as yeast mannan.

Nutrient	BIGG ID	Uptake Rate [mmol.g_{Dw}^{-1}.hr^{-1}]
Calcium	ca2	1
Cob(I)alamin	cbl1	1
Co^{2+}	cobalt2	1
Fe^{2+}	fe2	1
Fe^{3+}	fe3	1
Hydrogen sulfide	h2s	1
potassium	k	1
magnesium	mg2	1
Mn^{2+}	mn2	1
Sodium	na1	1
Protoheme	pheme	1
hydrogenphosphate	pi	1
Zinc	zn2	1
Ammonium	nh4	10
CO_2	co2	10
H_2O	h2o	10
D-Glucose	glc-D	10
Alpha-mannan (yeast)	amannan140	10
4-Aminobutanoate	4abut	10
Acetate	ac	10
Adenosine	adn	10
L-Alanine	ala-L	10
L-Arginine	arg-L	10
L-Asparagine	asn-L	10
L-Aspartate	asp-L	10
Cys-Gly	cgly	10
Citrate	cit	10
L-Cysteine	cys-L	10
Cytidine	cytd	10
Deoxyadenosine	dad-2	10
Deoxycytidine	dcyt	10
Deoxyguanosine	dgsn	10
Deoxyinosine	din	10
Deoxyuridine	duri	10
Ethanol	etoh	10
Formate	for	10
Fumarate	fum	10
D-Galactose	gal	10
L-Glutamine	gln-L	10
L-Glutamate	glu-L	10
Glycine	gly	10
Guanosine	gsn	10
proton	h	10
L-Histidine	his-L	10
L-Isoleucine	ile-L	10
Inosine	ins	10
D-Lactate	lac-D	10
L-Lactate	lac-L	10
L-Leucine	leu-L	10
L-Lysine	lys-L	10
L-Methionine	met-L	10
Methylglyoxal	mthgxl	10
NMN	nmn	10
Ornithine	orn	10
Phenylacetic acid	pac	10
L-Phenylalanine	phe-L	10
L-Proline	pro-L	10
Putrescine	ptrc	10
Pyridoxine	pydxn	10
pyruvate	pyr	10
Riboflavin	ribflv	10
L-Serine	ser-L	10
Sulfate	so4	10
Spermidine	spmd	10
Succinate	succ	10
Taurine	taur	10
taurocholic acid	tchola	10
Thiamin	thm	10
L-Threonine	thr-L	10
Thymidine	thymd	10
L-Tryptophan	trp-L	10
L-Tyrosine	tyr-L	10
Uracil	ura	10
Urea	urea	10
Uridine	uri	10
L-Valine	val-L	10
Xanthine	xan	10

[2] Mo ML, Palsson BO, Herrgard MJ. Connecting extracellular metabolomic measurements to intracellular flux states in yeast. BMC Syst Biol 2009; 3:37.

Table S7: Reactions showing increased flux in the *B. thetaiotaomicron*-associated mouse model when orotic aciduria, AICA-ribosiduria and ribose-5-phosphate isomerase deficiency were simulated.

B. thetaiotaomicron and mouse reactions with a fold change in flux > 3 (rounded) compared to the healthy model are shown. The fluxes were calculated using flux variability analysis for optimization of mouse growth on Western Diet.

a) Orotic aciduria

	Reaction ID	Reaction Description	Subsystem	Fold Change in minimal flux	Fold Change in maximal flux
B. thetaiotaomicron reactions	IEX_BTcytd[u]tr	Cytidine exchange (internal)	Exchange Reactions	0,00	4,36
	IEX_BTdcyt[u]tr	Deoxycytidine exchange (internal)	Exchange Reactions	0,00	4,33
	IEX_BTuri[u]tr	Uridine exchange (internal)	Exchange Reactions	Zero to 0,06 (absolute value)	5,54
	BTASPCT	Aspartate carbamoyltransferase	Purine and Pyrimidine Biosynthesis	10,02	3,74
	BTCBPS	Carbamoyl-phosphate synthase (glutamine-hydrolysing)	Purine and Pyrimidine Biosynthesis	10,02	3,38
	BTCYTDt2r	Cytidine transport in via proton symport, reversible	Transport, Extracellular	4,36	0,00
	BTCYTK1	Cytidylate kinase (CMP)	Nucleotide Salvage Pathway	11,71	1,04
	BTDCYTt2r	Deoxycytidine transport in via proton symport reversible	Transport, Extracellular	4,33	0,00
	BTDHORDfum	Fumarate-dependent dihydroorotate dehydrogenase	Purine and Pyrimidine Biosynthesis	10,02	3,74
	BTDHORTS	Dihydroorotase	Purine and Pyrimidine Biosynthesis	3,74	10,02
	BTNDPK3	Nucleoside-diphosphate kinase (ATP:CDP)	Nucleotide Salvage Pathway	11,71	1,04
	BTNDPK6	Nucleoside-diphosphate kinase (ATP:dUDP)	Nucleotide Salvage Pathway	3,97	0,98
	BTOMPDC	Orotidine-5-phosphate decarboxylase	Purine and Pyrimidine Biosynthesis	10,02	3,74
	BTORPT	Orotate phosphoribosyltransferase	Purine and Pyrimidine Biosynthesis	3,74	10,02
	BTRNTR4	Ribonucleoside-triphosphate reductase (UTP)	Nucleotide Salvage Pathway	0,00	3,97
	BTTRDRr	Thioredoxin reductase	Nucleotide Metabolism (BIGG database)	1,04	3,70
	BTURIDK2r	Uridylate kinase (dUMP)	Nucleotide Salvage Pathway	3,97	0,98
	BTURIt2r	Uridine transport in via proton symport reversible	Transport, Extracellular	5,54	Zero to 0,06 (absolute value)
Mouse reactions	IEX_MMcytd[u]tr	Cytidine exchange (internal)	Exchange Reactions	4,36	0,00
	IEX_MMdcyt[u]tr	Deoxycytidine exchange (internal)	Exchange Reactions	4,33	0,00
	IEX_MMuri[u]tr	Uridine exchange (internal)	Exchange Reactions	5,54	Zero to 0,06 (absolute value)
	MMCYTDt	Cytidine facilated transport in cytosol	Transport, Extracellular	0,00	4,36
	MMCYTDt4	Cytidine transport in via sodium symport	Transport, Extracellular	0,00	4,36
	MMCYTDt5	Cytidine transport (1:2 Na/cytd cotransport)	Transport, Extracellular	0,00	4,36
	MMDCYTD	Deoxycytidine deaminase	Nucleotide Salvage Pathway	0,00	4,33
	MMDCYTt	Deoxycytidine transport via diffusion	Transport, Extracellular	0,00	4,33
	MMURIt	Uridine facilated transport in cytosol	Transport, Extracellular	0,00	5,54
	MMURIt4	Uridine transport in via sodium symport	Transport, Extracellular	0,00	5,54
	MMURIt5	Uridine transport in via sodium symport (1:2)	Transport, Extracellular	0,00	5,54

b) AICA-ribosiduria

	Reaction ID	Reaction Description	Subsystem	Fold Change in minimal flux	Fold Change in maximal flux
B. thetaiotaomicron reactions	IEX_BTdad-2[u]tr	Deoxyadenosine exchange (internal)	Exchange Reactions	0,00	4,71
	IEX_BTgsn[u]tr	Guanosine exchange (internal)	Exchange Reactions	0,00	6,90
	IEX_BTins[u]tr	Inosine exchange (internal)	Exchange Reactions	Zero to 0,08 (absolute value)	8,26
	BTADSL2r	Adenylosuccinate lyase	Purine and Pyrimidine Biosynthesis	7,53	3,98
	BTAIRCr	Phosphoribosylaminoimidazole carboxylase	Purine and Pyrimidine Biosynthesis	0,09	3,98
	BTDADK	Deoxyadenylate kinase	Nucleotide Salvage Pathway	4,71	0,00
	BTDADNt2r	Deoxyadenosine transport in via proton symport reversible	Transport, Extracellular	4,71	0,00
	BTDGK1	Deoxyguanylate kinase (dGMP:ATP)	Nucleotide Salvage Pathway	3,91	0,97
	BTDURIPP	Deoxyuridine phosphorylase	Nucleotide Salvage Pathway	0,00	3,91
	BTGARFTi	Phosphoribosylglycinamide formyltransferase, irreversible	Purine and Pyrimidine Biosynthesis	0,00	3,97
	BTGART	GAR transformylase-T	Purine and Pyrimidine Biosynthesis	0,00	4,04
	BTGLUPRT	Glutamine phosphoribosyldiphosphate amidotransferase	Purine and Pyrimidine Biosynthesis	7,47	3,97
	BTGMPS2	GMP synthase	Purine and Pyrimidine Biosynthesis	1,04	4,10
	BTGSNt2r	Guanosine transport in via proton symport reversible	Transport, Extracellular	6,90	0,00
	BTIMPD	IMP dehydrogenase	Purine and Pyrimidine Biosynthesis	1,04	4,10
	BTINSt2	Inosine transport in via proton symport reversible	Transport, Extracellular	8,26	Zero to 0,08 (absolute value)
	BTNTD6	5-nucleotidase (dAMP)	Nucleotide Salvage Pathway	0,00	4,71
	BTNTD8	5-nucleotidase (dGMP)	Nucleotide Salvage Pathway	0,00	3,91
	BTNTPTP1	Nucleoside triphosphate tripolyhydrolase	Nucleotide Salvage Pathway	0,00	3,91
	BTPRAGS	Phosphoribosylglycinamide synthetase	Purine and Pyrimidine Biosynthesis	7,47	3,97
	BTPRAIS	Phosphoribosylaminoimidazole synthase	Purine and Pyrimidine Biosynthesis	7,47	3,97
	BTPRASCSi	Phosphoribosylaminoimidazolesuccinocarboxamide synthase	Purine and Pyrimidine Biosynthesis	7,53	3,98
	BTPRFGS	Phosphoribosylformylglycinamidine synthase	Purine and Pyrimidine Biosynthesis	7,47	3,97
	BTPUNP2	Purine-nucleoside phosphorylase (Deoxyadenosine)	Nucleotide Salvage Pathway	3,91	0,00
	BTPUNP4	Purine-nucleoside phosphorylase (Deoxyguanosine)	Nucleotide Salvage Pathway	0,00	3,91
	BTRNTR1	Ribonucleoside-triphosphate reductase (ATP)	Nucleotide Salvage Pathway	1,04	4,42
	BTRNTR2	Ribonucleoside-triphosphate reductase (GTP)	Nucleotide Salvage Pathway	1,04	3,67
	BTUPPRT	Uracil phosphoribosyltransferase	Nucleotide Salvage Pathway	0,00	3,91
Mouse reactions	IEX_MMdad-2[u]tr	Deoxyadenosine exchange (internal)	Exchange Reactions	4,71	0,00
	IEX_MMgsn[u]tr	Guanosine exchange (internal)	Exchange Reactions	6,90	0,00
	IEX_MMins[u]tr	Inosine exchange (internal)	Exchange Reactions	8,26	Zero to 0,08 (absolute value)
	MMDADAe	Deoxyadenosine deaminase, extracellular	Nucleotide Salvage Pathway	0,00	4,63
	MMDADNt4	Deoxyadenosine transport via diffusion	Transport, Extracellular	0,00	4,71
	MMDINt	Deoxyinosine transport via diffusion	Transport, Extracellular	0,00	4,63
	MMGSNt	Guanosine facilated transport in cytosol	Transport, Extracellular	0,00	6,90
	MMGSNt4	Guanosine transport in via sodium symport	Transport, Extracellular	0,00	6,90
	MMGSNt5	Guanosine transport in via sodium (1:2) symport	Transport, Extracellular	0,00	6,90
	MMINSt	Inosine transport (diffusion)	Transport, Extracellular	0,00	8,26
	MMINSt4	Inosine transport in via sodium symport	Transport, Extracellular	0,00	8,26
	MMINSt5	Inosine transport in via sodium (1:2) symport	Transport, Extracellular	0,00	8,26

c) Ribose-5-phosphate isomerase deficiency

	Reaction ID	Reaction Description	Subsystem	Fold Change in minimal flux	Fold Change in maximal flux
B. thetaiotaomicron reactions	IEX_BTrib-D[u]tr	D-ribose exchange (internal)	Exchange Reactions	Zero to 0,61 (absolute value)	3,33
	BTADNUC	Adenosine hydrolase	Nucleotide Salvage Pathway	0,00	3,57
	BTGNNUC	Guanosine hydrolase	Nucleotide Salvage Pathway	0,00	3,57
	BTGUAPRT	Guanine phosphoribosyltransferase	Nucleotide Salvage Pathway	0,00	3,60
	BTHXPRT	Hypoxanthine phosphoribosyltransferase	Nucleotide Salvage Pathway	0,00	3,60
	BTINSH	Inosine hydrolase	Purine and Pyrimidine Biosynthesis	0,00	3,57
	BTNTD10	5'-nucleotidase (XMP)	Nucleotide Salvage Pathway	0,00	3,60
	BTNTD11	5'-nucleotidase (IMP)	Nucleotide Salvage Pathway	0,00	3,60
	BTNTD7	5'-nucleotidase (AMP)	Nucleotide Salvage Pathway	0,00	3,60
	BTNTD9	5'-nucleotidase (GMP)	Nucleotide Salvage Pathway	0,00	3,60
	BTPUNP1	Purine-nucleoside phosphorylase (Adenosine)	Nucleotide Salvage Pathway	3,60	3,57
	BTPUNP3	Purine-nucleoside phosphorylase (Guanosine)	Nucleotide Salvage Pathway	3,57	3,60
	BTPUNP5	Purine-nucleoside phosphorylase (Inosine)	Nucleotide Salvage Pathway	3,57	3,60
	BTPUNP7	Purine-nucleoside phosphorylase (Xanthosine)	Nucleotide Salvage Pathway	3,57	3,60
	BTXPPT	Xanthine phosphoribosyltransferase	Nucleotide Salvage Pathway	0,00	3,60
	BTXTSNH	Xanthosine hydrolase	Purine and Pyrimidine Biosynthesis	0,00	3,57
Mouse reactions	IEX_MMrib-D[u]tr	D-ribose exchange (internal)	Exchange Reactions	3,33	Zero to 0,61 (absolute value)
	MMRBK	Ribokinase	Pentose Phosphate Pathway	Zero to 0,61 (absolute value)	3,33
	MMRIBt	Ribose transport via diffusion	Transport, Extracellular	1,00	3,33

Table S9: Simulation constraints for the five diets used this study for analysis of the joint model iexG*MM Bθ*.

Uptake of metabolites at a certain rate is allowed by constraining the lower bound of the respective exchange reaction to the corresponding negative value. For nutrients which are not provided in the simulated medium, the lower bund of exchange reactions is constrained to zero.

Nutrient	BIGG ID	High-protein diet	High-carbohydrate diet	High-fat diet	Ketogenic diet	Western diet
Carbohydrate		Uptake Rate [mmol.gDw-1.hr-1]	Uptake Rate [mmol.gDw-1.hr-1]	Uptake Rate [mmol.gDw-1.hr-1]	Uptake Rate [mmol.gDw-1.hr-1]	Uptake Rate [mmol.gDw-1.hr-1]
D-Fructose	fru	0,1	1,5	0,1	0,01	1
glc	glc	0,1	1,5	0,1	0,01	1
Lactose	lcts	0,05	0,75	0,05	0.005	0,5
Maltose	malt	0,05	0,75	0,05	0.005	0,5
Sucrose	sucr	0,05	0,75	0,05	0,005	0,5
Dextran 40, 1,6-alpha-D-Glucan	dextran40	0,000625	0,009375	0,000625	0,000063	0,00625
Starch n=1200 repeat units (300 repeat units amylose, 900 repeat units amylopectin)	starch1200	0,000042	0,000626	0,000042	0,000004	0,00042
Pullulan (n=1200 repeat units, alpha-1,4 and alph-1,6 bounds)	pullulan1200	0,000042	0,000626	0,000042	0,000004	0,00042
Pectins	pect	0,000118	0,001775	0,000118	0,0000118	0,00118
Amylose (n=300 repeat units, alpha-1,4-glc)	amylose300	0,000167	0,002501	0,000167	0,000017	0,00167
Larch arabinogalactan	arabinogal	0,000078	0,001167	0,000078	0,000008	0,00078
Mannopentaose	manpt	0,01	0,15	0,01	0,001	0,1
Laminarin (n=30 repeat units, beta -1,3 glc)	lmn30	0,001667	0,025005	0,001667	0,000167	0,01667
Levan, 1000 fructose units	levan1000	0,00005	0,00075	0,00005	0,000005	0,0005
Raffinose	raffin	0,01667	0,25005	0,01667	0,001667	0,1667
Total percentage		**5%**	**75%**	**5%**	**0.5%**	**50%**
Fat		Uptake Rate [mmol.gDw-1.hr-1]	Uptake Rate [mmol.gDw-1.hr-1]	Uptake Rate [mmol.gDw-1.hr-1]	Uptake Rate [mmol.gDw-1.hr-1]	Uptake Rate [mmol.gDw-1.hr-1]
tetradecanoate (n-C14:0)	ttdca	0,14228	0,03557	0,53355	0,67583	0,24899
Hexadecanoate (n-C16:0)	hdca	0,1245	0,031125	0,466875	0,591375	0,21788
octadecanoate (n-C18:0)	ocdca	0,110668	0,027667	0,415005	0,525673	0,19367
Arachidic acid	arach	0,0996	0,0249	0,3735	0,4731	0,1743
octanoate (n-C8:0)	octa	0.249	0,06225	0,93375	1,18275	0,43575
Glycerol	glyc	0.664	0.166	2,49	3.154	1.162
Cholesterol	chsterol	0,07376	0,01844	0,2766	0,35036	0,12908
Hexadecenoate (n-C16:1)	hdcea	0,1245	0,031125	0,466875	0,591375	0,21788
octadecenoate (n-C18:1)	ocdcea	0,110668	0,027667	0,415005	0,525673	0,19367
arachidonic acid	arachd	0,0996	0,0249	0,3735	0,4731	0,1743
linoleic acid (all cis C18:2) n-6	lnlc	0,110668	0,027667	0,415005	0,525673	0,19367
alpha-Linolenic acid, C18:3, n-3	lnlnca	0,110668	0,027667	0,415005	0,525673	0,19367
Total percentage		**20%**	**5%**	**75%**	**95%**	**35%**
Protein		Uptake Rate [mmol.gDw-1.hr-1]	Uptake Rate [mmol.gDw-1.hr-1]	Uptake Rate [mmol.gDw-1.hr-1]	Uptake Rate [mmol.gDw-1.hr-1]	Uptake Rate [mmol.gDw-1.hr-1]
L-Alanine	ala-L	1,5	0,4	0,4	0,09	0,3
L-Arginine	arg-L	0,75	0,2	0,2	0.045	0,15
L-Glutamate	glu-L	0,9	0,24	0,24	0.054	0,18
Glycine	gly	2,25	0,6	0,6	0.135	0,45
L-Isoleucine	ile-L	0,75	0,2	0,2	0.045	0,15
L-Leucine	leu-L	0,75	0,2	0,2	0.045	0,15
L-Lysine	lys-L	0,75	0,2	0,2	0.045	0,15
L-Methionine	met-L	0,9	0,24	0,24	0.054	0,18
L-Proline	pro-L	0,9	0,24	0,24	0.054	0,18
L-Asparagine	asn-L	1.125	0,3	0,3	0,0675	0.225
L-Aspartate	asp-L	1.125	0,3	0,3	0,0675	0.225
L-Histidine	his-L	0,75	0,2	0,2	0.045	0,15
L-Phenylalanine	phe-L	0.495	0.132	0.132	0,0297	0.099
L-Serine	ser-L	1,5	0,4	0,4	0,09	0,3
L-Threonine	thr-L	1.125	0,3	0,3	0,0675	0.225
L-Tryptophan	trp-L	0.405	0.108	0.108	0,0243	0.081
L-Tyrosine	tyr-L	0.495	0.132	0.132	0,0297	0.099
L-Glutamine	gln-L	0,9	0,24	0,24	0.054	0,18
L-Valine	val-L	0,9	0,24	0,24	0.054	0,18
L-Cysteine	cys-L	1,5	0,4	0,4	0,09	0,3
Total percentage		**75%**	**20%**	**20%**	**4.5%**	**15%**
Minerals and cofactors		Uptake Rate [mmol.gDw-1.hr-1]	Uptake Rate [mmol.gDw-1.hr-1]	Uptake Rate [mmol.gDw-1.hr-1]	Uptake Rate [mmol.gDw-1.hr-1]	Uptake Rate [mmol.gDw-1.hr-1]
Calcium	ca2	1	1	1	1	1
Cob(I)alamin	cbl1	1	1	1	1	1
Co2+	cobalt2	1	1	1	1	1
Fe2+	fe2	1	1	1	1	1
Fe3+	fe3	1	1	1	1	1
Hydrogen sulfide	h2s	1	1	1	1	1
Potassium	k	1	1	1	1	1
Magnesium	mg2	1	1	1	1	1
Mn2+	mn2	1	1	1	1	1
Sodium	na1	1	1	1	1	1
Protoheme	pheme	1	1	1	1	1
Zinc	zn2	1	1	1	1	1
Ammonium	nh4	100	100	100	100	100
Phosphate	pi	100	100	100	100	100

Table S10: Description of *Bacteroides thetaiotaomicron reconstruction* iAH991.

Table S10a: All reactions included in iAH991. Rev = Reversibility (1 = reversible, 0 = irreversible), GA = Gene association, CS = Cofidence score, LB = Lower bound, UB = Upper Bound

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	12ETHDt	1,2-Ethanediol facilitated transport	12ethd[e] <=> 12ethd[c]	1		-1000	1000	1	Transport, Extracellular		KEGG Pathway suggests that this metabolite is formed.	
	12PPDRt	R-Propane-1,2-diol facilitated transport	12ppd-R[e] <=> 12ppd-R[c]	1		-1000	1000	2	Transport, Extracellular	PMID:18848625, PMID:8370454	Fermentation of rhamnose leads to secretion of propane-1,2-diol as end product. R-propane-1,2-diol is formed via methylglyoxal (PMID:8370454). Gene is unknown.	
	12PPDt	S-Propane-1,2-diol facilitated transport	12ppd-S[e] <=> 12ppd-S[c]	1		-1000	1000	2	Transport, Extracellular	PMID:17448155, PMID:18848625	Fermentation of fucose and rhamnose leads to secretion of propane-1,2-diol as end product. Gene is unknown.	
rxn02522	23PDE2	2,3-Cyclic UMP 3-nucleotidohydrolase	h2o[c] + 23cump[c] => h[c] + 3ump[c]	0	BT_1236	0	1000	2	Nucleotide Salvage Pathway			3.1.4.16
rxn02762	23PDE4	2,3-Cyclic CMP 3-nucleotidohydrolase	h2o[c] + 23ccmp[c] => h[c] + 3cmp[c]	0	BT_1236	0	1000	2	Nucleotide Salvage Pathway			3.1.4.16
rxn02521	23PDE7	2,3-Cyclic AMP 3-nucleotidohydrolase	h2o[c] + 23camp[c] => h[c] + 3amp[c]	0	BT_1236	0	1000	2	Nucleotide Salvage Pathway			3.1.4.16
rxn03483	23PDE9	2,3-Cyclic GMP 3-nucleotidohydrolase	h2o[c] + 23cgmp[c] => h[c] + 3gmp[c]	0	BT_1236	0	1000	2	Nucleotide Salvage Pathway			3.1.4.16
rxn07441	26DAPLLATi	L,L-diaminopimelate aminotransferase (irreversible)	h2o[c] + h[c] + thdp[c] + glu-L[c] => 26dap-LL[c] + akg[c]	0	BT_0547	0	1000	2	Threonine and Lysine Metabolism		Reversible in SEED database, however KEGG states that this reaction runs in the direction of 26dap-LL in vivo.	2.6.1.83

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn02900	2AMEPHPAT	2-aminoethylphosphonate:pyruvate aminotransferase	2ameph[c] + pyr[c] <=> ala-L[c] + pald[c]	1	BT_1718	-1000	1000	3	Capsular Polysaccharide Biosynthesis	PMID:12904299	PEPM, 3OPDC and 2AMEPHPAT form the biosynthetic pathway of 2-aminoethylphosphonate, a component of the capsular polysaccharide complex of Bacteroides fragilis, and most likely other Bacteroides species.	2.6.1.37
	2FUCLAC_FUCASEe	alpha-fucosidase, 2-fucosyllactose (extracellular)	2fuclac[e] + h2o[e] => fuc-L[e] + lcts[e]	0	((BT_1625 or BT_4136) and ((BT_4134 and BT_4135) or (BT_1630 and BT_1631)))	0	1000	4	HMO Degradation	PMID: 22036470	B. thetaiotaomicron grows on human milk oligosaccharides (HMOs); numerous glycosidase hydrolases are upregulated during growth on HMOs. Involves alpha-fucosidase and susC/SusD (binding proteins).	
rxn05358	2MBCOATA	2-methylbutanoyl-CoA[acyl-carrier-protein] transferase	2mbcoa[c] + ACP[c] <=> coa[c] + 2mbutACP[c]	1	BT_0789	-1000	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.180
	2MMALD	(R)-2-methylmalate dehydratase	2mmal[c] <=> h2o[c] + 2mmale[c]	1	(BT_1859 and BT_1860)	-1000	1000	2	Valine, Leucine, and Isoleucine Metabolism		Added based on annotation from KEGG	4.2.1.35
	2MMALD2	3-isopropylmalate/(R)-2-methylmalate dehydratase	h2o[c] + 2mmale[c] <=> e3mmal[c]	1	(BT_1859 and BT_1860)	-1000	1000	2	Valine, Leucine, and Isoleucine Metabolism		Added based on annotation from KEGG	4.2.1.35

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	3DSPHR	3-Dehydrosphinganine reductase	h[c] + nadph[c] + 3dsphgn[c] => nadp[c] + sphgn[c]	0		0	1000	2	Sphingolipid Metabolism	PMID:16887518, PMID:20855611	Bacteroides are well established to produce sphingolipids. However, no homolog of human 3DSPHR was found in Bacteroides species. Either Bacteroides have structural homologs of this enzyme, which are not revealed by BLASTP search, or sphingolipids are synthesized by another mechanism.	1.1.1.102
	3FUCLAC_FUCASEe	alpha-fucosidase, 3-fucosyllactose (extracellular)	h2o[e] + 3fuclac[e] => fuc-L[e] + lcts[e]	0	((BT_1625 or BT_4136) and ((BT_4134 and BT_4135) or (BT_1630 and BT_1631)))	0	1000	4	HMO Degradation	PMID: 22036470	B. thetaiotaomicron grows on human milk oligosaccharides (HMOs); numerous glycosidase hydrolases are upregulated during growth on HMOs. Involves alpha-fucosidase and susC/ SusD (binding proteins).	3.2.1.51
	3HACPR1	3-hydroxyacyl-ACP-dehydratase (FabZ)	3hgACPm[c] => h2o[c] + egACPm[c]	0	BT_4206	0	1000	3	Biotin Metabolism	PMID:20693992	Based on biotin synthesis described in PMID:20693992 for E. coli.	
	3HACPR2	3-hydroxyacyl-ACP-dehydratase (FabZ)	3hpACPm[c] => h2o[c] + epACPm[c]	0	BT_4206	0	1000	3	Biotin Metabolism	PMID:20693992	Based on biotin synthesis described in PMID:20693992 for E. coli	
rxn05333	3HAD100	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C10:0)	3hdecACP[c] => h2o[c] + tdec2eACP[c]	0	BT_4206	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	4.2.1.61

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05423	3HAD10M11	10-methyl-3-hydroxy-undecanoyl-ACP hydro-lyase	10m3hundecACP[c] => h2o[c] + 10mtundec2eACP[c]	0	BT_4206	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	4.2.1.61
rxn05373	3HAD10M12	10-methyl-3-hydroxy-dodecanoyl-ACP hydro-lyase	10m3hddcaACP[c] => h2o[c] + 10mtddec2eACP[c]	0	BT_4206	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	4.2.1.61
rxn05398	3HAD11M12	11-methyl-3-hydroxy-dodecanoyl-ACP hydro-lyase	11m3hddcaACP[c] => h2o[c] + 11mtddec2eACP[c]	0	BT_4206	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	4.2.1.61
rxn05331	3HAD120	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C12:0)	3hddecACP[c] => h2o[c] + tddec2eACP[c]	0	BT_4206	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	4.2.1.61

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	3HAD121	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C12:1)	3hcddec5eACP[c] => h2o[c] + t3c5ddeceACP[c]	0	BT_4206	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	4.2.1.61
rxn05427	3HAD12M13	12-methyl-3-hydroxy-tridecanoyl-ACP hydro-lyase	12m3htridecACP[c] => h2o[c] + 12mttritec2eACP[c]	0	BT_4206	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	4.2.1.61
rxn05377	3HAD12M14	12-methyl-3-hydroxy-tetra-decanoyl-ACP hydro-lyase	12m3hmyrsACP[c] => h2o[c] + 12mtmrs2eACP[c]	0	BT_4206	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	4.2.1.61
rxn05402	3HAD13M14	13-methyl-3-hydroxy-tetra-decanoyl-ACP hydro-lyase	13m3hmyrsACP[c] => h2o[c] + 13mtmrs2eACP[c]	0	BT_4206	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	4.2.1.61

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05335	3HAD140	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C14:0)	3hmrsACP[c] => h2o[c] + tmrs2eACP[c]	0	BT_4206	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	4.2.1.61
	3HAD141	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C14:1)	3hcmrs7eACP[c] => h2o[c] + t3c7mrseACP[c]	0	BT_4206	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	4.2.1.61
rxn05431	3HAD14M15	14-methyl-3-hydroxy-pentadecanoyl-ACP hydro-lyase	14m3hpentdecACP[c] => h2o[c] + 14mtpentdec2eACP[c]	0	BT_4206	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	4.2.1.61
rxn05381	3HAD14M16	14-methyl-3-hydroxy-hexa-decanoyl-ACP hydro-lyase	14m3hpalmACP[c] => h2o[c] + 14mtpalm2eACP[c]	0	BT_4206	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	4.2.1.61

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05406	3HAD15M16	15-methyl-3-hydroxy-hexa-decanoyl-ACP hydro-lyase	15m3hpalmACP[c] => h2o[c] + 15mtpalm2eACP[c]	0	BT_4206	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	4.2.1.61
rxn05332	3HAD160	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C16:0)	3hpalmACP[c] => h2o[c] + tpalm2eACP[c]	0	BT_4206	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	4.2.1.61
	3HAD161	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C16:1)	3hcpalm9eACP[c] => h2o[c] + t3c9palmeACP[c]	0	BT_4206	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	4.2.1.61
rxn05462	3HAD180	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C18:0)	3hoctaACP[c] => h2o[c] + toctd2eACP[c]	0	BT_4206	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	4.2.1.61
	3HAD181	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C18:1)	3hcvac11eACP[c] => h2o[c] + t3c11vaceACP[c]	0	BT_4206	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	4.2.1.61
rxn05329	3HAD40	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C4:0)	3haACP[c] => h2o[c] + but2eACP[c]	0	BT_4206	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	4.2.1.61

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05411	3HAD4M5	4-methyl-3-hydroxy-pentanoyl-ACP hydro-lyase	4m3hpentACP[c] => h2o[c] + 4mtpent2eACP[c]	0	BT_4206	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	4.2.1.61
rxn05361	3HAD4M6	4-methyl-3-hydroxy-hexanoyl-ACP hydro-lyase	4m3hhexACP[c] => h2o[c] + 4mthex2eACP[c]	0	BT_4206	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	4.2.1.61
rxn05386	3HAD5M6	5-methyl-3-hydroxy-hexanoyl-ACP hydro-lyase	5m3hhexACP[c] => h2o[c] + 5mthex2eACP[c]	0	BT_4206	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	4.2.1.61
rxn05330	3HAD60	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C6:0)	3hhexACP[c] => h2o[c] + thex2eACP[c]	0	BT_4206	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	4.2.1.61

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05415	3HAD6M7	6-methyl-3-hydroxy-heptanoyl-ACP hydro-lyase	6m3hheptACP[c] => h2o[c] + 6mthept2eACP[c]	0	BT_4206	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	4.2.1.61
rxn05365	3HAD6M8	6-methyl-3-hydroxy-octanoyl-ACP hydro-lyase	6m3hocACP[c] => h2o[c] + 6mtoct2eACP[c]	0	BT_4206	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	4.2.1.61
rxn05390	3HAD7M8	7-methyl-3-hydroxy-octanoyl-ACP hydro-lyase	7m3hocACP[c] => h2o[c] + 7mtoct2eACP[c]	0	BT_4206	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	4.2.1.61
rxn05334	3HAD80	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C8:0)	3hoctACP[c] => h2o[c] + toct2eACP[c]	0	BT_4206	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	4.2.1.61

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05369	3HAD8M10	8-methyl-3-hydroxy-decanoyl-ACP hydro-lyase	8m3hdcaACP[c] => h2o[c] + 8mtdec2eACP[c]	0	BT_4206	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	4.2.1.61
rxn05419	3HAD8M9	8-methyl-3-hydroxy-nonanoyl-ACP hydro-lyase	8m3hnonACP[c] => h2o[c] + 8mtnon2eACP[c]	0	BT_4206	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	4.2.1.61
rxn05394	3HAD9M10	9-methyl-3-hydroxy-decanoyl-ACP hydro-lyase	9m3hdcaACP[c] => h2o[c] + 9mtdec2eACP[c]	0	BT_4206	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	4.2.1.61

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	3OAACPR1	3-ketoacyl-ACP-reductase (FabG)	h[c] + nadph[c] + 3ogACPm[c] => nadp[c] + 3hgACPm[c]	0	BT_0409	0	1000	3	Biotin Metabolism	PMID:20693992	Based on biotin synthesis described in PMID:20693992 for E. coli. BT_0409 was considered the most likely putatively annotated gene for FabG.	
	3OAACPR2	3-ketoacyl-ACP-reductase (FabG)	h[c] + nadph[c] + 3opACPm[c] => nadp[c] + 3hpACPm[c]	0	BT_0409	0	1000	3	Biotin Metabolism	PMID:20693992	Based on biotin synthesis described in PMID:20693992 for E. coli. BT_0409 was considered the most likely putatively annotated gene for FabG.	
rxn05338	3OAR100	3-oxoacyl-[acyl-carrier-protein] reductase (n-C10:0)	h[c] + nadph[c] + 3odecACP[c] <=> nadp[c] + 3hdecACP[c]	1	(BT_0972 or BT_2380)	-1000	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	1.1.1.100
rxn05422	3OAR10M11	10-methyl-3-oxo-undecanoyl-ACPNADP+ oxidoreductase	h[c] + nadph[c] + 10m3oundecACP[c] <=> nadp[c] + 10m3hundecACP[c]	1	(BT_0972 or BT_2380)	-1000	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.1.1.100

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05372	3OAR10M12	10-methyl-3-oxo-dodecanoyl-ACPNADP+ oxidoreductase	h[c] + nadph[c] + 10m3oddcaACP[c] <=> nadp[c] + 10m3hddcaACP[c]	1	(BT_0972 or BT_2380)	-1000	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.1.1.100
rxn05397	3OAR11M12	11-methyl-3-oxo-dodecanoyl-ACPNADP+ oxidoreductase	h[c] + nadph[c] + 11m3oddcaACP[c] <=> nadp[c] + 11m3hddcaACP[c]	1	(BT_0972 or BT_2380)	-1000	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.1.1.100
rxn05340	3OAR120	3-oxoacyl-[acyl-carrier-protein] reductase (n-C12:0)	h[c] + nadph[c] + 3oddecACP[c] <=> nadp[c] + 3hddecACP[c]	1	(BT_0972 or BT_2380)	-1000	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	1.1.1.100
	3OAR121	3-oxoacyl-[acyl-carrier-protein] reductase (n-C12:1)	h[c] + nadph[c] + 3ocddec5eACP[c] => nadp[c] + 3hcddec5eACP[c]	0	(BT_0972 or BT_2380)	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	1.1.1.100

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05426	3OAR12M13	12-methyl-3-oxo-tridecanoyl-ACPNADP+ oxidoreductase	h[c] + nadph[c] + 12m3otridecACP[c] <=> nadp[c] + 12m3htridecACP[c]	1	(BT_0972 or BT_2380)	-1000	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.1.1.100
rxn05376	3OAR12M14	12-methyl-3-oxo-tetra-decanoyl-ACPNADP+ oxidoreductase	h[c] + nadph[c] + 12m3omyrsACP[c] <=> nadp[c] + 12m3hmyrsACP[c]	1	(BT_0972 or BT_2380)	-1000	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.1.1.100
rxn05401	3OAR13M14	13-methyl-3-oxo-tetra-decanoyl-ACPNADP+ oxidoreductase	h[c] + nadph[c] + 13m3omyrsACP[c] <=> nadp[c] + 13m3hmyrsACP[c]	1	(BT_0972 or BT_2380)	-1000	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 720433	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.1.1.100
rxn05342	3OAR140	3-oxoacyl-[acyl-carrier-protein] reductase (n-C14:0)	h[c] + nadph[c] + 3omrsACP[c] <=> nadp[c] + 3hmrsACP[c]	1	(BT_0972 or BT_2380)	-1000	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	1.1.1.100

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	3OAR141	3-oxoacyl-[acyl-carrier-protein] reductase (n-C14:1)	h[c] + nadph[c] + 3ocmrs7eACP[c] => nadp[c] + 3hcmrs7eACP[c]	0	(BT_0972 or BT_2380)	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	1.1.1.100
rxn05430	3OAR14M15	14-methyl-3-oxo-pentadecanoyl-ACPNADP+ oxidoreductase	h[c] + nadph[c] + 14m3opentdecACP[c] <=> nadp[c] + 14m3hpentdecACP[c]	1	(BT_0972 or BT_2380)	-1000	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.1.1.100
rxn05380	3OAR14M16	14-methyl-3-oxo-hexa-decanoyl-ACPNADP+ oxidoreductase	h[c] + nadph[c] + 14m3opalmACP[c] <=> nadp[c] + 14m3hpalmACP[c]	1	(BT_0972 or BT_2380)	-1000	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.1.1.100
rxn05405	3OAR15M16	15-methyl-3-oxo-hexa-decanoyl-ACPNADP+ oxidoreductase	h[c] + nadph[c] + 15m3opalmACP[c] <=> nadp[c] + 15m3hpalmACP[c]	1	(BT_0972 or BT_2380)	-1000	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.1.1.100

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05336	3OAR160	3-oxoacyl-[acyl-carrier-protein] reductase (n-C16:0)	h[c] + nadph[c] + 3opalmACP[c] <=> nadp[c] + 3hpalmACP[c]	1	(BT_0972 or BT_2380)	-1000	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	1.1.1.100
	3OAR161	3-oxoacyl-[acyl-carrier-protein] reductase (n-C16:1)	h[c] + nadph[c] + 3ocpalm9eACP[c] => nadp[c] + 3hcpalm9eACP[c]	0	(BT_0972 or BT_2380)	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	1.1.1.100
rxn05461	3OAR180	3-oxoacyl-[acyl-carrier-protein] reductase (n-C18:0)	h[c] + nadph[c] + 3ooctdACP[c] <=> nadp[c] + 3hoctaACP[c]	1	(BT_0972 or BT_2380)	-1000	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	1.1.1.100
	3OAR181	3-oxoacyl-[acyl-carrier-protein] reductase (n-C18:1)	h[c] + nadph[c] + 3ocvac11eACP[c] => nadp[c] + 3hcvac11eACP[c]	0	(BT_0972 or BT_2380)	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	1.1.1.100
rxn05339	3OAR40	3-oxoacyl-[acyl-carrier-protein] reductase (n-C4:0)	h[c] + nadph[c] + actACP[c] <=> nadp[c] + 3haACP[c]	1	(BT_0972 or BT_2380)	-1000	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	1.1.1.100
rxn05410	3OAR4M5	4-methyl-3-oxo-pentanoyl-ACPNADP+ oxidoreductase	h[c] + nadph[c] + 4m3opentACP[c] <=> nadp[c] + 4m3hpentACP[c]	1	(BT_0972 or BT_2380)	-1000	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.1.1.100

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05360	3OAR4M6	4-methyl-3-oxo-hexanoyl-ACPNADP+ oxidoreductase	h[c] + nadph[c] + 4m3ohexACP[c] <=> nadp[c] + 4m3hhexACP[c]	1	(BT_0972 or BT_2380)	-1000	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.1.1.100
rxn05385	3OAR5M6	5-methyl-3-oxo-hexanoyl-ACPNADP+ oxidoreductase	h[c] + nadph[c] + 5m3ohexACP[c] <=> nadp[c] + 5m3hhexACP[c]	1	(BT_0972 or BT_2380)	-1000	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.1.1.100
rxn05337	3OAR60	3-oxoacyl-[acyl-carrier-protein] reductase (n-C6:0)	h[c] + nadph[c] + 3ohexACP[c] <=> nadp[c] + 3hhexACP[c]	1	(BT_0972 or BT_2380)	-1000	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	1.1.1.100
rxn05414	3OAR6M7	6-methyl-3-oxo-heptanoyl-ACPNADP+ oxidoreductase	h[c] + nadph[c] + 6m3oheptACP[c] <=> nadp[c] + 6m3hheptACP[c]	1	(BT_0972 or BT_2380)	-1000	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.1.1.100

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05364	3OAR6M8	6-methyl-3-oxo-octanoyl-ACPNADP+ oxidoreductase	h[c] + nadph[c] + 6m3oocACP[c] <=> nadp[c] + 6m3hocACP[c]	1	(BT_0972 or BT_2380)	-1000	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.1.1.100
rxn05389	3OAR7M8	7-methyl-3-oxo-octanoyl-ACPNADP+ oxidoreductase	h[c] + nadph[c] + 7m3oocACP[c] <=> nadp[c] + 7m3hocACP[c]	1	(BT_0972 or BT_2380)	-1000	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.1.1.100
rxn05341	3OAR80	3-oxoacyl-[acyl-carrier-protein] reductase (n-C8:0)	h[c] + nadph[c] + 3ooctACP[c] <=> nadp[c] + 3hoctACP[c]	1	(BT_0972 or BT_2380)	-1000	1000	2	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	1.1.1.100
rxn05368	3OAR8M10	8-methyl-3-oxo-decanoyl-ACPNADP+ oxidoreductase	h[c] + nadph[c] + 8m3odcaACP[c] <=> nadp[c] + 8m3hdcaACP[c]	1	(BT_0972 or BT_2380)	-1000	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.1.1.100

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05418	3OAR8M9	8-methyl-3-oxo-nonanoyl-ACPNADP+ oxidoreductase	h[c] + nadph[c] + 8m3ononACP[c] <=> nadp[c] + 8m3hnonACP[c]	1	(BT_0972 or BT_2380)	-1000	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.1.1.100
rxn05393	3OAR9M10	9-methyl-3-oxo-decanoyl-ACPNADP+ oxidoreductase	h[c] + nadph[c] + 9m3odcaACP[c] <=> nadp[c] + 9m3hdcaACP[c]	1	(BT_0972 or BT_2380)	-1000	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.1.1.100
rxn05343	3OAS100	3-oxoacyl-[acyl-carrier-protein] synthase (n-C10:0)	h[c] + malACP[c] + ocACP[c] => ACP[c] + 3odecACP[c] + co2[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	2.3.1.41
rxn05425	3OAS10M11	10-methyl-undecanoyl-ACPmalonyl-[acyl-carrier-protein] C-acyltransferase (decarboxylating)	h[c] + malACP[c] + 10mundecACP[c] => ACP[c] + 12m3otridecACP[c] + co2[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.41

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05375	3OAS10M12	10-methyl-dodecanoyl-ACPmalonyl-[acyl-carrier-protein] C-acyltransferase (decarboxylating)	h[c] + malACP[c] + 10mddcaACP[c] => ACP[c] + 12m3omyrsACP[c] + co2[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.41
rxn05400	3OAS11M12	11-methyl-dodecanoyl-ACPmalonyl-[acyl-carrier-protein] C-acyltransferase (decarboxylating)	h[c] + malACP[c] + 11mddcaACP[c] => ACP[c] + 13m3omyrsACP[c] + co2[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.41
rxn05348	3OAS120	3-oxoacyl-[acyl-carrier-protein] synthase (n-C12:0)	h[c] + malACP[c] + dcaACP[c] => ACP[c] + 3oddecACP[c] + co2[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	2.3.1.41
	3OAS121	3-oxoacyl-[acyl-carrier-protein] synthase (n-C12:1)	h[c] + malACP[c] + cdec3eACP[c] => ACP[c] + 3ocddec5eACP[c] + co2[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	2.3.1.41

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05429	3OAS12M13	12-methyl-tridecanoyl-ACPmalonyl-[acyl-carrier-protein] C-acyltransferase (decarboxylating)	h[c] + malACP[c] + 12mtridecACP[c] => ACP[c] + 14m3opentdecACP[c] + co2[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.41
rxn05379	3OAS12M14	12-methyl-tetra-decanoyl-ACPmalonyl-[acyl-carrier-protein] C-acyltransferase (decarboxylating)	h[c] + malACP[c] + 12mmyrsACP[c] => ACP[c] + 14m3opalmACP[c] + co2[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.41
rxn05404	3OAS13M14	13-methyl-tetra-decanoyl-ACPmalonyl-[acyl-carrier-protein] C-acyltransferase (decarboxylating)	h[c] + malACP[c] + 13mmyrsACP[c] => ACP[c] + 15m3opalmACP[c] + co2[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.41
rxn05345	3OAS140	3-oxoacyl-[acyl-carrier-protein] synthase (n-C14:0)	h[c] + malACP[c] + ddcaACP[c] => ACP[c] + 3omrsACP[c] + co2[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	2.3.1.41

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	3OAS141	3-oxoacyl-[acyl-carrier-protein] synthase (n-C14:1)	h[c] + malACP[c] + cddec5eACP[c] => ACP[c] + 3ocmrs7eACP[c] + co2[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	2.3.1.41
rxn05344	3OAS160	3-oxoacyl-[acyl-carrier-protein] synthase (n-C16:0)	h[c] + malACP[c] + myrsACP[c] => ACP[c] + 3opalmACP[c] + co2[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	2.3.1.41
	3OAS161	3-oxoacyl-[acyl-carrier-protein] synthase (n-C16:1)	h[c] + malACP[c] + tdeACP[c] => ACP[c] + 3ocpalm9eACP[c] + co2[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	2.3.1.41
rxn05460	3OAS180	3-oxoacyl-[acyl-carrier-protein] synthase (n-C18:0)	h[c] + malACP[c] + palmACP[c] => ACP[c] + 3ooctdACP[c] + co2[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	2.3.1.41
	3OAS181	3-oxoacyl-[acyl-carrier-protein] synthase (n-C18:1)	h[c] + malACP[c] + hdeACP[c] => ACP[c] + 3ocvac11eACP[c] + co2[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	2.3.1.41
rxn05409	3OAS2M3	2-methylpropionyl-ACPmalonyl-[acyl-carrier-protein] C-acyltransferase (decarboxylating)	h[c] + malACP[c] + 2mpropACP[c] => ACP[c] + 4m3opentACP[c] + co2[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.41

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05384	3OAS3M4	3-methylbutanoyl-ACPmalonyl-[acyl-carrier-protein] C-acyltransferase (decarboxylating)	h[c] + malACP[c] + 3mbutACP[c] => ACP[c] + 5m3ohexACP[c] + co2[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.41
rxn05359	3OAS4M3O6	4-methyl-3-oxo-hexanoyl-ACPmalonyl-[acyl-carrier-protein] C-acyltransferase (decarboxylating)	h[c] + 2mbutACP[c] + malACP[c] => ACP[c] + 4m3ohexACP[c] + co2[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.41
rxn05413	3OAS4M5	4-methyl-pentanoyl-ACPmalonyl-[acyl-carrier-protein] C-acyltransferase (decarboxylating)	h[c] + malACP[c] + 4mpentACP[c] => ACP[c] + 6m3oheptACP[c] + co2[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.41

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05363	3OAS4M6	4-methyl-hexanoyl-ACPmalonyl-[acyl-carrier-protein] C-acyltransferase (decarboxylating)	h[c] + malACP[c] + 4mhexACP[c] => ACP[c] + 6m3oocACP[c] + co2[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.41
rxn05388	3OAS5M6	5-methyl-hexanoyl-ACPmalonyl-[acyl-carrier-protein] C-acyltransferase (decarboxylating)	h[c] + malACP[c] + 5mhexACP[c] => ACP[c] + 7m3oocACP[c] + co2[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.41
rxn05346	3OAS60	3-oxoacyl-[acyl-carrier-protein] synthase (n-C6:0)	h[c] + malACP[c] + butACP[c] => ACP[c] + 3ohexACP[c] + co2[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	2.3.1.41
rxn05417	3OAS6M7	6-methyl-heptanoyl-ACPmalonyl-[acyl-carrier-protein] C-acyltransferase (decarboxylating)	h[c] + malACP[c] + 6mheptACP[c] => ACP[c] + 8m3ononACP[c] + co2[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.41

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05367	3OAS6M8	6-methyl-octanoyl-ACPmalonyl-[acyl-carrier-protein] C-acyltransferase (decarboxylating)	h[c] + malACP[c] + 6mocACP[c] => ACP[c] + 8m3odcaACP[c] + co2[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.41
rxn05392	3OAS7M8	7-methyl-octanoyl-ACPmalonyl-[acyl-carrier-protein] C-acyltransferase (decarboxylating)	h[c] + malACP[c] + 7mocACP[c] => ACP[c] + 9m3odcaACP[c] + co2[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.41
rxn05350	3OAS80	3-oxoacyl-[acyl-carrier-protein] synthase (n-C8:0)	h[c] + malACP[c] + hexACP[c] => ACP[c] + 3ooctACP[c] + co2[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	2.3.1.41
rxn05371	3OAS8M10	8-methyl-decanoyl-ACPmalonyl-[acyl-carrier-protein] C-acyltransferase (decarboxylating)	h[c] + malACP[c] + 8mdcaACP[c] => ACP[c] + 10m3oddcaACP[c] + co2[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.41

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05421	3OAS8M9	8-methyl-nonanoyl-ACPmalonyl-[acyl-carrier-protein] C-acyltransferase (decarboxylating)	h[c] + malACP[c] + 8mnonACP[c] => ACP[c] + 10m3oundecACP[c] + co2[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.41
rxn05396	3OAS9M10	9-methyl-decanoyl-ACPmalonyl-[acyl-carrier-protein] C-acyltransferase (decarboxylating)	h[c] + malACP[c] + 9mdcaACP[c] => ACP[c] + 11m3oddcaACP[c] + co2[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.41

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	3POPDC	phosphonopyruvate decarboxylase	h[c] + 3pop[c] => pald[c] + co2[c]	0	BT_1719	0	1000	3	Capsular Polysaccharide Biosynthesis	PMID:12904299	The enzyme catalyses a step in the biosynthetic pathway of 2-aminoethylphosphonate, a component of the capsular polysaccharide complex of Bacteroides fragilis and most likely other Bacteroides species. Requires thiamine diphosphate and Mg2+ as cofactors. The enzyme is activated by the divalent cations Mg2+, Ca2+ and Mn2+. Pyruvate and sulfopyruvate can also act as substrates, but more slowly. This enzyme drives the reaction catalysed by EC 5.4.2.9, phosphoenolpyruvate mutase, in the thermodynamically unfavourable direction of 3-phosphonopyruvate formation.	4.1.1.82
rxn03446	4HTHRS	4-Hydroxy-L-threonine synthase	h2o[c] + phthr[c] => 4hthr[c] + pi[c]	0	BT_2401	0	1000	2	Cofactor and Prosthetic Group Biosynthesis			4.2.3.1
	5DOAN	5'-deoxyadenosine nuclosidase	h2o[c] + dad-5[c] => 5drib[c] + ade[c]	0	BT_4451	0	1000	2	Cofactor and Prosthetic Group Biosynthesis	PMID:21166890	This reaction is catalyzed by Methylthioadenosine/S-adenosylhomocysteine nucleosidase.	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	7AHSDH	7-alpha-hydroxysteroid dehydrogenase	cholate[c] + nad[c] <=> h[c] + 7ocholate[c] + nadh[c]	1	BT_1911	-1000	1000	4	Bile Acid Metabolism	PMID:189820	Partly purified and characterized (PMID:189820) and annotated in B. thetaiotaomicron genome	1.1.1.159
	7OCHOLATEt2	3alpha,12alpha-Dihydroxy-7-oxo-5beta-cholanate transport out via sodium cotransport	7ocholate[c] + 2 na1[c] => 7ocholate[e] + 2 na1[e]	0		0	1000	2	Transport, Extracellular	PMID:16299351	B. thetaiotaomicron cannot completely epimerize bile acids. Further biotransformation of bile acid is performed by other gut bacteria (reviewed in PMID:16299351). Therefore, secretion of metabolized bile acid assumed.	
	A_MANASEe	alpha-mannosidase, extracellular	2 h2o[e] + m2mn[e] => 2 man[e] + mn[e]	0	(BT_3774 or BT_3990 or BT_2199 or BT_2105 or BT_4072 or BT_4092 or BT_3784 or BT_3527 or BT_3530 or BT_3962)	0	1000	3	N-Glycan Degradation	PMID: 20081828	B. thetaiotaomicron is known to degrade host N-glycans. The cleaved bound in this case is alpha-1,2. the mannosidases of the GH92 family included in the GPR were shown to be active agianst alpha-1,2 bounds in alpha-mannan.	3.2.1.24
rxn01117	A5PISO	arabinose-5-phosphate isomerase	ru5p-D[c] <=> ara5p[c]	1	BT_3306	-1000	1000	2	Alternate Carbon Metabolism			5.3.1.13
rxn00533	ACCOAC	acetyl-CoA carboxylase	accoa[c] + atp[c] + hco3[c] => h[c] + pi[c] + adp[c] + malcoa[c]	0	((BT_1915 and BT_1916 and BT_2238) or (BT_1448 and BT_1449 and BT_2238))	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330		6.4.1.2
	ACETOLt	Acetol facilitated transport	acetol[e] <=> acetol[c]	1		-1000	1000	2	Transport, Extracellular	PMID:11260473	B. thetaiotaomicron produces acetol.	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	ACGALK3	N-acetylgalactosamine kinase (6-phosphate)	atp[c] + acgal[c] => h[c] + adp[c] + acgal6p[c]	0		0	1000	2	Aminosugar Metabolism	PMID:2845859	B. thetaiotaomicron grows on N-acetylgalactosamine: PMID:2845859. However, the utilization pathway is poorly understood.	
	ACGALr	N-acetylgalactosamine reversible transport via proton symport	2 h[e] + acgal[e] <=> 2 h[c] + acgal[c]	1		-1000	1000	2	Transport, Extracellular	PMID:2845859	B. thetaiotaomicron grows on N-acetylgalactosamine: PMID:2845859. However, the utilization pathway is poorly understood.	
rxn00897	ACGAM2E	N-Acyl-D-glucosamine 2-epimerase	acgam[c] <=> acmana[c]	1	(BT_0437 or BT_0453 or BT_3605)	-1000	1000	2	Aminosugar Metabolism			5.1.3.8
rxn00892	ACGAMK	N-acetylglucosamine kinase	atp[c] + acgam[c] => h[c] + adp[c] + acgam6p[c]	0	(BT_2493 or BT_4654)	0	1000	3	Aminosugar Metabolism	PMID:15659667		2.7.1.59
rxn01505	ACGAMPM	phosphoacetylglucosamine mutase	acgam6p[c] <=> acgam1p[c]	1		-1000	1000	1	Aminosugar Metabolism	PMID:7240086	Manually filled in based on KEGG Pathway to to make N-acetylglucosamine, a substrate known to support growth, usable.	5.4.2.3
rxn08040	ACGAMT	UDP-N-acetylglucosamine:undecaprenylphosphate N-acetylglucosamine -1-phosphate transferase	uacgam[c] + udcpp[c] => ump[c] + unaga[c]	0	(BT_1339 or BT_2888)	0	1000	2	Cell Envelope Biosynthesis		Reversible in SEED	
	ACGAMtr	Na-acetylglucosamine transport in via proton symport, reversible	2 h[e] + acgam[e] <=> 2 h[c] + acgam[c]	1	(BT_3180 or BT_3619)	-1000	1000	4	Transport, Extracellular	PMID:7240086	B. thetaiotaomicron grows on N-acetylglucosamine as sole carbon source. Gene annotation taken from The SEED Viewer (last checked 01.07.11).	
rxn01917	ACGK	acetylglutamate kinase	atp[c] + acglu[c] => adp[c] + acg5p[c]	0	BT_3395	0	1000	2	Arginine and Proline Metabolism		Putative annotation (NCBI). Reversible in SEED.	2.7.2.8

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn00192	ACGS	N-acetylglutamate synthase	glu-L[c] + accoa[c] => h[c] + coa[c] + acglu[c]	0		0	1000	1	Arginine and Proline Metabolism		No GPR association available, but all reaction following up from this reaction to acetylornithine deacetylase are present, so a complete pathway was assumed.	2.3.1.1
rxn03194	ACHBS	2-aceto-2-hydroxybutanoate synthase	h[c] + pyr[c] + 2obut[c] => co2[c] + 2ahbut[c]	0	(BT_2076 and BT_2077)	0	1000	2	Valine, Leucine, and Isoleucine Metabolism		ACHBS and ACLS replace SEED reactions rxn00011, rxn02185 and rxn03194	2.2.1.6
rxn00225	ACKr	acetate kinase	atp[c] + ac[c] <=> adp[c] + actp[c]	1	BT_3693	-1000	1000	3	Central Metabolism	PMID: 16349240	Present in related organism Bacteroides xylanolyticus.	2.7.2.1
	ACLS	acetolactate synthase	h[c] + 2 pyr[c] => co2[c] + alac-S[c]	0	(BT_2076 and BT_2077)	0	1000	2	Valine, Leucine, and Isoleucine Metabolism		ACHBS and ACLS replace SEED reactions rxn00011, rxn02185 and rxn03194	4.1.3.18
	ACNAM9PL2	2-keto-3-deoxy-d-glycero-d-galacto-9-phosphonononic acid (KDN-9-P) synthase	h2o[c] + man6p[c] + pep[c] => pi[c] + kdnp[c]	0	BT_1714	0	1000	4	Capsular Polysaccharide Biosynthesis	PMID: 18804026	B. thetaiotaomicron forms and cytidylates 2-keto-3-deoxy-D-glycero-D-galacto-nononic acid (KDN), most likely for inclusion in its capsular polysaccharides.	2.5.1.56
rxn05487	ACNAMt2r	N-acetylneuraminate proton symport, reversible	h[e] + acnam[e] => h[c] + acnam[c]	0		0	1000	1	Transport, Extracellular			

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn10212	ACOAAGPAT140	myristoyl-1-acylglycerol-3-phosphate O-acyltransferase	1tdecg3p[c] + tdcoa[c] => coa[c] + pa140[c]	0	(BT_0243 or BT_4462)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.51
rxn10211	ACOAAGPAT160	palmitoyl-1-acylglycerol-3-phosphate O-acyltransferase	pmtcoa[c] + 1hdecg3p[c] => coa[c] + pa160[c]	0	(BT_0243 or BT_4462)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.51
rxn10213	ACOAAGPAT180	stearoyl-1-acylglycerol-3-phosphate O-acyltransferase	stcoa[c] + 1odecg3p[c] => coa[c] + pa180[c]	0	(BT_0243 or BT_4462)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.51

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn10218	ACOAAGPATAI15	anteisopentadecanoyl-1-acylglycerol-3-phosphate O-acyltransferase	1aipdecg3p[c] + aipdcoa[c] => h[c] + coa[c] + paai15[c]	0	(BT_0243 or BT_4462)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.51
rxn10214	ACOAAGPATAI17	anteisoheptadecanoyl-1-acylglycerol-3-phosphate O-acyltransferase	aihpdcoa[c] + 1aihpdecg3p[c] => coa[c] + paai17[c]	0	(BT_0243 or BT_4462)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.51
rxn10216	ACOAAGPATI14	isotetradecanoyl-1-acylglycerol-3-phosphate O-acyltransferase	itdcoa[c] + 1itdecg3p[c] => h[c] + coa[c] + pai14[c]	0	(BT_0243 or BT_4462)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.51

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn10217	ACOAAGPATI15	isopentadecanoyl-1-acylglycerol-3-phosphate O-acyltransferase	ipdcoa[c] + 1ipdecg3p[c] => h[c] + coa[c] + pai15[c]	0	(BT_0243 or BT_4462)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.51
rxn10219	ACOAAGPATI16	isohexadecanoyl-1-acylglycerol-3-phosphate O-acyltransferase	ihdcoa[c] + 1ihdecg3p[c] => h[c] + coa[c] + pai16[c]	0	(BT_0243 or BT_4462)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.51
rxn10215	ACOAAGPATI17	isoheptadecanoyl-1-acylglycerol-3-phosphate O-acyltransferase	ihpdcoa[c] + 1ihpdecg3p[c] => coa[c] + pai17[c]	0	(BT_0243 or BT_4462)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.51
rxn05349	ACOATA	Acetyl-CoA ACP transacylase	ACP[c] + accoa[c] <=> coa[c] + acACP[c]	1	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	-1000	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330		2.3.1.38

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn00469	ACODA	acetylornithine deacetylase	h2o[c] + acorn[c] => ac[c] + orn[c]	0	BT_3549	0	1000	2	Arginine and Proline Metabolism		Reversible in SEED	3.5.1.16
rxn00974	ACONTa	aconitase (half-reaction A, Citrate hydro-lyase)	cit[c] <=> h2o[c] + acon-C[c]	1	BT_2072	-1000	1000	4	TCA Cycle	PMID:11260473, PMID:11880608	This enzyme was demonstrated in B. thetaiotaomicron. The Bacteroides aconitase is mitochondrial-like.	4.2.1.3
rxn01388	ACONTb	aconitase (half-reaction B, Isocitrate hydro-lyase)	h2o[c] + acon-C[c] <=> icit[c]	1	BT_2072	-1000	1000	4	TCA Cycle	PMID:11260473, PMID:11880608	This enzyme was demonstrated in B. thetaiotaomicron. The Bacteroides aconitase is mitochondrial-like.	4.2.1.3
rxn01637	ACOTA	acetylornithine transaminase	akg[c] + acorn[c] <=> glu-L[c] + acg5sa[c]	1	BT_3758	-1000	1000	2	Arginine and Proline Metabolism			2.6.1.11
rxn06023	ACPS1	acyl-carrier protein synthase	coa[c] + apoACP[c] => h[c] + ACP[c] + pap[c]	0		0	1000	1	Cofactor and Prosthetic Group Biosynthesis		Reaction is reversible in SEED. Added by Model SEED during auto-completion step in pipeline. The reaction is essential for lipid metabolism.	2.7.8.7
rxn00175	ACS	acetyl-CoA synthetase	coa[c] + atp[c] + ac[c] => accoa[c] + amp[c] + ppi[c]	0	BT_2924	0	1000	2	Glycolysis/Gluconeogenesis		Annotation from NCBI Gene, last updated 21.05.11	6.2.1.1
	ACS2	acetyl-CoA synthase (propionate)	coa[c] + atp[c] + ppa[c] => amp[c] + ppi[c] + ppcoa[c]	0	BT_2924	0	1000	2	Glycolysis/Gluconeogenesis		Annotation from NCBI Gene, last updated 21.05.11	6.2.1.1
rxn09953	ACTNDH	acetoin dehydrogenase complex	coa[c] + nad[c] + actn-R[c] <=> h[c] + nadh[c] + accoa[c] + acald[c]	1	(BT_0309 and BT_0311 and BT_0312)	-1000	1000	2	Unassigned		Added manually based on SEED database and KEGG	2.3.1.190
	ACtr	acetate transporter	ac[e] <=> ac[c]	1		-1000	1000	2	Transport, Extracellular	PMID:19321416, PMID:12740060	Bacteroides species are well established to produce short-chain fatty acids (SCFAs).	
rxn03841	ADCL	4-aminobenzoate synthase	4adcho[c] => h[c] + pyr[c] + 4abz[c]	0	BT_0768	0	1000	2	Cofactor and Prosthetic Group Biosynthesis			4.1.3.38

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn00097	ADK1	adenylate kinase	atp[c] + amp[c] <=> 2 adp[c]	1	BT_4387	-1000	1000	2	Nucleotide Salvage Pathway			2.7.4.3
rxn10052	ADK2	adenylate kinase (Inorganic triphosphate)	amp[c] + pppi[c] <=> adp[c] + ppi[c]	1	BT_4387	-1000	1000	2	Nucleotide Salvage Pathway			2.7.4.3
rxn05318	ADNt2	adenosine transport in via proton symport	h[e] + adn[e] => h[c] + adn[c]	0	BT_4330	0	1000	2	Transport, Extracellular		Reversible in SEED	
rxn00927	ADNUC	adenosine hydrolase	h2o[c] + adn[c] => ade[c] + rib-D[c]	0	BT_2808	0	1000	2	Alternate Carbon Metabolism		Reversible in SEED	3.2.2.8
rxn05187	ADOCBLabc	Adenosylcobalamin transport via ABC system	h2o[c] + atp[c] + adocbl[e] => h[c] + pi[c] + adp[c] + adocbl[c]	0	(BT_1799 or BT_1489)	0	1000	4	Transport, Extracellular	PMID:4853401, PMID: 19748469	B. thetaiotaomicron requires cobalamin (vitamin B12) for growth. Gene annotation is putatively based on NCBI Gene. Cob(I)alamin adenosyltransferase gene is not essential in vitro, seems to suggest that adenosylcobalamine can also be transported.	
rxn00139	ADPT	adenine phosphoribosyltransferase	ade[c] + prpp[c] => amp[c] + ppi[c]	0	BT_3267	0	1000	2	Nucleotide Salvage Pathway			2.4.2.7
rxn00361	ADSK	adenylyl-sulfate kinase	atp[c] + aps[c] => h[c] + adp[c] + paps[c]	0	BT_0413	0	1000	2	Cysteine Metabolism		Putative annotation (NCBI Gene). Reversible in SEED	2.7.1.25
rxn00800	ADSL1r	adenylsuccinate lyase	dcamp[c] <=> amp[c] + fum[c]	1	BT_3871	-1000	1000	2	Purine and Pyrimidine Biosynthesis			4.3.2.2
rxn03136	ADSL2r	adenylosuccinate lyase	25aics[c] <=> fum[c] + aicar[c]	1	BT_3871	-1000	1000	2	Purine and Pyrimidine Biosynthesis			4.3.2.2
rxn00838	ADSS	adenylosuccinate synthase	asp-L[c] + gtp[c] + imp[c] => 2 h[c] + pi[c] + dcamp[c] + gdp[c]	0	BT_1843	0	1000	2	Purine and Pyrimidine Biosynthesis			6.3.4.4
rxn01484	AGDC	N-acetylglucosamine-6-phosphate deacetylase	h2o[c] + acgam6p[c] => ac[c] + gam6p[c]	0	(BT_0675 or BT_0676 or BT_3588)	0	1000	2	Aminosugar Metabolism			3.5.1.25

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	AGDC2	N-acetylgalactosamine-6-phosphate amidohydrolase	h2o[c] + acgal6p[c] => ac[c] + galam6p[c]	0	(BT_0675 or BT_0676 or BT_3588)	0	1000	3	Aminosugar Metabolism	PMID:2845859	B. thetaiotaomicron grows on N-acetylgalactosamine. Utilization pathway is based on assumption.	3.5.1.25
rxn01029	AGMD	Agmantine deiminase	h2o[c] + agm[c] => nh4[c] + ncptrc[c]	0	BT_0876	0	1000	3	Arginine and Proline Metabolism	PMID:10801923	This reaction is involved in the putrescine secretion pathway.	3.5.3.12
rxn03511	AGMHE	ADP-D-glycero-D-manno-heptose epimerase	adphep-DD[c] => adphep-LD[c]	0		0	1000	2	Lipopolysaccharide Biosynthesis	PMID:20974832	No gene found, but this reaction is required for lipopolysaccharide synthesis. The structure of B. thetaiotaomicron LPS has been studied.	5.1.3.20
rxn08083	AGPAT120	1-tetradecanoyl-sn-glycerol 3-phosphate O-acyltransferase (n-C12:0)	ddcaACP[c] + 1ddecg3p[c] => ACP[c] + pa120[c]	0	(BT_0243 or BT_4462)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	2.3.1.51
rxn08084	AGPAT140	1-tetradecanoyl-sn-glycerol 3-phosphate O-acyltransferase (n-C14:0)	myrsACP[c] + 1tdecg3p[c] => ACP[c] + pa140[c]	0	(BT_0243 or BT_4462)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	2.3.1.51
rxn08086	AGPAT160	1-hexadecanoyl-sn-glycerol 3-phosphate O-acyltransferase (n-C16:0)	palmACP[c] + 1hdecg3p[c] => ACP[c] + pa160[c]	0	(BT_0243 or BT_4462)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	2.3.1.51
rxn08088	AGPAT180	1-octadecanoyl-sn-glycerol 3-phosphate O-acyltransferase (n-C18:0)	1odecg3p[c] + ocdcaACP[c] => ACP[c] + pa180[c]	0	(BT_0243 or BT_4462)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	2.3.1.51
rxn08089	AGPAT181	1-octadec-7-enoyl-sn-glycerol 3-phosphate O-acyltransferase (n-C18:1)	1odec11eg3p[c] + octeACP[c] => ACP[c] + pa181[c]	0	(BT_0243 or BT_4462)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	2.3.1.51
rxn02465	AGPR	N-acetyl-g-glutamyl-phosphate reductase	nadp[c] + pi[c] + acg5sa[c] <=> h[c] + nadph[c] + acg5p[c]	1	BT_3759	-1000	1000	2	Arginine and Proline Metabolism			1.2.1.38

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn00141	AHC	adenosylhomocysteinase	h2o[c] + ahcys[c] <=> adn[c] + hcys-L[c]	1	BT_2797	-1000	1000	2	Methionine Metabolism			3.3.1.1
rxn00143	AHCYSNS_r	S-adenosylhomocysteine nucleosidase reversible	h2o[c] + ahcys[c] <=> ade[c] + rhcys[c]	1	BT_4451	-1000	1000	2	Methionine Metabolism			3.2.2.9
	AHEXASE2e	N-acetylglucosaminidase, N-glycans, extracellular	h2o[e] + s2l2n2m2m[e] => acgam[e] + s2l2n2m2mn[e]	0	(BT_4394 or BT_4395 or BT_4337 or BT_3598 or BT_1627 or BT_3868 or BT_0459 or BT_0460 or BT_0506 or BT_4681 or BT_1621 or BT_3178 or BT_0456 or BT_1051 or BT_2459)	0	1000	4	N-Glycan Degradation	PMID:16565725, PMID: 20689974	BT_4395 gene product was purified and characterized.	
	AHEXASE3e	beta-N-acetylhexosaminidase, extracellular	h2o[e] + chtbs[e] => 2 acgam[e]	0	(BT_4394 or BT_4395 or BT_4337 or BT_3598 or BT_1627 or BT_3868 or BT_0459 or BT_0460 or BT_0506 or BT_4681 or BT_1621 or BT_3178 or BT_0456 or BT_1051 or BT_2459)	0	1000	4	N-Glycan Degradation	PMID:16565725, PMID: 20689974	BT_4395 gene product was purified and characterized.	3.2.1.52

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	AHEXASEe	beta-N-acetylhexosaminidase, extracellular	2 h2o[e] + n2m2mn[e] => 2 acgam[e] + m2mn[e]	0	(BT_4394 or BT_4395 or BT_4337 or BT_3598 or BT_1627 or BT_3868 or BT_0459 or BT_0460 or BT_0506 or BT_4681 or BT_1621 or BT_3178 or BT_0456 or BT_1051 or BT_2459)	0	1000	4	N-Glycan Degradation	PMID:16565725, PMID: 20689974	BT_4395 gene product was purified and characterized.	3.2.1.52
rxn09997	AHMMPS	4-amino-5-hydroxymethyl-2-methylpyrimidine synthetase	2 h[c] + air[c] => pi[c] + 4ahmmp[c] + gcald[c]	0	BT_0650	0	1000	2	Thiamine Metabolism			
rxn00952	AHSERL2	O-acetylhomoserine (thiol)-lyase	achms[c] + h2s[c] => h[c] + ac[c] + hcys-L[c]	0	(BT_1923 or BT_2387)	0	1000	2	Methionine Metabolism			2.5.1.49
rxn06078	AHSERL3	O-Acetyl-L-homoserine acetate-lyase (adding methanethiol)	achms[c] + trdrd[c] + tsul[c] <=> h[c] + ac[c] + hcys-L[c] + trdox[c] + so3[c]	1	(BT_1923 or BT_2387)	-1000	1000	2	Methionine Metabolism		Added manually to BIGG database based on SEED database	2.5.1.49
rxn03137	AICART	phosphoribosylaminoimidazolecarboxamide formyltransferase	aicar[c] + 10fthf[c] <=> fprica[c] + thf[c]	1	BT_3812	-1000	1000	2	Purine and Pyrimidine Biosynthesis			2.1.2.3
rxn05452	AIHPDCOATA	14-methyl-hexa-decanoyl-ACP[acyl-carrier-protein] transferase	coa[c] + 14mpalmACP[c] <=> ACP[c] + aihpdcoa[c]	1	BT_0789	-1000	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.180

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05451	AIPDCOATA	12-methyl-tetra-decanoyl-ACP[acyl-carrier-protein] transferase	coa[c] + 12mmyrsACP[c] <=> ACP[c] + aipdcoa[c]	1	BT_0789	-1000	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.180
rxn05229	AIRC2	phosphoribosylaminoimidazole carboxylase	atp[c] + hco3[c] + air[c] => h[c] + pi[c] + adp[c] + 5caiz[c]	0	BT_2518	0	1000	2	Purine and Pyrimidine Biosynthesis			4.1.1.21
	AIRC3	phosphoribosylaminoimidazole carboxylase (mutase rxn)	5aizc[c] <=> 5caiz[c]	1	BT_2518	-1000	1000	2	Purine and Pyrimidine Biosynthesis		According to KEGG and BIGG databases, phosphoribosylamino imidazole carboxylase also catalyzes NCAIR mutase reaction.	4.1.1.21
rxn02938	AIRCr	phosphoribosylaminoimidazole carboxylase	co2[c] + air[c] <=> h[c] + 5aizc[c]	1	BT_2518	-1000	1000	2	Purine and Pyrimidine Biosynthesis		Irreversible in SEED	4.1.1.21
rxn03167	AKP1	alkaline phosphatase (Dihydroneopterin)	3 h2o[c] + ahdt[c] => 2 h[c] + 3 pi[c] + dhnpt[c]	0	(BT_0028 or BT_3708 or BT_4363)	0	1000	4	Folate Metabolism	PMID:3968032	Appears to be largely membrane-bound in B. thetaiotaomicron (unpublished data mentioned in PMID:3968032).	3.1.3.1
rxn00851	ALAALA	D-alanine--D-alanine ligase	atp[c] + 2 ala-D[c] => h[c] + pi[c] + adp[c] + alaala[c]	0	BT_3713	0	1000	2	Cell Envelope Biosynthesis			6.3.2.4
	ALAALADe	D-alanine-D-alanine dipeptidase, extracellular	h2o[e] + alaala[e] => 2 ala-D[e]	0	(BT_3007 or BT_3187)	0	1000	2	Peptide Degradation	PMID:12663928	Predicted non-cytosolic in PMID:12663928. Assumed to be extracellular for modeling purposes.	3.4.17.14

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn12633	ALAASP1c	Hydrolysis of L-alanyl-L-aspartate	h2o[c] + alaasp[c] <=> ala-L[c] + asp-L[c]	1	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314 or BT_1838)	-1000	1000	2	Peptide Degradation			
	ALAASPt	L-alanyl-L-aspartate transport via proton symport	h[e] + alaasp[e] => h[c] + alaasp[c]	0	(BT_0580 or BT_4385 or BT_1086)	0	1000	2	Transport, Extracellular		Genes added based on TransportDB (last consulted 06.06.12).	
rxn00278	ALAD_R	Alanine dehydrogenase	h2o[c] + ala-L[c] + nad[c] <=> h[c] + pyr[c] + nadh[c] + nh4[c]	1	BT_1554	-1000	1000	2	Alanine and Aspartate Metabolism			1.4.1.1
rxn12639	ALAGLN1c	Hydrolysis of L-alanyl-L-glutamine	h2o[c] + alagln[c] <=> ala-L[c] + gln-L[c]	1	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314 or BT_1838)	-1000	1000	2	Peptide Degradation			
	ALAGLNt	L-alanyl-L-glutamine transport via proton symport	h[e] + alagln[e] => h[c] + alagln[c]	0	(BT_0580 or BT_4385 or BT_1086)	0	1000	2	Transport, Extracellular		Genes added based on TransportDB (last consulted 06.06.12).	
rxn12640	ALAGLU1c	Hydrolysis of L-alanyl-L-glutamate	h2o[c] + alaglu[c] <=> glu-L[c] + ala-L[c]	1	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314 or BT_1838)	-1000	1000	2	Peptide Degradation			
	ALAGLUt	L-alanyl-L-glutamate transport via proton symport	h[e] + alaglu[e] => h[c] + alaglu[c]	0	(BT_0580 or BT_4385 or BT_1086)	0	1000	2	Transport, Extracellular		Genes added based on TransportDB (last consulted 06.06.12).	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn12641	ALAGLY1c	Hydrolysis of L-alanylglycine	h2o[c] + alagly[c] <=> ala-L[c] + gly[c]	1	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314 or BT_1838)	-1000	1000	2	Peptide Degradation			
	ALAGLYt	L-alanylglycine transport via proton symport	h[e] + alagly[e] => h[c] + alagly[c]	0	(BT_0580 or BT_4385 or BT_1086)	0	1000	2	Transport, Extracellular		Genes added based on TransportDB (last consulted 06.06.12).	
rxn12642	ALAHIS1c	Hydrolysis of L-alanyl-L-histidine	h2o[c] + alahis[c] <=> ala-L[c] + his-L[c]	1	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314 or BT_1838)	-1000	1000	2	Peptide Degradation			
	ALAHISt	L-alanyl-L-histidine transport via proton symport	h[e] + alahis[e] => h[c] + alahis[c]	0	(BT_0580 or BT_4385 or BT_1086)	0	1000	2	Transport, Extracellular		Genes added based on TransportDB (last consulted 06.06.12).	
rxn12643	ALALEU1c	Hydrolysis of L-alanyl-L-leucine	h2o[c] + alaleu[c] <=> ala-L[c] + leu-L[c]	1	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314 or BT_1838)	-1000	1000	2	Peptide Degradation			
	ALALEUt	L-alanyl-L-leucine transport via proton symport	h[e] + alaleu[e] => h[c] + alaleu[c]	0	(BT_0580 or BT_4385 or BT_1086)	0	1000	2	Transport, Extracellular		Genes added based on TransportDB (last consulted 06.06.12).	
rxn00283	ALAR	alanine racemase	ala-L[c] <=> ala-D[c]	1	BT_4101	-1000	1000	2	Alanine and Aspartate Metabolism		Annotation from KEGG and NCBI Gene (last updated 01.01.11)	5.1.1.1

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05496	ALAt4r	Alanine-Sodium symporter	na1[e] + ala-L[e] <=> ala-L[c] + na1[c]	1	BT_4476	-1000	1000	2	Transport, Extracellular		Annotation from TransportDB (www.membranetransport.org).	
rxn12644	ALATHR1c	Hydrolysis of L-alanyl-L-threonine	h2o[c] + alathr[c] <=> ala-L[c] + thr-L[c]	1	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314 or BT_1838)	-1000	1000	2	Peptide Degradation			
	ALATHRt	L-alanyl-L-threonine transport via proton symport	h[e] + alathr[e] => h[c] + alathr[c]	0	(BT_0580 or BT_4385 or BT_1086)	0	1000	2	Transport, Extracellular		Genes added based on TransportDB (last consulted 06.06.12).	
rxn00763	ALCD19	alcohol dehydrogenase (glycerol)	h[c] + nadh[c] + glyald[c] <=> nad[c] + glyc[c]	1	(BT_0535 or BT_4512)	-1000	1000	2	Alternate Carbon Metabolism		This reaction was included by Model SEED, but may not take place. in B. thetaiotaomicron.	1.1.1.1
rxn00543	ALCD2x	alcohol dehydrogenase (ethanol)	nad[c] + etoh[c] <=> h[c] + nadh[c] + acald[c]	1	(BT_0535 or BT_4512)	-1000	1000	2	Central Metabolism	PMID:17563350 supports genome annotation		1.1.1.1
rxn00743	ALKP	alkaline phosphatase	h2o[c] + dhap[c] => pi[c] + dha[c]	0	(BT_0028 or BT_3708 or BT_4363)	0	1000	4	Glycerophospholipid Metabolism	PMID:3968032	Appears to be largely membrane-bound in B. thetaiotaomicron (unpublished data mentioned in PMID:3968032).	3.1.3.1

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	ALR2	aldose reductase (methylglyoxal)	h[c] + nadph[c] + mthgxl[c] => nadp[c] + acetol[c]	0		0	1000	2	Central Metabolism	PMID:18848625, PMID:8370454, PMID:11260473	No GPR is known. The reaction is putatively added to reconcile the results by PMID:18848625, which suggest the presence of a second pathway for 1,2-propanediol formation in B. thetaiotaomicron. Also based on pathways described by PMID:8370454. There is evidence for acetol production in B. thetaiotaomicron (PMID:11260473).	1.1.1.21
	ALR4x	aldose reductase (acetol)	h[c] + nadh[c] + acetol[c] => 12ppd-R[c] + nad[c]	0	(BT_3617 or BT_4424)	0	1000	3	Glycerophospholipid Metabolism	PMID:18848625, PMID:8370454	The reaction is carried out by sorbitol dehydrogenase. Added to reconcile the results by PMID:18848625, which suggest the presence of a second pathway for 1,2-propanediol formation in B. thetaiotaomicron. Also based on pathways described by PMID:8370454.	
rxn01122	ALTRH	altronate hydrolase	altrn[c] => h2o[c] + 2ddglcn[c]	0	BT_0486	0	1000	2	Alternate Carbon Metabolism			4.2.1.7

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn02875	AMAA	N-acetylmuramoyl-L-alanine amidase	h2o[c] + acmama[c] => ala-L[c] + acmam[c]	0	(BT_1991 or BT_2027 or BT_2141 or BT_3200 or BT_4736 or BT_0706 or BT_1168 or BT_1519 or BT_1641 or BT_1706 or BT_4031)	0	1000	2	Cell Envelope Biosynthesis			3.5.1.28
rxn08126	AMALT1	Amylomaltase (maltotriose)	malt[c] + malttr[c] => glc-D[c] + maltttr[c]	0	BT_2146	0	1000	2	Alternate Carbon Metabolism		Reversible in SEED	2.4.1.25
rxn08127	AMALT2	Amylomaltase (maltotetraose)	malt[c] + maltttr[c] => glc-D[c] + maltpt[c]	0	BT_2146	0	1000	2	Alternate Carbon Metabolism		Reversible in SEED	2.4.1.25
rxn08128	AMALT3	Amylomaltase (maltopentaose)	malt[c] + maltpt[c] => glc-D[c] + malthx[c]	0	BT_2146	0	1000	2	Alternate Carbon Metabolism		Reversible in SEED	2.4.1.25
rxn08129	AMALT4	Amylomaltase (maltohexaose)	malt[c] + malthx[c] => glc-D[c] + malthp[c]	0	BT_2146	0	1000	2	Alternate Carbon Metabolism		Reversible in SEED	2.4.1.25

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	AMANNANASEe	Alpha-mannan degradation, extracellular	139 h2o[e] + amannan140[e] <=> 140 man[e]	1	((BT_3990 or BT_2629 or BT_2199 or BT_3784 or BT_3962 or BT_4092) and (BT_3991 or BT_3858 or BT_1769 or BT_1878 or BT_3130 or BT_3773) and (BT_3994 or BT_3792 or BT_2623 or BT_2949 or BT_3501 or BT_1883 or BT_3524 or BT_3301 or BT_3521) and ((BT_2625 and BT_2626) or (BT_3788 and BT_3789) or (BT_3854 and BT_3855)))	-1000	1000	4	N-Glycan Degradation	PMID: 22205877, PMID: 20081828	B. thetaiotaomicron grows on yeast alpha-mannan.The enzymes carrying out the reaction are assumed to be secreted. The reaction involves cleaving of alpha-1,2, -1,3 and -1,6 bonds. Several susC and susD are upregulated during growth on alpha-mannan (included in the GPR).	
rxn02312	AMAOTr	adenosylmethionine-8-amino-7-oxononanoate transaminase	8aonn[c] + amet[c] <=> amob[c] + dann[c]	1	BT_1442	-1000	1000	4	Cofactor and Prosthetic Group Biosynthesis	PMID:4853401, PMID:20693992	B. thetaiotaomicron does not require biotin (PMID:4853401). Most likely, biotin is synthesized as described in PMID:20693992.	2.6.1.62
	AMMQLT8	S-adenosylmethione:2-demthylmenaquinole methyltransferase (menaquinone 8)	amet[c] + 2dmmql8[c] => h[c] + ahcys[c] + mql8[c]	0	(BT_0853 or BT_4216)	0	1000	3	Cofactor and Prosthetic Group Biosynthesis	PMID:6102980	B. thetaiotaomicron produces menaquinone 8.	2.1.1.-

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	AMMQT10	S-adenosylmethione:2-demthylmenaquinone methyltransferase (menaquinone 10)	h[c] + amet[c] + 2dmmq10[c] => ahcys[c] + mql10[c]	0	(BT_0853 or BT_4216)	0	1000	4	Cofactor and Prosthetic Group Biosynthesis	PMID:6102980	B. thetaiotaomicron produces menaquinone 7,8,9,10 and 11. MK-10 and MK-11 are the main components. Reaction is not charge balanced. Needs to be fixed. AH	
	AMMQT11	S-adenosylmethione:2-demthylmenaquinone methyltransferase (menaquinone 11)	h[c] + amet[c] + 2dmmq11[c] => ahcys[c] + mql11[c]	0	(BT_0853 or BT_4216)	0	1000	4	Cofactor and Prosthetic Group Biosynthesis	PMID:6102980	B. thetaiotaomicron produces menaquinone 7,8,9,10 and 11. MK-10 and MK-11 are the main components. Reaction is not charge balanced. Needs to be fixed. AH	
	AMMQT7	S-adenosylmethione:2-demthylmenaquinone methyltransferase (menaquinone 7)	h[c] + amet[c] + 2dmmq7[c] => ahcys[c] + mql7[c]	0	(BT_0853 or BT_4216)	0	1000	4	Cofactor and Prosthetic Group Biosynthesis	PMID:6102980	B. thetaiotaomicron produces menaquinone 7,8,9,10 and 11. MK-10 and MK-11 are the main components. Reaction is not charge balanced. Needs to be fixed. AH	
rxn10094	AMMQT8	S-adenosylmethione:2-demthylmenaquinone methyltransferase (menaquinone 8)	h[c] + amet[c] + 2dmmq8[c] => ahcys[c] + mql8[c]	0	(BT_0853 or BT_4216)	0	1000	4	Cofactor and Prosthetic Group Biosynthesis	PMID:6102980	B. thetaiotaomicron produces menaquinone 7,8,9,10 and 11. MK-10 and MK-11 are the main components. Reaction is not charge balanced. Needs to be fixed. AH	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	AMMQT9	S-adenosylmethione:2-demthylmenaquinone methyltransferase (menaquinone 9)	h[c] + amet[c] + 2dmmq9[c] => ahcys[c] + mql9[c]	0	(BT_0853 or BT_4216)	0	1000	4	Cofactor and Prosthetic Group Biosynthesis	PMID:6102980	B. thetaiotaomicron produces menaquinone 7,8,9,10 and 11. MK-10 and MK-11 are the main components. Reaction is not charge balanced. Needs to be fixed. AH	
rxn00131	AMPN	AMP nucleosidase	h2o[c] + amp[c] => ade[c] + r5p[c]	0	BT_0888	0	1000	2	Nucleotide Salvage Pathway		Reversible in SEED	3.2.2.4
rxn00650	AMPTASECG	alanyl aminopeptidase (cys-gly)	h2o[c] + cgly[c] => gly[c] + cys-L[c]	0	(BT_0638 or BT_1615 or BT_2706 or BT_4045)	0	1000	2	Peptide Degradation			3.4.11.2
	AMPTASEPG	aminopeptidase (pro-gly)	h2o[c] + progly[c] => gly[c] + pro-L[c]	0	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314)	0	1000	2	Peptide Degradation			
	AMPTASEPGe	hydrolysis of Prolylglycine by predicted non-cytosolic proline peptidase	h2o[e] + progly[e] => pro-L[e] + gly[e]	0	BT_0587	0	1000	2	Peptide Degradation	PMID:12663928	Predicted non-cytosolic in PMID:12663928. Assumed to be extracellular for modeling purposes.	3.4.13.9
	AMY1e	alpha-amylase, extracellular (strch1 -> strch2)	8 h2o[e] + strch1[e] => 8 glc-D[e] + strch2[e]	0	((BT_3698 and BT_3701 and BT_3702) or (BT_0773 and BT_3701 and BT_3702) or (BT_4305 and BT_3701 and BT_3702))	0	1000	4	Plant Polysaccharide Degradation	PMID:10986238, PMID:2722747, PMID:8955399, PMID: 18981178, PMID:18611383	Starch utilization by B. thetaiotaomicron as sole carbon source is well established.	3.2.1.1

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	AMYe	starch hydrolysis by alpha-1,4-amylase and alpha-1,6 pullulanase	499 h2o[e] + starch1200[e] => 100 glc-D[e] + 100 malt[e] + 300 malttr[e]	0	((BT_3698 and BT_3701 and BT_3702) or (BT_0773 and BT_3701 and BT_3702) or (BT_4305 and BT_3701 and BT_3702))	0	1000	4	Plant Polysaccharide Degradation	PMID:10986238, PMID:2722747, PMID:8955399, PMID: 18981178, PMID:18611383	Starch utilization by B. thetaiotaomicron as sole carbon source is well established.	3.2.1.1
	AMYLe	amylose hydrolysis by alpha-1,4-amylase	199 h2o[e] + amylose300[e] => 100 glc-D[e] + 100 malt[e]	0	((BT_3698 and BT_3701 and BT_3702) or (BT_0773 and BT_3701 and BT_3702) or (BT_4305 and BT_3701 and BT_3702))	0	1000	4	Plant Polysaccharide Degradation	PMID:10986238, PMID:2722747, PMID:8955399, PMID: 18981178, PMID:18611383	Starch utilization by B. thetaiotaomicron as sole carbon source is well established.	3.2.1.1
rxn00791	ANPRT	anthranilate phosphoribosyltransferase	prpp[c] + anth[c] => ppi[c] + pran[c]	0	BT_0530	0	1000	2	Tyrosine, Tryptophan, and Phenylalanine Metabolism			2.4.2.18
rxn00727	ANS	anthranilate synthase	gln-L[c] + chor[c] => h[c] + glu-L[c] + pyr[c] + anth[c]	0	(BT_0531 and BT_0532)	0	1000	2	Tyrosine, Tryptophan, and Phenylalanine Metabolism			4.1.3.27
rxn00726	ANS2	anthranilate synthase 2	nh4[c] + chor[c] => h2o[c] + h[c] + pyr[c] + anth[c]	0	(BT_0531 and BT_0532)	0	1000	2	Tyrosine, Tryptophan, and Phenylalanine Metabolism			4.1.3.27
rxn02666	AOBUTDs	L-2-amino-3-oxobutanoate decarboxylation (spontaneous)	h[c] + 2aobut[c] => co2[c] + aact[c]	0		0	1000	1	Threonine and Lysine Metabolism			
rxn02297	AOXSr	8-amino-7-oxononanoate synthase	h[c] + ala-L[c] + pmcoa[c] <=> coa[c] + co2[c] + 8aonn[c]	1	(BT_0870 or BT_1443)	-1000	1000	4	Cofactor and Prosthetic Group Biosynthesis	PMID:20693992	Irreversible reaction in SEED. This enzyme was recently shown to use pimeloyl-ACP. It is assumed to utilize both substrates.	2.3.1.47

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	AOXSr2	8-amino-7-oxononanoate synthase (pimeloyl-ACP)	h[c] + ala-L[c] + pmACP[c] <=> ACP[c] + co2[c] + 8aonn[c]	1	(BT_0870 or BT_1443)	-1000	1000	4	Biotin Metabolism	PMID:20693992	This enzyme is generally believed to utilize pimeloyl-CoA. Use of pimeloyl-ACP was recently shown.	2.3.1.47
rxn02474	APRAUR	5-amino-6-(5-phosphoribosylamino)uracil reductase	h[c] + nadph[c] + 5apru[c] => nadp[c] + 5aprbu[c]	0	BT_3728	0	1000	2	Cofactor and Prosthetic Group Biosynthesis			1.1.1.193
rxn09988	ARABASE3e	arabinotriose arabinosidase	2 h2o[e] + arabttr[e] => 3 arab-L[e]	0	(BT_0348 or BT_3096 or BT_3657)	0	1000	4	Plant Polysaccharide Degradation	PMID: 21339299	Takes place in periplasm. Extracellular for modelling purposes.	3.2.1.55
	ARABINANASEe	Arabinan degradation, extracellular	100 h2o[e] + arabinan101[e] <=> 97 arab-L[e] + gal[e] + rmn[e] + 2 galur[e]	1	((BT_0360 or BT_0367 or BT_0368 or BT_0369) and (BT_4152 or BT_4667 or BT_4668) and (BT_4153 or BT_4170) and (BT_4175 or BT_4176) and ((BT_0361 and BT_0362) or (BT_4164 and BT_4165) or (BT_0363 and BT_0364) or (BT_4670 and BT_4671) or (BT_3680 and BT_3681)))	-1000	1000	4	Plant Polysaccharide Degradation	PMID: 22205877, PMID: 21339299	B. thetaiotaomicron grows on arabinan. BT_0360, BT_0367 and BT_0369 are active against sugar beet arabinan. susC/susD homologs and enzymes for galactose, galacturonate and L-rhamnose degradation (included in GPR) are upregulated during growth on arabinan.	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	ARABINOGALASEe	Arabinogalactan degradation by beta-galactosidase, endo-arabinofuranosidase and beta-glucuronidase, extracellular/periplasmatic	659 h2o[e] + arabinogal[e] => 15 h[e] + 92 arab-L[e] + 552 gal[e] + 15 glcur[e]	0	((BT_0348 or BT_0265 or BT_3675 or BT_3685) and BT_0290 and BT_3687 and ((BT_3045 and BT_3046) or (BT_0268 and BT_0269) or (BT_0272 and BT_0273) or (BT_3680 and BT_3681)))	0	1000	4	Plant Polysaccharide Degradation	PMID:848954, PMID:7251978, PMID:16887514 PMID:10820072, PMID: 22205877	B. thetaiotaomicron degrades larch arabinogalactan, which consists of galactose/arabinose (6:1) and small amounts of glucuronic acid. Larch AG is likely degraded via beta-galactosidase, Arabinan endo-1,5-alpha-L-arabinosidase (EC 3.2.1.99) and Alpha-N-arabinofuranosidase (EC 3.2.1.55) and involves susC/ susD. The genes included in the GPR are upregulated during growth on arabinogalactan.	
rxn01292	ARAI	L-arabinose isomerase	arab-L[c] <=> rbl-L[c]	1	BT_0351	-1.000	1000	2	Alternate Carbon Metabolism			5.3.1.4
rxn05500	ARBt2r	L-arabinose transport via proton symport	h[e] + arab-L[e] <=> h[c] + arab-L[c]	1	BT_0454	-1000	1000	4	Transport, Extracellular	PMID: 21339299, PMID: 16887504	PMID: 21339299: evidence for arabinose uptake. B. thetaiotaomicron grows on arabinose (i.e. PMID: 16887504)	
rxn05154	ARGabc	L-arginine transport via ABC system	h2o[c] + atp[c] + arg-L[e] => h[c] + pi[c] + adp[c] + arg-L[c]	0	BT_4049	0	1000	2	Transport, Extracellular		Annotation from NCBI Gene (last updated 01.01.11)	
	ARGARG1c	Hydrolysis of L-argininyl-L-arginine	h2o[c] + argarg[c] <=> 2 arg-L[c]	1	BT_1846	-1000	1000	4	Peptide Degradation	PMID: 22628297	B. thetaiotaomicron peptidase M49 was characterized and shown to hydrolyze Arg-Arg and Phe-Arg specifically.	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	ARGARGt	L-argininyl-L-arginine transport via proton symport	h[e] + argarg[e] <=> h[c] + argarg[c]	1	(BT_0580 or BT_4385 or BT_1086)	-1000	1000	4	Transport, Extracellular	PMID: 22628297	B. thetaiotaomicron peptidase M49 was characterized and shown to hydrolyze Arg-Arg and Phe-Arg specifically.	
rxn00405	ARGDC	arginine decarboxylase	h[c] + arg-L[c] => co2[c] + agm[c]	0	BT_3394	0	1000	2	Arginine and Proline Metabolism			4.1.1.19
rxn00394	ARGN	arginase	h2o[c] + arg-L[c] => orn[c] + urea[c]	0	BT_1099	0	1000	2	Arginine and Proline Metabolism		Putative gene annotation	3.5.3.1
rxn00802	ARGSL	argininosuccinate lyase	argsuc[c] <=> fum[c] + arg-L[c]	1	BT_3733	-1000	1000	2	Alanine and Aspartate Metabolism			4.3.2.1
rxn01434	ARGSSr	argininosuccinate synthase, reversible	atp[c] + asp-L[c] + citr-L[c] <=> h[c] + amp[c] + ppi[c] + argsuc[c]	1	BT_3760	-1000	1000	2	Arginine and Proline Metabolism			6.3.4.5
	AROH	L-Arogenate hydro-lyase	Largn[c] => h2o[c] + co2[c] + phe-L[c]	0	BT_3936	0	1000	2	Tyrosine, Tryptophan, and Phenylalanine Metabolism		Added based on KEGG Pathway	4.2.1.51
	AS3TASE_HS1	N-acetylglucosamine-3-sulfatase, heparin degradation	h2o[e] + hspg_degr_4[e] => h[e] + hspg_degr_5[e] + so4[e]	0		0	1000	2	Glycosaminoglycan Degradation	PMID:19801541, PMID:7574611	B.thetaiotaomicron specific putative heparin sulfate degradation pathway. It is unknown which sulfatase catalyzes this reaction.	3.1.6.14
	AS3TASE_HS2	N-acetylglucosamine-3-sulfatase, heparin degradation	h2o[e] + hspg_degr_9[e] => h[e] + so4[e] + hspg_degr_10[e]	0		0	1000	2	Glycosaminoglycan Degradation	PMID:19801541, PMID:7574611	B.thetaiotaomicron specific putative heparin sulfate degradation pathway. It is unknown which sulfatase catalyzes this reaction.	3.1.6.14

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	AS6TASE_HS1	N-acetylglucosamine-6-sulfatase, heparin degradation	2 h2o[e] + hspg_degr_3[e] => 2 h[e] + hspg_degr_4[e] + 2 so4[e]	0	(BT_4656 and BT_0238)	0	1000	4	Glycosaminoglycan Degradation	PMID:19801541, PMID:7574611, PMID:21507958	B. thetaiotaomicron specific putative heparin sulfate degradation pathway. Requires sulfatase-maturing enzyme (BT_0238) to be functional.	3.1.6.14
	AS6TASE_HS2	N-acetylglucosamine-6-sulfatase, heparin degradation	h2o[e] + hspg_degr_8[e] => h[e] + so4[e] + hspg_degr_9[e]	0	(BT_4656 and BT_0238)	0	1000	4	Glycosaminoglycan Degradation	PMID:19801541, PMID:7574611, PMID:21507958	B. thetaiotaomicron specific putative heparin sulfate degradation pathway. Requires sulfatase-maturing enzyme (BT_0238) to be functional.	3.1.6.14
rxn01643	ASADi	Aspartate-semialdehyde dehydrogenase	h[c] + nadph[c] + 4pasp[c] => nadp[c] + pi[c] + aspsa[c]	0	BT_3636	0	1000	2	Threonine and Lysine Metabolism			1.2.1.11
rxn00342	ASNN	L-asparaginase	h2o[c] + asn-L[c] => asp-L[c] + nh4[c]	0	(BT_0526 or BT_2404 or BT_2757)	0	1000	2	Alanine and Aspartate Metabolism			3.5.1.1
rxn00416	ASNS1	asparagine synthase (glutamine-hydrolysing)	h2o[c] + atp[c] + asp-L[c] + gln-L[c] => h[c] + glu-L[c] + amp[c] + ppi[c] + asn-L[c]	0	BT_0551	0	1000	2	Alanine and Aspartate Metabolism			6.3.5.4
rxn00340	ASNS2	asparagine synthetase	atp[c] + asp-L[c] + nh4[c] => h[c] + amp[c] + ppi[c] + asn-L[c]	0	BT_2129	0	1000	2	Alanine and Aspartate Metabolism			6.3.1.1
	ASNt2r	L-asparagine reversible transport via proton symport	h[e] + asn-L[e] <=> h[c] + asn-L[c]	1		-1000	1000	2	Transport, Extracellular	Dworkin, M. and S. Falkow (2006). The prokaryotes : a handbook on the biology of bacteria. New York ; [London], Springer	B. thetaiotaomicron is weakly proteolytic, so a transport reaction for all amino acids is assumed.	
rxn00346	ASP1DC	aspartate 1-decarboxylase	h[c] + asp-L[c] => co2[c] + ala-B[c]	0	BT_4309	0	1000	2	Cofactor and Prosthetic Group Biosynthesis			4.1.1.15

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn01018	ASPCT	aspartate carbamoyltransferase	asp-L[c] + cbp[c] => h[c] + pi[c] + cbasp[c]	0	(BT_0741 and BT_0742)	0	1000	2	Purine and Pyrimidine Biosynthesis			2.1.3.2
rxn00337	ASPK	aspartate kinase	atp[c] + asp-L[c] <=> adp[c] + 4pasp[c]	1	(BT_1375 or BT_1901 or BT_2403)	-1000	1000	2	Threonine and Lysine Metabolism			2.7.2.4
rxn00262	ASPO1	L-aspartate oxidase	h2o[c] + asp-L[c] + o2[c] => nh4[c] + h2o2[c] + oaa[c]	0	BT_3184	0	1000	2	Cofactor and Prosthetic Group Biosynthesis	PMID:11863440	O2 can be replaced by fumarate as electron acceptor, yielding succinate. The ability of the enzyme to use both O2 and fumarate in cofactor reoxidation enables it to function under both aerobic and anaerobic conditions.	1.4.3.16
	ASPO5	L-aspartate oxidase	fum[c] + asp-L[c] => h[c] + iasp[c] + succ[c]	0	BT_3184	0	1000	2	Cofactor and Prosthetic Group Biosynthesis	PMID:11863440	O2 can be replaced by fumarate as electron acceptor, yielding succinate. The ability of the enzyme to use both O2 and fumarate in cofactor reoxidation enables it to function under both aerobic and anaerobic conditions.	1.4.3.16
rxn00338	ASPO6	L-aspartate oxidase	asp-L[c] + o2[c] => h[c] + h2o2[c] + iasp[c]	0	BT_3184	0	1000	2	Cofactor and Prosthetic Group Biosynthesis			1.4.3.16
rxn00347	ASPT	L-aspartase	asp-L[c] => fum[c] + nh4[c]	0	BT_2755	0	1000	2	Alanine and Aspartate Metabolism			4.3.1.1
	ASPt2r	L-aspartate reversible transport via proton symport	h[e] + asp-L[e] <=> h[c] + asp-L[c]	1		-1000	1000	2	Transport, Extracellular	Dworkin, M. and S. Falkow (2006). The prokaryotes : a handbook on the biology of bacteria. New York ; [London], Springer	B. thetaiotaomicron is weakly proteolytic, so a transport reaction for all amino acids is assumed.	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn00260	ASPTA	aspartate transaminase	akg[c] + asp-L[c] <=> glu-L[c] + oaa[c]	1	(BT_3935 or BT_3720 or BT_3375 or BT_0666 or BT_1077 or BT_1476 or BT_2415)	-1000	1000	2	Alanine and Aspartate Metabolism			2.6.1.1
	ATPM	ATP maintenance requirement	h2o[c] + atp[c] => h[c] + pi[c] + adp[c]	0		84.300	1000	0	Unassigned		Added based on published reconstructions in BIGG database	
rxn00789	ATPPRT	ATP phosphoribosyltransferase	atp[c] + prpp[c] => ppi[c] + prbatp[c]	0	BT_0200	0	1000	2	Histidine Metabolism			2.4.2.17
rxn10042	ATPS4	ATP synthase (four protons for one ATP)	pi[c] + adp[c] + 4 h[e] => h2o[c] + 3 h[c] + atp[c]	0	(BT_0711 and BT_0712 and BT_0714 and BT_0715 and BT_0716 and BT_0717 and BT_0718 and BT_0719)	0	1000	2	Central Metabolism		UniProt: Reviewed, ATPase is confirmed to be made up of the present 8 SUs	3.6.3.14
	B_MANNASEe	beta-mannosidase, extracellular	h2o[e] + mn[e] => acgam[e] + man[e]	0	(BT_0458 or BT_2855 or BT_4074 or BT_2432 or BT_3599)	0	1000	4	N-Glycan Degradation	PMID:17287210	BT_0458 gene product was purified and characterized. Shown to have beta-mannosidase activity on human N-glycans.	3.2.1.25
rxn00792	BACCL	biotin-[acetyl-CoA-carboxylase] ligase	h[c] + atp[c] + btn[c] => ppi[c] + btamp[c]	0	BT_2238	0	1000	2	Biotin Metabolism			6.3.4.15
rxn00020	BGLA	1,4-beta-D-Glucan glucohydrolase	h2o[c] + cellb[c] => 2 glc-D[c]	0	(BT_3009 or BT_3300 or BT_3314 or BT_1778)	0	1000	4	Alternate Carbon Metabolism	PMID:879772	Beta-glucosidase activity and cellobiose degradation was shown experimentally in B. thetaiotaomicron.	3.2.1.21

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
			34.7965 h2o[c] + 0.25601 glu-L[c] + 0.50006 ala-L[c] + 0.004668 ACP[c] + 0.004668 coa[c] + 0.004668 nadp[c] + 0.004668 nad[c] + 0.004668 na1[c] + 40.1701 atp[c] + 0.004668 adocbl[c] + 0.23468 asp-L[c] + 0.2091 gtp[c] + 0.004668 10fthf[c] + 0.004668 thf[c] + 0.25601 gln-L[c] + 0.5958 gly[c] + 0.092623 his-L[c] + 0.43866 leu-L[c] + 0.24665 thr-L[c] + 0.004668 amet[c] + 0.004668 mql8[c] + 0.004668 mql10[c] + 0.004668 mql11[c] + 0.004668 mql7[c] + 0.004668 mql9[c] + 0.08898 cys-L[c] + 0.21543 pro-L[c] + 0.28828 arg-L[c] + 0.18056 phe-L[c] + 0.23468 asn-L[c] + 0.004668 btn[c] + 0.14934 met-L[c] + 0.004668 ca2[c] + 0.12988 ctp[c] + 0.010648 pg140[c] + 0.010648 clpn140[c] + 0.010648 pg160[c] +									

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn00137	BPNT	3',5'-bisphosphate nucleotidase	h2o[c] + pap[c] => pi[c] + amp[c]	0		0	1000	1	Cysteine Metabolism		Added by Model SEED during auto-completion step in pipeline.	3.1.3.7
rxn06673	BTNPL	holocarboxylase synthestase (biotin protein ligase)	btamp[c] + apoC_Lys[c] => h[c] + amp[c] + apoC_Lys_btn[c]	0	(BT_1450 or BT_1917)	0	1000	2	Biotin Metabolism		Not sure about synthesis of apoC_Lys in B. thetaiotaomicron.	6.4.1.1
	BTNt2	Biotin reversible transport via proton symport	h[e] + btn[e] <=> h[c] + btn[c]	1		-1000	1000	2	Transport, Extracellular	PMID: 19748469	B. thetaiotaomicron mutants in biotin biosynthesis are not essential in vitro on tryptone-yeast extract-glucose medium, suggesting that B. thetaiotaomicron can uptake biotin from yeast extract.	
rxn08180	BTS4	Biotin synthase	amet[c] + dtbt[c] + s[c] => h[c] + dad-5[c] + btn[c] + met-L[c]	0	BT_1442	0	1000	4	Cofactor and Prosthetic Group Biosynthesis	PMID:4853401, PMID:20693992	B. thetaiotaomicron does not require biotin (PMID:4853401). Most likely, biotin is synthesized as described in PMID:20693992.	2.8.1.6
rxn01236	BUTK	Butyrate kinase	atp[c] + but[c] => adp[c] + butpi[c]	0	BT_2552	0	1000	2	Butanoate Metabolism		Reversible in SEED	2.7.2.7
rxn10447	CA2abc	calcium transport via ABC system	h2o[c] + atp[c] + ca2[e] => h[c] + pi[c] + adp[c] + ca2[c]	0	BT_2541	0	1000	3	Transport, Extracellular	PMID:4472783	B. thetaiotaomicron requires calcium in medium. Gene annotation added manually based on NCBI Gene.	
	CARNCNc	hydrolysis of L-Carnosine for uptake	h2o[c] + carn[c] <=> his-L[c] + ala-B[c]	1	(BT_4045 or BT_1615)	-1000	1000	2	Histidine Metabolism	PMID:3543210, PMID:12663928	B. thetaiotaomicron is weakly proteolytic. Has a predicted cytosolic Nalpha-(beta-alanyl)-L-histidine hydrolase.	3.4.13.20 or 3.4.13.18

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	CARPEPT1tr	Reversible transport of L-Carnosine by Di-/tripeptide transporter	h[e] + carn[e] <=> h[c] + carn[c]	1	(BT_4385 or BT_0580)	-1000	1000	2	Transport, Extracellular	PMID:3543210, PMID:12663928	B. thetaiotaomicron is weakly proteolytic. Has a predicted cytosolic Nalpha-(beta-alanyl)-L-histidine hydrolase.	
rxn00006	CAT	catalase	2 h2o2[c] => 2 h2o[c] + o2[c]	0	BT_1971	0	1000	4	ROS Detoxification	PMID:9371450		1.11.1.6
	CAt7r	calcium / sodium antiporter (1:3), reversible	3 na1[e] + ca2[c] <=> 3 na1[c] + ca2[e]	1	BT_3019	-1000	1000	3	Transport, Extracellular	PMID: 19748469	BT_2541 KO appears to be viable in vitro, which suggest that another calcium transporter exists.	
rxn10147	CBL1abc	Cob(1)alamin transport via ABC system	h2o[c] + atp[c] + cbl1[e] => h[c] + pi[c] + adp[c] + cbl1[c]	0	(BT_1799 or BT_1489)	0	1000	4	Transport, Extracellular	PMID:4853401	B. thetaiotaomicron requires cobalamin (vitamin B12) for growth. Gene annotation is putatively based on NCBI Gene.	
rxn08194	CBLAT	cob(I)alamin adenosyltransferase	h[c] + atp[c] + cbl1[c] <=> pppi[c] + adocbl[c]	1	BT_2760	-1000	1000	3	Cofactor and Prosthetic Group Biosynthesis	PMID:148460	B. thetaiotaomicron requires Vitamin B12 in medium.	2.5.1.17
rxn00414	CBPS	carbamoyl-phosphate synthase (glutamine-hydrolysing)	h2o[c] + 2 atp[c] + hco3[c] + gln-L[c] => 2 h[c] + glu-L[c] + pi[c] + 2 adp[c] + cbp[c]	0	(BT_0556 and BT_0557 and BT_3866)	0	1000	2	Purine and Pyrimidine Biosynthesis			6.3.5.5
	CCP	Cytochrome c peroxidase	2 h[c] + h2o2[c] + 2 focytcc553[c] => 2 h2o[c] + 2 ficytcc553[c]	0	BT_1606	0	1000	2	ROS Detoxification		Added based on annotation from NCBI Gene.	1.11.1.5
rxn05516	CD2abc1	cadmium transport out via ABC system	h2o[c] + atp[c] + cd2[c] => h[c] + pi[c] + adp[c] + cd2[e]	0	BT_1091	0	1000	2	Transport, Extracellular			
rxn01750	CDPGHL	CDPglucose 4,6-hydro-lyase	cdpglc[c] => h2o[c] + cdpddg[c]	0	BT_1350	0	1000	2	Alternate Carbon Metabolism		Added based on KEGG Pathway. The product's function and further metabolic fate seems to be unknown.	4.2.1.45

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn03908	CDPMEK	4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase	atp[c] + 4c2me[c] => h[c] + adp[c] + 2p4c2me[c]	0	BT_0624	0	1000	2	Cofactor and Prosthetic Group Biosynthesis		Reversible in SEED	2.7.1.148
	CEPTC_BT	choline phosphotransferase	cdpchol[c] + cer1_bt[c] => h[c] + cmp[c] + sphmyln_bt[c]	0		0	1000	2	Sphingolipid Metabolism	PMID:6102980, PMID:16887518, PMID:20855611, Anaerobe (2001) 07, 103?112 doi:10.1006/anae.2001.0376	Bacteroides are well established to produce sphingolipids. Pathway added manually to BIGG database to represent known structural differences between eukaryotic and bacterial sphingolipids. The main sphingolipid types in B. thetaiotaomicron are ceramide-1-phosphoethanolamine and ceramide-1-phosphocholine. The fatty acid is usually branched. In B. thetaiotaomicron, the main FA is iso-branched C17. However, no homolog of human ceramide synthase was found in Bacteroides species. Either Bacteroides have structural homologs of this enzyme, which are not revealed by BLASTP search, or sphingolipids are synthesized by another mechanism.	2.7.8.3

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	CEPTE_BT	ethanolamine phosphotransferase (B.thetaiotaomicron specific)	cer1_bt[c] + cdpea[c] => h[c] + cmp[c] + pe_cer1_bt[c]	0		0	1000	2	Sphingolipid Metabolism	PMID:6102980, PMID:16887518, PMID:20855611, Anaerobe (2001) 07, 103?112 doi:10.1006/anae.2001.0376	Bacteroides are well established to produce sphingolipids. Pathway added manually to BIGG database to represent known structural differences between eukaryotic and bacterial sphingolipids. The main sphingolipid types in B. thetaiotaomicron are ceramide-1-phosphoethanolamine and ceramide-1-phosphocholine. The fatty acid is usually branched. In B. thetaiotaomicron, the main FA is iso-branched C17. However, no homolog of human ceramide synthase was found in Bacteroides species. Either Bacteroides have structural homologs of this enzyme, which are not revealed by BLASTP search, or sphingolipids are synthesized by another mechanism.	2.7.8.1

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	CERS_BT	Ceramide-1 synthase (B.thetaioataomicron specific)	sphgn[c] + ihpdcoa[c] => h[c] + coa[c] + cer1_bt[c]	0		0	1000	2	Sphingolipid Metabolism	PMID:6102980, PMID:16887518, PMID:20855611, Anaerobe (2001) 07, 103?112 doi:10.1006/anae .2001.0376	Bacteroides are well established to produce sphingolipids. Pathway added manually to BIGG database to represent known structural differences between eukaryotic and bacterial sphingolipids. The main sphingolipid types in B. thetaiotaomicron are ceramide-1-phosphoethanolamine and ceramide-1-phosphocholine. The fatty acid is usually branched. In B. thetaiotaomicron, the main FA is iso-branched C17. However, no homolog of human ceramide synthase was found in Bacteroides species. Either Bacteroides have structural homologs of this enzyme, which are not revealed by BLASTP search, or sphingolipids are synthesized by another mechanism.	
	CGLYt3_2_	Cys-Gly transport in via proton symport	2 h[e] + cgly[e] => 2 h[c] + cgly[c]	0	(BT_0580 or BT_4385 or BT_1086)	0	1000	2	Transport, Extracellular		Genes added based on TransportDB (last consulted 06.06.12).	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	CHLPCTD	choline phosphate cytididyltransferase	h[c] + ctp[c] + cholp[c] => ppi[c] + cdpchol[c]	0	BT_1721	0	1000	2	Sphingolipid Metabolism	PMID:6102980, PMID:16887518, PMID:20855611, Anaerobe (2001) 07, 103?112 doi:10.1006/anae .2001.0376	May also be glucose-1-phosphate-cytidylyltransferase (NCBI Gene, last updated 04.03.10). This reaction is needed for sphingolipid synthesis. Sphingolipids are known to be synthesized in B. thetaiotaomicron.	
	CHOLK	Choline kinase	atp[c] + chol[c] => h[c] + adp[c] + cholp[c]	0		0	1000	2	Sphingolipid Metabolism	PMID:6102980, PMID:16887518, PMID:20855611, Anaerobe (2001) 07, 103?112 doi:10.1006/anae .2001.0376	No gene is known. Added to allow sphingolipid synthesis.	2.7.1.32
rxn00756	CHOLSH	Choline sulfate sulfohydrolase	h2o[c] + chols[c] => h[c] + chol[c] + so4[c]	0	(BT_1918 or BT_3349)	0	1000	2	Glycine, Serine, and Threonine Metabolism			3.1.6.6
rxn01256	CHORM	chorismate mutase	chor[c] => pphn[c]	0	BT_3934	0	1000	2	Tyrosine, Tryptophan, and Phenylalanine Metabolism		putative gene annotation	5.4.99.5
rxn01255	CHORS	chorismate synthase	3psme[c] => pi[c] + chor[c]	0	BT_2084	0	1000	2	Tyrosine, Tryptophan, and Phenylalanine Metabolism			4.2.3.5
	CITRAMALS	citramalate synthase	h2o[c] + pyr[c] + accoa[c] <=> h[c] + coa[c] + 2mmal[c]	1	BT_1858	-1000	1000	2	Valine, Leucine, and Isoleucine Metabolism		One of the enzymes involved in a novel pyruvate pathway for isoleucine biosynthesis that is found in some, mainly archaeal, bacteria (KEGG). It is also annotated in B. thetaiotaomicron's genome.	2.3.1.182

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	CKDNS	CMP-3-deoxy-D-glycero-D-galacto-nonulosonic acid (CMP-KDN) synthetase	ctp[c] + kdn[c] => ppi[c] + ckdn[c]	0	BT_1715	0	1000	4	Capsular Polysaccharide Biosynthesis	PMID:18804026	B. thetaiotaomicron forms and cytidylates 2-keto-3-deoxy-D-glycero-D-galacto-nononic acid (KDN), most likely for inclusion in its capsular polysaccharides.	
rxn10335	CLPNS140	myristoyl-cardiolipin synthase	2 pg140[c] <=> glyc[c] + clpn140[c]	1	(BT_2046 or BT_2382 or BT_3978)	-1000	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	2.7.8.-
rxn10334	CLPNS160	palmitoyl-cardiolipin synthase	2 pg160[c] <=> glyc[c] + clpn160[c]	1	(BT_2046 or BT_2382 or BT_3978)	-1000	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	2.7.8.-
rxn10336	CLPNS180	stearoyl-cardiolipin synthase	2 pg180[c] <=> glyc[c] + clpn180[c]	1	(BT_2046 or BT_2382 or BT_3978)	-1000	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	2.7.8.-
rxn10341	CLPNSAI15	anteisopentadecanoyl-cardiolipin synthase	2 pgai15[c] <=> glyc[c] + clpnai15[c]	1	(BT_2046 or BT_2382 or BT_3978)	-1000	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.7.8.-

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn10338	CLPNSAI17	anteisoheptadecanoyl-cardiolipin synthase	2 pgai17[c] <=> glyc[c] + clpnai17[c]	1	(BT_2046 or BT_2382 or BT_3978)	-1000	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.7.8.-
rxn10339	CLPNSI14	isotetradecanoyl-cardiolipin synthase	2 pgi14[c] <=> glyc[c] + clpni14[c]	1	(BT_2046 or BT_2382 or BT_3978)	-1000	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.7.8.-
rxn10340	CLPNSI15	isopentadecanoyl-cardiolipin synthase	2 pgi15[c] <=> glyc[c] + clpni15[c]	1	(BT_2046 or BT_2382 or BT_3978)	-1000	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.7.8.-

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn10342	CLPNSI16	isohexadecanoyl-cardiolipin synthase	2 pgi16[c] <=> glyc[c] + clpni16[c]	1	(BT_2046 or BT_2382 or BT_3978)	-1000	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.7.8.-
rxn10337	CLPNSI17	isoheptadecanoyl-cardiolipin synthase	2 pgi17[c] <=> glyc[c] + clpni17[c]	1	(BT_2046 or BT_2382 or BT_3978)	-1000	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.7.8.-
rxn10473	Clt	chlorideion transport out via diffusion	cl[e] <=> cl[c]	1	BT_3944	-1000	1000	2	Transport, Extracellular		Putative annotation (NCBI)	
rxn02483	CMLDC	4-carboxymuconolactone decarboxylase	2c25dho[c] => h[c] + co2[c] + 5odhf2a[c]	0	BT_1393	0	1000	2	Benzoate Degradation			4.1.1.44
rxn05467	CO2t	CO2 transporter via diffusion	co2[e] <=> co2[c]	1		-1000	1000	1	Transport, Extracellular			
rxn10474	COBALTt5	cobalt transport in/out via permease (no H+)	cobalt2[c] <=> cobalt2[e]	1	BT_4679	-1000	1000	2	Transport, Extracellular		Irreversible in SEED	
	CPS_BT_ABC	Capsule polysaccharide (B.thetaiotaomicron specific) export	h2o[c] + atp[c] + cps_bt[c] => h[c] + pi[c] + adp[c] + cps_bt[e]	0	(BT_0057 and BT_0398 and BT_0481 and BT_0613 and BT_1356 and BT_2863)	0	1000	4	Capsular Polysaccharide Biosynthesis	PMID:17579514	Not sure if ABC transporter is correct. See comments for reaction CPSS_BT for more details on B. thetaiotaomicron CPS. Genes taken from Table S5 in PMID:17579514.	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	CPSS_BT	Capsular polysaccharide synthesis (B. thetaiotaomicron specific)	2ameph[c] + ckdn[c] + gdpfuc[c] + dtdprmn[c] + uacmamu[c] => cps_bt[c]	0	(BT_0033 and BT_0378 and BT_0381 and BT_0382 and BT_0391 and BT_0394 and BT_0598 and BT_1343 and BT_1346 and BT_1355 and BT_1644 and BT_1653 and BT_1708 and BT_1722 and BT_2872)	0	1000	4	Capsular Polysaccharide Biosynthesis	PMID:12904299, PMID:18804026, PMID:15774760, PMID:17579514, PMID:18263721 PMID:19403529	Putative reaction and product formula, no information about exact reaction stochiometry and structure of B. thetaiotaomicron CPS found. B. thetaiotaomicron most likely synthesizes 2-aminoethylphosphonate (PMID:12904299) and CMP-KDN (PMID:18804026) for inclusion into CPS. Annotation is based on Table S5 in PMID:17579514. Boolean rules may be incorrect. There are eight CPS biosynthesis loci in the B. thetaiotaomicron genome. dTDP-L-rhamnose is also generally involved in capsule polysaccharide synthesis. The capsules of gram-negative bacteria also include N-acetylmannosaminuronate (ManNAcA) (PMID:18263721). Bacteroides also incorporate GDP-fucose synthesized from host-derived fucose into their capsular polysaccharides (PMID:15774760).	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn00256	CS	citrate synthase	h2o[c] + accoa[c] + oaa[c] => h[c] + coa[c] + cit[c]	0	BT_2070	0	1000	2	TCA Cycle			2.3.3.1
	CS4TASE	chondro-4-sulfatase	h2o[e] + cspg_a_degr[e] => h[e] + so4[e] + acgalglcur[e]	0	((BT_0238 and BT_3095) or (BT_0238 and BT_3051) or (BT_0238 and BT_3177))	0	1000	4	Glycosaminoglycan Degradation	PMID:21507958	BT_0238 encodes anSME (anaerobic Sulfatase-Maturing Enzyme).	3.1.6.9
	CS4TASE2	chondro-4-sulfatase	h2o[e] + cspg_b_degr[e] => h[e] + so4[e] + acgalidour2s[e]	0	((BT_0238 and BT_3095) or (BT_0238 and BT_3051) or (BT_0238 and BT_3177))	0	1000	4	Glycosaminoglycan Degradation	PMID:21507958	BT_0238 encodes anSME (anaerobic Sulfatase-Maturing Enzyme).	3.1.6.9
	CS6TASE	chondro-6-sulfatase	h2o[e] + cspg_c_degr[e] => h[e] + so4[e] + acgalglcur[e]	0	((BT_0238 and BT_1622) or (BT_3057 and BT_0238) or (BT_4656 and BT_0238) or (BT_3486 and BT_0238))	0	1000	4	Glycosaminoglycan Degradation	PMID:21507958	BT_0238 encodes anSME (anaerobic Sulfatase-Maturing Enzyme).	3.1.6.4

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	CSABCASE_A_e	Chondroitin sulfate lyase ABC, CS_A	2 h2o[e] + cspg_a[e] => 2 cspg_a_degr[e] + cspg_ab_rest[e]	0	(BT_3331 and BT_3332 and BT_3348)	0	1000	4	Glycosaminoglycan Degradation	PMID:6782076, PMID:7574611, PMID:18512954, PMID:18992215, PMID:18996345	B. thetaiotaomicron ferments chondroitin sulfate. The polysaccharide utilization locus (PUL) BT3324 - BT3350 is upregulated in its presence. BT_3348 degrades chondroitin sulfate to oligosaccharides, which requires BT_3331 (sus C homolog) and BT_3332 (csuF). BT_3324 and BT_3350 degrade the desulfated oligosaccharides to monosaccharides. Based on Figure 3, PMID:18996345. It is assumed that the proteoglycan rest is undegradable for B. thetaiotaomicron.	4.2.2.20

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	CSABCASE_B_e	Chondroitin sulfate lyase ABC, CS_B	2 h2o[e] + cspg_b[e] => cspg_a_degr[e] + cspg_b_degr[e] + cspg_ab_rest[e]	0	(BT_3331 and BT_3332 and BT_3348)	0	1000	4	Glycosaminoglycan Degradation	PMID:6782076, PMID:7574611, PMID:18512954, PMID:18992215, PMID:18996345	B. thetaiotaomicron ferments chondroitin sulfate. The polysaccharide utilization locus (PUL) BT3324 - BT3350 is upregulated in its presence. BT_3348 degrades chondroitin sulfate to oligosaccharides, which requires BT_3331 (sus C homolog) and BT_3332 (csuF). BT_3324 and BT_3350 degrade the desulfated oligosaccharides to monosaccharides. Based on Figure 3, PMID:18996345. It is assumed that the proteoglycan rest is undegradable for B. thetaiotaomicron.	4.2.2.20

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	CSABCASE_C_e	Chondroitin sulfate lyase ABC, CS_C	2 h2o[e] + cspg_c[e] => 2 cspg_c_degr[e] + cspg_c_rest[e]	0	(BT_3331 and BT_3332 and BT_3348)	0	1000	4	Glycosaminoglycan Degradation	PMID:6782076, PMID:7574611, PMID:18512954, PMID:18992215, PMID:18996345	B. thetaiotaomicron ferments chondroitin sulfate. The polysaccharide utilization locus (PUL) BT3324 - BT3350 is upregulated in its presence. BT_3348 degrades chondroitin sulfate to oligosaccharides, which requires BT_3331 (sus C homolog) and BT_3332 (csuF). BT_3324 and BT_3350 degrade the desulfated oligosaccharides to monosaccharides. Based on Figure 3, PMID:18996345. It is assumed that the proteoglycan rest is undegradable for B. thetaiotaomicron.	4.2.2.20
	CSPMDDC	carboxyspermidine decarboxylase	2 h[c] + cspmd[c] => co2[c] + spmd[c]	0	BT_0674	0	1000	3	Spermidine and Putrescine Biosynthesis	PMID:10801923	Annotation from NCBI Gene, last updated 02.04.11	4.1.1.-
	CSPMDDH	carboxyspermidine:NADP+ oxidoreductase	nadph[c] + aspsa[c] + ptrc[c] <=> h2o[c] + nadp[c] + cspmd[c]	1		-1000	1000	2	Spermidine and Putrescine Biosynthesis	PMID:10801923	Added to allow B. thetaiotaomicron to secrete putrescine (shown in vivo). Annotated for Bacteroides helcogenes (Bache_1714).	4.1.1.-
rxn05192	CTBTabc	Crotono-betaine ABC transport	h2o[c] + atp[c] + ctbt[e] => h[c] + pi[c] + adp[c] + ctbt[c]	0	(BT_1749 and BT_1750 and BT_1751)	0	1000	2	Transport, Extracellular			
rxn00410	CTPS1	CTP synthase (NH3)	atp[c] + nh4[c] + utp[c] => 2 h[c] + pi[c] + adp[c] + ctp[c]	0	BT_0590	0	1000	2	Purine and Pyrimidine Biosynthesis		Reversible in SEED	6.3.4.2

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn00412	CTPS2	CTP synthase (glutamine)	h2o[c] + atp[c] + gln-L[c] + utp[c] => 2 h[c] + glu-L[c] + pi[c] + adp[c] + ctp[c]	0	BT_0590	0	1000	2	Purine and Pyrimidine Biosynthesis			6.3.4.2
rxn10481	Cuabc	Copper transport via ABC system	h2o[c] + atp[c] + cu2[e] => h[c] + pi[c] + adp[c] + cu2[c]	0	BT_1091	0	1000	2	Transport, Extracellular			
rxn05528	Cut1	Copper export via ATPase	h2o[c] + atp[c] + cu2[c] => h[c] + pi[c] + adp[c] + cu2[e]	0	BT_1091	0	1000	2	Transport, Extracellular			
	CYSDS	Cysteine Desulfhydrase	h2o[c] + cys-L[c] => pyr[c] + nh4[c] + h2s[c]	0	(BT_1923 or BT_2387)	0	1000	2	Cysteine Metabolism	PMID:4853401	Added to allow B. thetaiotaomicron to use cysteine as sulfur source.	4.1.99.1
rxn00649	CYSS	cysteine synthase	h2s[c] + acser[c] => h[c] + ac[c] + cys-L[c]	0	(BT_1852 or BT_3080)	0	1000	3	Cysteine Metabolism	PMID:4853401	Cysteine can be synthesized de novo and serve as sulfur source.	2.5.1.47
rxn05733	CYSS3r	cysteine synthase (Thiosulfate)	trdrd[c] + tsul[c] + acser[c] <=> h[c] + ac[c] + trdox[c] + so3[c] + cys-L[c]	1	(BT_1852 or BT_3080)	-1000	1000	2	Cysteine Metabolism		Added manually to BIGG database based on SEED database	2.5.1.47
	CYSt2r	L-cysteine reversible transport via proton symport	h[e] + cys-L[e] <=> h[c] + cys-L[c]	1		-1000	1000	2	Transport, Extracellular	PMID:4853401	Cysteine is required as sulfur source if sulfide is not available.	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn10113	CYTBD	cytochrome oxidase bd (ubiquinol-8: 2 protons)	2 h[c] + 0.5 o2[c] + q8h2[c] => h2o[c] + 2 h[e] + q8[c]	0	(BT_3053 or (BT_1209 and BT_1210))	0	1000	4	Central Metabolism	PMID: 1474983, PMID: 893348	B. fragilis, and most likely B. thetaiotaomicron, is stimulated by nanomolar concentrations of oxygen due to cytochrome bd oxidase acitivity (PMID:14749831). It is unclear whether B. thetaiotaomicron uses ubiquinone, menaquinone or both. PMID: 893348 states that only menaquinone is present, however ubiquinone-using enzymes are annotated in B. thetaiotaomicron genome.	1.10.3.-
rxn10806	CYTBD2	cytochrome oxidase bd (menaquinol-8: 2 protons)	2 h[c] + mql8[c] + 0.5 o2[c] => h2o[c] + 2 h[e] + mqn8[c]	0	(BT_3053 or (BT_1209 and BT_1210))	0	1000	4	Central Metabolism	PMID:14749831, PMID: 893348	B. fragilis, and most likely B. thetaiotaomicron, is stimulated by nanomolar concentrations of oxygen due to cytochrome bd oxidase acitivity (PMID:14749831). It is unclear whether B. thetaiotaomicron uses ubiquinone, menaquinone or both. PMID: 893348 states that only menaquinone is present, however ubiquinone-using enzymes are annotated in B. thetaiotaomicron genome.	1.10.3.-

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn01368	CYTD	cytidine deaminase	h2o[c] + h[c] + cytd[c] => nh4[c] + uri[c]	0	BT_1539	0	1000	2	Nucleotide Salvage Pathway		SEED rxn utilizes 2.5 h	3.5.4.5
rxn00365	CYTDK1	ATPcytidine 5-phosphotransferase	atp[c] + cytd[c] => h[c] + adp[c] + cmp[c]	0	(BT_0184 or BT_2527)	0	1000	2	Nucleotide Salvage Pathway			2.7.1.48
rxn00369	CYTDK2	cytidine kinase (GTP)	gtp[c] + cytd[c] => h[c] + gdp[c] + cmp[c]	0	(BT_0184 or BT_2527)	0	1000	2	Nucleotide Salvage Pathway		Reversible in SEED	2.7.1.48
rxn00707	CYTDK3	ITPcytidine 5-phosphotransferase	cytd[c] + itp[c] => h[c] + cmp[c] + idp[c]	0	(BT_2060 or BT_2093)	0	1000	2	Nucleotide Salvage Pathway		Reversible in SEED	2.7.4.14
rxn00368	CYTDK4	UTPcytidine 5-phosphotransferase	utp[c] + cytd[c] => h[c] + cmp[c] + udp[c]	0	(BT_0184 or BT_2527)	0	1000	2	Nucleotide Salvage Pathway			2.7.1.48
rxn05198	CYTDt2r	cytidine transport in via proton symport, reversible	h[e] + cytd[e] <=> h[c] + cytd[c]	1	BT_4330	-1000	1000	2	Transport, Extracellular			
rxn00364	CYTK1	cytidylate kinase (CMP)	atp[c] + cmp[c] <=> adp[c] + cdp[c]	1	(BT_2060 or BT_2093)	-1000	1000	2	Nucleotide Salvage Pathway			2.7.4.14
rxn01219	CYTK2	cytidylate kinase (dCMP)	atp[c] + dcmp[c] <=> adp[c] + dcdp[c]	1	(BT_2060 or BT_2093)	-1000	1000	2	Nucleotide Salvage Pathway			2.7.4.14
	D_LACt2	D-lactate transport via proton symport	h[e] + lac-D[e] <=> h[c] + lac-D[c]	1		-1000	1000	2	Transport, Extracellular	PMID:438119, PMID:148460, PMID:12740060, PMID:11260473	Bacteroides produce lactate under certain circumstances.	
rxn01127	DADK	deoxyadenylate kinase	atp[c] + damp[c] <=> adp[c] + dadp[c]	1	BT_4387	-1000	1000	2	Nucleotide Salvage Pathway			2.7.4.11
rxn05317	DADNt2r	deoxyadenosine transport in via proton symport reversible	h[e] + dad-2[e] <=> h[c] + dad-2[c]	1	BT_4330	-1000	1000	2	Transport, Extracellular			
rxn08297	DAGK160	diacylglycerol kinase (n-C16:0)	atp[c] + 12dgr160[c] => h[c] + adp[c] + pa160[c]	0		0	1000	2	Sphingolipid Metabolism		Not sure if this enzyme is present. It is annotated for most Bacteroides species except B. thetaiotaomicron. Needed for degradation of diacylglycerol and sphingolipid synthesis.	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	DALAt2r	D-alanine transport via proton symport	h[e] + ala-D[e] <=> h[c] + ala-D[c]	1		-1000	1000	2	Transport, Extracellular	PMID:12663928	Added by Model SEED during auto-completion. No gene annotation for ala-D transport available, but B. thetaiotaomicron is believed to possess a non-cytosolic D-alanine-D-alanine dipeptidase.	
rxn00313	DAPDC	diaminopimelate decarboxylase	h[c] + 26dap-M[c] => co2[c] + lys-L[c]	0	BT_1374	0	1000	2	Threonine and Lysine Metabolism			4.1.1.20
rxn01974	DAPE	diaminopimelate epimerase	26dap-LL[c] <=> 26dap-M[c]	1	BT_0548	-1000	1000	2	Threonine and Lysine Metabolism			5.1.1.7
rxn01991	DAPMDH	Meso-diaminopimelate D-dehydrogenase	h2o[c] + nadp[c] + 26dap-M[c] <=> h[c] + nadph[c] + nh4[c] + l2a6o[c]	1	BT_1979	-1000	1000	2	Folate Metabolism			1.4.1.16
rxn08306	DASYN120	CDP-diacylglycerol synthetase (n-C12:0)	h[c] + pa120[c] + ctp[c] => ppi[c] + cdpdddecg[c]	0	(BT_4006 or BT_4463)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Reversible in reaction in Model SEED. The fatty acid composition of B. thetaiotaomicron was determined experimentally.	2.7.7.41
rxn08307	DASYN140	CDP-diacylglycerol synthetase (n-C14:0)	h[c] + pa140[c] + ctp[c] => ppi[c] + cdpdtdecg[c]	0	(BT_4006 or BT_4463)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Reversible in reaction in Model SEED. The fatty acid composition of B. thetaiotaomicron was determined experimentally.	2.7.7.41
rxn08309	DASYN160	CDP-diacylglycerol synthetase (n-C16:0)	h[c] + pa160[c] + ctp[c] => ppi[c] + cdpdhdecg[c]	0	(BT_4006 or BT_4463)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Reversible in reaction in Model SEED. The fatty acid composition of B. thetaiotaomicron was determined experimentally.	2.7.7.41

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn08311	DASYN180	CDP-diacylglycerol synthetase (n-C18:0)	h[c] + pa180[c] + ctp[c] => ppi[c] + cdpdodecg[c]	0	(BT_4006 or BT_4463)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Reversible in reaction in Model SEED. The fatty acid composition of B. thetaiotaomicron was determined experimentally.	2.7.7.41
rxn08312	DASYN181	CDP-diacylglycerol synthetase (n-C18:1)	h[c] + pa181[c] + ctp[c] => ppi[c] + cdpdodec11eg[c]	0	(BT_4006 or BT_4463)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Reversible in reaction in Model SEED. The fatty acid composition of B. thetaiotaomicron was determined experimentally.	2.7.7.41
rxn10224	DASYNAI15	anteisopentadecanoyl-phosphatidate cytidylyltransferase	h[c] + paai15[c] + ctp[c] => ppi[c] + cdpdaipdecg[c]	0	(BT_4006 or BT_4463)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.7.7.41
rxn10221	DASYNAI17	anteisoheptadecanoyl-phosphatidate cytidylyltransferase	h[c] + paai17[c] + ctp[c] => ppi[c] + cdpdaihpdecg[c]	0	(BT_4006 or BT_4463)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.7.7.41

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn10222	DASYNI14	isotetradecanoyl-phosphatidate cytidylyltransferase	h[c] + pai14[c] + ctp[c] => ppi[c] + cdpditdecg[c]	0	(BT_4006 or BT_4463)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.7.7.41
rxn10223	DASYNI15	isopentadecanoyl-phosphatidate cytidylyltransferase	h[c] + pai15[c] + ctp[c] => ppi[c] + cdpdipdecg[c]	0	(BT_4006 or BT_4463)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.7.7.41
rxn10225	DASYNI16	isohexadecanoyl-phosphatidate cytidylyltransferase	h[c] + pai16[c] + ctp[c] => ppi[c] + cdpdihdecg[c]	0	(BT_4006 or BT_4463)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.7.7.41

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn10220	DASYNI17	isoheptadecanoyl-phosphatidate cytidylyltransferase	h[c] + pai17[c] + ctp[c] => ppi[c] + cdpdihpdecg[c]	0	(BT_4006 or BT_4463)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.7.7.41
rxn05040	DB4PS	3,4-Dihydroxy-2-butanone-4-phosphate synthase	ru5p-D[c] => h[c] + db4p[c] + for[c]	0	BT_2416	0	1000	2	Cofactor and Prosthetic Group Biosynthesis			4.1.99.12
rxn02277	DBTS	dethiobiotin synthase	co2[c] + atp[c] + dann[c] => 3 h[c] + pi[c] + adp[c] + dtbt[c]	0	BT_1446	0	1000	4	Cofactor and Prosthetic Group Biosynthesis	PMID:4853401, 20693992	B. thetaiotaomicron does not require biotin (PMID:4853401). Most likely, biotin is synthesized as described in PMID:20693992.	6.3.3.3
rxn01217	DCMPDA	dCMP deaminase	h2o[c] + h[c] + dcmp[c] <=> nh4[c] + dump[c]	1	BT_4260	-1000	1000	2	Nucleotide Salvage Pathway		Irreversible in SEED	3.5.4.12
rxn01800	DCYTD	deoxycytidine deaminase	h2o[c] + h[c] + dcyt[c] => nh4[c] + duri[c]	0	BT_1539	0	1000	2	Nucleotide Salvage Pathway			3.5.4.14
rxn05205	DCYTt2r	deoxycytidine transport in via proton symport reversible	h[e] + dcyt[e] <=> h[c] + dcyt[c]	1	BT_4330	-1000	1000	2	Transport, Extracellular			
rxn01123	DDGLKr	2-dehydro-3-deoxygluconate kinase	atp[c] + 2ddglcn[c] <=> h[c] + adp[c] + 2ddg6p[c]	1	BT_0488	-1000	1000	2	Pentose and Glucuronate Interconversions			2.7.1.45
rxn01332	DDPA	3-deoxy-D-arabino-heptulosonate 7-phosphate synthetase	h2o[c] + pep[c] + e4p[c] => pi[c] + 2dda7p[c]	0	BT_3934	0	1000	2	Tyrosine, Tryptophan, and Phenylalanine Metabolism		putative gene annotation	4.1.2.15
rxn00328	DDPGA	2-dehydro-3-deoxy-phosphogluconate aldolase	4h2oglt[c] <=> pyr[c] + glx[c]	1	BT_0489	-1000	1000	2	Arginine and Proline Metabolism			4.1.2.14

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	DEXTRAN40e	alpha-dextrin endo-1,6-alpha-glucosidase/ pullulanase	40 h2o[e] + dextran40[e] => 40 malt[e]	0	(BT_1663 or BT_4689)	0	1000	4	Plant Polysaccharide Degradation	PMID:848954	Assumed to perform dextran (alpha-1,6-glucan) degradation. Maltose is the smallest sugar that it can release from an alpha-(1->6)-linkage (KEGG Enzyme). B. thetaiotaomicron ferments dextran.	3.2.1.41
	DGC3D	2-deoxy-D-gluconate 3-dehydrogenase	nad[c] + 2dglcn[c] => h[c] + nadh[c] + 3ddgc[c]	0	(BT_3232 or BT_1015)	0	1000	2	Pentose and Glucuronate Interconversions		Gene annotation was drawn from The SEED.	1.1.1.125
	DGC3D2	2-deoxy-D-gluconate 3-dehydrogenase	nad[c] + 2ddglcn[c] <=> h[c] + nadh[c] + dkdglcn[c]	1	(BT_3232 or BT_1015)	-1000	1000	2	Pentose and Glucuronate Interconversions		Gene annotation was drawn from The SEED.	1.1.1.125
rxn01509	DGK1	deoxyguanylate kinase (dGMP:ATP)	atp[c] + dgmp[c] <=> adp[c] + dgdp[c]	1	BT_2009	-1000	1000	2	Nucleotide Salvage Pathway			2.7.4.8
rxn09688	DGSNt2	deoxyguanosine transport in via proton symport	h[e] + dgsn[e] => h[c] + dgsn[c]	0	BT_4330	0	1000	2	Transport, Extracellular			
rxn00898	DHAD1	dihydroxy-acid dehydratase (2,3-dihydroxy-3-methylbutanoate)	23dhmb[c] => h2o[c] + 3mob[c]	0	BT_2078	0	1000	2	Valine, Leucine, and Isoleucine Metabolism			4.2.1.9
rxn03437	DHAD2	Dihydroxy-acid dehydratase (2,3-dihydroxy-3-methylpentanoate)	23dhmp[c] => h2o[c] + 3mop[c]	0	BT_2078	0	1000	2	Valine, Leucine, and Isoleucine Metabolism			4.2.1.9
rxn02929	DHDPRy	dihydrodipicolinate reductase (NADPH)	h[c] + nadph[c] + 23dhdp[c] => thdp[c] + nadp[c]	0	BT_3320	0	1000	2	Threonine and Lysine Metabolism		Reversible reaction in Model SEED	1.3.1.26
rxn01644	DHDPS	dihydrodipicolinate synthase	pyr[c] + aspsa[c] => 2 h2o[c] + h[c] + 23dhdp[c]	0	(BT_0895 or BT_2814)	0	1000	2	Threonine and Lysine Metabolism			4.2.1.52
rxn00686	DHFR	dihydrofolate reductase	h[c] + nadph[c] + dhf[c] <=> nadp[c] + thf[c]	1	(BT_0106 or BT_2048)	-1000	1000	2	Folate Metabolism			1.5.1.3
rxn01603	DHFS	dihydrofolate synthase	glu-L[c] + atp[c] + dhpt[c] => h[c] + pi[c] + adp[c] + dhf[c]	0	BT_1335	0	1000	2	Cofactor and Prosthetic Group Biosynthesis			6.3.2.12

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	DHNAOT10	1,4-dihydroxy-2-naphthoate octaprenyltransferase (demethylmenaquinone 10)	dhna[c] + octdp[c] => h[c] + 2 co2[c] + ppi[c] + 2dmmq10[c]	0		0	1000	3	Cofactor and Prosthetic Group Biosynthesis	PMID:6102980	B. thetaiotaomicron produces menaquinone 7,8,9,10 and 11. MK-10 and MK-11 are the main components.Note: Reaction is unbalanced, but I don't know to fix this. KEGG doesn't have any information. AH	
	DHNAOT11	1,4-dihydroxy-2-naphthoate octaprenyltransferase (demethylmenaquinone 11)	dhna[c] + octdp[c] => h[c] + 8 co2[c] + ppi[c] + 2dmmq11[c]	0		0	1000	3	Cofactor and Prosthetic Group Biosynthesis	PMID:6102980	B. thetaiotaomicron produces menaquinone 7,8,9,10 and 11. MK-10 and MK-11 are the main components.Note: Reaction is unbalanced, but I don't know to fix this. KEGG doesn't have any information. AH	
rxn08333	DHNAOT4	1,4-dihydroxy-2-naphthoate octaprenyltransferase	h[c] + dhna[c] + octdp[c] => co2[c] + ppi[c] + 2dmmql8[c]	0	(BT_2014 or BT_2015)	0	1000	3	Cofactor and Prosthetic Group Biosynthesis	PMID:6102980	B. thetaiotaomicron produces menaquinone 7,8,9,10 and 11. MK-10 and MK-11 are the main components.Note: Reaction is unbalanced, but I don't know to fix this. KEGG doesn't have any information. AH	2.5.1.-

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	DHNAOT7	1,4-dihydroxy-2-naphthoate octaprenyltransferase (demethylmenaquinone 7)	dhna[c] + octdp[c] => h[c] + co2[c] + ppi[c] + 2dmmq7[c]	0	(BT_2014 or BT_2015)	0	1000	3	Cofactor and Prosthetic Group Biosynthesis	PMID:6102980	B. thetaiotaomicron produces menaquinone 7,8,9,10 and 11. MK-10 and MK-11 are the main components.Note: Reaction is unbalanced, but I don't know to fix this. KEGG doesn't have any information. AH	
	DHNAOT9	1,4-dihydroxy-2-naphthoate octaprenyltransferase (demethylmenaquinone 9)	dhna[c] + octdp[c] => h[c] + co2[c] + ppi[c] + 2dmmq9[c]	0	(BT_2014 or BT_2015)	0	1000	3	Cofactor and Prosthetic Group Biosynthesis	PMID:6102980	B. thetaiotaomicron produces menaquinone 7,8,9,10 and 11. MK-10 and MK-11 are the main components.Note: Reaction is unbalanced, but I don't know to fix this. KEGG doesn't have any information. AH	
rxn02504	DHNPA	dihydroneopterin aldolase	dhnpt[c] => h[c] + gcald[c] + 2ahhmp[c]	0	BT_2149	0	1000	2	Folate Metabolism			4.1.2.25
	DHORDfum	Fumarate dependent DHORD	fum[c] + dhor-S[c] => succ[c] + orot[c]	0	(BT_1009 or (BT_0891 and BT_0892))	0	1000	2	Purine and Pyrimidine Biosynthesis		Gene was incorrectly annotated by Model SEED, correct: dihydroorotate dehydrogenase (fumarate)	1.3.98.1
rxn01360	DHORDi	(S)-Dihydroorotateoxygen oxidoreductase	o2[c] + dhor-S[c] => h2o2[c] + orot[c]	0	(BT_1009 or (BT_0891 and BT_0892))	0	1000	2	Purine and Pyrimidine Biosynthesis			1.3.3.1
rxn01465	DHORTS	dihydroorotase	h2o[c] + dhor-S[c] <=> h[c] + cbasp[c]	1	BT_0250	-1000	1000	2	Purine and Pyrimidine Biosynthesis			3.5.2.3
rxn02475	DHPPDA	diaminohydroxyphosphoribosylaminopyrimidine deaminase	h2o[c] + h[c] + 25dhpp[c] => nh4[c] + 5apru[c]	0	BT_3728	0	1000	2	Cofactor and Prosthetic Group Biosynthesis			3.5.4.26
rxn02200	DHPS	dihydropteroate synthase	4abz[c] + 2ahhmp[c] => h2o[c] + dhpt[c]	0	BT_3646	0	1000	2	Folate Metabolism		Reversible reaction in Model SEED	2.5.1.15

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	DHPS3	7,8 dihydropteroate synthase (methanopterin)	6hmhptpp[c] + Brfap[c] => ppi[c] + dhrfap[c]	0	BT_1410	0	1000	2	Cofactor and Prosthetic Group Biosynthesis		Gene annotation was drawn from The SEED.	2.5.1.15
rxn02212	DHQS	3-dehydroquinate synthase	2dda7p[c] => pi[c] + 3dhq[c]	0	BT_3975	0	1000	2	Tyrosine, Tryptophan, and Phenylalanine Metabolism			4.2.3.4
rxn02213	DHQTi	3-dehydroquinate dehydratase, irreversible	3dhq[c] => h2o[c] + 3dhsk[c]	0	BT_2842	0	1000	2	Tyrosine, Tryptophan, and Phenylalanine Metabolism			4.2.1.10
rxn09687	DINSt2	deoxyinosine transport in via proton symport	h[e] + din[e] => h[c] + din[c]	0	BT_4330	0	1000	2	Transport, Extracellular		Reversible reaction in Model SEED	
	DM_4HBA	Sink needed to allow 4-hydroxy-benzoate to leave system	4hba[c] =>	0		0	1000	0	exchange/demand reaction			
	DM_5DRIB	Sink needed to allow 5'-deoxyribose to leave system	5drib[c] =>	0		0	1000	0	exchange/demand reaction			
	DM_AMOB	Sink needed to allow S-Adenosyl-4-methylthio-2-oxobutanoate to leave the system	amob[c] =>	0		0	1000	0	exchange/demand reaction			
rxn01213	DMATT	dimethylallyltranstransferase	dmpp[c] + ipdp[c] => ppi[c] + grdp[c]	0	(BT_3261 or BT_2058)	0	1000	2	Cofactor and Prosthetic Group Biosynthesis			2.5.1.1
rxn08352	DMPPS	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate reductase (dmpp)	h[c] + nadh[c] + h2mb4p[c] => h2o[c] + nad[c] + dmpp[c]	0	BT_2061	0	1000	2	Cofactor and Prosthetic Group Biosynthesis			1.17.1.2
rxn04996	DMPPS2	4-hydroxy-3-methylbut-2-enyl diphosphate reductase (NADP)	h[c] + nadph[c] + h2mb4p[c] => h2o[c] + nadp[c] + dmpp[c]	0	BT_2061	0	1000	2	Cofactor and Prosthetic Group Biosynthesis		Added manually to BIGG database based on SEED database. Reviewed gene (NCBI Gene, updated 08.01.11).	1.17.1.2

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn11946	DMQMT	3-Dimethylubiquinonol 3-methyltransferase	amet[c] + 2omhmbl[c] => h[c] + ahcys[c] + q8h2[c]	0	BT_3209	0	1000	2	Cofactor and Prosthetic Group Biosynthesis	PMID: 893348	It is not clear whether only menaquinone or mq and ubiquinone are synthesized. PMID: 893348 states that only menaquinone is present, however ubiquinone-using enzymes are annotated in B. thetaiotaomicron genome.	2.1.1.64
rxn00100	DPCOAK	dephospho-CoA kinase	atp[c] + dpcoa[c] => h[c] + coa[c] + adp[c]	0	BT_4594	0	1000	2	Cofactor and Prosthetic Group Biosynthesis		Putative annotation (NCBI)	2.7.1.24
rxn01790	DPR	2-dehydropantoate 2-reductase	h[c] + nadph[c] + 2dhp[c] => nadp[c] + pant-R[c]	0	(BT_2074 or BT_3117)	0	1000	2	Cofactor and Prosthetic Group Biosynthesis		Reversible in SEED	1.1.1.169
rxn01987	DRBKr	Deoxyribokinase	h[c] + adp[c] + 2dr5p[c] <=> atp[c] + drib[c]	1	(BT_2799 or BT_3576 or (BT_2803 and BT_2804))	-1000	1000	2	Pentose Phosphate Pathway			2.7.1.15
rxn00784	DRPAr	2-Deoxy-D-ribose-5-phosphate acetaldehyde-lyase	2dr5p[c] <=> acald[c] + g3p[c]	1	(BT_3263 or BT_4425)	-1000	1000	2	Alternate Carbon Metabolism			4.1.2.4
	DT5HSUt2r	5-Dehydro-4-deoxy-D-glucuronate transport in via proton symport, reversible	h[e] + dt5hsu[e] <=> h[c] + dt5hsu[c]	1	BT_4105	-1000	1000	2	Transport, Extracellular	PMID:3968032	Added to allow complete degradation of pectin, not sure if this degradation product is generated in periplasm or cytosol. Degradation pathway may be slightly different. Added based on NCBI Gene (annotation: hexouronate transporter).	
rxn01513	DTMPK	dTMP kinase	atp[c] + dtmp[c] <=> adp[c] + dtdp[c]	1		-1000	1000	1	Nucleotide Salvage Pathway		Added by Model SEED during auto-completion step in pipeline.	2.7.4.9

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn01518	DURIK1	deoxyuridine kinase (ATP:Deoxyuridine)	atp[c] + duri[c] => h[c] + adp[c] + dump[c]	0	BT_2275	0	1000	2	Nucleotide Salvage Pathway		Reversible in SEED	2.7.1.21
rxn01799	DURIPP	deoxyuridine phosphorylase	pi[c] + duri[c] <=> 2dr1p[c] + ura[c]	1	(BT_1881 or BT_4554)	-1000	1000	2	Nucleotide Salvage Pathway			
rxn09685	DURIt2	deoxyuridine transport in via proton symport	h[e] + duri[e] => h[c] + duri[c]	0	BT_4330	0	1000	2	Transport, Extracellular		Reversible in SEED	
rxn01519	DUTPDP	dUTP diphosphatase	h2o[c] + dutp[c] => h[c] + ppi[c] + dump[c]	0	(BT_3461 or BT_4350)	0	1000	2	Nucleotide Salvage Pathway			3.6.1.23
rxn03958	DXPRIi	1-deoxy-D-xylulose reductoisomerase	h[c] + nadph[c] + dxyl5p[c] => nadp[c] + 2me4p[c]	0	BT_2002	0	1000	2	Cofactor and Prosthetic Group Biosynthesis			
rxn03909	DXPS	1-deoxy-D-xylulose 5-phosphate synthase	h[c] + pyr[c] + g3p[c] => co2[c] + dxyl5p[c]	0	(BT_1403 or BT_4099)	0	1000	2	Cofactor and Prosthetic Group Biosynthesis			
rxn01331	E4PD	Erythrose 4-phosphate dehydrogenase	h2o[c] + nad[c] + e4p[c] <=> 2 h[c] + nadh[c] + 4per[c]	1	BT_4263	-1000	1000	2	Cofactor and Prosthetic Group Biosynthesis			1.2.1.72
	EACPR1	Enoyl-ACP-reductase (FabI)	h[c] + nadph[c] + egACPm[c] => nadp[c] + gACPm[c]	0	BT_4188	0	1000	3	Biotin Metabolism	PMID:20693992	Based on biotin synthesis described in PMID:20693992 for E. coli	
	EACPR2	Enoyl-ACP-reductase (FabI)	h[c] + nadph[c] + epACPm[c] => nadp[c] + pmACPm[c]	0	BT_4188	0	1000	3	Biotin Metabolism	PMID:20693992	Based on biotin synthesis described in PMID:20693992 for E. coli	
rxn05327	EAR100x	enoyl-[acyl-carrier-protein] reductase (NADH) (n-C10:0)	h[c] + tdec2eACP[c] + nadh[c] => dcaACP[c] + nad[c]	0	BT_4188	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	1.3.1.9

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05448	EAR10M11x	10-methyl-trans-undec-2-enoyl-ACPNAD+ oxidoreductase (A-specific)	h[c] + 10mtundec2eACP[c] + nadh[c] => 10mundecACP[c] + nad[c]	0	BT_4188	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.3.1.9
rxn05436	EAR10M12x	10-methyl-trans-dodec-2-enoyl-ACPNAD+ oxidoreductase (A-specific)	h[c] + 10mtddec2eACP[c] + nadh[c] => 10mddcaACP[c] + nad[c]	0	BT_4188	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.3.1.9
rxn05442	EAR11M12x	11-methyl-trans-dodec-2-enoyl-ACPNAD+ oxidoreductase (A-specific)	h[c] + 11mtddec2eACP[c] + nadh[c] => 11mddcaACP[c] + nad[c]	0	BT_4188	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.3.1.9
rxn05324	EAR120x	enoyl-[acyl-carrier-protein] reductase (NADH) (n-C12:0)	h[c] + tddec2eACP[c] + nadh[c] => ddcaACP[c] + nad[c]	0	BT_4188	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	1.3.1.9

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	EAR121x	enoyl-[acyl-carrier-protein] reductase (NADH) (n-C12:1)	h[c] + t3c5ddeceACP[c] + nadh[c] => cddec5eACP[c] + nad[c]	0	BT_4188	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	1.3.1.9
rxn05449	EAR12M13x	12-methyl-trans-tridec-2-enoyl-ACPNAD+ oxidoreductase (A-specific)	h[c] + 12mttritec2eACP[c] + nadh[c] => 12mtridecACP[c] + nad[c]	0	BT_4188	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.3.1.9
rxn05437	EAR12M14x	12-methyl-trans-tetra-dec-2-enoyl-ACPNAD+ oxidoreductase (A-specific)	h[c] + 12mtmrs2eACP[c] + nadh[c] => 12mmyrsACP[c] + nad[c]	0	BT_4188	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.3.1.9
rxn05443	EAR13M14x	13-methyl-trans-tetra-dec-2-enoyl-ACPNAD+ oxidoreductase (A-specific)	h[c] + 13mtmrs2eACP[c] + nadh[c] => 13mmyrsACP[c] + nad[c]	0	BT_4188	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.3.1.9

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05323	EAR140x	enoyl-[acyl-carrier-protein] reductase (NADH) (n-C14:0)	h[c] + tmrs2eACP[c] + nadh[c] => myrsACP[c] + nad[c]	0	BT_4188	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	1.3.1.9
	EAR141x	enoyl-[acyl-carrier-protein] reductase (NADH) (n-C14:1)	h[c] + t3c7mrseACP[c] + nadh[c] => tdeACP[c] + nad[c]	0	BT_4188	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	1.3.1.9
rxn05450	EAR14M15x	14-methyl-trans-pentadec-2-enoyl-ACPNAD+ oxidoreductase (A-specific)	h[c] + 14mtpentdec2eACP[c] + nadh[c] => nad[c] + 14mpentdecACP[c]	0	BT_4188	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.3.1.9
rxn05438	EAR14M16x	14-methyl-trans-hexa-dec-2-enoyl-ACPNAD+ oxidoreductase (A-specific)	h[c] + 14mtpalm2eACP[c] + nadh[c] => nad[c] + 14mpalmACP[c]	0	BT_4188	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.3.1.9

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05444	EAR15M16x	15-methyl-trans-hexa-dec-2-enoyl-ACPNAD+ oxidoreductase (A-specific)	h[c] + 15mtpalm2eACP[c] + nadh[c] => nad[c] + 15mpalmACP[c]	0	BT_4188	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.3.1.9
rxn05328	EAR160x	enoyl-[acyl-carrier-protein] reductase (NADH) (n-C16:0)	h[c] + tpalm2eACP[c] + nadh[c] => palmACP[c] + nad[c]	0	BT_4188	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	1.3.1.9
	EAR161x	enoyl-[acyl-carrier-protein] reductase (NADH) (n-C16:1)	h[c] + t3c9palmeACP[c] + nadh[c] => hdeACP[c] + nad[c]	0	BT_4188	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	1.3.1.9
rxn05464	EAR180x	enoyl-[acyl-carrier-protein] reductase (NADH) (n-C18:0)	h[c] + toctd2eACP[c] + nadh[c] => nad[c] + ocdcaACP[c]	0	BT_4188	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	1.3.1.9
	EAR181x	enoyl-[acyl-carrier-protein] reductase (NADH) (n-C18:1)	h[c] + t3c11vaceACP[c] + nadh[c] => nad[c] + octeACP[c]	0	BT_4188	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	1.3.1.9
rxn05322	EAR40x	enoyl-[acyl-carrier-protein] reductase (NADH) (n-C4:0)	h[c] + but2eACP[c] + nadh[c] => butACP[c] + nad[c]	0	BT_4188	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	1.3.1.9

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05445	EAR4M5x	4-methyl-trans-pent-2-enoyl-ACPNAD+ oxidoreductase (A-specific)	h[c] + 4mtpent2eACP[c] + nadh[c] => 4mpentACP[c] + nad[c]	0	BT_4188	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.3.1.9
rxn05433	EAR4M6x	4-methyl-trans-hex-2-enoyl-ACPNAD+ oxidoreductase (A-specific)	h[c] + 4mthex2eACP[c] + nadh[c] => 4mhexACP[c] + nad[c]	0	BT_4188	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.3.1.9
rxn05439	EAR5M6x	5-methyl-trans-hex-2-enoyl-ACPNAD+ oxidoreductase (A-specific)	h[c] + 5mthex2eACP[c] + nadh[c] => 5mhexACP[c] + nad[c]	0	BT_4188	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.3.1.9
rxn05326	EAR60x	enoyl-[acyl-carrier-protein] reductase (NADH) (n-C6:0)	h[c] + thex2eACP[c] + nadh[c] => hexACP[c] + nad[c]	0	BT_4188	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	1.3.1.9

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05446	EAR6M7x	6-methyl-trans-hept-2-enoyl-ACPNAD+ oxidoreductase (A-specific)	h[c] + 6mthept2eACP[c] + nadh[c] => 6mheptACP[c] + nad[c]	0	BT_4188	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.3.1.9
rxn05434	EAR6M8x	6-methyl-trans-oct-2-enoyl-ACPNAD+ oxidoreductase (A-specific)	h[c] + 6mtoct2eACP[c] + nadh[c] => 6mocACP[c] + nad[c]	0	BT_4188	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.3.1.9
rxn05440	EAR7M8x	7-methyl-trans-oct-2-enoyl-ACPNAD+ oxidoreductase (A-specific)	h[c] + 7mtoct2eACP[c] + nadh[c] => 7mocACP[c] + nad[c]	0	BT_4188	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.3.1.9
rxn05325	EAR80x	enoyl-[acyl-carrier-protein] reductase (NADH) (n-C8:0)	h[c] + toct2eACP[c] + nadh[c] => ocACP[c] + nad[c]	0	BT_4188	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	1.3.1.9

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05435	EAR8M10x	8-methyl-trans-dec-2-enoyl-ACPNAD+ oxidoreductase (A-specific)	h[c] + 8mtdec2eACP[c] + nadh[c] => 8mdcaACP[c] + nad[c]	0	BT_4188	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.3.1.9
rxn05447	EAR8M9x	8-methyl-trans-non-2-enoyl-ACPNAD+ oxidoreductase (A-specific)	h[c] + 8mtnon2eACP[c] + nadh[c] => 8mnonACP[c] + nad[c]	0	BT_4188	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.3.1.9
rxn05441	EAR9M10x	9-methyl-trans-dec-2-enoyl-ACPNAD+ oxidoreductase (A-specific)	h[c] + 9mtdec2eACP[c] + nadh[c] => 9mdcaACP[c] + nad[c]	0	BT_4188	0	1000	3	Cell Envelope Biosynthesis	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	1.3.1.9
rxn03884	EDA_R	2-dehydro-3-deoxy-D-gluconate-6-phosphate	2ddg6p[c] <=> pyr[c] + g3p[c]	1	BT_0489	-1000	1000	2	Pentose Phosphate Pathway			4.1.2.14

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	EDTXS1_BT	Endotoxin Synthesis (lauroyl transferase)	ddcaACP[c] + kdolipid4_bt[c] => ACP[c] + kdolipid4L_bt[c]	0	BT_2152	0	1000	3	Lipopolysaccharide Biosynthesis	PMID:18931137, PMID:19460428, PMID:20974832	LPS biosynthesis partly based on reconstruction of the related microbe P. gingivalis (PMID:18931137). Based on structural information taken from (PMID:19460428, PMID:20974832). Could not find information, though, if laurate is really added to kdolipid IV in B. thetaiotaomicron.	
rxn02339	EHGLAT	L-erythro-4-Hydroxyglutamate:2-oxoglutarate aminotransferase	akg[c] + e4hglu[c] => glu-L[c] + 4h2oglt[c]	0	(BT_0666 or BT_1077 or BT_1476 or BT_2415 or BT_3375 or BT_3720 or BT_3935)	0	1000	2	Arginine and Proline Metabolism		Reversible in SEED	2.6.1.1
rxn00459	ENO	enolase	2pg[c] <=> h2o[c] + pep[c]	1	BT_4572	-1000	1000	2	Glycolysis/Gluconeogenesis			4.2.1.11
	ETOHt	ethanol reversible transport	etoh[e] <=> etoh[c]	1		-1000	1000	2	Transport, Extracellular	PMID:438119, PMID:17563350	Bacteroides produce weak amounts of ethanol under certain circumstances.	
	EX_12ethd(e)	1,2-Ethanediol exchange	12ethd[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_12ppd_R(e)	(R)-Propane-1,2-diol exchange	12ppd-R[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_12ppd_S(e)	(S)-Propane-1,2-diol exchange	12ppd-S[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_2fuclac(e)	2-Fucosyllactose exchange	2fuclac[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_2omfuc(e)	2-o-methylfucose exchange	2omfuc[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_2omxyl(e)	2-O-methylxylose exchange	2omxyl[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_3ddlhept(e)	3-deoxy-d-lyxo-heptulosaric acid exchange	3ddlhept[e] <=>	1		-1000	1000	0	exchange/demand reaction			

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	EX_3fuclac(e)	3-Fucosyllactose exchange	3fuclac[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_4abut(e)	4-Aminobutanoate exchange	4abut[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_7ocholate(e)	alpha,12alpha-Dihydroxy-7-oxo-5beta-cholanate exchange	7ocholate[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_ac(e)	Acetate exchange	ac[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_acerA(e)	Aceric acid (3-C-carboxy-5-deoxy-l-xylose) exchange	acerA[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_acetol(e)	Acetol exchange	acetol[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_acgal(e)	N-Acetyl-D-galactosamine exchange	acgal[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_acgalglcur(e)	desulfated disaccharide acgalglcur exchange	acgalglcur[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_acgalidour(e)	desulfated disaccharide acgalidour exchange	acgalidour[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_acgalidour2s(e)	partly desulfated disaccharide acgalidour exchange	acgalidour2s[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00122(e)	EX_acgam(e)	N-Acetyl-D-glucosamine exchange	acgam[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00232(e)	EX_acnam(e)	N-Acetylneuraminate exchange	acnam[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00182(e)	EX_adn(e)	Adenosine exchange	adn[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_adocbl(e)	Adenosylcobalamin exchange	adocbl[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00117(e)	EX_ala_D(e)	D-Alanine exchange	ala-D[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00035(e)	EX_ala_L(e)	L-Alanine exchange	ala-L[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_alaala(e)	D-Alanyl-D-alanine exchange	alaala[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd11593(e)	EX_alaasp(e)	L-alanyl-L-aspartate exchange	alaasp[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd11587(e)	EX_alagln(e)	L-alanyl-L-glutamine exchange	alagln[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd11586(e)	EX_alaglu(e)	L-alanyl-L-glutamate exchange	alaglu[e] <=>	1		-1000	1000	0	exchange/demand reaction			

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
EX_cpd11585(e)	EX_alagly(e)	L-alanylglycine exchange	alagly[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd11584(e)	EX_alahis(e)	L-alanyl-L-histidine exchange	alahis[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd11583(e)	EX_alaleu(e)	L-alanyl-L-leucine exchange	alaleu[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd11582(e)	EX_alathr(e)	L-alanyl-L-threonine exchange	alathr[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_amannan140(e)	Alpha-mannan exchange	amannan140[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_amylose300(e)	Amylose exchange	amylose300[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_apio-D(e)	D-apiose exchange	apio-D[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00224(e)	EX_arab_L(e)	L-Arabinose exchange	arab-L[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_arabinan101(e)	Arabinan exchange	arabinan101[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_arabinogal(e)	Larch arabinogalactan exchange	arabinogal[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_arabttr(e)	Arabinotriose exchange	arabttr[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00051(e)	EX_arg_L(e)	L-Arginine exchange	arg-L[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_argarg(e)	L-argininyl-L-arginine exchange	argarg[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_asn_L(e)	L-Asparagine exchange	asn-L[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_asp_L(e)	L-Aspartate exchange	asp-L[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00104(e)	EX_btn(e)	Biotin exchange	btn[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00063(e)	EX_ca2(e)	Calcium exchange	ca2[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_carn(e)	Carnosine exchange	carn[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00635(e)	EX_cbl1(e)	Cob(I)alamin exchange	cbl1[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd01012(e)	EX_cd2(e)	Cadmium exchange	cd2[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd01017(e)	EX_cgly(e)	Cys-Gly exchange	cgly[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_chtbs(e)	Chitobiose exchange	chtbs[e] <=>	1		-1000	1000	0	exchange/demand reaction			

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EX_cpd00137(e)	EX_cit(e)	Citrate exchange	cit[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00099(e)	EX_cl(e)	Chloride exchange	cl[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00011(e)	EX_co2(e)	CO2 exchange	co2[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00149(e)	EX_cobalt2(e)	Co2+ exchange	cobalt2[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_core2(e)	Core2 (mucin O-glycan) exchange	core2[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_core3(e)	Core3 (mucin O-glycan) exchange	core3[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_core4(e)	Core4 (mucin O-glycan) exchange	core4[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_core5(e)	Core 5 exchange	core5[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_core6(e)	Core6 (mucin O-glycan) exchange	core6[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_core7(e)	Core 7 exchange	core7[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_core8(e)	Core 8 exchange	core8[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_cps_bt(e)	Capsule polysaccharide (B.thetaiotaomicron specific) exchange	cps_bt[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_cspg_a(e)	Chondroitin sulfate A exchange	cspg_a[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_cspg_a_degr(e)	GalNAc4S-GlcA exchange	cspg_a_degr[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_cspg_ab_rest(e)	Chondroitin sulfate lyase AB degradation product exchange	cspg_ab_rest[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_cspg_b(e)	Chondroitin sulfate B exchange	cspg_b[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_cspg_b_degr(e)	GalNAc4S-IdoA2S exchange	cspg_b_degr[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_cspg_c(e)	Chondroitin sulfate C exchange	cspg_c[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_cspg_c_degr(e)	GalNAc6S-GlcA exchange	cspg_c_degr[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_cspg_c_rest(e)	Chondroitin sulfate lyase C degradation product exchange	cspg_c_rest[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd08305(e)	EX_ctbt(e)	Crotonobetaine exchange	ctbt[e] <=>	1		-1000	1000	0	exchange/demand reaction			

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EX_cpd00058(e)	EX_cu2(e)	Cu2+ exchange	cu2[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00084(e)	EX_cys_L(e)	L-Cysteine exchange	cys-L[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00367(e)	EX_cytd(e)	Cytidine exchange	cytd[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00438(e)	EX_dad_2(e)	Deoxyadenosine exchange	dad-2[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00654(e)	EX_dcyt(e)	Deoxycytidine exchange	dcyt[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_dextran40(e)	Dextran 40, (1,6-alpha-D-Glucan) exchange	dextran40[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00277(e)	EX_dgsn(e)	Deoxyguanosine exchange	dgsn[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd03279(e)	EX_din(e)	Deoxyinosine exchange	din[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_dsT_antigen(e)	disialyl-T antigen exchange	dsT_antigen[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_dt5hsu(e)	5-Dehydro-4-deoxy-D-glucuronate exchange	dt5hsu[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00412(e)	EX_duri(e)	Deoxyuridine exchange	duri[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_etoh(e)	Ethanol exchange	etoh[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_f1a(e)	F1alpha (mucin O-glycan) exchange	f1a[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd10515(e)	EX_fe2(e)	Fe2+ exchange	fe2[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd10516(e)	EX_fe3(e)	Fe3+ exchange	fe3[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd03725(e)	EX_fe3dcit(e)	Fe(III)dicitrate exchange	fe3dcit[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00393(e)	EX_fol(e)	Folate exchange	fol[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00047(e)	EX_for(e)	Formate exchange	for[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00082(e)	EX_fru(e)	D-Fructose exchange	fru[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_fuc_L(e)	L-Fucose exchange	fuc-L[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_fucneulacnhx(e)	Monofucosyl-monosialyl-lacto-N-hexaose exchange	fucneulacnhx[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00106(e)	EX_fum(e)	Fumarate exchange	fum[e] <=>	1		-1000	1000	0	exchange/demand reaction			

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EX_cpd00108(e)	EX_gal(e)	D-Galactose exchange	gal[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_galam(e)	Galactosamine exchange	galam[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00280(e)	EX_galur(e)	D-Galacturonate exchange	galur[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_gam(e)	D-Glucosamine exchange	gam[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_gam26s(e)	Glucosamine 2,6-sulfate exchange	gam26s[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_gchola(e)	Glycocholate exchange	gchola[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00027(e)	EX_glc(e)	D-Glucose exchange	glc-D[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00164(e)	EX_glcur(e)	D-Glucuronate exchange	glcur[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00053(e)	EX_gln_L(e)	L-Glutamine exchange	gln-L[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00023(e)	EX_glu_L(e)	L-Glutamate exchange	glu-L[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00033(e)	EX_gly(e)	Glycine exchange	gly[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd11581(e)	EX_glyasn(e)	Glycyl-L-asparagine exchange	glyasn[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd11589(e)	EX_glyasp(e)	Glycyl-L-aspartate exchange	glyasp[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00540(e)	EX_glyb(e)	Glycine betaine exchange	glyb[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_glycogen1500(e)	Glycogen exchange	glycogen1500[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd11580(e)	EX_glygln(e)	Glycyl-L-glutamine exchange	glygln[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd11592(e)	EX_glyglu(e)	Glycyl-L-glutamate exchange	glyglu[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_glygly(e)	exchange reaction for glycylglycine	glygly[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd15604(e)	EX_glyleu(e)	Glycylleucine exchange	glyleu[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd11591(e)	EX_glymet(e)	Glycyl-L-methionine exchange	glymet[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd15605(e)	EX_glyphe(e)	exchange reaction for glycylphenylalaine	glyphe[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd11588(e)	EX_glypro(e)	Glycylproline exchange	glypro[e] <=>	1		-1000	1000	0	exchange/demand reaction			

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EX_cpd15606(e)	EX_glytyr(e)	Glycyl-L-tyrosine exchange	glytyr[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_gncore1(e)	gncore1 (mucin O-glycan) exchange	gncore1[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_gncore2(e)	GlcNAc-alpha-1,4-Core 2 exchange	gncore2[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00311(e)	EX_gsn(e)	Guanosine exchange	gsn[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00067(e)	EX_h(e)	H+ exchange	h[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_h2(e)	H2 exchange	h2[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00001(e)	EX_h2o(e)	H2O exchange	h2o[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_h2s(e)	Hydrogen sulfide exchange	h2s[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_ha(e)	hyaluronan exchange	ha[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_ha_deg1(e)	hyaluronan degradation product 1 exchange	ha_deg1[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_ha_pre1(e)	hyaluronan biosynthesis, precursor 1 exchange	ha_pre1[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00531(e)	EX_hg2(e)	Hg2+ exchange	hg2[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00119(e)	EX_his_L(e)	L-Histidine exchange	his-L[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_homogal(e)	Homogalacturonan exchange	homogal[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_hspg(e)	heparan sulfate proteoglycan exchange	hspg[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_hspg_degr_1(e)	heparan sulfate proteoglycan degradation product 1 exchange	hspg_degr_1[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_hspg_degr_10(e)	heparan sulfate proteoglycan degradation product 10 exchange	hspg_degr_10[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_hspg_degr_11(e)	heparan sulfate proteoglycan degradation product 11 exchange	hspg_degr_11[e] <=>	1		-1000	1000	0	exchange/demand reaction			

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	EX_hspg_degr_12(e)	heparan sulfate proteoglycan degradation product 12 exchange	hspg_degr_12[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_hspg_degr_13(e)	heparan sulfate proteoglycan degradation product 13 exchange	hspg_degr_13[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_hspg_degr_14(e)	heparan sulfate proteoglycan degradation product 14 exchange	hspg_degr_14[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_hspg_degr_15(e)	heparan sulfate proteoglycan degradation product 15 exchange	hspg_degr_15[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_hspg_degr_2(e)	heparan sulfate proteoglycan degradation product 2 exchange	hspg_degr_2[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_hspg_degr_3(e)	heparan sulfate proteoglycan degradation product 3 exchange	hspg_degr_3[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_hspg_degr_4(e)	heparan sulfate proteoglycan degradation product 4 exchange	hspg_degr_4[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_hspg_degr_5(e)	heparan sulfate proteoglycan degradation product 5 exchange	hspg_degr_5[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_hspg_degr_6(e)	heparan sulfate proteoglycan degradation product 6 exchange	hspg_degr_6[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_hspg_degr_7(e)	heparan sulfate proteoglycan degradation product 7 exchange	hspg_degr_7[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_hspg_degr_8(e)	heparan sulfate proteoglycan degradation product 8 exchange	hspg_degr_8[e] <=>	1		-1000	1000	0	exchange/demand reaction			

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	EX_hspg_degr_9(e)	heparan sulfate proteoglycan degradation product 9 exchange	hspg_degr_9[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_hspg_rest(e)	hspg_undegradable_rest exchange	hspg_rest[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_idour(e)	Iduronate exchange	idour[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00322(e)	EX_ile_L(e)	L-Isoleucine exchange	ile-L[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00246(e)	EX_ins(e)	Inosine exchange	ins[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_inulin(e)	Inulin exchange	inulin[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_isobut(e)	Isobutyrate exchange	isobut[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_isocapr(e)	Isocaproate exchange	isocapr[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_isoval(e)	Isovalerate exchange	isoval[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00205(e)	EX_k(e)	K+ exchange	k[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_kdo(e)	3-Deoxy-D-manno-2-octulosonate exchange	kdo[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_kesto(e)	Kestose exchange	kesto[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_kestopt(e)	Kestopentaose exchange	kestopt[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_kestottr(e)	Kestotetraose exchange	kestottr[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_l2n2m2mn(e)	de-Fuc, reducing GlcNAc removed, de-Sia form of PA6 (w/o peptide linkage) exchange	l2n2m2mn[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00221(e)	EX_lac_D(e)	D-lactate exchange	lac-D[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00159(e)	EX_lac_L(e)	L-Lactate exchange	lac-L[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_lacdfucttr(e)	Lactodifucotetraose exchange	lacdfucttr[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_lacndfuchx(e)	Lacto-N-difucohexaose exchange	lacndfuchx[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_lacnfucpt(e)	Lacto-N-fucopentaose exchange	lacnfucpt[e] <=>	1		-1000	1000	0	exchange/demand reaction			

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	EX_lacnnttr(e)	Lacto-N-neotetraose exchange	lacnnttr[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_lacnttr(e)	Lacto-N-tetraose exchange	lacnttr[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00208(e)	EX_lcts(e)	Lactose exchange	lcts[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00107(e)	EX_leu_L(e)	L-Leucine exchange	leu-L[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_leugly(e)	exchange reaction for leucylglycine	leugly[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_leuleu(e)	Leucylleucine exchange	leuleu[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_levan1000(e)	Levan exchange	levan1000[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_levanb(e)	Levanbiose exchange	levanb[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_levanttr(e)	Levantriose exchange	levanttr[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_levantttr(e)	Levantetraose exchange	levantttr[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_lmn2(e)	Laminaribiose exchange	lmn2[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_lmn30(e)	Laminarin exchange	lmn30[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_lps_bt(e)	Lipopolysaccharide exchange	lps_bt[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00039(e)	EX_lys_L(e)	L-Lysine exchange	lys-L[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_m2mn(e)	(alpha-D-mannosyl)2-beta-D-mannosyl-N-acetylglucosamine exchange	m2mn[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00179(e)	EX_malt(e)	Maltose exchange	malt[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_malthp(e)	Maltoheptaose exchange	malthp[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd01329(e)	EX_malthx(e)	Maltohexaose exchange	malthx[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_maltpt(e)	Maltopentaose exchange	maltpt[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd01262(e)	EX_malttr(e)	Maltotriose exchange	malttr[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_maltttr(e)	Maltotetraose exchange	maltttr[e] <=>	1		-1000	1000	0	exchange/demand reaction			

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EX_cpd00138(e)	EX_man(e)	D-Mannose exchange	man[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_manb(e)	Mannobiose exchange	manb[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_manpt(e)	Mannopentaose exchange	manpt[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_mantr(e)	Mannotriose exchange	mantr[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_manttr(e)	Mannotetraose exchange	manttr[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd03198(e)	EX_melib(e)	Melibiose exchange	melib[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_meoh(e)	methanol exchange	meoh[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00060(e)	EX_met_L(e)	L-Methionine exchange	met-L[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd11590(e)	EX_metala(e)	L-methionyl-L-alanine exchange	metala[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00254(e)	EX_mg2(e)	Mg exchange	mg2[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_mn(e)	beta-1,4-mannose-N-acetylglucosamine exchange	mn[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00030(e)	EX_mn2(e)	Mn2+ exchange	mn2[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_mqn10(e)	Menaquinone 10 exchange	mqn10[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_mqn11(e)	Menaquinone 11 exchange	mqn11[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_mqn7(e)	Menaquinone 7 exchange	mqn7[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_mqn8(e)	Menaquinone 8 exchange	mqn8[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_mqn9(e)	Menaquinone 9 exchange	mqn9[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_mthgxl(e)	Methylglyoxal exchange	mthgxl[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_n2m2mn(e)	de-Fuc, reducing GlcNAc removed, de-Sia, de-Gal form of PA6 (w/o peptide linkage) exchange	n2m2mn[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00971(e)	EX_na1(e)	Sodium exchange	na1[e] <=>	1		-1000	1000	0	exchange/demand reaction			

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	EX_nac(e)	Nicotinate exchange	nac[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_neulacnttr(e)	Sialyllacto-N-tetraose exchange	neulacnttr[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00013(e)	EX_nh4(e)	Ammonia exchange	nh4[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_nmn(e)	NMN exchange	nmn[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00075(e)	EX_no2(e)	Nitrite exchange	no2[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00007(e)	EX_o2(e)	O2 exchange	o2[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_oligofru4(e)	Oligofructose exchange	oligofru4[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_orn(e)	Ornithine exchange	orn[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_pac(e)	Phenylacetic acid exchange	pac[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_pb(e)	Lead exchange	pb[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_pe_cer1_BT(e)	Ceramide phosphoethanolamine (B.thetaiotaomicron specific) exchange	pe_cer1_bt[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_pect(e)	exchange reaction for pectins	pect[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_pecticgal(e)	Pectic galactan (potato) exchange	pecticgal[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00066(e)	EX_phe_L(e)	L-Phenylalanine exchange	phe-L[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_phearg(e)	L-phenylalanyl-L-arginine exchange	phearg[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_pheme(e)	Protoheme exchange	pheme[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00009(e)	EX_pi(e)	Phosphate exchange	pi[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00644(e)	EX_pnto_R(e)	(R)-Pantothenate exchange	pnto-R[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_ppa(e)	Propionate exchange	ppa[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00129(e)	EX_pro_L(e)	L-Proline exchange	pro-L[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_progly(e)	L-Prolinylglycine exchange	progly[e] <=>	1		-1000	1000	0	exchange/demand reaction			

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
EX_cpd00118(e)	EX_ptrc(e)	Putrescine exchange	ptrc[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_pullulan1200(e)	Pullulan exchange	pullulan1200[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_pydxn(e)	Pyridoxine exchange	pydxn[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_pyr(e)	Pyruvate exchange	pyr[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_raffin(e)	Raffinose exchange	raffin[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_rhamnogalurI(e)	Rhamnogalacturonan I exchange	rhamnogalurI[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_rhamnogalurII(e)	Rhamnogalacturonan II exchange	rhamnogalurII[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_rib_D(e)	D-Ribose exchange	rib-D[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00220(e)	EX_ribflv(e)	Riboflavin exchange	ribflv[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00396(e)	EX_rmn(e)	L-Rhamnose exchange	rmn[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_s2l2fn2m2masn(e)	PA6 exchange	s2l2fn2m2masn[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_s2l2n2m2m(e)	de-Fuc form of PA6 (w/o peptide linkage) exchange	s2l2n2m2m[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_s2l2n2m2masn(e)	de-Fuc form of PA6 exchange	s2l2n2m2masn[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_s2l2n2m2mn(e)	de-Fuc, reducing GlcNAc removed form of PA6 (w/o peptide linkage) exchange	s2l2n2m2mn[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00054(e)	EX_ser_L(e)	L-Serine exchange	ser-L[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_Ser_Thr(e)	protein-linked serine or threonine residue (O-glycosylation site) exchange	Ser_Thr[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00048(e)	EX_so4(e)	Sulfate exchange	so4[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_sphmyln_BT(e)	Sphingomyelin (B.thetaiotaomicron specific) exchange	sphmyln_bt[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00264(e)	EX_spmd(e)	Spermidine exchange	spmd[e] <=>	1		-1000	1000	0	exchange/demand reaction			

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	EX_sT_antigen(e)	sT_antigen (mucin O-glycan) exchange	sT_antigen[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_starch1200(e)	Starch exchange	starch1200[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_sTn_antigen(e)	sialyl-Tn antigen exchange	sTn_antigen[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_strch1(e)	starch, structure 1 (1,6-{7[1,4-Glc], 4[1,4-Glc]}) exchange	strch1[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_strch2(e)	starch, structure 2 (1,6-{2[1,4-Glc], [1,4-Glc]}) exchange	strch2[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_stys(e)	Stachyose exchange	stys[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00036(e)	EX_succ(e)	Succinate exchange	succ[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00076(e)	EX_sucr(e)	Sucrose exchange	sucr[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_T_antigen(e)	T antigen (core 1) exchange	T_antigen[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00210(e)	EX_taur(e)	Taurine exchange	taur[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_tchola(e)	Taurocholate exchange	tchola[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00305(e)	EX_thm(e)	Thiamin exchange	thm[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_thr_L(e)	L-Threonine exchange	thr-L[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00184(e)	EX_thymd(e)	Thymidine exchange	thymd[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_Tn_antigen(e)	Tn_antigen (mucin O-glycan) exchange	Tn_antigen[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00794(e)	EX_tre(e)	Trehalose exchange	tre[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00065(e)	EX_trp_L(e)	L-Tryptophan exchange	trp-L[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00069(e)	EX_tyr_L(e)	L-Tyrosine exchange	tyr-L[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	EX_unsdigalur(e)	4-(4-Deoxy-alpha-D-gluc-4-enuronosyl)-D-galacturonate, Unsaturated digalacturonate exchange	unsdigalur[e] <=>	1		-1000	1000	0	exchange/demand reaction			

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
EX_cpd00092(e)	EX_ura(e)	Uracil exchange	ura[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00073(e)	EX_urea(e)	Urea exchange	urea[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00249(e)	EX_uri(e)	Uridine exchange	uri[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00156(e)	EX_val_L(e)	L-Valine exchange	val-L[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00309(e)	EX_xan(e)	Xanthine exchange	xan[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00154(e)	EX_xyl_D(e)	D-Xylose exchange	xyl-D[e] <=>	1		-1000	1000	0	exchange/demand reaction			
EX_cpd00034(e)	EX_zn2(e)	Zinc exchange	zn2[e] <=>	1		-1000	1000	0	exchange/demand reaction			
	F1PGT	fucose-1-phosphate guanylyltransferase	h[c] + gtp[c] + fuc1p-L[c] <=> ppi[c] + gdpfuc[c]	1	BT_2128	-1000	1000	4	Alternate Carbon Metabolism	PMID:15774760, PMID:19379697	Bacteroides use host-derived fucose for cell surface decoration.	2.7.7.30
rxn05736	FACOAL140	fatty-acid--CoA ligase (tetradecanoate)	coa[c] + atp[c] + ttdca[c] <=> tdcoa[c] + amp[c] + ppi[c]	1	(BT_0684 or BT_1226 or BT_2154 or BT_2782 or BT_3550)	-1000	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Reaction is irreversible in SEED. This reaction is involved in fatty acid biosynthesis.	6.2.1.3
rxn00947	FACOAL160	fatty-acid--CoA ligase (hexadecanoate)	coa[c] + atp[c] + hdca[c] <=> pmtcoa[c] + amp[c] + ppi[c]	1	(BT_0684 or BT_1226 or BT_2154 or BT_2782 or BT_3550)	-1000	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Reaction is irreversible in SEED. This reaction is involved in fatty acid biosynthesis.	6.2.1.3
rxn09450	FACOAL161	fatty-acid--CoA ligase (hexadecenoate)	coa[c] + atp[c] + hdcea[c] <=> amp[c] + ppi[c] + hdcoa[c]	1	(BT_0684 or BT_1226 or BT_2154 or BT_2782 or BT_3550)	-1000	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Reaction is irreversible in SEED. This reaction is involved in fatty acid biosynthesis.	6.2.1.3
rxn09449	FACOAL180	fatty-acid--CoA ligase (octadecanoate)	coa[c] + atp[c] + ocdca[c] <=> stcoa[c] + amp[c] + ppi[c]	1	(BT_0684 or BT_1226 or BT_2154 or BT_2782 or BT_3550)	-1000	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Reaction is irreversible in SEED. This reaction is involved in fatty acid biosynthesis.	6.2.1.3
rxn09448	FACOAL181	fatty-acid--CoA ligase (octadecenoate)	coa[c] + atp[c] + ocdcea[c] <=> amp[c] + ppi[c] + odecoa[c]	1	(BT_0684 or BT_1226 or BT_2154 or BT_2782 or BT_3550)	-1000	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Reaction is irreversible in SEED. This reaction is involved in fatty acid biosynthesis.	6.2.1.3

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05248	FACOALAI15	fatty-acid--CoA ligase (ANTEISO15)	coa[c] + atp[c] + fa4[c] <=> aipdcoa[c] + amp[c] + ppi[c]	1	(BT_0684 or BT_1226 or BT_2154 or BT_2782 or BT_3550)	-1000	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	6.2.1.3
rxn05251	FACOALAI17	fatty-acid--CoA ligase (ANTEISO17)	coa[c] + atp[c] + fa12[c] <=> aihpdcoa[c] + amp[c] + ppi[c]	1	(BT_0684 or BT_1226 or BT_2154 or BT_2782 or BT_3550)	-1000	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	6.2.1.3
rxn05247	FACOALI14	fatty-acid--CoA ligase (ISO14)	coa[c] + atp[c] + fa1[c] <=> itdcoa[c] + amp[c] + ppi[c]	1	(BT_0684 or BT_1226 or BT_2154 or BT_2782 or BT_3550)	-1000	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	6.2.1.3

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05249	FACOALI15	fatty-acid--CoA ligase (ISO15)	coa[c] + atp[c] + fa3[c] <=> ipdcoa[c] + amp[c] + ppi[c]	1	(BT_0684 or BT_1226 or BT_2154 or BT_2782 or BT_3550)	-1000	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	6.2.1.3
rxn05250	FACOALI16	fatty-acid--CoA ligase (ISO16)	coa[c] + atp[c] + fa6[c] <=> ihdcoa[c] + amp[c] + ppi[c]	1	(BT_0684 or BT_1226 or BT_2154 or BT_2782 or BT_3550)	-1000	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	6.2.1.3
rxn05252	FACOALI17	fatty-acid--CoA ligase (ISO17)	coa[c] + atp[c] + fa11[c] <=> ihpdcoa[c] + amp[c] + ppi[c]	1	(BT_0684 or BT_1226 or BT_2154 or BT_2782 or BT_3550)	-1000	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	6.2.1.3
rxn00786	FBA	fructose-bisphosphate aldolase	fdp[c] <=> dhap[c] + g3p[c]	1	(BT_1106 or BT_1659 or BT_1691)	-1000	1000	4	Glycolysis/Gluconeogenesis	PMID:73363, PMID:148460	Demonstrated by enzyme assay in B. thetaiotaomicron/ close relative B. fragilis.	4.1.2.13

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn01870	FBA2	D-Fructose 1-phosphate D-glyceraldehyde-3-phosphate-lyase	f1p[c] <=> glyald[c] + dhap[c]	1	(BT_1106 or BT_1659 or BT_1691)	-1000	1000	2	Alternate Carbon Metabolism	PMID:73363, PMID:148460	This reaction was included by Model SEED, but may not take place. in B. thetaiotaomicron.	4.1.2.13
rxn01334	FBA3	Sedoheptulose 1,7-bisphosphate D-glyceraldehyde-3-phosphate-lyase	s17bp[c] <=> dhap[c] + e4p[c]	1	(BT_1106 or BT_1659 or BT_1691)	-1000	1000	4	Pentose Phosphate Pathway	PMID:73363, PMID:148460		4.1.2.13
rxn00549	FBP	fructose-bisphosphatase	h2o[c] + fdp[c] => pi[c] + f6p[c]	0	BT_1228	0	1000	2	Glycolysis/Gluconeogenesis			3.1.3.11
rxn02319	FCI	L-fucose isomerase	fuc-L[c] <=> fcl-L[c]	1	BT_1273	-1000	1000	4	Alternate Carbon Metabolism	PMID:10449780	The L-fucose utilization operon was characterized experimentally.	5.3.1.25
	FCLK	L-fuculokinase	atp[c] + fcl-L[c] => h[c] + adp[c] + fc1p[c]	0	BT_1275	0	1000	4	Alternate Carbon Metabolism	PMID:10449780	The L-fucose utilization operon was characterized experimentally.	2.7.1.51
rxn01620	FCLPA	L-fuculose 1-phosphate aldolase	fc1p[c] <=> dhap[c] + lald-L[c]	1	BT_1274	-1000	1000	4	Alternate Carbon Metabolism	PMID:10449780	The L-fucose utilization operon was characterized experimentally.	4.1.2.17

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	FDNADOX	ferredoxin:NAD+ oxidoreductase	nad[c] + fdxrd[c] <=> h[c] + nadh[c] + fdxox[c]	1		-1000	1000	2	Unassigned	PMID:760499, PMID:12740060, PMID:20444704	In the gut, this reaction allows primary fermenters, such as B. thetaiotaomicron, to regenerate NAD+. Also involves a ferredoxin-dependent hydrogenase (HYD4). The pathway only takes place if the end product hydrogen is removed from the environment because the equilibrium of the reaction favors the formation of NADH. B. thetaiotaomicron generates hydrogen as one of its fermentation end products; accumulation of hydrogen inhibits reoxidation of NADH. It is therefore assumed that it regenerates NAD+ via this pathway, which leads to increased hydrogen partial pressure. Removal of hydrogen allows B. thetaiotaomicron to regenerate NAD+. No gene is known, reaction was added during manual gapfilling.	1.18.1.3
rxn05555	FE2abc	iron (II) transport via ABC system	h2o[c] + atp[c] + fe2[e] => h[c] + pi[c] + adp[c] + fe2[c]	0	(BT_1592 or (BT_2098 and BT_2099) or (BT_1950 and BT_1952))	0	1000	4	Transport, Extracellular	BT requires Fe2: PMID:4472783	Putative annotation (NCBI)	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05189	FE3abc	iron (III) transport via ABC system	h2o[c] + atp[c] + fe3[e] => h[c] + pi[c] + adp[c] + fe3[c]	0	((BT_2098 and BT_2099) or (BT_1950 and BT_1952))	0	1000	2	Transport, Extracellular		Added by Model SEED during auto-completion step in pipeline. Gene annotation was added from NCBI Gene during manual curation.	
rxn05195	FE3DCITabc	iron transport from ferric-dicitrate via ABC system	h2o[c] + atp[c] + fe3dcit[e] => h[c] + pi[c] + adp[c] + 2 cit[c] + fe3[c]	0	BT_1951	0	1000	2	Transport, Extracellular		Added based on BIGG database	
rxn05557	FEDCabc	iron (III) dicitrate transport via ABC system	h2o[c] + atp[c] + 2 cit[e] + fe3[e] => h[c] + pi[c] + adp[c] + 2 cit[c] + fe3[c]	0	BT_1951	0	1000	2	Transport, Extracellular			
rxn00056	FERO	ferroxidase	4 h[c] + o2[c] + 4 fe2[c] => 2 h2o[c] + 4 fe3[c]	0	BT_4715	0	1000	2	Porphyrin and Chlorophyll Metabolism			1.16.3.1
	FK	Fucokinase	atp[c] + fuc-L[c] => h[c] + adp[c] + fuc1p-L[c]	0	BT_2128	0	1000	4	Alternate Carbon Metabolism	PMID:15774760	The pathway was demonstrated experimentally in Bacteroides fragilis.	2.7.1.52
rxn00122	FMNAT	FMN adenylyltransferase	h[c] + atp[c] + fmn[c] => ppi[c] + fad[c]	0	BT_2543	0	1000	2	Cofactor and Prosthetic Group Biosynthesis			2.7.7.2
rxn02201	FOLD3	dihydropteroate synthase	4abz[c] + 2ahhmd[c] => ppi[c] + dhpt[c]	0	BT_3646	0	1000	2	Folate Metabolism			2.5.1.15
	FOLR	tetrahydrofolate NADP oxidoreductase	2 nadp[c] + thf[c] <=> h[c] + 2 nadph[c] + fol[c]	1	(BT_0106 or BT_2048)	-1000	1000	2	Folate Metabolism	PMID:4853401, PMID:9167138	Added to allow folate biosynthesis. B. thetaiotaomicron does not require folate in medium.	1.5.1.3

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05255	FOLt	FOLt	h[e] + fol[e] <=> h[c] + fol[c]	1		-1000	1000	2	Transport, Extracellular	PMID:9167138	It is well established that the gut microbiota produces folic acid. Colonic absorption of bacterial folate seems to be significant. It is assumed that B. thetaiotaomicron is one of the sources of folate supply.	
	FOMETR	aminomethyltransferase	h[c] + 5fthf[c] <=> h2o[c] + methf[c]	1	BT_4584	-1000	1000	2	Cofactor and Prosthetic Group Biosynthesis		One of several reactions catalyzed by aminomethyltransferase (EC 2.1.2.10). Added based on KEGG Pathway.	2.1.2.10
	FORt	formate transport via diffusion	for[c] <=> for[e]	1		0	1000	2	Transport, Extracellular	PMID:9178362	B. thetaiotaomicron produces formate under certain circumstances.	
rxn00689	FPGS_tm	TetrahydrofolateL-glutamate gamma-ligase (ADP-forming)	glu-L[c] + atp[c] + thf[c] => h[c] + pi[c] + adp[c] + thfglu[c]	0	BT_1335	0	1000	2	Folate Metabolism			6.3.2.17
rxn01210	FPGS7	10-Formyltetrahydrofolate L-glutamate ligase (ADP-forming)	4 glu-L[c] + 4 atp[c] + 10fthf[c] => 4 h[c] + 4 pi[c] + 4 adp[c] + 10fthf5glu[c]	0	BT_1335	0	1000	2	Folate Metabolism			6.3.2.17
	FRD10	fumarate reductase	fum[c] + mql10[c] => succ[c] + mqn10[c]	0	(BT_3054 and BT_3055)	0	1000	4	TCA Cycle	PMID:12777495, PMID:11260473	Bacteroides have both succinate dehydrogenase and fumarate reductase acitivity. Fumarate reductase is a key enzyme in central metabolism. AH	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	FRD11	fumarate reductase	fum[c] + mql11[c] => succ[c] + mqn11[c]	0	(BT_3054 and BT_3055)	0	1000	4	TCA Cycle	PMID:12777495, PMID:11260473	Bacteroides have both succinate dehydrogenase and fumarate reductase acitivity. Fumarate reductase is a key enzyme in central metabolism. AH	
rxn08527	FRD2	fumarate reductase	fum[c] + mql8[c] => succ[c] + mqn8[c]	0	(BT_3054 and BT_3055)	0	1000	4	TCA Cycle	PMID:12777495, PMID:11260473	Bacteroides have both succinate dehydrogenase and fumarate reductase acitivity. Fumarate reductase is a key enzyme in central metabolism. AH	1.3.99.1
rxn08528	FRD3	fumarate reductase	fum[c] + 2dmmql8[c] => 2dmmq8[c] + succ[c]	0	(BT_3054 and BT_3055)	0	1000	3	TCA Cycle	PMID:12777495, PMID:11260473	Bacteroides have both succinate dehydrogenase and fumarate reductase acitivity. Fumarate reductase is a key enzyme in central metabolism. It is not known if B. thetaiotaomicron uses demethylmenaquinone or only menaquinone.	1.3.99.1
	FRD8	fumarate reductase	fum[c] + mql7[c] => succ[c] + mqn7[c]	0	(BT_3054 and BT_3055)	0	1000	4	TCA Cycle	PMID:12777495, PMID:11260473	Bacteroides have both succinate dehydrogenase and fumarate reductase acitivity. Fumarate reductase is a key enzyme in central metabolism. AH	
	FRD9	fumarate reductase	fum[c] + mql9[c] => succ[c] + mqn9[c]	0	(BT_3054 and BT_3055)	0	1000	4	TCA Cycle	PMID:12777495, PMID:11260473	Bacteroides have both succinate dehydrogenase and fumarate reductase acitivity. Fumarate reductase is a key enzyme in central metabolism. AH	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn01486	FRTT	trans,trans-Farnesyl-diphosphateisopentenyl-diphosphate	ipdp[c] + frdp[c] => ppi[c] + ggdp[c]	0	(BT_3261 or BT_2058)	0	1000	2	Cofactor and Prosthetic Group Biosynthesis			2.5.1.29
	FRUASE3	Intracellular endofructanase	h2o[c] + levanb[c] => 2 fru[c]	0	BT_1765	0	1000	4	Plant Polysaccharide Degradation	PMID:20603004	Intracellular fructanase acitivity was demonstrated in B. thetaiotaomicron.	3.2.1.65
	FRUt2r	D-fructose transport in via proton symport reversible	h[e] + fru[e] <=> h[c] + fru[c]	1	BT_1758	-1000	1000	4	Transport, Extracellular	PMID: 20603004	B. thetaiotaomicron grows on D-fructose.	
rxn01654	FTCD_r	Formiminotetrahydrofolate cyclodeaminase (EC 4.3.1.4)	2 h[c] + 5forthf[c] <=> nh4[c] + methf[c]	1	BT_2691	-1000	1000	2	Folate Metabolism			4.3.1.4
rxn01653	FTHFCL	5-formethyltetrahydrofolate cyclo-ligase	atp[c] + 5fthf[c] => pi[c] + adp[c] + methf[c]	0	BT_4258	0	1000	2	Folate Metabolism		Putative annotation (NCBI)	6.3.3.2
rxn00691	FTHFD	formyltetrahydrofolate deformylase	h2o[c] + 10fthf[c] => h[c] + thf[c] + for[c]	0	BT_1381	0	1000	2	Folate Metabolism			3.5.1.10
rxn00690	FTHFLi	formate-tetrahydrofolate ligase	atp[c] + thf[c] + for[c] => pi[c] + adp[c] + 10fthf[c]	0	BT_0737	0	1000	2	Folate Metabolism			6.3.4.3
	FUCASEe	alpha-fucosidase, extracellular	h2o[e] + s2l2fn2m2masn[e] => fuc-L[e] + s2l2n2m2masn[e]	0	(BT_1842 or BT_2970 or BT_3665)	0	1000	4	N-Glycan Degradation	PMID:15774760, PMID:19379697'	Bacteroides use host-derived fucose for cell surface decoration.	3.2.1.51

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	FUCNEULACNHX_DEGe	monofucosyl-monosialyl-lacto-N-hexaose degradation by alpha-fucosidase, sialidase, N-acetylglutaminidase and beta-galactosidase (extracellular)	8 h2o[e] + 2 fucneulacnhx[e] => 2 fuc-L[e] + 2 acgam[e] + 2 acnam[e] + 2 gal[e] + lacnnttr[e] + lacnttr[e]	0	((BT_1625 or BT_4136) and (BT_0455 or BT_2194 or BT_2892) and (BT_1626 or BT_0461) and (BT_1627 or BT_1632 or BT_4132 or BT_0459 or BT_0460 or BT_1038 or BT_1044 or BT_1048 or BT_1051 or BT_4295 or BT_2825) and ((BT_1630 and BT_1631) or (BT_4134 and BT_4135) or (BT_1039 and BT_1040) or (BT_1042 and BT_1043) or (BT_1046 and BT_1047) or (BT_4297 and BT_4298) or (BT_2818 and BT_2819) or (BT_2820 and BT_2821)))	0	1000	3	HMO Degradation	PMID: 22036470, PMID: 20679197	B. thetaiotaomicron grows on human milk oligosaccharides (HMOs); numerous glycosidase hydrolases are upregulated during growth on HMOs. Lacto-N-tetraose and Lacto-N-neotetraose are poorly metabolized and accumulate if BT is grown on HMOs. Putative reaction. Structure based on PMID: 20679197. Involves beta-galactosidase, alpha-fucosidase, sialidase, N-acetylglucosaminidase, susC, susD (binding proteins).	
	FUCt	L-fucose transport via proton symport	fuc-L[e] + h[e] <=> h[c] + fuc-L[c]	1	(BT_1277 or BT_3616)	-1000	1000	4	Transport, Extracellular	PMID:10449780	B. thetaiotaomicron can use L-fucose as carbon source.	
rxn00799	FUM	fumarase	h2o[c] + fum[c] <=> mal-L[c]	1	BT_2256	-1000	1000	4	TCA Cycle	PMID: 12777495	Role of enzyme was characterized experimentally in Bacteroides fragilis.	4.2.1.2
rxn05561	FUMt2r	fumarate reversible transport via symport	h[e] + fum[e] <=> h[c] + fum[c]	1	BT_2756	-1000	1000	2	Transport, Extracellular		Annotation from NCBI Gene.	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn03638	G1PACT	glucosamine-1-phosphate N-acetyltransferase	accoa[c] + gam1p[c] => h[c] + coa[c] + acgam1p[c]	0		0	1000	1	Cell Envelope Biosynthesis		This enzyme was added to allow synthesis of N-acetylglucosamine from glucose . This role might also be fulfilled by glucosamine-6-phosphate-acetyltransferase (EC 2.3.1.4), it is unclear which pathway is used by B. thetaiotaomicron.	2.3.1.157
rxn00702	G1PCT	Glucose-1-phosphate cytidylyltransferase (EC 2.7.7.33)	h[c] + ctp[c] + g1p[c] <=> ppi[c] + cdpglc[c]	1	BT_1351	-1000	1000	2	Alternate Carbon Metabolism			2.7.7.33
rxn01675	G1PTT	glucose-1-phosphate thymidylyltransferase	h[c] + dttp[c] + g1p[c] => ppi[c] + dtdpglu[c]	0	(BT_0463 or BT_2017)	0	1000	2	Capsular Polysaccharide Biosynthesis		Reversible in SEED	2.7.7.24
rxn08546	G3PAT120	glycerol-3-phosphate acyltransferase (C12:0)	ddcaACP[c] + glyc3p[c] => ACP[c] + 1ddecg3p[c]	0		0	1000	2	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added during manual gapfilling to allow lipid biosynthesis to take place. GPR is unknown.	2.3.1.15
rxn08547	G3PAT140	glycerol-3-phosphate acyltransferase (C14:0)	myrsACP[c] + glyc3p[c] => ACP[c] + 1tdecg3p[c]	0		0	1000	2	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added during manual gapfilling to allow lipid biosynthesis to take place. GPR is unknown.	2.3.1.15
rxn08549	G3PAT160	glycerol-3-phosphate acyltransferase (C16:0)	palmACP[c] + glyc3p[c] => ACP[c] + 1hdecg3p[c]	0		0	1000	2	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added during manual gapfilling to allow lipid biosynthesis to take place. GPR is unknown.	2.3.1.15
rxn08551	G3PAT180	glycerol-3-phosphate acyltransferase (C18:0)	ocdcaACP[c] + glyc3p[c] => ACP[c] + 1odecg3p[c]	0		0	1000	2	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added during autocompletion step by Model SEED to allow lipid biosynthesis to take place. GPR is unknown.	2.3.1.15

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn08552	G3PAT181	glycerol-3-phosphate acyltransferase (C18:1)	octeACP[c] + glyc3p[c] => ACP[c] + 1odec11eg3p[c]	0		0	1000	2	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added during manual gapfilling to allow lipid biosynthesis to take place. GPR is unknown.	2.3.1.15
rxn10209	G3PATAI15	anteisopentadecanoyl-glycerol-3-phosphate O-acyltransferase	h[c] + aipdcoa[c] + glyc3p[c] => coa[c] + 1aipdecg3p[c]	0		0	1000	2	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added during manual gapfilling to allow lipid biosynthesis to take place. GPR is unknown.	2.3.1.15
rxn10206	G3PATAI17	anteisoheptadecanoyl-glycerol-3-phosphate O-acyltransferase	aihpdcoa[c] + glyc3p[c] => coa[c] + 1aihpdecg3p[c]	0		0	1000	2	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added during autocompletion step by Model SEED to allow lipid biosynthesis to take place. GPR is unknown.	2.3.1.15
rxn10207	G3PATI14	isotetradecanoyl-glycerol-3-phosphate O-acyltransferase	h[c] + itdcoa[c] + glyc3p[c] => coa[c] + 1itdecg3p[c]	0		0	1000	2	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added during manual gapfilling to allow lipid biosynthesis to take place. GPR is unknown.	2.3.1.15
rxn10208	G3PATI15	isopentadecanoyl-glycerol-3-phosphate O-acyltransferase	h[c] + ipdcoa[c] + glyc3p[c] => coa[c] + 1ipdecg3p[c]	0		0	1000	2	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added during manual gapfilling to allow lipid biosynthesis to take place. GPR is unknown.	2.3.1.15
rxn10210	G3PATI16	isohexadecanoyl-glycerol-3-phosphate O-acyltransferase	h[c] + ihdcoa[c] + glyc3p[c] => coa[c] + 1ihdecg3p[c]	0		0	1000	2	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added during manual gapfilling to allow lipid biosynthesis to take place. GPR is unknown.	2.3.1.15
rxn10205	G3PATI17	isoheptadecanoyl-glycerol-3-phosphate O-acyltransferase	ihpdcoa[c] + glyc3p[c] => coa[c] + 1ihpdecg3p[c]	0		0	1000	2	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added during autocompletion step by Model SEED to allow lipid biosynthesis to take place. GPR is unknown.	2.3.1.15
rxn00611	G3PD1	glycerol-3-phosphate dehydrogenase (NAD)	nad[c] + glyc3p[c] <=> h[c] + nadh[c] + dhap[c]	1	BT_2123	-1000	1000	2	Glycerophospholipid Metabolism			1.1.1.94

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn02374	G5SADs	L-glutamate 5-semialdehyde dehydratase (spontaneous)	glu5sa[c] <=> h2o[c] + h[c] + 1pyr5c[c]	1		-1000	1000	1	Arginine and Proline Metabolism			
rxn02373	G5SD	glutamate-5-semialdehyde dehydrogenase	h[c] + nadph[c] + glu5p[c] => nadp[c] + pi[c] + glu5sa[c]	0	BT_3718	0	1000	2	Arginine and Proline Metabolism			1.2.1.41
rxn01975	G6PBDH	beta-D-Glucose-6-phosphateNADP+ 1-oxoreductase	nadp[c] + g6p-B[c] <=> h[c] + nadph[c] + 6pgl[c]	1	BT_1221	-1000	1000	4	Pentose Phosphate Pathway	PMID: 7183748	Demonstrated biochemically.	1.1.1.49
rxn00552	G6PDA	glucosamine-6-phosphate deaminase	h2o[c] + gam6p[c] => nh4[c] + f6p[c]	0	(BT_0258 or BT_3587 or BT_3601 or BT_4127)	0	1000	4	Aminosugar Metabolism	PMID: 7240086	B. thetaiotaomicron metabolizes glucosamine.	3.5.99.6
rxn00604	G6PDH2r	glucose 6-phosphate dehydrogenase	nadp[c] + g6p[c] <=> h[c] + nadph[c] + 6pgl[c]	1	BT_1221	-1000	1000	4	Pentose Phosphate Pathway	PMID: 7183748	Demonstrated biochemically.	1.1.1.49
rxn01977	G6PI	alpha-D-Glucose 6-phosphate ketol-isomerase	g6p[c] <=> g6p-B[c]	1	BT_2124	-1000	1000	4	Glycolysis/Gluconeogenesis	PMID: 6804433	Measured by enzyme assay for B. thetaiotaomicron.	5.3.1.9
rxn02380	G6PI3	beta-D-Glucose 6-phosphate ketol-isomerase	g6p-B[c] <=> f6p[c]	1	BT_2124	-1000	1000	4	Glycolysis/Gluconeogenesis	PMID: 6804433	Measured by enzyme assay for B. thetaiotaomicron.	5.3.1.9
	GACPCD	Glutaryl-ACP condensation catalyzed by FabB or FabF	h[c] + malACP[c] + gACPm[c] => ACP[c] + 3opACPm[c] + co2[c]	0	BT_3358	0	1000	3	Biotin Metabolism	PMID:20693992	Based on biotin synthesis described in PMID:20693992 for E. coli. The authors are unsure if this reaction is carried out by FabB or FabF. Here, FabF is assumed to carry out the reaction.	
	GALAM6PDA	Galactosamine-6-phosphate deaminase	h2o[c] + galam6p[c] => nh4[c] + tag6p-D[c]	0		0	1000	2	Aminosugar Metabolism	PMID:2845859	B. thetaiotaomicron grows on N-acetylgalactosamine: PMID:2845859. However, the utilization pathway is poorly understood.	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	GALAMt2r	galactosamine transport (proton symport)	h[e] + galam[e] <=> h[c] + galam[c]	1		-1000	1000	2	Transport, Extracellular	PMID: 6367911	B. thetaiotaomicron metabolizes galactosamine to some extent (though the compound does not support growth in vivo).	
	GALASE_HSe	Extracellular beta-galactosidase, heparin degradation	2 h2o[e] + hspg_degr_15[e] => 2 gal[e] + hspg_rest[e]	0	(BT_0290 or BT_0461 or BT_0757 or BT_0983 or BT_0992 or BT_0993 or BT_0996 or BT_1626 or BT_2190 or BT_2680 or BT_2922 or BT_2969 or BT_3092 or BT_3114 or BT_3179 or BT_3293 or BT_3340 or BT_3513 or BT_3654 or BT_4050 or BT_4152 or BT_4156 or BT_4160 or BT_4181 or BT_4241 or BT_4667 or BT_4684)	0	1000	4	Glycosaminoglycan Degradation	PMID:19801541, PMID:7574611	B. thetaiotaomicron specific putative heparin sulfate degradation pathway.	3.2.1.23

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	GALASE_OGLYCAN1e	Beta-galactosidase, mucin-type O-glycans, extracellular	h2o[e] + f1a[e] => gal[e] + core6[e]	0	BT_4241 and BT_4246 and BT_4247	0	1000	4	O-Glycan Degradation	PMID: 18996345, PMID: 10430883, PMID: 848954	B. thetaiotaomicron is well known to degrade mucin, the genes included in the GPR are upregulated during growth on mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis. Involves beta-galactosidase, susC, susD (binding proteins).	
	GALASE_OGLYCAN2e	Beta-galactosidase, mucin-type O-glycans, extracellular	h2o[e] + T_antigen[e] => gal[e] + Tn_antigen[e]	0	BT_4241 and BT_4246 and BT_4247	0	1000	4	O-Glycan Degradation	PMID: 18996345, PMID: 10430883, PMID: 848954	B. thetaiotaomicron is well known to degrade mucin, the genes included in the GPR are upregulated during growth on mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis. Involves beta-galactosidase, susC, susD (binding proteins).	
	GALASE_OGLYCAN3e	Beta-galactosidase, mucin-type O-glycans, extracellular	h2o[e] + core8[e] => gal[e] + Tn_antigen[e]	0	BT_4241 and BT_4246 and BT_4247	0	1000	4	O-Glycan Degradation	PMID: 18996345, PMID: 10430883, PMID: 848954	B. thetaiotaomicron is well known to degrade mucin, the genes included in the GPR are upregulated during growth on mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis. Involves beta-galactosidase, susC, susD (binding proteins).	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	GALASE1e	beta-galactosidase, extracellular	2 h2o[e] + l2n2m2mn[e] => n2m2mn[e] + 2 gal[e]	0	(BT_0290 or BT_0461 or BT_0757 or BT_0983 or BT_0992 or BT_0993 or BT_0996 or BT_1626 or BT_2190 or BT_2680 or BT_2922 or BT_2969 or BT_3092 or BT_3114 or BT_3179 or BT_3293 or BT_3340 or BT_3513 or BT_3654 or BT_4050 or BT_4152 or BT_4156 or BT_4160 or BT_4181 or BT_4241 or BT_4667 or BT_4684)	0	1000	3	N-Glycan Degradation	PMID:16968696, PMID:17132046	B. thetaiotaomicron ferments host-derived N-glycans.	3.2.1.23
rxn00808	GALK	galactokinase	atp[c] + gal[c] => h[c] + adp[c] + gal1p[c]	0	BT_0370	0	1000	4	Alternate Carbon Metabolism	PMID:16887504	B. thetaiotaomicron grows on galactose as sole carbon source.	2.7.1.6
rxn01171	GALM1r	aldose 1-epimerase (glucose), reversible	glc-bD[c] <=> glc-D[c]	1	(BT_0372 or BT_0356 or BT_2849 or BT_3529 or BT_3532)	-1000	1000	2	Alternate Carbon Metabolism			5.1.3.3

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	GALNACASE_OGLYCAN1e	N-acetylgalactosaminidase, mucin-type O-glycans, extracellular	h2o[e] + Tn_antigen[e] => acgal[e] + Ser_Thr[e]	0	BT_0065	0	1000	4	O-Glycan Degradation	PMID: 19403529, PMID: 18996345, PMID: 10430883, PMID: 848954	B. thetaiotaomicron is well known to degrade mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis. BT_0065 is N-acetylgalactosaminidase according to PMID: 19403529. There may be other enzymes performing this function.	
	GALNACASE_OGLYCAN2e	N-acetylgalactosaminidase, mucin-type O-glycans, extracellular	h2o[e] + core5[e] => acgal[e] + Tn_antigen[e]	0	BT_0065	0	1000	4	O-Glycan Degradation	PMID: 19403529, PMID: 18996345, PMID: 10430883, PMID: 848954	B. thetaiotaomicron is well known to degrade mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis. BT_0065 is N-acetylgalactosaminidase according to PMID: 19403529. There may be other enzymes performing this function.	
	GALNACASE_OGLYCAN3e	N-acetylgalactosaminidase, mucin-type O-glycans, extracellular	h2o[e] + core7[e] => acgal[e] + Tn_antigen[e]	0	BT_0065	0	1000	4	O-Glycan Degradation	PMID: 19403529, PMID: 18996345, PMID: 10430883, PMID: 848954	B. thetaiotaomicron is well known to degrade mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis. BT_0065 is N-acetylgalactosaminidase according to PMID: 19403529. There may be other enzymes performing this function.	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	GALOX	Galactose oxidase	h2o[c] + o2[c] + gal[c] <=> h[c] + h2o2[c] + galctn-D[c]	1	BT_4040 or BT_4632	-1000	1000	2	Alternate Carbon Metabolism	PMID: 22036470	Reaction R01098 in KEGG. The gene may be wrongly annotated and have a different function (upregulated during growth on human milk oligosaccharides).	1.1.3.9
rxn00817	GALS3	a-galactosidase (melibiose)	h2o[c] + melib[c] => glc-D[c] + gal[c]	0	(BT_1871 or BT_2851 or BT_3065 or BT_3131 or BT_3133 or BT_3410)	0	1000	4	Plant Polysaccharide Degradation	PMID:19646996, PMID:18848471, PMID:2557798	Growth on melibiose was demonstrated for B. thetaiotaomicron.	3.2.1.22
rxn05566	GALt2_2	D-galactose transport in via proton symport	h[e] + gal[e] <=> h[c] + gal[c]	1	(BT_3589 or BT_1758 or BT_0371 or BT_4311 or BT_4653)	-1000	1000	4	Transport, Extracellular	i.e. PMID: 16887504	Annotation based on NCBI Gene (last updated 14.05.11). B. thetaiotaomicron grows on galactose.	
	GALUi	UTP-glucose-1-phosphate uridylyltransferase (irreversible)	h[c] + utp[c] + g1p[c] => ppi[c] + udpg[c]	0		0	1000	2	Cell Envelope Biosynthesis	PMID:19460428	This reaction is neccessary to produce UDP-glucose for lipopolysaccharide biosynthesis. No gene annotation is available, however. The structure of B. thetaiotaomicron LPS is described in PMID:19460428.	2.7.7.9
rxn05673	GALURt2r	galacturonate transport in via proton symport	h[c] + galur[c] <=> h[e] + galur[e]	1	BT_4105	-1000	1000	2	Transport, Extracellular	PMID:563214	B. thetaiotaomicron grows on galacturonate as sole carbon source.	
	GAM2STASE_HS1	N-sulfoglucosamine sulfohydrolase, heparin degradation	2 h2o[e] + gam26s[e] => h[e] + 2 so4[e] + gam[e]	0	((BT_1624 and BT_0238) or (BT_3796 and BT_0238))	0	1000	3	Glycosaminoglycan Degradation	PMID:21507958, PMID:19801541, PMID:7574611	B. thetaiotaomicron specific putative heparin sulfate degradation pathway. Requires sulfatase-maturing enzyme (BT_0238) to be functional. Not sure if annotation (putative secreted sulfatase) is correct.	3.10.1.1

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	GAM2STASE_HS2	N-sulfoglucosamine sulfohydrolase, heparin degradation	2 h2o[e] + hspg_degr_5[e] => 2 h[e] + 2 so4[e] + hspg_degr_6[e]	0	((BT_1624 and BT_0238) or (BT_3796 and BT_0238))	0	1000	2	Glycosaminoglycan Degradation	PMID:19801541, PMID:7574611	B. thetaiotaomicron specific putative heparin sulfate degradation pathway. Not sure if annotation (putative secreted sulfatase) is correct.	3.10.1.1
	GAM2STASE_HS3	N-sulfoglucosamine sulfohydrolase, heparin degradation	h2o[e] + hspg_degr_10[e] => h[e] + so4[e] + hspg_degr_11[e]	0	((BT_1624 and BT_0238) or (BT_3796 and BT_0238))	0	1000	2	Glycosaminoglycan Degradation	PMID:19801541, PMID:7574611	B. thetaiotaomicron specific putative heparin sulfate degradation pathway. Not sure if annotation (putative secreted sulfatase) is correct.	3.10.1.1
	GAMt2r	glucosamine transport (proton symport)	h[e] + gam[e] <=> h[c] + gam[c]	1		-1000	1000	2	Transport, Extracellular	PMID:7240086	B. thetaiotaomicron metabolizes glucosamine.	
rxn00781	GAPD	glyceraldehyde-3-phosphate dehydrogenase	pi[c] + nad[c] + g3p[c] <=> h[c] + nadh[c] + 13dpg[c]	1	BT_4263	-1000	1000	4	Glycolysis/Gluconeogenesis	PMID: 11260473	Activity measured by enzyme assay in B. thetaiotaomicron.	1.2.1.12
rxn03004	GARFTi	phosphoribosylglycinamide formyltransferase, irreversible	10fthf[c] + gar[c] => h[c] + thf[c] + fgam[c]	0	(BT_2883 or BT_3360)	0	1000	2	Purine and Pyrimidine Biosynthesis			2.1.2.2
rxn04783	GART	GAR transformylase-T	atp[c] + for[c] + gar[c] => h[c] + pi[c] + adp[c] + fgam[c]	0	BT_0704	0	1000	2	Purine and Pyrimidine Biosynthesis			2.1.2.-
rxn06377	GCCa	glycine-cleavage complex	h[c] + gly[c] + lpro[c] => co2[c] + alpro[c]	0	BT_1147	0	1000	2	Glycine, Serine, and Threonine Metabolism			1.4.4.2
rxn06600	GCCb	glycine cleavage complex	thf[c] + alpro[c] => nh4[c] + dhlpro[c] + mlthf[c]	0	(BT_2519 and BT_4584)	0	1000	2	Glycine, Serine, and Threonine Metabolism			2.1.2.10
rxn06493	GCCc	glycine-cleavage complex	nad[c] + dhlpro[c] => h[c] + nadh[c] + lpro[c]	0	(BT_2519 or BT_3186 or (BT_1147 and BT_2519))	0	1000	2	Glycine, Serine, and Threonine Metabolism		Reversible in SEED	1.8.1.4

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	GCHOLAH	Bile acid hydrolase (glycocholate)	h2o[c] + gchola[c] => h[c] + cholate[c] + gly[c]	0	(BT_1259 or BT_2086)	0	1000	4	Bile Acid Metabolism	PMID:10993, Dworkin, M. and S. Falkow (2006). The prokaryotes : a handbook on the biology of bacteria. New York ; [London], Springer	Enzyme was demonstrated experimentally (PMID:10993). Growth of B. thetaiotaomicron is stimulated by 20% bile.	3.5.1.24
	GCHOLAt2	glycocholate transport via sodium cotransport	2 na1[e] + gchola[e] => 2 na1[c] + gchola[c]	0		0	1000	2	Transport, Extracellular	PMID:10993	B. thetaiotaomicron metabolizes glycocholate and taurocholate. A bile acid/ sodium symporter is annotated for Bacteroides salanitronis.	
rxn00555	GF6PTAr	Glutamine-fructose-6-phosphate transaminase	gln-L[c] + f6p[c] <=> glu-L[c] + gam6p[c]	1	BT_0554	-1000	1000	2	Aminosugar Metabolism			2.6.1.16
rxn03962	GFUCS	GDP-L-fucose synthase	h[c] + nadph[c] + gdpddman[c] => nadp[c] + gdpfuc[c]	0	BT_1225	0	1000	4	Alternate Carbon Metabolism	DOI: 10.1007/s10068-010-0120-0	Gene was cloned and gene product was characterized.	1.1.1.271
rxn05287	GGTT	geranylgeranyltransferase	ipdp[c] + ggdp[c] => ppi[c] + pendp[c]	0	(BT_3261 or BT_2058)	0	1000	2	Cofactor and Prosthetic Group Biosynthesis			
rxn00692	GHMT2r	glycine hydroxymethyltransferase, reversible	thf[c] + ser-L[c] <=> h2o[c] + gly[c] + mlthf[c]	1	BT_0738	-1000	1000	2	Glycine, Serine, and Threonine Metabolism			2.1.2.1
rxn00239	GK1	guanylate kinase (GMP:ATP)	atp[c] + gmp[c] <=> adp[c] + gdp[c]	1	BT_2009	-1000	1000	2	Nucleotide Salvage Pathway			2.7.4.8
rxn09562	GK2	guanylate kinase (GMPdATP)	datp[c] + gmp[c] <=> gdp[c] + dadp[c]	1	BT_2009	-1000	1000	2	Nucleotide Salvage Pathway			2.7.4.8
	GLCAASE_HSe	Beta-glucuronidase, heparin degradation	h2o[e] + hspg_degr_12[e] => glcur[e] + hspg_degr_13[e]	0	(BT_3292 or BT_4151)	0	1000	4	Glycosaminoglycan Degradation	PMID:19801541, PMID:7574611	B. thetaiotaomicron specific putative heparin sulfate degradation pathway.	3.2.1.31

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	GLCAASE8e	beta-glucuronidase, hyaluronan degradation	h2o[e] + ha[e] => glcur[e] + ha_deg1[e]	0	(BT_3292 or BT_4151)	0	1000	4	Glycosaminoglycan Degradation	PMID:848954, PMID:18996345	B. thetaiotaomicron ferments hyaluronan. The polysaccharide utilization locus (PUL) BT3324 - BT3350 is upregulated in its presence.	3.2.1.31
	GLCAASE9e	beta-glucuronidase, hyaluronan degradation	2 h2o[e] + ha_pre1[e] => acgam[e] + glcur[e]	0	(BT_3292 or BT_4151)	0	1000	4	Glycosaminoglycan Degradation	PMID:848954, PMID:18996345	B. thetaiotaomicron ferments hyaluronan. The polysaccharide utilization locus (PUL) BT3324 - BT3350 is upregulated in its presence.	3.2.1.31

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	GLCAASEe	beta-glucuronidase/ chondroitinase	h2o[e] + acgalglcur[e] => acgal[e] + glcur[e]	0	(BT_3292 or BT_4151 or BT_3324 or BT_3350)	0	1000	4	Glycosaminoglycan Degradation	PMID:6782076, PMID:7574611, PMID:848954, PMID:18996345	B. thetaiotaomicron ferments chondroitin sulfate. The polysaccharide utilization locus (PUL) BT3324 - BT3350 is upregulated in its presence. BT_3348 degrades chondroitin sulfate to oligosaccharides, which requires BT_3331 (sus C homolog) and BT_3332 (csuF). BT_3324 and BT_3350 degrade the desulfated oligosaccharides to monosaccharides. Based on Figure 3, PMID:18996345. BT_3292 and BT_4151 were added based on gene annotation, not sure they perform this role. Reaction takes place in periplasm (extracellular for modeling purposes).	3.2.1.31
	GLCNACASE_HS1	Alpha-N-acetylglucosaminidase, heparin degradation	2 h2o[e] + 2 h[e] + hspg_degr_6[e] => 2 acgam[e] + glcur[e]	0	(BT_0438 or BT_3590 or BT_4359)	0	1000	4	Glycosaminoglycan Degradation	PMID:19801541, PMID:7574611	B. thetaiotaomicron specific putative heparin sulfate degradation pathway.	3.2.1.50
	GLCNACASE_HS2	Alpha-N-acetylglucosaminidase, heparin degradation	h2o[e] + h[e] + hspg_degr_11[e] => gam[e] + hspg_degr_12[e]	0	(BT_0438 or BT_3590 or BT_4359)	0	1000	4	Glycosaminoglycan Degradation	PMID:19801541, PMID:7574611	B. thetaiotaomicron specific putative heparin sulfate degradation pathway.	3.2.1.50
	GLCNACASE_HS3	Alpha-N-acetylglucosaminidase, heparin degradation	h2o[e] + hspg_degr_13[e] => acgam[e] + hspg_degr_14[e]	0	(BT_0438 or BT_3590 or BT_4359)	0	1000	4	Glycosaminoglycan Degradation	PMID:19801541, PMID:7574611	B. thetaiotaomicron specific putative heparin sulfate degradation pathway.	3.2.1.50

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	GLCNACASE_OGLYCAN1e	N-acetylglucosaminidase, mucin-type O-glycans, extracellular	h2o[e] + core6[e] => acgam[e] + Tn_antigen[e]	0	(BT_2825 or BT_1038 or BT_1044 or BT_1048 or BT_0865 or BT_1282 or BT_3753 or BT_4132 or BT_4406 or BT_3985 or BT_3987) and ((BT_1039 and BT_1040) or (BT_1042 and BT_1043) or (BT_1046 and BT_1047) or (BT_4134 and BT_4135) or (BT_4404 and BT_4405) or (BT_3983 and BT_3984) or (BT_0866 and BT_0867) or (BT_3751 and BT_3752) or (BT_1280 and BT_1281) or (BT_3958 and BT_3959) or (BT_4633 and BT_4634) or (BT_2818 and BT_2819) or (BT_2820 and BT_2821))	0	1000	4	O-Glycan Degradation	PMID: 18996345, PMID: 10430883, PMID: 848954	B. thetaiotaomicron is well known to degrade mucin, the genes included in the GPR are upregulated during growth on mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis. Involves N-acetylglucosaminidase, susC, susD (binding proteins).	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	GLCNACASE_OGLYCAN2e	N-acetylglucosaminidase, mucin-type O-glycans, extracellular	h2o[e] + gncore2[e] => acgam[e] + core2[e]	0	(BT_2825 or BT_1038 or BT_1044 or BT_1048 or BT_0865 or BT_1282 or BT_3753 or BT_4132 or BT_4406 or BT_3985 or BT_3987) and ((BT_1039 and BT_1040) or (BT_1042 and BT_1043) or (BT_1046 and BT_1047) or (BT_4134 and BT_4135) or (BT_4404 and BT_4405) or (BT_3983 and BT_3984) or (BT_0866 and BT_0867) or (BT_3751 and BT_3752) or (BT_1280 and BT_1281) or (BT_3958 and BT_3959) or (BT_4633 and BT_4634) or (BT_2818 and BT_2819) or (BT_2820 and BT_2821))	0	1000	4	O-Glycan Degradation	PMID: 18996345, PMID: 10430883, PMID: 848954	B. thetaiotaomicron is well known to degrade mucin, the genes included in the GPR are upregulated during growth on mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis. Involves N-acetylglucosaminidase, susC, susD (binding proteins).	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	GLCNACASE_OGLYCAN3e	N-acetylglucosaminidase, mucin-type O-glycans, extracellular	h2o[e] + core2[e] => acgam[e] + T_antigen[e]	0	(BT_2825 or BT_1038 or BT_1044 or BT_1048 or BT_0865 or BT_1282 or BT_3753 or BT_4132 or BT_4406 or BT_3985 or BT_3987) and ((BT_1039 and BT_1040) or (BT_1042 and BT_1043) or (BT_1046 and BT_1047) or (BT_4134 and BT_4135) or (BT_4404 and BT_4405) or (BT_3983 and BT_3984) or (BT_0866 and BT_0867) or (BT_3751 and BT_3752) or (BT_1280 and BT_1281) or (BT_3958 and BT_3959) or (BT_4633 and BT_4634) or (BT_2818 and BT_2819) or (BT_2820 and BT_2821))	0	1000	4	O-Glycan Degradation	PMID: 18996345, PMID: 10430883, PMID: 848954	B. thetaiotaomicron is well known to degrade mucin, the genes included in the GPR are upregulated during growth on mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis. Involves N-acetylglucosaminidase, susC, susD (binding proteins).	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	GLCNACASE_OGLYCAN4e	N-acetylglucosaminidase, mucin-type O-glycans, extracellular	h2o[e] + gncore1[e] => acgam[e] + T_antigen[e]	0	(BT_2825 or BT_1038 or BT_1044 or BT_1048 or BT_0865 or BT_1282 or BT_3753 or BT_4132 or BT_4406 or BT_3985 or BT_3987) and ((BT_1039 and BT_1040) or (BT_1042 and BT_1043) or (BT_1046 and BT_1047) or (BT_4134 and BT_4135) or (BT_4404 and BT_4405) or (BT_3983 and BT_3984) or (BT_0866 and BT_0867) or (BT_3751 and BT_3752) or (BT_1280 and BT_1281) or (BT_3958 and BT_3959) or (BT_4633 and BT_4634) or (BT_2818 and BT_2819) or (BT_2820 and BT_2821))	0	1000	4	O-Glycan Degradation	PMID: 18996345, PMID: 10430883, PMID: 848954	B. thetaiotaomicron is well known to degrade mucin, the genes included in the GPR are upregulated during growth on mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis. Involves N-acetylglucosaminidase, susC, susD (binding proteins).	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	GLCNACASE_OGLYCAN5e	N-acetylglucosaminidase, mucin-type O-glycans, extracellular	h2o[e] + core4[e] => acgam[e] + core3[e]	0	(BT_2825 or BT_1038 or BT_1044 or BT_1048 or BT_0865 or BT_1282 or BT_3753 or BT_4132 or BT_4406 or BT_3985 or BT_3987) and ((BT_1039 and BT_1040) or (BT_1042 and BT_1043) or (BT_1046 and BT_1047) or (BT_4134 and BT_4135) or (BT_4404 and BT_4405) or (BT_3983 and BT_3984) or (BT_0866 and BT_0867) or (BT_3751 and BT_3752) or (BT_1280 and BT_1281) or (BT_3958 and BT_3959) or (BT_4633 and BT_4634) or (BT_2818 and BT_2819) or (BT_2820 and BT_2821))	0	1000	4	O-Glycan Degradation	PMID: 18996345, PMID: 10430883, PMID: 848954	B. thetaiotaomicron is well known to degrade mucin, the genes included in the GPR are upregulated during growth on mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis. Involves N-acetylglucosaminidase, susC, susD (binding proteins).	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	GLCNACASE_OGLYCAN6e	N-acetylglucosaminidase, mucin-type O-glycans, extracellular	h2o[e] + core3[e] => acgam[e] + Tn_antigen[e]	0	(BT_2825 or BT_1038 or BT_1044 or BT_1048 or BT_0865 or BT_1282 or BT_3753 or BT_4132 or BT_4406 or BT_3985 or BT_3987) and ((BT_1039 and BT_1040) or (BT_1042 and BT_1043) or (BT_1046 and BT_1047) or (BT_4134 and BT_4135) or (BT_4404 and BT_4405) or (BT_3983 and BT_3984) or (BT_0866 and BT_0867) or (BT_3751 and BT_3752) or (BT_1280 and BT_1281) or (BT_3958 and BT_3959) or (BT_4633 and BT_4634) or (BT_2818 and BT_2819) or (BT_2820 and BT_2821))	0	1000	4	O-Glycan Degradation	PMID: 18996345, PMID: 10430883, PMID: 848954	B. thetaiotaomicron is well known to degrade mucin, the genes included in the GPR are upregulated during growth on mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis. Involves N-acetylglucosaminidase, susC, susD (binding proteins).	
rxn05740	GLCP	glycogen phosphorylase	pi[c] + glycogen[c] => g1p[c]	0	(BT_1100 or BT_1293)	0	1000	3	Alternate Carbon Metabolism	PMID:37285	Glycogen synthesis was demonstrated in B. thetaiotaomicron.	2.4.1.1

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	GLCS2	glycogen synthase (UDPGlc)	udpg[c] => h[c] + udp[c] + glycogen[c]	0	(BT_1294 or BT_4307)	0	1000	3	Alternate Carbon Metabolism	PMID:37285	Gene annotation from NCBI Gene (last updated 01.01.11). It was demonstrated that B. thetaiotaomicron produces a glycogen.	2.4.1.11
	GLCt2r	GLCt2r	h[e] + glc-D[e] <=> h[c] + glc-D[c]	1	(BT_3589 or BT_1758 or BT_0371 or BT_4311 or BT_4653)	-1000	1000	4	Transport, Extracellular	PMID: 16887504	B. thetaiotaomicron grows on glucose, does not utilize a phosphotransferase system for uptake. Annotation from KEGG.	
	GLCt4	glucose transport via sodium symport	na1[e] + glc-D[e] <=> na1[c] + glc-D[c]	1	BT_0355	-1000	1000	4	Transport, Extracellular	PMID: 4853401	B. thetaiotaomicron uses glucose as sole carbon source.	
rxn05574	GLCURt2r	glucuronate transport in via proton symport	h[e] + glcur[e] <=> h[c] + glcur[c]	1	BT_4105	-1000	1000	4	Transport, Extracellular	PMID:7240086	B. thetaiotaomicron grows on glucuronate as sole carbon source.	
rxn00187	GLNS	glutamine synthetase	glu-L[c] + atp[c] + nh4[c] => h[c] + pi[c] + adp[c] + gln-L[c]	0	(BT_0453 or BT_0543 or BT_0785 or BT_4339)	0	1000	4	Glutamate metabolism	PMID:2576872	Characterized for close relative B. fragilis.	6.3.1.2
	GLNt2r	L-glutamine reversible transport via proton symport	h[e] + gln-L[e] <=> h[c] + gln-L[c]	1		-1000	1000	1	Transport, Extracellular	Dworkin, M. and S. Falkow (2006). The prokaryotes : a handbook on the biology of bacteria. New York ; [London], Springer	B. thetaiotaomicron is weakly proteolytic, so a transport reaction for all amino acids is assumed to be present.	
rxn00179	GLU5K	glutamate 5-kinase	glu-L[c] + atp[c] => adp[c] + glu5p[c]	0	BT_3719	0	1000	2	Arginine and Proline Metabolism		Reversible in SEED	2.7.2.11
rxn10136	GLUABUTt7	4-aminobutyrate/glutamate antiport	glu-L[e] + 4abut[c] <=> glu-L[c] + 4abut[e]	1	BT_2573	-1000	1000	2	Transport, Extracellular		Annotation from TransportDB (www.membranetransport.org).	
rxn00194	GLUDC	Glutamate Decarboxylase	h[c] + glu-L[c] => co2[c] + 4abut[c]	0	BT_2570	0	1000	2	Glutamate Metabolism			4.1.1.15

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn00182	GLUDxi	glutamate dehydrogenase (NAD)	h2o[c] + glu-L[c] + nad[c] => h[c] + akg[c] + nadh[c] + nh4[c]	0	(BT_1970 or BT_1973)	0	1000	2	Glutamate Metabolism	PMID: 8955404	B. thetaiotaomicron has two glutamate dehydrogenases, one one of which uses only NAD and one which uses both NAD and NADP.	1.4.1.4
rxn00184	GLUDy	glutamate dehydrogenase (NADP)	h2o[c] + glu-L[c] + nadp[c] <=> h[c] + akg[c] + nadph[c] + nh4[c]	1	BT_1970	-1000	1000	4	Glutamate Metabolism	PMID: 8955404	B. thetaiotaomicron has two glutamate dehydrogenases, one one of which uses only NAD and one which uses both NAD and NADP.	1.4.1.4
rxn01641	GLUFORT	Glutamate formiminotransferase (EC 2.1.2.5) @ Glutamate formyltransferase	glu-L[c] + 5forthf[c] <=> h[c] + thf[c] + forglu[c]	1	BT_2693	-1000	1000	2	Folate Metabolism			2.1.2.5
rxn00189	GLUN	glutaminase	h2o[c] + gln-L[c] => glu-L[c] + nh4[c]	0	BT_2571	0	1000	2	Glutamate Metabolism			3.5.1.2
rxn00790	GLUPRT	glutamine phosphoribosyldiphosphate amidotransferase	h2o[c] + prpp[c] + gln-L[c] => glu-L[c] + ppi[c] + pram[c]	0	(BT_0555 or BT_4582)	0	1000	2	Purine and Pyrimidine Biosynthesis			2.4.2.14
rxn00193	GLUR	glutamate racemase	glu-D[c] <=> glu-L[c]	1	BT_3722	-1000	1000	2	Cell Envelope Biosynthesis			5.1.1.3
rxn00085	GLUSy	glutamate synthase (NADPH)	h[c] + akg[c] + nadph[c] + gln-L[c] => 2 glu-L[c] + nadp[c]	0	(BT_0552 and BT_0553)	0	1000	2	Glutamate Metabolism		Reversible in SEED	1.4.1.13
rxn12645	GLYASN1c	Hydrolysis of Glycyl-L-asparagine	h2o[c] + glyasn[c] <=> gly[c] + asn-L[c]	1	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314)	-1000	1000	2	Peptide Degradation			
	GLYASNt	Glycyl-L-asparagine transport via proton symport	h[e] + glyasn[e] => h[c] + glyasn[c]	0	(BT_0580 or BT_4385 or BT_1086)	0	1000	2	Transport, Extracellular		Genes added based on TransportDB (last consulted 06.06.12).	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn12637	GLYASP1c	Hydrolysis of Glycyl-L-aspartate	h2o[c] + glyasp[c] <=> asp-L[c] + gly[c]	1	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314)	-1000	1000	2	Peptide Degradation			
	GLYASPt	Glycyl-L-aspartate transport via proton symport	h[e] + glyasp[e] => h[c] + glyasp[c]	0	(BT_0580 or BT_4385 or BT_1086)	0	1000	2	Transport, Extracellular		Genes added based on TransportDB (last consulted 06.06.12).	
rxn00274	GLYAT	glycine C-acetyltransferase	accoa[c] + gly[c] <=> coa[c] + 2aobut[c]	1	BT_1371	-1000	1000	2	Glycine, Serine, and Threonine Metabolism			2.3.1.29
rxn05181	GLYBabc	Glycine betaine transport via ABC system	h2o[c] + atp[c] + glyb[e] => h[c] + pi[c] + adp[c] + glyb[c]	0	(BT_1749 and BT_1750 and BT_1751)	0	1000	2	Transport, Extracellular			
rxn01102	GLYCK	glycerate kinase	atp[c] + glyc-R[c] => h[c] + adp[c] + 3pg[c]	0	BT_1437	0	1000	2	Glycine, Serine, and Threonine Metabolism		Reversible reaction in Model SEED.	2.7.1.31
	GLYCOe	glycogen hydrolysis by samylases	1124 h2o[e] + glycogen1500[e] => 750 glc-D[e] + 375 malt[e]	0	(BT_3698 and BT_3701 and BT_3702)	0	1000	3	Alternate Carbon Metabolism	Dworkin, M. and S. Falkow (2006). The prokaryotes : a handbook on the biology of bacteria. New York ; [London], Springer, PMID:16788175	B. thetaiotaomicron ferments glycogen. In B. fragilis, glycogen utilization seems to be performed by the starch utilization operon. It is assumed this is also the case in B. thetaiotaomicron.	
rxn01011	GLYD	glycerate dehydrogenase	h[c] + nadh[c] + hpyr[c] <=> nad[c] + glyc-R[c]	1	BT_1207	-1000	1000	2	Glycine, Serine, and Threonine Metabolism		Gene was annotated by Model SEED as phosphoglycerate oxidoreductase (EC 1.1.1.95). NCBI Gene (last updated 21.05.11) confirms annotation as glycerate dehydrogenase.	1.1.1.29

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn12646	GLYGLN1c	Hydrolysis of Glycyl-L-glutamine	h2o[c] + glygln[c] <=> gln-L[c] + gly[c]	1	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314)	-1000	1000	2	Peptide Degradation			
	GLYGLNt	Glycyl-L-glutamine transport via proton symport	h[e] + glygln[e] => h[c] + glygln[c]	0	(BT_0580 or BT_4385 or BT_1086)	0	1000	2	Transport, Extracellular		Genes added based on TransportDB (last consulted 06.06.12).	
rxn12634	GLYGLU1c	Hydrolysis of Glycyl-L-glutamate	h2o[c] + glyglu[c] <=> glu-L[c] + gly[c]	1	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314)	-1000	1000	2	Peptide Degradation			
	GLYGLUt	Glycyl-L-glutamate transport via proton symport	h[e] + glyglu[e] => h[c] + glyglu[c]	0	(BT_0580 or BT_4385 or BT_1086)	0	1000	2	Transport, Extracellular		Genes added based on TransportDB (last consulted 06.06.12).	
	GLYGLYHyi	hydrolysis of glycylycine, irreversible	h2o[c] + glygly[c] => 2 gly[c]	0	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314)	0	1000	2	Peptide Degradation			
	GLYGLYt	Glycylglycine transport	h[e] + glygly[e] <=> h[c] + glygly[c]	1	(BT_0580 or BT_4385 or BT_1086)	-1000	1000	2	Transport, Extracellular		Genes added based on TransportDB (last consulted 06.06.12).	
rxn00615	GLYKr	glycerol kinase (reversible)	atp[c] + glyc[c] <=> h[c] + adp[c] + glyc3p[c]	1		-1000	1000	1	Glycerophospholipid Metabolism		Added by Model SEED during auto-completion step in pipeline.	2.7.1.30

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn12845	GLYLEUHYDROc	hydrolysis of Glycylleucine in the small intestine for cellular uptake	h2o[c] + glyleu[c] <=> gly[c] + leu-L[c]	1	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314)	-1000	1000	2	Peptide Degradation	PMID: 4074331, PMID: 964683	BRENDA also lists beta-Ala-His dipeptidase (E.C. 3.4.13.20) as another enzyme catalyzing this reaction, but no literature evidence found.	3.4.13.19 or 3.4.13.18
	GLYLEUHYDROe	hydrolysis of Glycylleucine by predicted non-cytosolic leucine peptidase	h2o[e] + glyleu[e] => gly[e] + leu-L[e]	0	BT_2548	0	1000	2	Peptide Degradation	PMID:12663928	Predicted non-cytosolic in PMID:12663928. Assumed to be extracellular for modeling purposes.	3.4.11.15
rxn12849	GLYLEUPEPT1t	transport of Glycylleucine (extracellular)	h[e] + glyleu[e] => h[c] + glyleu[c]	0	(BT_0580 or BT_4385 or BT_1086)	0	1000	2	Transport, Extracellular		Genes added based on TransportDB (last consulted 06.06.12).	
rxn12635	GLYMET1c	Hydrolysis of Glycyl-L-methionine	h2o[c] + glymet[c] <=> gly[c] + met-L[c]	1	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314)	-1000	1000	2	Peptide Degradation			
	GLYMETt	Glycyl-L-methionine transport via proton symport	h[e] + glymet[e] => h[c] + glymet[c]	0	(BT_0580 or BT_4385 or BT_1086)	0	1000	2	Transport, Extracellular		Genes added based on TransportDB (last consulted 06.06.12).	
	GLYPHEHYi	hydrolysis of glycylphenylalanine, irreversible	h2o[c] + glyphe[c] => gly[c] + phe-L[c]	0	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314)	0	1000	2	Peptide Degradation			
	GLYPHEt	Glycylphenylalanine transport	h[e] + glyphe[e] <=> h[c] + glyphe[c]	1	(BT_0580 or BT_4385 or BT_1086)	-1000	1000	2	Transport, Extracellular		Genes added based on TransportDB (last consulted 06.06.12).	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn12638	GLYPROPRO1c	hydrolysis of Prolylglycine in the small intestine for cellular uptake	h2o[c] + glypro[c] <=> gly[c] + pro-L[c]	1	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314)	-1000	1000	2	Peptide Degradation			3.4.13.9
	GLYPROPRO1e	hydrolysis of Glycylproline by predicted non-cytosolic proline peptidase	h2o[e] + glypro[e] => pro-L[e] + gly[e]	0	BT_0587	0	1000	2	Peptide Degradation	PMID:12663928	Predicted non-cytosolic in PMID:12663928. Assumed to be extracellular for modeling purposes.	3.4.13.9
	GLYPROt	Glycyl-L-proline transport via proton symport	h[e] + glypro[e] => h[c] + glypro[c]	0	(BT_0580 or BT_4385 or BT_1086)	0	1000	2	Transport, Extracellular		Genes added based on TransportDB (last consulted 06.06.12).	
rxn05582	GLYt2r	glycine reversible transport via proton symport	h[e] + gly[e] <=> h[c] + gly[c]	1		-1000	1000	2	Transport, Extracellular			
rxn12847	GLYTYR1c	Hydrolysis of Glycyl-L-tyrosine	h2o[c] + glytyr[c] <=> gly[c] + tyr-L[c]	1	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314)	-1000	1000	2	Peptide Degradation			
	GLYTYRt	Glycyl-L-tyrosine transport via proton symport	h[e] + glytyr[e] => h[c] + glytyr[c]	0	(BT_0580 or BT_4385 or BT_1086)	0	1000	2	Transport, Extracellular		Genes added based on TransportDB (last consulted 06.06.12).	
rxn00642	GMAND	GDP-D-mannose dehydratase	gdpmann[c] => h2o[c] + gdpddman[c]	0	BT_1224	0	1000	4	Alternate Carbon Metabolism	DOI: 10.1007/s10068-010-0120-0	Gene was cloned and gene product was characterized.	4.2.1.47
rxn03916	GMHEPAT	D-glycero-D-manno-hepose 1-phosphate adenyltransferase	h[c] + atp[c] + gmhep1p[c] => ppi[c] + adphep-DD[c]	0		0	1000	2	Lipopolysaccharide Biosynthesis	PMID:20974832, PMID:19460428	The structure of B. thetaiotaomicron LPS was studied, but the exact LPS synthesis pathway is unknown.	
rxn03918	GMHEPK	D-glycero-D-manno-heptose 7-phosphate kinase	atp[c] + gmhep7p[c] => h[c] + adp[c] + gmhep17bp[c]	0		0	1000	2	Lipopolysaccharide Biosynthesis	PMID:20974832, PMID:19460428	The structure of B. thetaiotaomicron LPS was studied, but the exact LPS synthesis pathway is unknown.	

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rxn03919	GMHEPPA	D-glycero-D-manno-heptose 1,7-bisphosphate phosphatase	h2o[c] + gmhep17bp[c] => pi[c] + gmhep1p[c]	0	BT_0477	0	1000	4	Lipopolysaccharide Biosynthesis	PMID:20050615	The enzyme was purified and enzyme kinetics were studied.	
rxn00917	GMPS2	GMP synthase	h2o[c] + atp[c] + gln-L[c] + xmp[c] => 2 h[c] + glu-L[c] + amp[c] + ppi[c] + gmp[c]	0	(BT_2419 or BT_4265)	0	1000	2	Purine and Pyrimidine Biosynthesis			6.3.5.2
rxn01115	GND	phosphogluconate dehydrogenase	nadp[c] + 6pgc[c] => nadph[c] + co2[c] + ru5p-D[c]	0	BT_1222	0	1000	4	Pentose Phosphate Pathway	PMID: 7183748	Presence of enzyme was demonstrated experimentally.	1.1.1.44
rxn01226	GNNUC	gnnuc	h2o[c] + gsn[c] => rib-D[c] + gua[c]	0	BT_2808	0	1000	2	Nucleotide Salvage Pathway		Reversible in SEED	
rxn00758	GPDDA1	Glycerophosphodiester phosphodiesterase (Glycerophosphocholine)	h2o[c] + g3pc[c] => h[c] + chol[c] + glyc3p[c]	0	(BT_0442 or BT_0550 or BT_0195 or BT_3162 or BT_4727)	0	1000	2	Glycerophospholipid Metabolism		BT_3162: Evidence at protein level (PDB entry 3i10)	3.1.4.46
rxn01073	GPDDA2	Glycerophosphodiester phosphodiesterase (Glycerophosphoethanolamine)	h2o[c] + g3pe[c] => h[c] + glyc3p[c] + etha[c]	0	(BT_0442 or BT_0550 or BT_0195 or BT_3162 or BT_4727)	0	1000	2	Glycerophospholipid Metabolism		BT_3162: Evidence at protein level (PDB entry 3i10)	3.1.4.46
rxn08669	GPDDA4	Glycerophosphodiester phosphodiesterase (Glycerophosphoglycerol)	h2o[c] + g3pg[c] => h[c] + glyc[c] + glyc3p[c]	0	(BT_0442 or BT_0550 or BT_0195 or BT_3162 or BT_4727)	0	1000	2	Glycerophospholipid Metabolism		BT_3162: Evidence at protein level (PDB entry 3i10)	3.1.4.46
rxn01466	GRTT	geranyltranstransferase	ipdp[c] + grdp[c] => ppi[c] + frdp[c]	0	(BT_3261 or BT_2058)	0	1000	2	Cofactor and Prosthetic Group Biosynthesis			2.5.1.10
rxn05204	GSNt2r	guanosine transport in via proton symport reversible	h[e] + gsn[e] <=> h[c] + gsn[c]	1	BT_4330	-1000	1000	2	Transport, Extracellular			
rxn00299	GTPCI	GTP cyclohydrolase I	h2o[c] + gtp[c] => h[c] + ahdt[c] + for[c]	0	BT_3931	0	1000	2	Cofactor and Prosthetic Group Biosynthesis			3.5.4.16

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn00300	GTPCII	GTP cyclohydrolase II	3 h2o[c] + gtp[c] => 2 h[c] + ppi[c] + for[c] + 25dhpp[c]	0	BT_2416	0	1000	2	Cofactor and Prosthetic Group Biosynthesis			3.5.4.25
	GTPDPDP	guanosine-5'-triphosphate,3'-diphosphate diphosphatase	h2o[c] + gdptp[c] => h[c] + pi[c] + ppgpp[c]	0	BT_0540	0	1000	2	Cofactor and Prosthetic Group Biosynthesis		Included based on KEGG and NCBI putative gene annotation.	3.6.1.40
rxn00303	GTPDPK	GTP diphosphokinase	atp[c] + gtp[c] => h[c] + amp[c] + gdptp[c]	0	(BT_0700 or BT_3998)	0	1000	2	Cofactor and Prosthetic Group Biosynthesis			2.7.6.5
rxn00915	GUAPRT	guanine phosphoribosyltransferase	prpp[c] + gua[c] => ppi[c] + gmp[c]	0	BT_4386	0	1000	2	Nucleotide Salvage Pathway			2.4.2.8,2.4.2.7
rxn01080	GUI1	glucuronate isomerase (D-glucuronate)	glcur[c] <=> fruur[c]	1	BT_0823	-1000	1000	2	Alternate Carbon Metabolism			5.3.1.12
rxn01457	GUI2	glucuronate isomerase (D-galacturonate)	galur[c] <=> tagur[c]	1	BT_0823	-1000	1000	2	Alternate Carbon Metabolism			5.3.1.12
rxn05319	H2Ot	H2O transport via diffusion	h2o[e] <=> h2o[c]	1	BT_4718	-1000	1000	2	Transport, Extracellular		Irreversible reaction in SEED. Gene was added based on NCBI Gene.	
	H2St	h2s transport (diffusion)	h2s[e] <=> h2s[c]	1		-1000	1000	2	Transport, Extracellular	PMID:4853401	Sulfide (alternatively cysteine) is required as sulfur source.	
	H2td	hydrogen transport	h2[c] <=> h2[e]	1		-1000	1000	1	Transport, Extracellular	PMID:20444704	B. thetaiotaomicron produces hydrogen.	
rxn00102	HCO3E	HCO3 equilibration reaction	h2o[c] + co2[c] <=> h[c] + hco3[c]	1	BT_1681	-1000	1000	2	Unassigned			4.2.1.1
	HCYSMT	homocysteine S-methyltransferase	hcys-L[c] + amet[c] => h[c] + ahcys[c] + met-L[c]	0	BT_0180	0	1000	2	Methionine Metabolism			

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	HEMEti	Heme transport via ABC system	h2o[c] + atp[c] + pheme[e] => h[c] + pi[c] + adp[c] + pheme[c]	0	((BT_0491 and BT_0492 and BT_0493 and BT_0494 and BT_0495 and BT_0496 and BT_0497 and BT_0498 and BT_0499) or (BT_1950 and BT_1951 and BT_1952))	0	1000	4	Transport, Extracellular	PMID:4853401, PMID:17074906, PMID: 19748469	B. thetaiotaomicron requires heme for growth. Lewis et al. (2006) characterized the putative heme uptake operon in the related species Porphyromonas gingivalis (Bacteroidales order) and located the genes in B. thetaiotaomicron by using BLAST search. AH 05/12: KOs in this heme uptake operon are nonessential in vitro (Goodman et al. 2009), thus another heme transporter (BT_1950 + BT_1951) was added.	
	HEPARL1_e	Heparin Lyase I, extracellular	2 h2o[e] + hspg[e] => 2 h[e] + gam26s[e] + hspg_degr_1[e] + hspg_degr_2[e]	0	BT_4675	0	1000	4	Glycosaminoglycan Degradation	PMID:19801541, PMID:7574611	Heparin Lyase I cleaves the glycosidic linkage to the nonreducing end of iduronate. B. thetaiotaomicron specific putative pathway.	4.2.2.7
rxn12008	HETT	all-trans-Heptaprenyltransferase	ipdp[c] + hepdp[c] => ppi[c] + octdp[c]	0	(BT_3261 or BT_2058)	0	1000	2	Cofactor and Prosthetic Group Biosynthesis		Added manually to BIGG database based on SEED database	2.5.1.90
rxn00216	HEX1	hexokinase (D-glucose:ATP)	atp[c] + glc-D[c] => h[c] + adp[c] + g6p[c]	0	(BT_2430 or BT_2493 or BT_4654)	0	1000	4	Glycolysis/Gluconeogenesis	PMID: 15659667, PMID:73363	Reversible in SEED	2.7.1.1
	HEX10	hexokinase (D-glucosamine:ATP)	atp[c] + gam[c] => h[c] + adp[c] + gam6p[c]	0	BT_2430	0	1000	3	Aminosugar Metabolism	PMID:7240086	B. thetaiotaomicron is able to ferment glucosamine. Proposed pathway, not sure if glucosamine is utilized in this way.	2.7.1.1

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	HEX11	hexokinase (D-galactosamine:ATP)	atp[c] + galam[c] => h[c] + adp[c] + galam6p[c]	0		0	1000	2	Aminosugar Metabolism	PMID: 6367911	Galactosamine is metabolized by B. thetaiotaomicron to some extent and appears to be phosphorylated (though the compound does not support growth in vivo).	
	HEX4	hexokinase (D-mannose:ATP)	atp[c] + man[c] => h[c] + adp[c] + man6p[c]	0	(BT_2430 or BT_2493 or BT_4654)	0	1000	3	Alternate Carbon Metabolism	PMID:15659667	Reversible reaction in SEED. Enzyme was characterized experimentally for B. fragilis.	2.7.1.7
rxn00547	HEX7	hexokinase (D-fructose:ATP)	atp[c] + fru[c] => h[c] + adp[c] + f6p[c]	0	(BT_1757 or BT_3305)	0	1000	3	Alternate Carbon Metabolism	PMID: 20603004	Reversible reaction in SEED. BT_1757 indirectly confirmed by gene expression study.	2.7.1.1
rxn01169	HEXb	ATPD-glucose 6-phosphotransferase	atp[c] + glc-bD[c] => h[c] + adp[c] + g6p-B[c]	0	(BT_2430 or BT_2493 or BT_4654)	0	1000	4	Glycolysis/Gluconeogenesis	PMID: 15659667, PMID:73363	Reversible reaction in SEED. Enzyme was characterized experimentally for B. fragilis.	2.7.1.1
rxn03891	HEXTT	trans-hexaprenyltranstransferase	ipdp[c] + hexdp[c] => ppi[c] + hepdp[c]	0	(BT_3261 or BT_2058)	0	1000	2	Cofactor and Prosthetic Group Biosynthesis			2.5.1.30
rxn10343	HG2abc	Mercury (Hg+2) ABC transporter	h2o[c] + atp[c] + hg2[c] => h[c] + pi[c] + adp[c] + hg2[e]	0	BT_1091	0	1000	2	Transport, Extracellular		Added manually to BIGG database based on SEED database	
rxn00867	HISD	Histidine ammonia-lyase (EC 4.3.1.3)	his-L[c] => nh4[c] + urcan[c]	0	BT_2690	0	1000	2	Histidine Metabolism			4.3.1.3
	HISt2r	L-histidine reversible transport via proton symport	h[e] + his-L[e] <=> h[c] + his-L[c]	1		-1000	1000	2	Transport, Extracellular	Dworkin, M. and S. Falkow (2006). The prokaryotes : a handbook on the biology of bacteria. New York ; [London], Springer.	B. thetaiotaomicron is weakly proteolytic, so a transport reaction for all amino acids is assumed to be present.	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn00863	HISTD	histidinol dehydrogenase	h2o[c] + 2 nad[c] + histd[c] => 3 h[c] + 2 nadh[c] + his-L[c]	0	BT_0201	0	1000	2	Histidine Metabolism		Originally two subreactions in SEED	1.1.1.23
rxn02160	HISTP	histidinol-phosphatase	h2o[c] + hisp[c] => pi[c] + histd[c]	0	(BT_0203 or BT_1478 or BT_4257)	0	1000	2	Histidine Metabolism		BT_0203: Histidine biosynthesis bifunctional protein hisB (reviewed in UniProt, updated 08.03.11)	3.1.3.15
rxn02484	HMPK1	hydroxymethylpyrimidine kinase (ATP)	atp[c] + 4ahmmp[c] => h[c] + adp[c] + 4ampm[c]	0	BT_0790	0	1000	2	Cofactor and Prosthetic Group Biosynthesis		Reversible reaction in SEED	2.7.1.49
	HOMOGALASEe	Homogalacturonan degradation (citrus HG, 100 residues)	100 h2o[e] + homogal[e] => 20 ac[e] + 100 galur[e] + 20 meoh[e]	0	((BT_4146 or BT_4149 or BT_4153 or BT_4155 or BT_4170 or BT_4183 or BT_4115 or BT_4116 or BT_4119 or BT_4123) and BT_4150 and BT_4175 and (BT_4109 or BT_4110) and ((BT_4670 and BT_4671) or (BT_4164 and BT_4165) or (BT_4113 and BT_4114) or (BT_4121 and BT_4122) or (BT_3680 and BT_3681)))	0	1000	4	Plant Polysaccharide Degradation	PMID: 22205877, PMID: 12913136	Bacteroides thetaiotaomicron grows on citrus homogalacturonan. The genes included in the GPR are upregulated during growth. Enzymes/ proteins assumed to be involved: galacturonisidase, rhamnogalactorunan esterase, rhamnogalacturonan lyase, pectinesterase, susC/ SusD	
rxn02503	HPPK	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase	atp[c] + 2ahhmp[c] => h[c] + amp[c] + 2ahhmd[c]	0	BT_3216	0	1000	2	Folate Metabolism		Reversible reaction in SEED	2.7.6.3

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn01301	HSDxi2	homoserine dehydrogenase (NADH), irreversible	h[c] + nadh[c] + aspsa[c] => nad[c] + hom-L[c]	0	BT_2403	0	1000	2	Glycine, Serine, and Threonine Metabolism			1.1.1.3
rxn01302	HSDyi2	homoserine dehydrogenase (NADPH), irreversible	h[c] + nadph[c] + aspsa[c] => nadp[c] + hom-L[c]	0	BT_2403	0	1000	2	Glycine, Serine, and Threonine Metabolism			1.1.1.3
rxn01300	HSK	homoserine kinase	atp[c] + hom-L[c] => h[c] + adp[c] + phom[c]	0	BT_2402	0	1000	2	Threonine and Lysine Metabolism			2.7.1.39
rxn01304	HSST	homoserine O-succinyltransferase	hom-L[c] + succoa[c] => coa[c] + suchms[c]	0	BT_2413	0	1000	2	Methionine Metabolism			2.3.1.46
rxn02320	HSTPTr	Histidinol-phosphate aminotransferase (EC 2.6.1.9)	akg[c] + hisp[c] <=> glu-L[c] + imacp[c]	1	BT_0202	-1000	1000	2	Histidine Metabolism			2.6.1.9
rxn00836	HXPRT	hypoxanthine phosphoribosyltransferase (Hypoxanthine)	prpp[c] + hxan[c] => ppi[c] + imp[c]	0	BT_4386	0	1000	2	Nucleotide Salvage Pathway			2.4.2.8

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn10118	HYD1	hydrogenase (ubiquinone-8: 2 protons)	2 h[c] + q8[c] + h2[c] => 2 h[e] + q8h2[c]	0	(BT_1210 or BT_0124 or BT_1834)	0	1000	4	Central Metabolism	PMID: 12777495	B. thetaiotaomicron generates hydrogen as one of its fermentation end products. Hydrogen also serves as an alternate electron donor for fumarate reduction via fumarate reductase (PMID:12777495). Gene annotation was proposed by the SEED Viewer, however, the reaction was not included in the draft model generated by Model SEED. NCBI Gene proposes NADH: ubiquinone oxidoreductase for BT_0124. According to KEGG, this reaction and ferredoxin hydrogenase (HYD4) are carried out by the same enzyme.	1.18.99.1

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	HYD4	hydrogen:ferredoxin oxidoreductase	fdxrd[c] <=> fdxox[c] + h2[c]	1	(BT_1210 or BT_0124 or BT_1834)	-1000	1000	4	Central Metabolism	PMID:893348, PMID:760499, PMID:12740060, PMID:11260473, PMID:12777495, PMID:20444704	In the gut, this reaction regenerates NAD+ via NADH:ferredoxin oxidoreductase (FDNADOX). B. thetaiotaomicron generates hydrogen as one of its fermentation end products; accumulation of hydrogen inhibits reoxidation of NADH. It is therefore assumed that it regenerates NAD+ via this pathway, which leads to increased hydrogen partial pressure. Removal of hydrogen allows B. thetaiotaomicron to regenerate NAD+. The reaction can also be linked to pyruvate:ferredoxin oxidoreductase (PMID:11260473). Hydrogen also serves as an alternate electron donor for fumarate reduction via fumarate reductase (PMID:12777495). Gene annotation was proposed by the SEED Viewer, however, the reaction was not included in the draft model generated by Model SEED. NCBI Gene proposes NADH: ubiquinone oxidoreductase for BT_0124. According to KEGG, this reaction and ubiquinone-dependent hydrogenase (HYD1)	1.12.7.2

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	HYPSUCORNS	putative succinylornithine synthesis (hypothetical reaction)	orn[c] + succ[c] => h2o[c] + sucorn[c]	0		0	1000	1	exchange/demand reaction		Hypothetical reaction, it is not known how this metabolite is synthesized.	
rxn05408	IBCOATA	2-methylpropionyl-CoA[acyl-carrier-protein] transferase	ACP[c] + ibcoa[c] <=> coa[c] + 2mpropACP[c]	1	BT_0789	-1000	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.180
rxn00199	ICDHyr	isocitrate dehydrogenase (NADP)	nadp[c] + icit[c] <=> akg[c] + nadph[c] + co2[c]	1	BT_2071	-1000	1000	3	TCA Cycle	PMID:11880608	Enzyme was characterized experimentally for B. fragilis.	1.1.1.42
rxn01258	ICHORS	isochorismate synthase	chor[c] <=> ichor[c]	1	BT_4700	-1000	1000	2	Cofactor and Prosthetic Group Biosynthesis			5.4.99.6
	IDOURASE	L-iduronidase	h2o[e] + acgalidour[e] => acgal[e] + idour[e]	0		0	1000	2	Glycosaminoglycan Degradation	PMID:18227125	Assumed to be present since B. thetaiotaomicron can degrade dermatan, which contains iduronate .	3.2.1.76
	IDOURASE_HS1	Iduronidase, heparin degradation	h2o[e] + hspg_degr_1[e] => hspg_degr_3[e] + idour[e]	0		0	1000	2	Glycosaminoglycan Degradation	PMID:19801541, PMID:7574611	B. thetaiotaomicron specific putative heparin sulfate degradation pathway. It is not known which enzyme performs this step.	3.2.1.76
	IDOURASE_HS2	Iduronidase, heparin degradation	h2o[e] + hspg_degr_7[e] => hspg_degr_8[e] + idour[e]	0		0	1000	2	Glycosaminoglycan Degradation	PMID:19801541, PMID:7574611	B. thetaiotaomicron specific putative heparin sulfate degradation pathway. It is not known which enzyme performs this step.	3.2.1.76

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	IDOURASE_HS3	Iduronidase, heparin degradation	h2o[e] + hspg_degr_14[e] => hspg_degr_15[e] + idour[e]	0		0	1000	2	Glycosaminoglycan Degradation	PMID:19801541, PMID:7574611	B. thetaiotaomicron specific putative heparin sulfate degradation pathway. It is not known which enzyme performs this step.	3.2.1.76
rxn03135	IG3PS	Imidazole-glycerol-3-phosphate synthase	gln-L[c] + prlp[c] => h[c] + glu-L[c] + aicar[c] + eig3p[c]	0	(BT_1378 and BT_1380)	0	1000	2	Histidine Metabolism			2.4.2.-
rxn02473	IGPDH	imidazoleglycerol-phosphate dehydratase	eig3p[c] => h2o[c] + imacp[c]	0	BT_0203	0	1000	2	Histidine Metabolism			4.2.1.19
rxn02507	IGPS	indole-3-glycerol-phosphate synthase	h[c] + 2cpr5p[c] => h2o[c] + co2[c] + 3ig3p[c]	0	BT_0529	0	1000	2	Tyrosine, Tryptophan, and Phenylalanine Metabolism			4.1.1.48
rxn05456	IHDCOATA	14-methyl-pentadecanoyl-ACP[acyl-carrier-protein] transferase	coa[c] + 14mpentdecACP[c] <=> ACP[c] + ihdcoa[c]	1	BT_0789	-1000	1000	2	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.180
rxn05454	IHPDCOATA	15-methyl-hexa-decanoyl-ACP[acyl-carrier-protein] transferase	coa[c] + 15mpalmACP[c] <=> ACP[c] + ihpdcoa[c]	1	BT_0789	-1000	1000	2	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.180

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05244	ILEt2r	L-isoleucine reversible transport via proton symport	h[e] + ile-L[e] <=> h[c] + ile-L[c]	1		-1000	1000	2	Transport, Extracellular	PMID:7462155	B. thetaiotaomicron incorporates leucine, valine and isoleucine into its phospholipids,which suggests the presence of a transporter for these amino acids. However, it is not known which gene encodes this transporter.	
rxn01575	ILETA	isoleucine transaminase	akg[c] + ile-L[c] <=> glu-L[c] + 3mop[c]	1	BT_3892	-1000	1000	2	Valine, Leucine, and Isoleucine Metabolism			2.6.1.42
rxn00832	IMPC	IMP cyclohydrolase	h2o[c] + imp[c] <=> fprica[c]	1	BT_3812	-1000	1000	2	Purine and Pyrimidine Biosynthesis			3.5.4.10
rxn00834	IMPD	IMP dehydrogenase	h2o[c] + nad[c] + imp[c] => h[c] + nadh[c] + xmp[c]	0	BT_3845	0	1000	2	Purine and Pyrimidine Biosynthesis		Reversible reaction in SEED	1.1.1.205
rxn01299	INSH	Inosine hydrolase	h2o[c] + ins[c] => rib-D[c] + hxan[c]	0	BT_2808	0	1000	2	Nucleotide Salvage Pathway		Reversible reaction in SEED	3.2.2.8
rxn05316	INSt2	inosine transport in via proton symport, reversible	h[e] + ins[e] <=> h[c] + ins[c]	1	BT_4330	-1000	1000	2	Transport, Extracellular		Reversible reaction in SEED	
	INULINASEe	Inulin degradation, extracellular	25 h2o[e] + inulin[e] => 25 fru[e] + kestopt[e]	0	(BT_1759 or BT_3082)	0	1000	4	Plant Polysaccharide Degradation	PMID: 19251883, PMID: 19321416, PMID:20603004	B. thetaiotaomicron grows on inulin (though slowly and less efficient than on levan).	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	IOR2	indolepyruvate ferredoxin oxidoreductase (phenylpyvurate)	coa[c] + 2 fdox[c] + phpyr[c] <=> h[c] + co2[c] + 2 fdred[c] + phaccoa[c]	1	(BT_0429 and BT_0430)	-1000	1000	3	Tyrosine, Tryptophan, and Phenylalanine Metabolism	PMID:18396344, PMID:16887608	Added based on annotation from NCBI Gene. B. thetaiotaomicron produces phenylacetate as a minor fermentation product (PMID:18396344). The indolepyruvate-dependent reaction of this enzyme may not take place since indoleacetate (a product of this pathway) was not found in B. thetaiotaomicron. Phenylacetate is also formed in the gut from aromatic acid metabolism (PMID:16887608).	1.2.7.8
rxn05453	IPDCOATA	13-methyl-tetra-decanoyl-ACP[acyl-carrier-protein] transferase	coa[c] + 13mmyrsACP[c] <=> ACP[c] + ipdcoa[c]	1	BT_0789	-1000	1000	2	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.180
rxn00830	IPDDI	isopentenyl-diphosphate D-isomerase	ipdp[c] <=> dmpp[c]	1	BT_3972	-1000	1000	2	Cofactor and Prosthetic Group Biosynthesis			5.3.3.2
rxn08756	IPDPS	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate reductase (ipdp)	h[c] + nadh[c] + h2mb4p[c] => h2o[c] + nad[c] + ipdp[c]	0	BT_2061	0	1000	2	Cofactor and Prosthetic Group Biosynthesis		Reviewed ispH 4-hydroxy-3-methylbut-2-enyl diphosphate reductase (NCBI Gene, updated 08.01.11)	1.17.1.2

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn04113	IPDPS2	isopentenyl-diphosphateNAD(P)+ oxidoreductase	h[c] + nadph[c] + h2mb4p[c] => h2o[c] + nadp[c] + ipdp[c]	0	BT_2061	0	1000	2	Cofactor and Prosthetic Group Biosynthesis		Reviewed ispH 4-hydroxy-3-methylbut-2-enyl diphosphate reductase (NCBI Gene, updated 08.01.11)	1.17.1.2
	IPMD2	(2R,3S)-3-methylmalate:NAD+ oxidoreductase	e3mmal[c] + nad[c] => co2[c] + nadh[c] + 2obut[c]	0	BT_1857	0	1000	2	Valine, Leucine, and Isoleucine Metabolism		Added based on annotation from KEGG Pathway	1.1.1.85
rxn03062	IPMDr	3-isopropylmalate dehydrogenase (EC 1.1.1.85)	nad[c] + 3c2hmp[c] <=> h[c] + nadh[c] + 3c4mop[c]	1	BT_1857	-1000	1000	3	Valine, Leucine, and Isoleucine Metabolism	PMID:8569539	Gene was cloned and characterized for Bacteroides fragilis.	1.1.1.85
rxn02789	IPPMIa	3-isopropylmalate dehydratase	3c2hmp[c] <=> h2o[c] + 2ippm[c]	1	(BT_1859 and BT_1860)	-1000	1000	2	Valine, Leucine, and Isoleucine Metabolism			4.2.1.33
rxn02811	IPPMIb	2-isopropylmalate hydratase	h2o[c] + 2ippm[c] <=> 3c3hmp[c]	1	(BT_1859 and BT_1860)	-1000	1000	2	Valine, Leucine, and Isoleucine Metabolism			4.2.1.33
rxn00902	IPPS	2-isopropylmalate synthase	h2o[c] + accoa[c] + 3mob[c] => h[c] + coa[c] + 3c3hmp[c]	0	BT_1861	0	1000	3	Valine, Leucine, and Isoleucine Metabolism	PMID:6440485	Demonstrated by enzyme assay in Bacteroides fragilis.	4.1.3.12
	IS2TASE	Iduronate 2-sulfatase	h2o[e] + acgalidour2s[e] => h[e] + so4[e] + acgalidour[e]	0	((BT_0238 and BT_0756) or (BT_0238 and BT_2914))	0	1000	4	Glycosaminoglycan Degradation	PMID:21507958	BT_0238 encodes anSME (anaerobic Sulfatase-Maturing Enzyme).	3.1.6.13
	IS2TASE_HS1	Iduronate 2-sulfatase, heparin degradation	2 h2o[e] + hspg_degr_2[e] => 4 h[e] + 2 so4[e] + hspg_degr_7[e]	0	((BT_0238 and BT_0756) or (BT_0238 and BT_2914))	0	1000	4	Glycosaminoglycan Degradation	PMID:21507958, PMID:19801541, PMID:7574611	B. thetaiotaomicron specific putative heparin sulfate degradation pathway. Requires sulfatase-maturing enzyme (BT_0238) to be functional.	3.1.6.13

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	ISOBUTt2r	Isobutyrate transport via proton symport	h[e] + isobut[e] <=> h[c] + isobut[c]	1		-1000	1000	2	Transport, Extracellular	Krieg, N. R. (2010). Bergey's manual of systematic bacteriology, 2nd ed., volume 4. New York, Springer.	Isobutyrate and isovalerate are known secretion products of B. thetaiotaomicron.It is not known if transport of these metabolites consumes energy, and which transporter carries out this function.	
	ISOCAPRt2r	Isocaproate transport via proton symport	h[e] + isocapr[e] <=> h[c] + isocapr[c]	1		-1000	1000	1	Transport, Extracellular	PMID:1541601, PMID:16887608	Isocaproate is a minor product in the large intestine from leucine reduction. It is not known if this metabolite is produced in B. thetaiotaomicron. Needed for reaction LEUO to be element and charge balanced.	
	ISOVALt2r	Isovalerate transport via proton symport	h[e] + isoval[e] <=> h[c] + isoval[c]	1		-1000	1000	2	Transport, Extracellular	Krieg, N. R. (2010). Bergey's manual of systematic bacteriology, 2nd ed., volume 4. New York, Springer.	Isobutyrate and isovalerate are known secretion products of B. thetaiotaomicron.It is not known if transport of these metabolites consumes energy, and which transporter carries out this function.	
rxn05455	ITDCOATA	12-methyl-tridecanoyl-ACP[acyl-carrier-protein] transferase	coa[c] + 12mtridecACP[c] <=> ACP[c] + itdcoa[c]	1	BT_0789	-1000	1000	2	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.180

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05383	IVCOATA	3-methylbutanoyl-CoA[acyl-carrier-protein] transferase	ACP[c] + ivcoa[c] <=> coa[c] + 3mbutACP[c]	1	BT_0789	-1000	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.180
rxn01642	IZPN	imidazolonepropionase	h2o[c] + 4izp[c] => h[c] + forglu[c]	0	BT_2692	0	1000	2	Histidine Metabolism			3.5.2.7
rxn10168	Kabc	Potassium ABC transporter	h2o[c] + atp[c] + k[e] => h[c] + pi[c] + adp[c] + k[c]	0	(BT_2423 and BT_2424 and BT_2425)	0	1000	2	Transport, Extracellular			
rxn02187	KARA1	ketol-acid reductoisomerase (2,3-dihydroxy-3-methylbutanoate)	nadp[c] + 23dhmb[c] <=> h[c] + nadph[c] + alac-S[c]	1	BT_2074	-1000	1000	2	Valine, Leucine, and Isoleucine Metabolism		Originally two subreactions in SEED	1.1.1.86
rxn02186	KARA2	ketol-acid reductoisomerase (2-Acetolactate)	h[c] + nadph[c] + 2ahbut[c] <=> nadp[c] + 23dhmp[c]	1	BT_2074	-1000	1000	2	Valine, Leucine, and Isoleucine Metabolism		Originally two subreactions in SEED	1.1.1.86
	KAS1	b-ketoacyl synthetase (Iso-C14:0)	14 h[c] + 10 nadph[c] + 5 malcoa[c] + ibcoa[c] => 4 h2o[c] + 6 coa[c] + 10 nadp[c] + 5 co2[c] + fa1[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Glycerophospholipid Metabolism	PMID:6102980, PMID:7440508, PMID: 7204330, PMID:19460428	B. thetaiotaomicron is well known to produce iso- and anteiso-branched fatty acids besides straight-chain fatty acids.	2.3.1.41
	KAS11	b-ketoacyl synthetase (Iso-C17:0)	17 h[c] + 12 nadph[c] + 6 malcoa[c] + ivcoa[c] => 5 h2o[c] + 7 coa[c] + 12 nadp[c] + 6 co2[c] + fa11[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Glycerophospholipid Metabolism	PMID:6102980, PMID:7440508, PMID: 7204330, PMID:19460428	B. thetaiotaomicron is well known to produce iso- and anteiso-branched fatty acids besides straight-chain fatty acids.	2.3.1.41

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	KAS12	b-ketoacyl synthetase (Anteiso-C17:0)	17 h[c] + 2mbcoa[c] + 12 nadph[c] + 6 malcoa[c] => 5 h2o[c] + 7 coa[c] + 12 nadp[c] + 6 co2[c] + fa12[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Glycerophospholipid Metabolism	PMID:6102980, PMID:7440508, PMID: 7204330, PMID:19460428	B. thetaiotaomicron is well known to produce iso- and anteiso-branched fatty acids besides straight-chain fatty acids.	2.3.1.41
	KAS13	b-ketoacyl synthetase (octadecanoate)	23 h[c] + 16 nadph[c] + accoa[c] + 8 malcoa[c] => 7 h2o[c] + 9 coa[c] + 16 nadp[c] + 8 co2[c] + ocdca[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Glycerophospholipid Metabolism	PMID:6102980, PMID:7440508, PMID: 7204330, PMID:19460428	B. thetaiotaomicron is well known to produce iso- and anteiso-branched fatty acids besides straight-chain fatty acids.	2.3.1.41
rxn05347	KAS14	beta-ketoacyl-ACP synthase	h[c] + malACP[c] + acACP[c] => ACP[c] + actACP[c] + co2[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Glycerophospholipid Metabolism	PMID:6102980, PMID:7440508, PMID: 7204330, PMID:19460428	B. thetaiotaomicron is well known to produce iso- and anteiso-branched fatty acids besides straight-chain fatty acids.	2.3.1.41
	KAS2	b-ketoacyl synthetase (n-C14:0)	17 h[c] + 12 nadph[c] + accoa[c] + 6 malcoa[c] => 5 h2o[c] + 7 coa[c] + 12 nadp[c] + 6 co2[c] + ttdca[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Glycerophospholipid Metabolism	PMID:6102980, PMID:7440508, PMID: 7204330, PMID:19460428	B. thetaiotaomicron is well known to produce iso- and anteiso-branched fatty acids besides straight-chain fatty acids.	2.3.1.41
	KAS3	b-ketoacyl synthetase (Iso-C15:0)	14 h[c] + 10 nadph[c] + 5 malcoa[c] + ivcoa[c] => 4 h2o[c] + 6 coa[c] + 10 nadp[c] + 5 co2[c] + fa3[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Glycerophospholipid Metabolism	PMID:6102980, PMID:7440508, PMID: 7204330, PMID:19460428	B. thetaiotaomicron is well known to produce iso- and anteiso-branched fatty acids besides straight-chain fatty acids.	2.3.1.41
	KAS4	b-ketoacyl synthetase (Anteiso-C15:0)	14 h[c] + 2mbcoa[c] + 10 nadph[c] + 5 malcoa[c] => 4 h2o[c] + 6 coa[c] + 10 nadp[c] + 5 co2[c] + fa4[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Glycerophospholipid Metabolism	PMID:6102980, PMID:7440508, PMID: 7204330, PMID:19460428	B. thetaiotaomicron is well known to produce iso- and anteiso-branched fatty acids besides straight-chain fatty acids.	2.3.1.41

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	KAS6	b-ketoacyl synthetase (Iso-C16:0)	17 h[c] + 12 nadph[c] + 6 malcoa[c] + ibcoa[c] => 5 h2o[c] + 7 coa[c] + 12 nadp[c] + 6 co2[c] + fa6[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Glycerophospholipid Metabolism	PMID:6102980, PMID:7440508, PMID: 7204330, PMID:19460428	B. thetaiotaomicron is well known to produce iso- and anteiso-branched fatty acids besides straight-chain fatty acids.	2.3.1.41
	KAS8	b-ketoacyl synthetase (palmitate, n-C16:0)	20 h[c] + 14 nadph[c] + accoa[c] + 7 malcoa[c] => 6 h2o[c] + 8 coa[c] + 14 nadp[c] + 7 co2[c] + hdca[c]	0	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	0	1000	3	Glycerophospholipid Metabolism	PMID:6102980, PMID:7440508, PMID: 7204330, PMID:19460428	B. thetaiotaomicron is well known to produce iso- and anteiso-branched fatty acids besides straight-chain fatty acids.	2.3.1.41
	KDNH	2-keto-3deoxy-D-glycero-D-galactononic acid phosphohydrolase	h2o[c] + kdnp[c] => pi[c] + kdn[c]	0	BT_1713	0	1000	4	Capsular Polysaccharide Biosynthesis	PMID:18804026	B. thetaiotaomicron forms and cytidylates 2-keto-3-deoxy-D-glycero-D-galacto-nononic acid (KDN), most likely for inclusion in its capsular polysaccharides.	
	KDOCT2	3-deoxy-manno-octulosonate cytidylyltransferase	ctp[c] + kdo[c] => ppi[c] + ckdo[c]	0	BT_0745	0	1000	2	Lipopolysaccharide Biosynthesis			2.7.7.38
rxn02404	KDOPP	3-deoxy-manno-octulosonate-8-phosphatase	h2o[c] + kdo8p[c] => pi[c] + kdo[c]	0	(BT_1677 or BT_1713)	0	1000	4	Lipopolysaccharide Biosynthesis	PMID: 18986982	BT_1713 gene product was purified and characterized.	3.1.3.45
rxn02331	KDOPS	3-deoxy -D-manno-octulosonic -acid 8-phosphate synthase	h2o[c] + ara5p[c] + pep[c] => pi[c] + kdo8p[c]	0	BT_4321	0	1000	2	Lipopolysaccharide Biosynthesis			4.1.2.16
	KDUI	5-keto-4-deoxyuronate isomerase	dt5hsu[c] => dkdglcn[c]	0	(BT_3231 or BT_4106)	0	1000	2	Pentose and Glucuronate Interconversions		Added based on annotation from KEGG Pathway	5.3.1.17
	KESTOASEe	Beta-2-1 fructan degradation, extracellular	2 h2o[e] + kesto[e] => glc-D[e] + 2 fru[e]	0	(BT_1759 or BT_3082)	0	1000	4	Plant Polysaccharide Degradation	PMID:20603004	B. thetaiotaomicron grows well on short chain beta-2-1 fructans.	3.2.1.65
	KESTOPTASEe	Beta-2-1 fructan degradation, extracellular	4 h2o[e] + kestopt[e] => glc-D[e] + 4 fru[e]	0	(BT_1759 or BT_3082)	0	1000	4	Plant Polysaccharide Degradation	PMID:20603004	B. thetaiotaomicron grows well on short chain beta-2-1 fructans.	3.2.1.65

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	KESTOTTRASEe	Beta-2-1 fructan degradation, extracellular	3 h2o[e] + kestottr[e] => glc-D[e] + 3 fru[e]	0	(BT_1759 or BT_3082)	0	1000	4	Plant Polysaccharide Degradation	PMID:20603004	B. thetaiotaomicron grows well on short chain beta-2-1 fructans.	3.2.1.65
rxn05596	Kt3r	potassium proton antiporter	h[e] + k[c] <=> h[c] + k[e]	1	((BT_4097 and BT_4098) or (BT_4665 and BT_4666))	-1000	1000	2	Transport, Extracellular			
rxn05602	L_LACt2r	L-lactate reversible transport via proton symport	h[e] + lac-L[e] <=> h[c] + lac-L[c]	1	BT_1453	-1000	1000	2	Transport, Extracellular			
rxn03012	L2A6OD2s	2,3,4,5-Tetrahydrodipicolinate conversion to L-2-Amino-6-oxopimelate (spontaneous)	h2o[c] + h[c] + thdp[c] => l2a6o[c]	0		0	1000	2	Folate Metabolism			
	LACDFUCTTR_FUCASEe	alpha-fucosidase, Lactodifucotetraose (extracellular)	h2o[e] + lacdfucttr[e] => 2fuclac[e] + fuc-L[e]	0	((BT_1625 or BT_4136) and ((BT_4134 and BT_4135) or (BT_1630 and BT_1631)))	0	1000	4	HMO Degradation	PMID: 22036470	B. thetaiotaomicron grows on human milk oligosaccharides (HMOs); numerous glycosidase hydrolases are upregulated during growth on HMOs. Involves alpha-fucosidase and susC/SusD (binding proteins).	3.2.1.51
	LACNDFUCHX_FUCASEe	alpha-fucosidase, Lacto-N-difucohexaose (extracellular)	h2o[e] + lacndfuchx[e] => fuc-L[e] + lacnfucpt[e]	0	((BT_1625 or BT_4136) and ((BT_4134 and BT_4135) or (BT_1630 and BT_1631)))	0	1000	4	HMO Degradation	PMID: 22036470	B. thetaiotaomicron grows on human milk oligosaccharides (HMOs); numerous glycosidase hydrolases are upregulated during growth on HMOs. Involves alpha-fucosidase and susC/SusD (binding proteins).	3.2.1.51

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	LACNFUCPT_FUCASEe	alpha-fucosidase, Lacto-N-fucopentaose (extracellular)	h2o[e] + lacnfucpt[e] => fuc-L[e] + lacnttr[e]	0	((BT_1625 or BT_4136) and ((BT_4134 and BT_4135) or (BT_1630 and BT_1631)))	0	1000	4	HMO Degradation	PMID: 22036470	B. thetaiotaomicron grows on human milk oligosaccharides (HMOs); numerous glycosidase hydrolases are upregulated during growth on HMOs. Involves alpha-fucosidase and susC/ SusD (binding proteins).	3.2.1.51
	LACNTTR_DEGe	Lacto-N-tetraose degradation by beta-galactosidase and N-acetylglucosaminidase, extracellular	2 h2o[e] + lacnttr[e] => lcts[e] + acgam[e] + gal[e]	0	((BT_1626 or BT_0461) and (BT_1627 or BT_1632 or BT_4132 or BT_0459 or BT_0460 or BT_1038 or BT_1044 or BT_1048 or BT_1051 or BT_4295 or BT_2825) and ((BT_1630 and BT_1631) or (BT_4134 and BT_4135) or (BT_1039 and BT_1040) or (BT_1042 and BT_1043) or (BT_1046 and BT_1047) or (BT_4297 and BT_4298) or (BT_2818 and BT_2819) or (BT_2820 and BT_2821)))	0	1000	3	HMO Degradation	MID: 22036470	Growth on this human milk oligosaccharide is very slow and inefficient, but detectable. No information on growth on Lacto-N-neotetraose is available. Involves beta-galactosidase, N-acetylglucosaminidase, susC, susD (binding proteins).	
	LACZe	b-galactosidase, extracellular	h2o[e] + lcts[e] => glc-D[e] + gal[e]	0	(BT_1626 or BT_4050)	0	1000	3	Alternate Carbon Metabolism	PMID:16968696	Genes are upregulated in the presence of lactose from mother's milk.	3.2.1.23

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn01270	LARGNAT	L-arogenate:2-oxoglutarate aminotransferase	Largn[c] + oaa[c] <=> h[c] + asp-L[c] + pphn[c]	1	BT_3935	-1000	1000	2	Tyrosine, Tryptophan, and Phenylalanine Metabolism		Added manually to BIGG database based on SEED database	2.6.1.57
	LCAR2	Lactaldehyde reductase (glycolaldehyde)	h[c] + nadh[c] + gcald[c] <=> 12ethd[c] + nad[c]	1	BT_3767	-1000	1000	2	Alternate Carbon Metabolism	PMID:3308886	Lactaldehyde dehydrogenase accepts glycolaldehyde as substrate (also shown in KEGG Pathway).	1.1.1.77
rxn01615	LCARS	lactaldehyde reductase (S-propane-1,2-diol forming)	h[c] + nadh[c] + lald-L[c] <=> 12ppd-S[c] + nad[c]	1	BT_3767	-1000	1000	4	Alternate Carbon Metabolism	PMID: 18848625, PMID:10449780	Demonstrated to be involved both in L-fucose and L-rhamnose utilization pathway.	1.1.1.77
rxn00500	LDH_D	D-lactate dehydrogenase	nad[c] + lac-D[c] <=> h[c] + pyr[c] + nadh[c]	1	BT_1575	-1000	1000	4	Central Metabolism	PMID:19525515	Demonstrated by biochemical assay for B. thetaiotaomicron.	1.1.1.28
rxn00499	LDH_L	L-lactate dehydrogenase	nad[c] + lac-L[c] <=> h[c] + pyr[c] + nadh[c]	1	(BT_4455 and BT_4456 and BT_4457)	-1000	1000	3	Central Metabolism	PMID:148460	Gene annotation was proposed by The SEED Viewer, however, the reaction was not included in the draft model generated by Model SEED. No other genome database confirms this annotation. However, L-lactate dehydrogenase was demonstrated in the closely related organism Bacteroides fragilis.	1.1.1.27
	LEUGLY1c	Hydrolysis of L-Leucylglycine	h2o[c] + leugly[c] => gly[c] + leu-L[c]	0	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314)	0	1000	2	Peptide Degradation			

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	LEUGLYLAPe	hydrolysis of Leucylglycine by predicted non-cytosolic leucine peptidase	h2o[e] + leugly[e] => gly[e] + leu-L[e]	0	BT_2548	0	1000	2	Peptide Degradation	PMID:12663928	Predicted non-cytosolic by Xu et al. (2003): "A Genomic View of the Human-B. thetaiotaomicron Symbiosis.". Assumed to be extracellular for modeling purposes.	3.4.11.15
	LEUGLYt	L-Leucylglycine transport via proton symport	h[e] + leugly[e] => h[c] + leugly[c]	0	(BT_0580 or BT_4385 or BT_1086)	0	1000	2	Transport, Extracellular		Genes added based on TransportDB (last consulted 06.06.12).	
	LEULEU1c	Hydrolysis of L-leucyl-L-leucine	h2o[c] + leuleu[c] => 2 leu-L[c]	0	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314)	0	1000	2	Peptide Degradation			
	LEULEULAPe	hydrolysis of Leucylleucine by predicted non-cytosolic leucine peptidase	h2o[e] + leuleu[e] => leu-L[e]	0	BT_2548	0	1000	2	Peptide Degradation	PMID:12663928	Predicted non-cytosolic by Xu et al. (2003): "A Genomic View of the Human-B. thetaiotaomicron Symbiosis.". Assumed to be extracellular for modeling purposes.	3.4.11.15
	LEULEUt	L-leucyl-L-leucine transport via proton symport	h[e] + leuleu[e] => h[c] + leuleu[c]	0	(BT_0580 or BT_4385 or BT_1086)	0	1000	2	Transport, Extracellular		Genes added based on TransportDB (last consulted 06.06.12).	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	LEUO	Leucine oxidation by gut bacteria	2 h2o[c] + 3 leu-L[c] => co2[c] + 3 nh4[c] + 2 isocapr[c] + isoval[c]	0		0	1000	2	Valine, Leucine, and Isoleucine Metabolism	PMID:1541601, PMID:3572204, PMID:16887608, Krieg, N. R. (2010). Bergey's manual of systematic bacteriology, 2nd ed., volume 4. New York, Springer.	Valine and leucine are oxidized by gut bacteria to BCFA (branched-chain fatty acids) with one less carbon atom (isobutyrate and isovalerate, respectively), CO2 and ammonia.Isocaproate is also formed in the large intestine by reduction of leucine. This reaction formula is hypothetical,no information on exact pathway and involved enzymes is avaiable. KEGG does not provide any pathway information either.Isobutyrate and isovalerate are known secretion products of B. thetaiotaomicron.	
rxn05243	LEUt2r	L-leucine reversible transport via proton symport	h[e] + leu-L[e] <=> h[c] + leu-L[c]	1		-1000	1000	2	Transport, Extracellular	PMID:7462155	B. thetaiotaomicron incorporates leucine, valine and isoleucine into its phospholipids,which suggests the presence of a transporter for these amino acids. However, it is not known which gene encodes this transporter.	
rxn00806	LEUTA	leucine transaminase	akg[c] + leu-L[c] <=> glu-L[c] + 4mop[c]	1	BT_3892	-1000	1000	2	Valine, Leucine, and Isoleucine Metabolism			2.6.1.6

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	LEVANASE_1e	Extracellular levanase	249 h2o[e] + levan1000[e] => 250 levantttr[e]	0	(BT_1760 and BT_1762 and BT_1763)	0	1000	4	Plant Polysaccharide Degradation	PMID:20603004	B. thetaiotaomicron utilizes levan from host's diet as carbon source. BT_1762 (susD homolog) is required for efficient levan binding, presumably also BT_1763 (susC homolog).	3.2.1.65
	LEVANASE_2e	Extracellular levanase	h2o[e] + levantttr[e] => fru[e] + levanttr[e]	0	(BT_1759 or BT_3082 or BT_1760)	0	1000	4	Plant Polysaccharide Degradation	PMID:20603004	B. thetaiotaomicron utilizes levanoligosaccharides.	3.2.1.65
	LEVANASE_3e	Extracellular levanase	h2o[e] + levanttr[e] => fru[e] + levanb[e]	0	(BT_1759 or BT_3082 or BT_1760)	0	1000	4	Plant Polysaccharide Degradation	PMID:20603004	B. thetaiotaomicron utilizes levanoligosaccharides.	3.2.1.65
	LEVANASE_4e	Extracellular levanase	h2o[e] + levanb[e] => 2 fru[e]	0	(BT_1759 or BT_3082 or BT_1760)	0	1000	4	Plant Polysaccharide Degradation	PMID:20603004	B. thetaiotaomicron utilizes levanoligosaccharides.	3.2.1.65
	LEVANB_ABC	levanbiose transport	h2o[c] + atp[c] + levanb[e] => h[c] + pi[c] + adp[c] + levanb[c]	0		0	1000	2	Plant Polysaccharide Degradation	PMID:20603004	B. thetaiotaomicron has an intracellular leavanbiose-degrading fructanase, therefore presence of a transport reaction is assumed.	
rxn01834	LGTHL	lactoylglutathione lyase	mthgxl[c] + gthrd[c] => lgt-S[c]	0	BT_1580	0	1000	2	Central Metabolism		Reversible reaction in Model SEED	4.4.1.5
	LMN2e	laminaribiase (extracellular)	h2o[e] + lmn2[e] => 2 glc-D[e]	0	(BT_2550 or BT_2824 or BT_3683)	0	1000	4	Plant Polysaccharide Degradation	PMID:879772, PMID:9178362	B. thetaiotaomicron grows on laminaran, products are laminaribiose and glucose.	3.2.1.6
	LMNe	Laminarinase (extracellular)	14 h2o[e] + lmn30[e] => 15 lmn2[e]	0	(BT_2550 or BT_2824 or BT_3683)	0	1000	4	Plant Polysaccharide Degradation	PMID:879772, PMID:9178362	B. thetaiotaomicron grows on laminaran, products are laminaribiose and glucose.	3.2.1.6

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	LPADSS_BT	lipidA_bt disaccaride synthase	lipidX_bt[c] + u2ga_bt[c] => 2 h[c] + udp[c] + lipidAds_bt[c]	0	BT_4004	0	1000	4	Lipopolysaccharide Biosynthesis	PMID:18931137, PMID:19460428, PMID:20974832	Based on H. pylori LPS biosynthesis (BIGG database), as in the P. gingivalis reconstruction (PMID:18931137). P. gingivalis' LPS is similar in structure to the Bacteroides LPS. Based on structural information taken from (PMID:19460428, PMID:20974832).	2.4.1.182
	LPS_BTabc	Lipopolysaccharide transport out via ABC system	h2o[c] + atp[c] + lps_bt[c] => h[c] + pi[c] + adp[c] + lps_bt[e]	0		0	1000	2	Transport, Extracellular	PMID:18931137, PMID:19460428, PMID:20974832	Based on H. pylori LPS biosynthesis (BIGG database), as in the P. gingivalis reconstruction (PMID:18931137). P. gingivalis' LPS is similar in structure to the Bacteroides LPS.	
	LPSSYN_BT	Formation for LPS from Core oligosaccharide-Lipid A and O-chain	2 uacgam[c] + adphep-DD[c] + 3 gdpfuc[c] + udpg[c] + core_lps_bt[c] + 2 udpgal[c] => adp[c] + 3 gdp[c] + 5 udp[c] + lps_bt[c]	0		0	1000	2	Lipopolysaccharide Biosynthesis	PMID:18931137, PMID:19460428, PMID:20974832. See also PMID:15774760	Based on H. pylori LPS biosynthesis (BIGG database), as in the P. gingivalis reconstruction (PMID:18931137). P. gingivalis' LPS is similar in structure to the Bacteroides LPS. Based on structural information taken from (PMID:19460428, PMID:20974832).	
rxn00321	LYSAM	Lysine 2,3-aminomutase (EC 5.4.3.2)	lys-L[c] <=> 36dahx[c]	1	BT_4474	-1000	1000	2	Threonine and Lysine Metabolism			5.4.3.2
rxn00322	LYSDC	lysine decarboxylase	h[c] + lys-L[c] => co2[c] + 15dap[c]	0	BT_3307	0	1000	2	Threonine and Lysine Metabolism		Added based on annotation from KEGG Pathway	4.1.1.18

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05305	LYSt3r	L-lysine transport out via proton antiport reversible	h[e] + lys-L[c] <=> h[c] + lys-L[e]	1	BT_1732	-1000	1000	2	Transport, Extracellular	PMID:10867063	The gut microbiota supplies the host with lysine (essential amino acid for humans).	
	MALCOACD	Malonyl-CoA condensation catalyzed by FabH	h[c] + malACP[c] + malcoam[c] => coa[c] + 3ogACPm[c] + co2[c]	0	(BT_0122 or BT_3834)	0	1000	3	Biotin Metabolism	PMID:20693992	Based on biotin synthesis described in PMID:20693992 for E. coli.	
	MALCOAMT	Malonyl-CoA methyltransferase BioC	malcoa[c] + amet[c] => ahcys[c] + malcoam[c]	0	BT_1445	0	1000	3	Biotin Metabolism	PMID:20693992	Based on biotin synthesis described in PMID:20693992 for E. coli. Malonyl-CoA is considered the most likely substrate.	
rxn00022	MALT	alpha-glucosidase	h2o[c] + malt[c] => 2 glc-D[c]	0	(BT_0132 or BT_0683 or BT_2620 or BT_3163 or BT_3169 or BT_3294 or BT_3299 or BT_3664 or BT_4581)	0	1000	3	Plant Polysaccharide Degradation	PMID: 10986238	The starch and maltooligosaccharide utilization system of B. thetaiotaomicron is well characterized.	3.2.1.20
	MALTe	alpha-glucosidase, extracellular	h2o[e] + malt[e] => 2 glc-D[e]	0	(BT_3704 or BT_3703)	0	1000	4	Plant Polysaccharide Degradation	PMID:18981178, PMID:18611383, PMID:10986238	The starch and maltooligosaccharide utilization system of B. thetaiotaomicron is well characterized.	3.2.1.20
	MALTt2r	maltose transport in via proton symport reversible	h[e] + malt[e] <=> h[c] + malt[c]	1		-1000	1000	2	Transport, Extracellular	PMID: 10986238	B. thetaiotaomicron grows on maltose.	
rxn00640	MAN1PT2r	mannose-1-phosphate guanylyltransferase (GDP) reversible	h[c] + gdp[c] + man1p[c] <=> pi[c] + gdpmann[c]	1	BT_0558	-1000	1000	2	Alternate Carbon Metabolism			2.7.7.22
rxn00559	MAN6PI	mannose-6-phosphate isomerase	man6p[c] <=> f6p[c]	1	BT_0373	-1000	1000	2	Alternate Carbon Metabolism			5.3.1.8

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	MANA1e	beta-mannosidase, mannobiose degradation	h2o[e] + manb[e] => 2 man[e]	0	(BT_0458 or BT_2855 or BT_4074 or BT_2432 or BT_3599 or BT_1769 or BT_1878 or BT_2199 or BT_3773 or BT_3784 or BT_3858 or BT_3962 or BT_3965 or BT_3990 or BT_3991 or BT_4073 or BT_4092 or BT_4093)	0	1000	4	Plant Polysaccharide Degradation	PMID:17287210, PMID: 20081828	BT_0458 gene product was purifed and characterized. Shown to have high activity on mannobiose and especially mannotriose,mannotetraose and mannopentaose. Most enzymes in this GPR of the GH92 family were shown to be active against mannobiose.	3.2.1.25
	MANA2e	beta-mannosidase, mannotriose degradation	h2o[e] + mantr[e] => man[e] + manb[e]	0	(BT_0458 or BT_2855 or BT_4074 or BT_2432 or BT_3599)	0	1000	4	Plant Polysaccharide Degradation	PMID:17287210	BT_0458 gene product was purifed and characterized. Shown to have high activity on mannobiose and especially mannotriose,mannotetraose and mannopentaose.	3.2.1.25
	MANA3e	beta-mannosidase, mannotetraose degradation	h2o[e] + manttr[e] => man[e] + mantr[e]	0	(BT_0458 or BT_2855 or BT_4074 or BT_2432 or BT_3599)	0	1000	4	Plant Polysaccharide Degradation	PMID:17287210	BT_0458 gene product was purifed and characterized. Shown to have high activity on mannobiose and especially mannotriose,mannotetraose and mannopentaose.	3.2.1.25
rxn03838	MANA4	mannase	h2o[c] + mantr[c] <=> gal[c] + melib[c]	1	(BT_1871 or BT_2851 or BT_3065 or BT_3131 or BT_3133 or BT_3410)	-1000	1000	4	Plant Polysaccharide Degradation	PMID:17287210	B. thetaiotaomicron grows on mannotriose.	3.2.1.22

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	MANA4e	beta-mannosidase, mannopentaose degradation	h2o[e] + manpt[e] => man[e] + manttr[e]	0	(BT_0458 or BT_2855 or BT_4074 or BT_2432 or BT_3599)	0	1000	4	Plant Polysaccharide Degradation	PMID:17287210	BT_0458 gene product was purifed and characterized. Shown to have high activity on mannobiose and especially mannotriose,mannotetraose and mannopentaose.	3.2.1.25
	MANabc	mannose transport via ABC transporter	h2o[c] + atp[c] + man[e] => h[c] + pi[c] + adp[c] + man[c]	0	BT_1536	0	1000	3	Transport, Extracellular	PMID: 22205877	B. thetaiotaomicron grows on mannose and alpha-mannan. The ABC transporter BT_1536 is upregulated during growth on alpha-mannan.	
rxn01775	MANAO	Mannonate oxidoreductase	nad[c] + mana[c] <=> h[c] + nadh[c] + fruur[c]	1	(BT_0130 or BT_1433)	-1000	1000	2	Alternate Carbon Metabolism			1.1.1.57
	MANTRabc	mannotriose transport via ABC transporter	h2o[c] + atp[c] + mantr[e] => h[c] + pi[c] + adp[c] + mantr[c]	0		0	1000	2	Transport, Extracellular	PMID:17287210	B. thetaiotaomicron grows on mannotriose.	
rxn05465	MCOATA	Malonyl-CoA-ACP transacylase	ACP[c] + malcoa[c] <=> coa[c] + malACP[c]	1	BT_0789	-1000	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330		2.3.1.85
rxn00248	MDH	malate dehydrogenase	nad[c] + mal-L[c] <=> h[c] + nadh[c] + oaa[c]	1	(BT_2510 or BT_3911)	-1000	1000	4	TCA Cycle	PMID: 11260473	Demonstrated by biochemical assay.	1.1.1.37
rxn00161	ME2	malic enzyme (NADP)	nadp[c] + mal-L[c] => pyr[c] + nadph[c] + co2[c]	0	BT_1969	0	1000	4	Central Metabolism	PMID:148460	Demonstrated in the close relative B. fragilis.	1.1.1.40
rxn05293	MECDPDH2	2C-methyl-D-erythritol 2,4 cyclodiphosphate dehydratase	nadh[c] + 2mecdp[c] => h2o[c] + nad[c] + h2mb4p[c]	0	BT_2517	0	1000	2	Cofactor and Prosthetic Group Biosynthesis			1.17.7.1
rxn03910	MECDPS	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	2p4c2me[c] => cmp[c] + 2mecdp[c]	0	BT_3884	0	1000	2	Cofactor and Prosthetic Group Biosynthesis		Reversible reaction in Model SEED	4.6.1.12

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	MELIBabc	melibiose transport via ABC system (import)	h2o[c] + atp[c] + melib[e] => h[c] + pi[c] + adp[c] + melib[c]	0		0	1000	2	Transport, Extracellular	PMID:2557798	B. thetaiotaomicron grows on melibiose.	
	MEOHt2	Methanol diffusion	meoh[e] <=> meoh[c]	1		-1000	1000	2	Transport, Extracellular	PMID:20693992	Biotin synthesis pathway as proposed by PMID:20693992 produces methanol.	
rxn03907	MEPCT	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	h[c] + ctp[c] + 2me4p[c] => ppi[c] + 4c2me[c]	0	(BT_1651 or BT_2881 or BT_3923)	0	1000	2	Cofactor and Prosthetic Group Biosynthesis		Reversible reaction in Model SEED	2.7.7.60
rxn12636	METALA1c	Hydrolysis of L-methionyl-L-alanine	h2o[c] + metala[c] <=> ala-L[c] + met-L[c]	1	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314 or BT_1838)	-1000	1000	2	Peptide Degradation			
	METALAt	L-methionyl-L-alanine transport via proton symport	h[e] + metala[e] => h[c] + metala[c]	0	(BT_0580 or BT_4385 or BT_1086)	0	1000	2	Transport, Extracellular		Genes added based on TransportDB (last consulted 06.06.12).	
rxn00126	METAT	methionine adenosyltransferase	h2o[c] + atp[c] + met-L[c] => pi[c] + ppi[c] + amet[c]	0	BT_3219	0	1000	2	Methionine Metabolism			2.5.1.6
	METOX1s	methionine oxidation (spontaneous)	h2o2[c] + met-L[c] => h2o[c] + metsox-S-L[c]	0		0	1000	1	Methionine Metabolism			
rxn06077	METSOXR1	L-methionine-S-oxide reductase	trdrd[c] + metsox-S-L[c] => h2o[c] + trdox[c] + met-L[c]	0	BT_2499	0	1000	2	Methionine Metabolism		Reversible reaction in Model SEED	1.8.4.5

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn00693	METSr	5-Methyltetrahydrofolate L-homocysteine S-methyltransferase	hcys-L[c] + 5mthf[c] <=> h[c] + thf[c] + met-L[c]	1	(BT_0180 or BT_0249 or BT_0342)	-1000	1000	3	Methionine Metabolism	Dworkin, M. and S. Falkow (2006). The prokaryotes : a handbook on the biology of bacteria. New York ; [London], Springer	BT_0180: Evidence at protein level (PDB entry 3k13). B. thetaiotaomicron is vitamin B12 dependent, vitamin B12 requirement can be replaced by methionine -> indirect evidence, since vitamin B12 is cofactor for this enzyme	2.1.1.13
	METt2r	L-methionine reversible transport via proton symport	h[e] + met-L[e] <=> h[c] + met-L[c]	1	BT_1270	-1000	1000	2	Transport, Extracellular	PMID:10867063	Gut microbiota contribute to host amino acid homeostasis. Methionine is an essential amino acid for humans. This annotation (Methionine transporter MetT) is only supported by The SEED.	
rxn10571	MG2abc	magnesium transport via ABC system	h2o[c] + atp[c] + mg2[e] => h[c] + pi[c] + adp[c] + mg2[c]	0	BT_0988	0	1000	4	Transport, Extracellular	PMID:4472783	Added by Model SEED during auto-completion step in pipeline. The reaction was confirmed during manual inspection: a gene for Mg2+ transport ATPase is annotated in its genome. B. thetaiotaomicron requires magnesium for growth.	
rxn00748	MGSA	methylglyoxal synthase	dhap[c] => pi[c] + mthgxl[c]	0	(BT_1098 or BT_2150)	0	1000	3	Central Metabolism	PMID:18848625	Supported by the observation that propanediol is still formed when lactaldehyde dehydrogenase is knocked out.	4.2.3.3

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05616	MGt5	magnesium transport in/out via permease (no H+)	mg2[c] <=> mg2[e]	1	(BT_4042 or BT_4679)	-1000	1000	4	Transport, Extracellular	PMID:4472783	Irreversible reaction in SEED. B. thetaiotaomicron requires magnesium for growth.	
rxn00881	MI1PP	myo-inositol 1-phosphatase	h2o[c] + mi1p-D[c] => pi[c] + inost[c]	0	BT_2801	0	1000	2	Inositol Phosphate Metabolism			3.1.3.25
rxn00609	MI1PS	myo-Inositol-1-phosphate synthase	g6p[c] => mi1p-D[c]	0	BT_1526	0	1000	2	Inositol Phosphate Metabolism		Reversible reaction in Model SEED	5.5.1.4
rxn00883	MI3PP	myo-inositol 3-phosphatase	h2o[c] + mi3p-D[c] => pi[c] + inost[c]	0	BT_2801	0	1000	2	Inositol Phosphate Metabolism			3.1.3.25
rxn00882	MI4PP	myo-inositol 4-phosphatase	h2o[c] + mi4p-D[c] => pi[c] + inost[c]	0	BT_2801	0	1000	2	Inositol Phosphate Metabolism			3.1.3.25
	MK10t	Menaquinone secretion/ uptake (menaquinone 10)	mqn10[c] <=> mqn10[e]	1		-1000	1000	2	Transport, Extracellular	PMID: 18841274	Gut microbiota, in particular Bacteroides, produce menaquinone, which contributes to host vitamin K homeostasis. AH	
	MK11t	Menaquinone secretion/ uptake (menaquinone 11)	mqn11[c] <=> mqn11[e]	1		-1000	1000	2	Transport, Extracellular	PMID: 18841274	Gut microbiota, in particular Bacteroides, produce menaquinone, which contributes to host vitamin K homeostasis. AH	
	MK7t	Menaquinone secretion/ uptake (menaquinone 7)	mqn7[c] <=> mqn7[e]	1		-1000	1000	2	Transport, Extracellular	PMID: 18841274	Gut microbiota, in particular Bacteroides, produce menaquinone, which contributes to host vitamin K homeostasis. AH	
	MK8t	Menaquinone secretion/ uptake (menaquinone 8)	mqn8[c] <=> mqn8[e]	1		-1000	1000	2	Transport, Extracellular	PMID: 18841274	Gut microbiota, in particular Bacteroides, produce menaquinone, which contributes to host vitamin K homeostasis. AH	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	MK9t	Menaquinone secretion/ uptake (menaquinone 9)	mqn9[c] <=> mqn9[e]	1		-1000	1000	2	Transport, Extracellular	PMID: 18841274	Gut microbiota, in particular Bacteroides, produce menaquinone, which contributes to host vitamin K homeostasis. AH	
rxn05746	MLTG1	Maltodextrin glucosidase (maltotriose)	h2o[c] + malttr[c] => malt[c] + glc-D[c]	0	BT_4690	0	1000	2	Plant Polysaccharide Degradation	PMID:848954	Added based on annotation from NCBI Gene. There may also be other cytoplasmatic enzymes carrying out this reaction. The starch and maltooligosaccharide utilization system of B. thetaiotaomicron is well characterized.	3.2.1.1
	MLTG1e	Maltodextrin glucosidase (maltotriose), extracellular	h2o[e] + malttr[e] => glc-D[e] + malt[e]	0	(BT_3703 or BT_3704)	0	1000	4	Plant Polysaccharide Degradation	PMID:10986238, PMID:2722747, PMID: 18981178, PMID:18611383	The starch and maltooligosaccharide utilization system of B. thetaiotaomicron is well characterized.	3.2.1.1
rxn08933	MLTG2	Maltodextrin glucosidase (maltotetraose)	h2o[c] + maltttr[c] => malttr[c] + glc-D[c]	0	BT_4690	0	1000	2	Plant Polysaccharide Degradation	PMID:848954	Added based on annotation from NCBI Gene. There may also be other cytoplasmatic enzymes carrying out this reaction. The starch and maltooligosaccharide utilization system of B. thetaiotaomicron is well characterized.	3.2.1.1
	MLTG2e	Maltodextrin glucosidase (maltotetraose), extracellular	h2o[e] + maltttr[e] => glc-D[e] + malttr[e]	0	(BT_3703 or BT_3704)	0	1000	4	Plant Polysaccharide Degradation	PMID: 18981178, PMID:18611383	The starch and maltooligosaccharide utilization system of B. thetaiotaomicron is well characterized.	3.2.1.1

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn08934	MLTG3	Maltodextrin glucosidase (maltopentaose)	h2o[c] + maltpt[c] => glc-D[c] + maltttr[c]	0	BT_4690	0	1000	2	Plant Polysaccharide Degradation	PMID:848954	Added based on annotation from NCBI Gene. There may also be other cytoplasmatic enzymes carrying out this reaction. The starch and maltooligosaccharide utilization system of B. thetaiotaomicron is well characterized.	3.2.1.1
	MLTG3e	Maltodextrin glucosidase (maltopentaose), extracellular	h2o[e] + maltpt[e] => glc-D[e] + maltttr[e]	0	(BT_3703 or BT_3704)	0	1000	4	Plant Polysaccharide Degradation	PMID: 18981178, PMID:18611383	The starch and maltooligosaccharide utilization system of B. thetaiotaomicron is well characterized.	3.2.1.1
rxn08935	MLTG4	Maltodextrin glucosidase (maltohexaose)	h2o[c] + malthx[c] => glc-D[c] + maltpt[c]	0	BT_4690	0	1000	2	Plant Polysaccharide Degradation	PMID:848954	Added based on annotation from NCBI Gene. There may also be other cytoplasmatic enzymes carrying out this reaction. The starch and maltooligosaccharide utilization system of B. thetaiotaomicron is well characterized.	3.2.1.1
	MLTG4e	Maltodextrin glucosidase (maltohexaose), extracellular	h2o[e] + malthx[e] => glc-D[e] + maltpt[e]	0	((BT_3698 and BT_3701 and BT_3702) or (BT_0773 and BT_3701 and BT_3702) or (BT_4305 and BT_3701 and BT_3702))	0	1000	4	Plant Polysaccharide Degradation	PMID:10986238, PMID:2722747, PMID:8955399, PMID: 18981178, PMID:18611383	The starch and maltooligosaccharide utilization system of B. thetaiotaomicron is well characterized.	3.2.1.1

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn08936	MLTG5	Maltodextrin glucosidase (maltoheptaose)	h2o[c] + malthp[c] => glc-D[c] + malthx[c]	0	BT_4690	0	1000	2	Plant Polysaccharide Degradation	PMID:848954	Added based on annotation from NCBI Gene. There may also be other cytoplasmatic enzymes carrying out this reaction. The starch and maltooligosaccharide utilization system of B. thetaiotaomicron is well characterized.	3.2.1.1
	MLTG5e	Maltodextrin glucosidase (maltoheptaose), extracellular	h2o[e] + malthp[e] => glc-D[e] + malthx[e]	0	((BT_3698 and BT_3701 and BT_3702) or (BT_0773 and BT_3701 and BT_3702) or (BT_4305 and BT_3701 and BT_3702))	0	1000	4	Plant Polysaccharide Degradation	PMID:10986238, PMID:2722747, PMID:8955399, PMID: 18981178, PMID:18611383	The starch and maltooligosaccharide utilization system of B. thetaiotaomicron is well characterized.	3.2.1.1
rxn00672	MMCD	Methylmalonyl-CoA decarboxylase	h[c] + mmcoa-S[c] => co2[c] + ppcoa[c]	0	(BT_1686 and BT_1689 and BT_4415)	0	1000	3	Central Metabolism	PMID: 148460	Demonstrated experimentally in Bacteroides fragilis.	4.1.1.9
rxn01996	MME	methylmalonyl-CoA epimerase	mmcoa-R[c] <=> mmcoa-S[c]	1	BT_1685	-1000	1000	2	Central Metabolism	PMID:148460	Demonstrated experimentally in Bacteroides fragilis.	5.1.99.1
rxn00602	MMM2r	Methylmalonyl-CoA mutase	succoa[c] <=> mmcoa-R[c]	1	(BT_2090 and BT_2091)	-1000	1000	3	Central Metabolism	PMID: 148460	Confirmed for B. fragilis, vitamin B12-dependent	5.4.99.2
rxn03885	MNNH	D-mannonate hydrolyase	mana[c] => h2o[c] + 2ddglcn[c]	0	(BT_0129 or BT_1432)	0	1000	2	Alternate Carbon Metabolism			4.2.1.8
rxn05618	MNt2	manganese transport in via proton symport	h[e] + mn2[e] => h[c] + mn2[c]	0	BT_0629	0	1000	2	Transport, Extracellular			

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	MOAT_BT	3-deoxy-D-manno-octulosonic acid transferase	ckdo[c] + lipidA_bt[c] => h[c] + cmp[c] + kdolipid4_bt[c]	0	BT_2747	0	1000	4	Lipopolysaccharide Biosynthesis	PMID:18931137, PMID:19460428, PMID:20974832	Based on H. pylori LPS biosynthesis (BIGG database), as in the P. gingivalis reconstruction (PMID:18931137). P. gingivalis' LPS is similar in structure to the Bacteroides LPS. Based on structural information taken from (PMID:19460428, PMID:20974832).	2.4.99.12
rxn00912	MOHMT	3-methyl-2-oxobutanoate hydroxymethyltransferase	h2o[c] + 3mob[c] + mlthf[c] => thf[c] + 2dhp[c]	0	BT_0698	0	1000	2	Cofactor and Prosthetic Group Biosynthesis		Reversible reaction in Model SEED	2.1.2.11
rxn01021	MTAN	methylthioadenosine nucleosidase	h2o[c] + 5mta[c] => ade[c] + 5mtr[c]	0	BT_4451	0	1000	2	Arginine and Proline Metabolism			3.2.2.16
rxn01211	MTHFC	methenyltetrahydrofolate cyclohydrolase	h2o[c] + methf[c] <=> h[c] + 10fthf[c]	1	(BT_0737 or BT_1607)	-1000	1000	2	Folate Metabolism			3.5.4.9
rxn00907	MTHFD	methylenetetrahydrofolate dehydrogenase (NADP)	nadp[c] + mlthf[c] <=> nadph[c] + methf[c]	1	BT_1607	-1000	1000	2	Folate Metabolism			1.5.1.5
rxn04954	MTHFR2	5,10-methylenetetrahydrofolate reductase (NADH)	2 h[c] + nadh[c] + mlthf[c] => nad[c] + 5mthf[c]	0	BT_3821	0	1000	2	Folate Metabolism		Reversible reaction in Model SEED	1.5.1.20
rxn00910	MTHFR3	5,10-methylenetetrahydrofolatereductase (NADPH)	2 h[c] + nadph[c] + mlthf[c] => nadp[c] + 5mthf[c]	0	BT_3821	0	1000	2	Folate Metabolism			1.5.1.20
	MTHGXLt	Methylglyoxal transport (cytosol to extracellular)	mthgxl[c] => mthgxl[e]	0		0	1000	2	Transport, Extracellular	PMID:11260473	B. thetaiotaomicron produces weak amounts of methylglyoxal.	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	NACHEX27e	beta-N-acetylhexosaminidase, hyaluronan degradation	h2o[e] + ha_deg1[e] => acgam[e] + ha_pre1[e]	0	(BT_4394 or BT_4395 or BT_4337 or BT_3598 or BT_1627 or BT_3868 or BT_0459 or BT_0460 or BT_0506 or BT_4681 or BT_1621 or BT_3178 or BT_0456 or BT_1051 or BT_2459)	0	1000	4	Glycosaminoglycan Degradation	PMID:16565725, PMID: 20689974, PMID:848954	BT_4395 gene product was purified and characterized. B. thetaiotaomicron ferments hyaluronan.	3.2.1.52
	NACt	Nicotinate secretion/ uptake	nac[c] <=> nac[e]	1		-1000	1000	2	Transport, Extracellular	PMID: 19748469	B. thetaiotaomicron mutants in NAD biosynthesis are not essential in vitro on tryptone-yeast extract-glucose medium, suggesting that B. thetaiotaomicron can uptake nicotinate from yeast extract.	
	NADDP	NAD diphosphatase	h2o[c] + nad[c] => 2 h[c] + amp[c] + nmn[c]	0	BT_1544	0	1000	2	Cofactor and Prosthetic Group Biosynthesis			3.6.1.22
rxn08971	NADH10	NADH dehydrogenase (menaquinone-8 & 0 protons)	h[c] + nadh[c] + mqn8[c] => nad[c] + mql8[c]	0	BT_1537	0	1000	2	Central Metabolism			1.6.5.3
	NADH17	NADH dehydrogenase (menaquinone-8 & 3 protons)	4 h[c] + nadh[c] + mqn8[c] => nad[c] + 3 h[e] + mql8[c]	0	(BT_4058 and BT_4059 and BT_4060 and BT_4061 and BT_4062 and BT_4063 and BT_4064 and BT_4065 and BT_4066 and BT_4067)	0	1000	4	Central Metabolism	PMID:12777495	The reaction is linked to fumarate reductase. The exact stochiometry is unkown, formula was putatively added based on E. coli iAF1260.	1.6.5.3

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn08975	NADH5	NADH dehydrogenase (ubiquinone-8)	h[c] + nadh[c] + q8[c] => nad[c] + q8h2[c]	0	BT_1537	0	1000	2	Central Metabolism	PMID: 893348	It is unclear whether B. thetaiotaomicron uses ubiquinone, menaquinone or both. PMID: 893348 states that only menaquinone is present, however ubiquinone-using enzymes are annotated in the genome.	1.6.5.3
rxn08976	NADH9	NADH dehydrogenase (demethylmenaquinone -8 & 0 protons)	h[c] + nadh[c] + 2dmmq8[c] => nad[c] + 2dmmql8[c]	0	BT_1537	0	1000	2	Central Metabolism	PMID: 893348	It is unclear whether B. thetaiotaomicron uses ubiquinone, menaquinone or both. PMID: 893348 states that only menaquinone is present, however ubiquinone-using enzymes are annotated in the genome.	1.6.5.3
rxn00077	NADK	NAD kinase	nad[c] + atp[c] => h[c] + nadp[c] + adp[c]	0	BT_3917	0	1000	2	NAD Metabolism			2.7.1.23
rxn10060	NADK2	NAD kinase (dTTP)	nad[c] + dttp[c] => h[c] + nadp[c] + dtdp[c]	0	BT_3917	0	1000	2	NAD Metabolism		Added manually to BIGG database based on SEED database.	2.7.1.23
rxn00138	NADS1	NAD synthase (nh3)	atp[c] + nh4[c] + dnad[c] => h[c] + nad[c] + amp[c] + ppi[c]	0	BT_0205	0	1000	2	Cofactor and Prosthetic Group Biosynthesis			6.3.1.5
rxn00190	NADS2	NAD synthase (glutamine-hydrolysing)	h2o[c] + atp[c] + gln-L[c] + dnad[c] => h[c] + glu-L[c] + nad[c] + amp[c] + ppi[c]	0	BT_0205	0	1000	2	NAD Metabolism			6.3.5.1
rxn01265	NAMNPP	nicotinic acid mononucleotide pyrophosphorylase	h2o[c] + atp[c] + prpp[c] + nac[c] => pi[c] + adp[c] + ppi[c] + nicrnt[c]	0	BT_1913	0	1000	2	Cofactor and Prosthetic Group Biosynthesis		Reversible reaction in Model SEED	2.4.2.11

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	NARK	Nitrite transport in	no2[c] => no2[e]	0		0	1000	2	ROS Detoxification	Dworkin, M. and S. Falkow (2006). The prokaryotes : a handbook on the biology of bacteria. New York ; [London], Springer, PMID:14665678, PMID:16183308	Nitrite appears to be produced from NH4 by nitrite reductase (the reaction does not seem to go the other way since nitrite does not serve as nitrogen source). Nitrite does not react further to nitric oxide (or only in very slight amounts) (PMID:16183308). It is assumed that nitrite is transported out via diffusion through porin (PMID:14665678).	
rxn05209	NAt3_1	sodium proton antiporter (H:NA is 1:1)	na1[c] + h[e] <=> h[c] + na1[e]	1	(BT_0634 or BT_3638)	-1000	1000	2	Transport, Extracellular			
rxn00853	NCPTRCA	N-Carbamoylputrescine amidase	h2o[c] + 2 h[c] + ncptrc[c] => co2[c] + nh4[c] + ptrc[c]	0	BT_0875	0	1000	3	Spermidine and Putrescine Biosynthesis	PMID:10801923	The reaction is involved in the putrescine secretion pathway.	3.5.1.53
rxn00237	NDPK1	nucleoside-diphosphate kinase (ATP:GDP)	atp[c] + gdp[c] <=> adp[c] + gtp[c]	1	BT_3925	-1000	1000	2	Nucleotide Salvage Pathway			2.7.4.6
rxn00117	NDPK2	nucleoside-diphosphate kinase (ATP:UDP)	atp[c] + udp[c] <=> adp[c] + utp[c]	1	BT_3925	-1000	1000	2	Nucleotide Salvage Pathway			2.7.4.6
rxn00409	NDPK3	nucleoside-diphosphate kinase (ATP:CDP)	atp[c] + cdp[c] <=> adp[c] + ctp[c]	1	BT_3925	-1000	1000	2	Nucleotide Salvage Pathway			2.7.4.6
rxn01512	NDPK4	nucleoside-diphosphate kinase (ATP:dTDP)	atp[c] + dtdp[c] <=> adp[c] + dttp[c]	1	BT_3925	-1000	1000	2	Nucleotide Salvage Pathway			2.7.4.6
rxn01353	NDPK5	nucleoside-diphosphate kinase (ATP:dGDP)	atp[c] + dgdp[c] <=> adp[c] + dgtp[c]	1	BT_3925	-1000	1000	2	Nucleotide Salvage Pathway			2.7.4.6
rxn01678	NDPK6	nucleoside-diphosphate kinase (ATP:dUDP)	atp[c] + dudp[c] <=> adp[c] + dutp[c]	1	BT_3925	-1000	1000	2	Nucleotide Salvage Pathway			2.7.4.6
rxn01673	NDPK7	nucleoside-diphosphate kinase (ATP:dCDP)	atp[c] + dcdp[c] <=> adp[c] + dctp[c]	1	BT_3925	-1000	1000	2	Nucleotide Salvage Pathway			2.7.4.6

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn00839	NDPK8	nucleoside-diphosphate kinase (ATP:dADP)	atp[c] + dadp[c] <=> adp[c] + datp[c]	1	BT_3925	-1000	1000	2	Nucleotide Salvage Pathway			2.7.4.6
rxn00515	NDPK9	nucleoside-diphosphate kinase (ATP:IDP)	atp[c] + idp[c] <=> adp[c] + itp[c]	1	BT_3925	-1000	1000	2	Nucleotide Salvage Pathway			2.7.4.6
	NEULACNTTR_SIASEe	sialidase, Sialyllacto-N-tetraose	h2o[e] + neulacnttr[e] => acnam[e] + lacnttr[e]	0	BT_0455 or BT_2194 or BT_2892	0	1000	4	HMO Degradation	PMID: 22036470	B. thetaiomicron liberates sialic acid from human milk oligosaccharides, though it cannot use it. Lacto-N-tetraose is poorly metabolized and accumulates if BT is grown on HMOs.	3.2.1.18
rxn05466	NH4t	ammonia reversible transport	nh4[e] <=> nh4[c]	1	BT_0544	-1000	1000	2	Transport, Extracellular			
	NMNt2r	NMN transport via proton symport reversible	h[c] + nmn[c] <=> h[e] + nmn[e]	1	BT_2396	-1000	1000	2	Transport, Extracellular		Annotation from NCBI Gene (last updated 01.01.11)	
rxn02155	NNATr	nicotinate-nucleotide adenylyltransferase	h[c] + atp[c] + nicrnt[c] <=> ppi[c] + dnad[c]	1	BT_2011	-1000	1000	2	NAD Metabolism			2.7.7.18
rxn02402	NNDPR	nicotinate-nucleotide diphosphorylase (carboxylating)	2 h[c] + prpp[c] + quln[c] => co2[c] + ppi[c] + nicrnt[c]	0	BT_1560	0	1000	2	NAD Metabolism			2.4.2.19
rxn01647	NP1_r	nucleotide phosphatase	h[c] + nac[c] + r1p[c] <=> pi[c] + nicrns[c]	1	(BT_1881 or BT_4554)	-1000	1000	2	NAD Metabolism			E2.4.2.1
rxn02898	NPHS	naphthoate synthase	sbzcoa[c] => coa[c] + dhna[c]	0	BT_4702	0	1000	2	Cofactor and Prosthetic Group Biosynthesis			4.1.3.36
rxn02400	NT5C	Nicotinate D-ribonucleotide phosphohydrolase	h2o[c] + nicrnt[c] => pi[c] + nicrns[c]	0	(BT_1236 or (BT_2440 and BT_2441))	0	1000	2	NAD Metabolism			3.1.3.5
rxn01521	NTD1	5'-nucleotidase (dUMP)	h2o[c] + dump[c] => pi[c] + duri[c]	0	(BT_1236 or BT_4003 or (BT_2440 and BT_2441))	0	1000	2	Nucleotide Salvage Pathway			3.1.3.5
rxn01961	NTD10	5'-nucleotidase (XMP)	h2o[c] + xmp[c] => pi[c] + xtsn[c]	0	(BT_1236 or (BT_2440 and BT_2441))	0	1000	2	Nucleotide Salvage Pathway			3.1.3.5

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rxn00831	NTD11	5'-nucleotidase (IMP)	h2o[c] + imp[c] => pi[c] + ins[c]	0	(BT_1236 or (BT_2440 and BT_2441))	0	1000	2	Nucleotide Salvage Pathway			3.1.3.5
rxn00708	NTD2	5'-nucleotidase (UMP)	h2o[c] + ump[c] => pi[c] + uri[c]	0	(BT_1236 or (BT_2440 and BT_2441))	0	1000	2	Nucleotide Salvage Pathway			3.1.3.5
rxn01218	NTD3	5'-nucleotidase (dCMP)	h2o[c] + dcmp[c] => pi[c] + dcyt[c]	0	(BT_1236 or (BT_2440 and BT_2441))	0	1000	2	Nucleotide Salvage Pathway			3.1.3.5
rxn00363	NTD4	5'-nucleotidase (CMP)	h2o[c] + cmp[c] => pi[c] + cytd[c]	0	(BT_1236 or (BT_2440 and BT_2441))	0	1000	2	Nucleotide Salvage Pathway			3.1.3.5
rxn01145	NTD5	5'-nucleotidase (dTMP)	h2o[c] + dtmp[c] => pi[c] + thymd[c]	0	(BT_1236 or (BT_2440 and BT_2441))	0	1000	2	Nucleotide Salvage Pathway			3.1.3.5
rxn01670	NTD5_a	Nicotinamide ribonucleotide phosphohydrolase	h2o[c] + nmn[c] => pi[c] + rnam[c]	0	(BT_1236 or (BT_2440 and BT_2441))	0	1000	2	NAD Metabolism			3.1.3.5
rxn01507	NTD6	5'-nucleotidase (dAMP)	h2o[c] + damp[c] => pi[c] + dad-2[c]	0	(BT_1236 or (BT_2440 and BT_2441))	0	1000	2	Nucleotide Salvage Pathway			3.1.3.5
rxn00132	NTD7	5'-nucleotidase (AMP)	h2o[c] + amp[c] => pi[c] + adn[c]	0	(BT_1236 or (BT_2440 and BT_2441))	0	1000	2	Nucleotide Salvage Pathway			3.1.3.5
rxn01445	NTD8	5'-nucleotidase (dGMP)	h2o[c] + dgmp[c] => pi[c] + dgsn[c]	0	(BT_1236 or (BT_2440 and BT_2441))	0	1000	2	Nucleotide Salvage Pathway			3.1.3.5
rxn00913	NTD9	5'-nucleotidase (GMP)	h2o[c] + gmp[c] => pi[c] + gsn[c]	0	(BT_1236 or (BT_2440 and BT_2441))	0	1000	2	Nucleotide Salvage Pathway			3.1.3.5
rxn00062	NTP1	nucleoside-triphosphatase (ATP)	h2o[c] + atp[c] => h[c] + pi[c] + adp[c]	0	BT_3128	0	1000	2	Nucleotide Salvage Pathway			3.6.1.15
rxn01351	NTPP1	Nucleoside triphosphate pyrophosphorylase (dgtp)	h2o[c] + dgtp[c] => h[c] + ppi[c] + dgmp[c]	0	BT_4350	0	1000	2	Nucleotide Salvage Pathway		Reviewed by NCBI Gene (updated 01.01.11)	3.6.1.19
rxn02518	NTPP10	Nucleoside triphosphate pyrophosphorylase (ditp)	h2o[c] + ditp[c] => h[c] + ppi[c] + dimp[c]	0	BT_4350	0	1000	2	Nucleotide Salvage Pathway		Reviewed by NCBI Gene (updated 01.01.11)	3.6.1.19
rxn01962	NTPP11	Nucleoside triphosphate pyrophosphorylase (xtp)	h2o[c] + xtp[c] => h[c] + ppi[c] + xmp[c]	0	BT_4350	0	1000	2	Nucleotide Salvage Pathway		Reviewed by NCBI Gene (updated 01.01.11)	3.6.1.19
rxn00301	NTPP2	Nucleoside triphosphate pyrophosphorylase (gtp)	h2o[c] + gtp[c] => h[c] + ppi[c] + gmp[c]	0	BT_4350	0	1000	2	Nucleotide Salvage Pathway		Reviewed by NCBI Gene (updated 01.01.11)	3.6.1.19

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rxn00463	NTPP8	Nucleoside triphosphate pyrophosphorylase (utp)	h2o[c] + utp[c] => h[c] + ump[c] + ppi[c]	0	BT_4350	0	1000	2	Nucleotide Salvage Pathway		Reviewed by NCBI Gene (updated 01.01.11)	3.6.1.19
rxn00514	NTPP9	Nucleoside triphosphate pyrophosphorylase (itp)	h2o[c] + itp[c] => h[c] + ppi[c] + imp[c]	0	BT_4350	0	1000	2	Nucleotide Salvage Pathway		Reviewed by NCBI Gene (updated 01.01.11)	3.6.1.19
rxn01352	NTPTP1	Nucleoside triphosphate tripolyhydrolase	h2o[c] + dgtp[c] => pppi[c] + dgsn[c]	0	(BT_3460 or BT_4208)	0	1000	2	Nucleotide Salvage Pathway		BT_4208: evidence at protein level (PDB entry 2q14)	3.1.5.1
rxn03978	NTRIR5	Cytochrome c nitrite reductase	2 h2o[c] + nh4[c] + 6 ficytcc553[c] <=> 8 h[c] + 6 focytcc553[c] + no2[c]	1	BT_1417	-1000	1000	2	Nitrogen Metabolism		Added manually to BIGG database based on SEED database	1.7.2.2
	O16G2e	oligo-1,6-glucosidase (strch2 ->strch3), extracellular	h2o[e] + strch2[e] => glc-D[e] + malt[e]	0	BT_3299	0	1000	4	Plant Polysaccharide Degradation	PMID:10986238, PMID:2722747, PMID:8955399, PMID: 18981178, PMID:18611383	Starch utilization by B. thetaiotaomicron as sole carbon source is well established.	3.2.1.10
rxn05468	O2t	o2 transport (diffusion)	o2[e] <=> o2[c]	1		-1000	1000	1	Transport, Extracellular			
rxn00162	OAADC	oxaloacetate decarboxylase	h[c] + oaa[c] => pyr[c] + co2[c]	0	((BT_1696 and BT_1697 and BT_1698) or BT_1689 or BT_4415)	0	1000	4	Central Metabolism	PMID: 148460	Confirmed for B. fragilis	4.1.1.3
rxn04794	OBTFL	2-Oxobutanoate formate lyase	coa[c] + 2obut[c] => ppcoa[c] + for[c]	0	((BT_1055 and BT_2955) or (BT_4738 and BT_1055) or (BT_2955 and BT_2956) or (BT_4737 and BT_4738))	0	1000	2	Alternate Carbon Metabolism	PMID: 8048843	Second reaction of pyruvate formate lyase. Presence of enzyme in Bacteroides xylanolyticus confirmed (PMID: 8048843).	2.3.1.54
	OGALURLe	Oligogalacturonate lyase (extracellular)	unsdigalur[e] => 2 dt5hsu[e]	0	(BT_4115 or BT_4116)	0	1000	2	Plant Polysaccharide Degradation	PMID:3968032	Oligogalacturonate lyase is not annotated in the B. thetaiotaomicron genome. Is assumed to also by carried out by pectate lyase to allow complete degradation of pectin.	4.2.2.6

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rxn03445	OHPBAT	O-Phospho-4-hydroxy-L-threonine:2-oxoglutarate aminotransferase	glu-L[c] + ohpb[c] <=> akg[c] + phthr[c]	1	BT_1153	-1000	1000	2	Cofactor and Prosthetic Group Biosynthesis			2.6.1.52
rxn03395	OHPHM	2-octaprenyl-6-hydroxyphenol methylase	amet[c] + 2ohph[c] => h[c] + ahcys[c] + 2omph[c]	0	BT_3209	0	1000	2	Cofactor and Prosthetic Group Biosynthesis	PMID: 893348	It is not clear whether only menaquinone or mq and ubiquinone are synthesized. PMID: 893348 states that only menaquinone is present, however ubiquinone-using enzymes are annotated in the genome.	
rxn01207	OIVD1r	2-oxoisovalerate dehydrogenase (acylating; 4-methyl-2-oxopentaoate)	coa[c] + nad[c] + 4mop[c] <=> co2[c] + nadh[c] + ivcoa[c]	1		-1000	1000	1	Valine, Leucine, and Isoleucine Metabolism		Added by Model SEED during auto-completion step in pipeline. Required for lipid metabolism, assumed to be correctly included.	1.2.1.25
	OIVD2	2-oxoisovalerate dehydrogenase (acylating; 3-methyl-2-oxobutanoate)	coa[c] + nad[c] + 3mob[c] => co2[c] + nadh[c] + ibcoa[c]	0		0	1000	1	Valine, Leucine, and Isoleucine Metabolism		Manual_Gapfilling based on reactions OIVD1r and OIVD3 added by Model SEED. Required for lipid metabolism.	1.2.1.25
rxn02269	OIVD3	2-oxoisovalerate dehydrogenase (acylating; 3-methyl-2-oxopentanoate)	coa[c] + nad[c] + 3mop[c] => 2mbcoa[c] + co2[c] + nadh[c]	0		0	1000	1	Valine, Leucine, and Isoleucine Metabolism		Reversible reaction in Model SEED. Added by Model SEED during auto-completion step in pipeline. Required for lipid metabolism, assumed to be correctly included.	1.2.1.25

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	OLIGOFRUASEe	Oligofructose degradation by extracellular fructanase	4 h2o[e] + oligofru4[e] => 4 fru[e]	0	(BT_1759 or BT_3082)	0	1000	4	Plant Polysaccharide Degradation	PMID:16461642, PMID:20603004	B. thetaiotaomicron grows on the prebiotic oligofructose. Degradation is carried out by exo-acting periplasmatic fructosidases (extracellular for modeling purposes).	
rxn01208	OMCDC	2-Oxo-4-methyl-3-carboxypentanoate decarboxylation	h[c] + 3c4mop[c] => co2[c] + 4mop[c]	0		0	1000	1	Valine, Leucine, and Isoleucine Metabolism			
rxn00710	OMPDC	orotidine-5'-phosphate decarboxylase	h[c] + orot5p[c] => co2[c] + ump[c]	0	BT_4209	0	1000	2	Purine and Pyrimidine Biosynthesis			4.1.1.23
rxn05939	OOR2r	2-oxoglutarate synthase (rev)	co2[c] + fdxrd[c] + succoa[c] <=> h[c] + akg[c] + coa[c] + fdxox[c]	1	((BT_0329 and BT_0330 and BT_0331 and BT_0333) or (BT_2836 and BT_2837))	-1000	1000	4	TCA Cycle	PMID: 533772, PMID:11880608	Demonstrated for several Bacteroides species. Neccessary for heme-dependent 2-oxoglutarate synthesis from oxaloacetate.	1.2.7.3
	OORr	2-oxoglutarate synthase (reversible)	akg[c] + coa[c] + 2 fdox[c] <=> h[c] + co2[c] + succoa[c] + 2 fdred[c]	1	((BT_0329 and BT_0330 and BT_0331 and BT_0333) or (BT_2836 and BT_2837))	-1000	1000	4	TCA Cycle	PMID: 533772, PMID:11880608	Demonstrated for several Bacteroides species. Neccessary for heme-dependent 2-oxoglutarate synthesis from oxaloacetate. OORr is an additional reaction catalyzed by 2-oxoglutarate synthase apart from OOR2r. Necessary to allow IOR2 to run. Not sure which form of ferredoxin is used.	1.2.7.3
	ORNabc	ornithine transport via ABC system	h2o[c] + atp[c] + orn[e] => h[c] + pi[c] + adp[c] + orn[c]	0	BT_4049	0	1000	2	Transport, Extracellular		Annotation from NCBI Gene (last updated 01.01.11)	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn00467	ORNTA	ornithine transaminase	akg[c] + orn[c] => glu-L[c] + glu5sa[c]	0	BT_3758	0	1000	2	Arginine and Proline Metabolism	PMID:238949	Acetylornithine transaminase catalyzes the transamination of N-2-acetyl-L-ornithine (ACOTA) as well as of L-ornithine (this reaction) with 2-oxoglutarate.	2.6.1.13
rxn01362	ORPT	orotate phosphoribosyltransferase	ppi[c] + orot5p[c] <=> prpp[c] + orot[c]	1	BT_3731	-1000	1000	2	Purine and Pyrimidine Biosynthesis		Irreversible reaction in Model SEED	2.4.2.10
rxn00503	P5CD	1-pyrroline-5-carboxylate dehydrogenase	2 h2o[c] + nad[c] + 1pyr5c[c] => h[c] + glu-L[c] + nadh[c]	0	BT_3115	0	1000	2	Arginine and Proline Metabolism	PMID: 18369526	Reversible reaction in Model SEED	1.5.1.12
rxn00931	P5CRyr	L-ProlineNADP+ 5-oxidoreductase	nadp[c] + pro-L[c] <=> 2 h[c] + nadph[c] + 1pyr5c[c]	1	(BT_1902 or BT_3757)	-1000	1000	2	Arginine and Proline Metabolism			1.5.1.2
rxn01257	PABB	Chorismate L-glutamine aminotransferase	nh4[c] + chor[c] => h2o[c] + 4adcho[c]	0	(BT_0531 or BT_0767)	0	1000	2	Folate Metabolism		Reversible reaction in Model SEED	2.6.1.85
	PACCOALr	phenylacetate-CoA ligase	coa[c] + atp[c] + pac[c] <=> amp[c] + ppi[c] + phaccoa[c]	1	(BT_0428 or BT_0571)	-1000	1000	3	Tyrosine, Tryptophan, and Phenylalanine Metabolism	PMID:18396344, PMID:16887608	B. thetaiotaomicron produces phenylacetate as a minor fermentation product (PMID:18396344). Phenylacetate is also formed in the gut from aromatic acid metabolism (PMID:16887608).	6.2.1.30
	PACt2r	phenylacetate transport in via proton symporter	h[e] + pac[e] <=> h[c] + pac[c]	1		-1000	1000	2	Transport, Extracellular	PMID:18396344	B. thetaiotaomicron produces phenylacetate as a minor fermentation product during growth on carbohydrates.	
rxn01791	PANTS	pantothenate synthase	atp[c] + ala-B[c] + pant-R[c] => h[c] + amp[c] + ppi[c] + pnto-R[c]	0	BT_4308	0	1000	3	Cofactor and Prosthetic Group Biosynthesis	PMID:4853401	Annotation from KEGG Pathway. B. thetaiotaomicron does not require patothenate.	6.3.2.1

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rxn03903	PAPPT2	phospho-N-acetylmuramoyl-pentapeptide-transferase (gamma-glutamate)	udcpp[c] + uGgla[c] => ump[c] + uaGgla[c]	0	BT_3451	0	1000	2	Cell Envelope Biosynthesis		Reversible reaction in Model SEED	2.7.8.13
rxn03904	PAPPT3	phospho-N-acetylmuramoyl-pentapeptide-transferase (meso-2,6-diaminopimelate)	udcpp[c] + ugmda[c] => ump[c] + uagmda[c]	0	BT_3451	0	1000	2	Cell Envelope Biosynthesis		Reversible reaction in Model SEED	2.7.8.13
rxn10344	PBt	Lead (Pb+2) ABC transporter	h2o[c] + atp[c] + pb[c] => h[c] + pi[c] + adp[c] + pb[e]	0	BT_1091	0	1000	2	Transport, Extracellular		Added manually to BIGG database based on SEED database	
rxn00871	PBUTT	Phosphate butyryltransferase	pi[c] + btcoa[c] <=> coa[c] + butpi[c]	1	BT_2551	-1000	1000	2	Butanoate Metabolism			2.3.1.19
rxn00250	PC	pyruvate carboxylase	pyr[c] + atp[c] + hco3[c] => h[c] + pi[c] + adp[c] + oaa[c]	0	BT_1196	0	1000	2	TCA Cycle			6.4.1.1
	PDHa	pyruvate dehydrogenase (lipoamide)	h[c] + pyr[c] + lpam[c] => co2[c] + adhlam[c]	0	BT_0311	0	1000	2	Glycolysis/Gluconeogenesis			
rxn01871	PDHbr	pyruvate dehydrogenase (dihydrolipoamide) reversible	coa[c] + adhlam[c] <=> accoa[c] + dhlam[c]	1	BT_0311	-1000	1000	2	Glycolysis/Gluconeogenesis			2.3.1.12
rxn01241	PDHcr	Pyruvate dehydrogenase (dihydrolipoamide dehydrogenase) reversible	nad[c] + dhlam[c] <=> h[c] + nadh[c] + lpam[c]	1	(BT_0309 or BT_1542 or BT_3186)	-1000	1000	2	Glycolysis/Gluconeogenesis			2.3.1.12
rxn00209	PDX5POi	pyridoxine 5'-phosphate oxidase	o2[c] + pdx5p[c] => h2o2[c] + pydx5p[c]	0	BT_1577	0	1000	2	Cofactor and Prosthetic Group Biosynthesis			1.4.3.5
	PDX5PS	Pyridoxine 5'-phosphate synthase	phthr[c] + nad[c] + dxyl5p[c] => 2 h2o[c] + h[c] + co2[c] + pi[c] + nadh[c] + pdx5p[c]	0	(BT_3918 and BT_4374)	0	1000	2	Cofactor and Prosthetic Group Biosynthesis		BIGG reaction PDX5PS replaces 3 SEED reactions.	2.6.99.2

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	PE_CER1_BTt	Ceramide phosphoethanolamine (B.thetaiotaomicron specific) export	pe_cer1_bt[c] <=> pe_cer1_bt[e]	1		-1000	1000	2	Sphingolipid Metabolism	PMID:16887518, PMID:20855611, Anaerobe (2001) 07, 103?112 doi:10.1006/anae.2001.0376	Bacteroides species are well established to produce sphingolipids.	
	PECTICGALASEe	Pectic galactan (potato) degradation, extracellular	99 h2o[e] + pecticgal[e] => 2 ac[e] + 9 arab-L[e] + 78 gal[e] + 4 rmn[e] + 9 galur[e] + 2 meoh[e]	0	((BT_0348 or BT_0360 or BT_0367 or BT_0368 or BT_0369) and (BT_4667 or BT_4668 or BT_4152) and (BT_4146 or BT_4149 or BT_4153 or BT_4155 or BT_4160 or BT_4170 or BT_4183 or BT_4115 or BT_4116 or BT_4119 or BT_4123) and (BT_4150 or BT_4173) and BT_4175 and (BT_4109 or BT_4110) and ((BT_0361 and BT_0362) or (BT_0363 and BT_0364) or (BT_4670 and BT_4671) or (BT_4164 and BT_4165) or (BT_4113 and BT_4114) or (BT_4121 and BT_4122)))	0	1000	4	Plant Polysaccharide Degradation	PMID: 22205877	B. thetaiotaomicron grows on pectic galactan. The genes included in the GPR are upregulated during growth. Enzymes/ proteins assumed to be involved: arabinosidase, galactosidase, galacturonisidase, rhamnogalactorunan esterase, rhamnogalacturonan lyase, pectinesterase, susC/ SusD	

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	PECTIN_DEG2e	Pectin degradation by extracellular pectate lyase and pectinesterase, gut microbiota specific	390 h[e] + pect[e] => 195 meoh[e] + 195 unsdigalur[e]	0	((BT_4115 or BT_4116) and BT_4110)	0	1000	4	Plant Polysaccharide Degradation	PMID:3968032	Purified and characterized by enzyme assay in B. thetaiotaomicron. Genome annotation from NCBI Gene. Appears to be located in periplasm (extracellular for modeling purposes).	
	PECTIN_DEGe	Pectin degradation by extracellular endopolygalacturonase and pectinesterase, gut microbiota specific	390 h2o[e] + pect[e] => 390 galur[e] + 195 meoh[e]	0	((BT_1018 or BT_2378 or BT_4123 or BT_4155 or BT_4187) and BT_4110)	0	1000	4	Plant Polysaccharide Degradation	PMID:3968032	Purified and characterized by enzyme assay. Genome annotation from NCBI Gene. Appears to be located in periplasm (extracellular for modeling purposes).	
	PEPM	phosphoenolpyruvate mutase	pep[c] <=> 3pop[c]	1	BT_1720	-1000	1000	3	Capsular Polysaccharide Biosynthesis	PMID:12904299	PEPM, 3OPDC and 2AMEPHPAT form the biosynthetic pathway of 2-aminoethylphosphonate, a component of the capsular polysaccharide complex of Bacteroides fragilis, and most likely other Bacteroides species.	5.4.2.9
	PEPT160	ethanolamine phosphotransferase (n-C16:0)	h[c] + pe160[c] + cmp[c] => cdpea[c] + 12dgr160[c]	0		0	1000	2	Sphingolipid Metabolism	PMID:16887518, PMID:20855611, Anaerobe (2001) 07, 103?112 doi:10.1006/anae.2001.0376	Reaction required for sphingolipid synthesis. The pathway mechanism may be different.	
rxn02939	PERD	Erythronate 4-phosphate (4per) dehydrogenase	nad[c] + 4per[c] <=> h[c] + nadh[c] + ohpb[c]	1	BT_3361	-1000	1000	2	Cofactor and Prosthetic Group Biosynthesis			1.1.1.290

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rxn00545	PFK	phosphofructokinase	atp[c] + f6p[c] => h[c] + adp[c] + fdp[c]	0	(BT_1102 or BT_2062 or BT_3356)	0	1000	4	Glycolysis/Gluconeogenesis	PMID:73363, PMID: 6122675	Reversible reaction in Model SEED. ATP- and pyrophosphate-linked phosphofructokinase activity was shown Bacteroides species.	2.7.1.11
rxn00551	PFK(ppi)	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase, beta subunit (EC 2.7.1.90)	ppi[c] + f6p[c] => h[c] + pi[c] + fdp[c]	0	BT_0307	0	1000	2	Glycolysis/Gluconeogenesis	PMID: 7240086, PMID: 6122675	Reversible reaction in Model SEED. ATP- and pyrophosphate-linked phosphofructokinase activity was shown Bacteroides species.	2.7.1.90
rxn02314	PFK_2	Phosphofructokinase	atp[c] + tag6p-D[c] => h[c] + adp[c] + tagdp-D[c]	0	(BT_1102 or BT_2062 or BT_3356)	0	1000	4	Alternate Carbon Metabolism	PMID:73363, PMID: 6122675	Reversible reaction in Model SEED. ATP- and pyrophosphate-linked phosphofructokinase activity was shown Bacteroides species.	2.7.1.11
rxn01343	PFK_3	ATPSedoheptulose 7-phosphate 1-phosphotransferase	atp[c] + s7p[c] => h[c] + adp[c] + s17bp[c]	0	(BT_1102 or BT_2062 or BT_3356)	0	1000	4	Pentose Phosphate Pathway	PMID:73363, PMID: 6122675	ATP- and pyrophosphate-linked phosphofructokinase activity was shown Bacteroides species.	2.7.1.11
rxn00157	PFL	pyruvate formate lyase	pyr[c] + coa[c] => accoa[c] + for[c]	0	((BT_1055 and BT_2955) or (BT_4738 and BT_1055) or (BT_2955 and BT_2956) or (BT_4737 and BT_4738))	0	1000	3	Central Metabolism	PMID: 8048843, PMID: 17563350	Presence of enzyme in Bacteroides xylanolyticus confirmed (PMID: 8048843), B. thetaiotaomicron produces formate (PMID: 17563350).	2.3.1.54
rxn01485	PGAMT	phosphoglucosamine mutase	gam1p[c] <=> gam6p[c]	1	BT_3950	-1000	1000	4	Cell Envelope Biosynthesis	PMID:18931137, PMID:19460428, PMID:20974832.	Reaction is needed for LPS biosynthesis, based on H. pylori LPS biosynthesis (BIGG database). Annotation from The SEED.	5.4.2.10
rxn01101	PGCDr	3-Phospho-D-glycerateNAD+ 2-oxidoreductase	nad[c] + 3pg[c] <=> h[c] + nadh[c] + 3php[c]	1	(BT_1152 or BT_1207)	-1000	1000	2	Glycine, Serine, and Threonine Metabolism			1.1.1.95

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn00558	PGI	glucose-6-phosphate isomerase	g6p[c] <=> f6p[c]	1	BT_2124	-1000	1000	4	Glycolysis/Gluconeogenesis	PMID: 6804433	Measured by enzyme assay in B. thetaiotaomicron.	5.3.1.9
rxn01100	PGK	phosphoglycerate kinase	atp[c] + 3pg[c] <=> adp[c] + 13dpg[c]	1	BT_1672	-1000	1000	2	Glycolysis/Gluconeogenesis			2.7.2.3
rxn01476	PGL	6-phosphogluconolactonase	h2o[c] + 6pgl[c] => h[c] + 6pgc[c]	0	BT_1220	0	1000	2	Pentose Phosphate Pathway			3.1.1.31
rxn00980	PGLYCP	Phosphoglycolate phosphatase	h2o[c] + 2pglyc[c] => pi[c] + glyclt[c]	0	(BT_4184 or BT_4315)	0	1000	2	Alternate Carbon Metabolism			3.1.3.18
rxn01106	PGM	phosphoglycerate mutase	2pg[c] <=> 3pg[c]	1	(BT_1105 or BT_1660 or BT_3419)	-1000	1000	2	Glycolysis/Gluconeogenesis			5.4.2.1
rxn00704	PGMT	phosphoglucomutase	g1p[c] <=> g6p[c]	1	(BT_1548 or BT_3950)	-1000	1000	2	Glycolysis/Gluconeogenesis		SEED annotation curated manually based on NCBI Gene.	5.4.2.2
rxn01967	PGMT2	phosphoglucomutase	g1p-B[c] <=> g6p-B[c]	1	BT_2127	-1000	1000	2	Glycolysis/Gluconeogenesis			E5.4.2.2
rxn09101	PGPP120	phosphatidylglycerol phosphate phosphatase (n-C14:0)	h2o[c] + pgp120[c] => pi[c] + pg120[c]	0	BT_1525	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	3.1.3.27
rxn09102	PGPP140	phosphatidylglycerol phosphate phosphatase (n-C14:0)	h2o[c] + pgp140[c] => pi[c] + pg140[c]	0	BT_1525	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	3.1.3.27
rxn09104	PGPP160	phosphatidylglycerol phosphate phosphatase (n-C16:0)	h2o[c] + pgp160[c] => pi[c] + pg160[c]	0	BT_1525	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	3.1.3.27
rxn09106	PGPP180	phosphatidylglycerol phosphate phosphatase (n-C18:0)	h2o[c] + pgp180[c] => pi[c] + pg180[c]	0	BT_1525	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	3.1.3.27
rxn09107	PGPP181	phosphatidylglycerol phosphate phosphatase (n-C18:1)	h2o[c] + pgp181[c] => pi[c] + pg181[c]	0	BT_1525	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	3.1.3.27

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn10269	PGPPAI15	anteisopentadecanoyl-Phosphatidylglycerophosphate phosphohydrolase	h2o[c] + pgpai15[c] => pi[c] + pgai15[c]	0	BT_1525	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	3.1.3.27
rxn10266	PGPPAI17	anteisoheptadecanoyl-Phosphatidylglycerophosphate phosphohydrolase	h2o[c] + pgpai17[c] => pi[c] + pgai17[c]	0	BT_1525	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	3.1.3.27
rxn10267	PGPPI14	isotetradecanoyl-Phosphatidylglycerophosphate phosphohydrolase	h2o[c] + pgpi14[c] => pi[c] + pgi14[c]	0	BT_1525	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	3.1.3.27

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn10268	PGPPI15	isopentadecanoyl-Phosphatidylglycerophosphate phosphohydrolase	h2o[c] + pgpi15[c] => pi[c] + pgi15[c]	0	BT_1525	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	3.1.3.27
rxn10270	PGPPI16	isohexadecanoyl-Phosphatidylglycerophosphate phosphohydrolase	h2o[c] + pgpi16[c] => pi[c] + pgi16[c]	0	BT_1525	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	3.1.3.27
rxn10265	PGPPI17	isoheptadecanoyl-Phosphatidylglycerophosphate phosphohydrolase	h2o[c] + pgpi17[c] => pi[c] + pgi17[c]	0	BT_1525	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	3.1.3.27
rxn09108	PGSA120	Phosphatidylglycerol synthase (n-C12:0)	cdpdddecg[c] + glyc3p[c] => h[c] + cmp[c] + pgp120[c]	0	(BT_1523 or BT_4464)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	2.7.8.5

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn09109	PGSA140	Phosphatidylglycerol synthase (n-C14:0)	cdpdtdecg[c] + glyc3p[c] => h[c] + cmp[c] + pgp140[c]	0	(BT_1523 or BT_4464)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	2.7.8.5
rxn09111	PGSA160	Phosphatidylglycerol synthase (n-C16:0)	cdpdhdecg[c] + glyc3p[c] => h[c] + cmp[c] + pgp160[c]	0	(BT_1523 or BT_4464)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	2.7.8.5
rxn09113	PGSA180	Phosphatidylglycerol synthase (n-C18:0)	cdpdodecg[c] + glyc3p[c] => h[c] + cmp[c] + pgp180[c]	0	(BT_1523 or BT_4464)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	2.7.8.5
rxn09114	PGSA181	Phosphatidylglycerol synthase (n-C18:1)	cdpdodec11eg[c] + glyc3p[c] => h[c] + cmp[c] + pgp181[c]	0	(BT_1523 or BT_4464)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	2.7.8.5
rxn10263	PGSAAI15	anteisopentadecanoyl-CDPdiacylglycerolsn-glycerol-3-phosphate 3-phosphatidyltransferase	cdpdaipdecg[c] + glyc3p[c] => h[c] + cmp[c] + pgpai15[c]	0	(BT_1523 or BT_4464)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.7.8.5
rxn10260	PGSAAI17	anteisoheptadecanoyl-CDPdiacylglycerolsn-glycerol-3-phosphate 3-phosphatidyltransferase	cdpdaihpdecg[c] + glyc3p[c] => h[c] + cmp[c] + pgpai17[c]	0	(BT_1523 or BT_4464)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.7.8.5

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn10261	PGSAI14	isotetradecanoyl-CDPdiacylglycerolsn-glycerol-3-phosphate 3-phosphatidyltransferase	cdpditdecg[c] + glyc3p[c] => h[c] + cmp[c] + pgpi14[c]	0	(BT_1523 or BT_4464)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.7.8.5
rxn10262	PGSAI15	isopentadecanoyl-CDPdiacylglycerolsn-glycerol-3-phosphate 3-phosphatidyltransferase	cdpdipdecg[c] + glyc3p[c] => h[c] + cmp[c] + pgpi15[c]	0	(BT_1523 or BT_4464)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.7.8.5
rxn10264	PGSAI16	isohexadecanoyl-CDPdiacylglycerolsn-glycerol-3-phosphate 3-phosphatidyltransferase	cdpdihdecg[c] + glyc3p[c] => h[c] + cmp[c] + pgpi16[c]	0	(BT_1523 or BT_4464)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.7.8.5

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn10259	PGSAI17	isoheptadecanoyl-CDPdiacylglycerolsn-glycerol-3-phosphate 3-phosphatidyltransferase	cdpdihpdecg[c] + glyc3p[c] => h[c] + cmp[c] + pgpi17[c]	0	(BT_1523 or BT_4464)	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.7.8.5
	PHCHGS	L-1-Pyrroline-3-hydroxy-5-carboxylate spontaneous conversion to L-4-Hydroxyglutamate semialdehyde	h2o[c] + h[c] + 1p3h5c[c] <=> 4hglusa[c]	1		-1000	1000	1	Arginine and Proline Metabolism		BIGG database suggests that this reaction occurs spontaneously.	
	PHEARG1c	Hydrolysis of L-phenylalanyl-L-arginine	h2o[c] + phearg[c] <=> arg-L[c] + phe-L[c]	1	BT_1846	-1000	1000	4	Peptide Degradation	PMID: 22628297	B. thetaiotaomicron peptidase M49 was characterized and shown to hydrolyze Arg-Arg and Phe-Arg specifically.	
	PHEARGt	L-phenylalanyl-L-arginine transport via proton symport	h[e] + phearg[e] <=> h[c] + phearg[c]	1	(BT_0580 or BT_4385 or BT_1086)	-1000	1000	4	Transport, Extracellular	PMID: 22628297	B. thetaiotaomicron peptidase M49 was characterized and shown to hydrolyze Arg-Arg and Phe-Arg specifically.	
rxn05306	PHEt2r	L-phenylalanine reversible transport via proton symport	h[e] + phe-L[e] <=> h[c] + phe-L[c]	1		-1000	1000	1	Transport, Extracellular	Dworkin, M. and S. Falkow (2006). The prokaryotes : a handbook on the biology of bacteria. New York ; [London], Springer	B. thetaiotaomicron is weakly proteolytic, so a transport reaction for all amino acids is assumed to be present.	
rxn00493	PHETA1	phenylalanine transaminase	akg[c] + phe-L[c] <=> glu-L[c] + phpyr[c]	1	(BT_0202 or BT_3935)	-1000	1000	2	Tyrosine, Tryptophan, and Phenylalanine Metabolism			2.6.1.58

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05145	PIabc	phosphate transport via ABC system	h2o[c] + atp[c] + pi[e] => h[c] + 2 pi[c] + adp[c]	0	((BT_1321 and BT_1322 and BT_1323 and BT_1324) or (BT_1321 and BT_1322 and BT_1323 and BT_0009))	0	1000	4	Transport, Extracellular	PMID:4472783	Reversible reaction in Model SEED. B. thetaiotaomicron requires inorganic phosphate for growth.	
rxn05312	PIt6	Phosphate transport out via proton symport	h[c] + pi[c] => h[e] + pi[e]	0	BT_4637	0	1000	2	Transport, Extracellular			
rxn05313	PIt8i	phosphate transport in via Na+ symporter, irreversible	1.5 na1[e] + pi[e] => pi[c] + 1.5 na1[c]	0	BT_2528	0	1000	2	Transport, Extracellular	PMID:4472783	B. thetaiotaomicron requires inorganic phosphate.	
rxn05144	PLPS	Pyridoxine biosynthesis glutamine amidotransferase	ru5p-D[c] + gln-L[c] + g3p[c] => 3 h2o[c] + h[c] + glu-L[c] + pi[c] + pydx5p[c]	0		0	1000	1	Vitamin B6 Metabolism		Reaction is reversible in SEED. Added by Model SEED during auto-completion step in pipeline.	2.4.2.-
	PMACPME	Cleavage of ester from pimeloyl-ACP methyl ester (BioH)	h2o[c] + pmACPm[c] => h[c] + pmACP[c] + meoh[c]	0		0	1000	2	Biotin Metabolism	PMID:20693992, PMID:4853401	Based on biotin synthesis described in PMID:20693992 for E. coli. Gene is not known, but the gap was filled to complete biotin synthesis pathway (biotin is not required by B. thetaiotaomicron, see PMID:4853401).	
rxn01329	PMANM	phosphomannomutase	man1p[c] <=> man6p[c]	1	(BT_3950 or BT_1548)	-1000	1000	2	Alternate Carbon Metabolism		Based on annotation from NCBI Gene (last updated 21.05.11)	5.4.2.8
rxn05039	PMDPHT	pyrimidine phosphatase	h2o[c] + 5aprbu[c] => pi[c] + 4r5au[c]	0		0	1000	1	Cofactor and Prosthetic Group Biosynthesis		Added by Model SEED during auto-completion step in pipeline.	3.1.3.-
rxn03108	PMPK	phosphomethylpyrimidine kinase	atp[c] + 4ampm[c] => adp[c] + 2mahmp[c]	0	BT_0790	0	1000	2	Cofactor and Prosthetic Group Biosynthesis		Reversible reaction in Model SEED	2.7.4.7

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05458	PMTCOATA	hexadecanoyl-ACP[acyl-carrier-protein] transferase	coa[c] + palmACP[c] <=> ACP[c] + pmtcoa[c]	1	BT_0789	-1000	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.180
rxn01646	PNP	purine-nucleoside phosphorylase	pi[c] + rnam[c] <=> h[c] + r1p[c] + ncam[c]	1	(BT_1881 or BT_4554)	-1000	1000	2	NAD Metabolism			3.4.2.1
rxn12510	PNTK	pantothenate kinase	atp[c] + pnto-R[c] => h[c] + adp[c] + 4ppan[c]	0	BT_4366	0	1000	2	Cofactor and Prosthetic Group Biosynthesis		Reversible reaction in Model SEED	2.7.1.33
	PNTOt2	Pantothenate reversible transport via proton symport	h[e] + pnto-R[e] <=> h[c] + pnto-R[c]	1		-1000	1000	2	Transport, Extracellular	PMID: 19748469	B. thetaiotaomicron mutants in panthotenate biosynthesis are not essential in vitro on tryptone-yeast extract-glucose medium, suggesting that B. thetaiotaomicron can uptake panthotenate from yeast extract.	
rxn05938	POR4	Pyruvate-flavodoxin oxidoreductase (EC 1.2.7.-)	co2[c] + accoa[c] + fdxrd[c] <=> h[c] + pyr[c] + coa[c] + fdxox[c]	1	BT_1747	-1000	1000	4	Central Metabolism	PMID: 11260473		1.2.7.1

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn09167	POX	pyruvate oxidase	h2o[c] + pyr[c] + q8[c] => co2[c] + ac[c] + q8h2[c]	0	(BT_1820 and BT_1822)	0	1000	4	Central Metabolism	PMID: 19525515, PMID: 893348	PMID: 19525515 demonstrates presence of this enzyme. It is unclear whether B. thetaiotaomicron uses ubiquinone, menaquinone or both. PMID: 893348 states that only menaquinone is present. Also, this enzyme is reported by KEGG not to accept menaquinone. However, ubiquinone-using enzymes are annotated in the B. thetaiotaomicron genome.	1.2.2.2
	PPA_1	inorganic diphosphatase (one proton translocation)	h2o[c] + ppi[c] => 2 pi[c] + h[e]	0	BT_3411	0	1000	2	Central Metabolism	PMID:10523139	Annotation based on NCBI Gene (last updated 28.05.11). Can cleave pyrophosphate to two phosphates; can generate a proton motive force and drive pyrophosphate synthesis when PMF is sufficient. General review in PMID:10523139.	3.6.1.1, T3.A.10
rxn00985	PPAKr	Propionate kinase	adp[c] + ppap[c] <=> atp[c] + ppa[c]	1	BT_3693	-1000	1000	3	Alternate Carbon Metabolism	PMID: 16349240		2.7.2.1
	PPAtr	Propionate transport, diffusion	ppa[e] <=> ppa[c]	1		-1000	1000	2	Transport, Extracellular	PMID:19321416, PMID:12740060	Bacteroides species are well established to produce short-chain fatty acids (SCFAs).	
rxn02341	PPCDC	phosphopantothenoylcysteine decarboxylase	h[c] + 4ppcys[c] => co2[c] + pan4p[c]	0	BT_1362	0	1000	2	Cofactor and Prosthetic Group Biosynthesis			4.1.1.36

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn00247	PPCKr	phosphoenolpyruvate carboxykinase	atp[c] + oaa[c] <=> co2[c] + adp[c] + pep[c]	1	BT_2790	-1000	1000	4	TCA Cycle	PMID:11260473, PMID:148460	Literature suggests that this reaction runs in the direction of oxaloacetate. The reaction was made reversible due to uncertainity.	4.1.1.49
rxn00151	PPDK	Pyruvate phosphate dikinase	pyr[c] + pi[c] + atp[c] => h[c] + pep[c] + amp[c] + ppi[c]	0	BT_0644	0	1000	2	Glycolysis/Gluconeogenesis		Reversible reaction in Model SEED	2.7.9.1
rxn00242	PPGPPDP	guanosine-3',5'-bis(diphosphate) 3'-diphosphatase	h2o[c] + ppgpp[c] => ppi[c] + gdp[c]	0	BT_3998	0	1000	2	Cofactor and Prosthetic Group Biosynthesis			3.1.7.2
	PPK2	polyphosphate kinase	atp[c] + ppi[c] => adp[c] + pppi[c]	0	(BT_0541 or BT_2019)	0	1000	2	Central Metabolism		Added based on annotation from NCBI Gene.	2.7.4.1
rxn09177	PPNCL2	phosphopantothenate-cysteine ligase	cys-L[c] + ctp[c] + 4ppan[c] => h[c] + ppi[c] + cmp[c] + 4ppcys[c]	0	BT_1362	0	1000	2	Cofactor and Prosthetic Group Biosynthesis			6.3.2.5
rxn12512	PPNCL3	phosphopantothenate-cysteine ligase	atp[c] + cys-L[c] + 4ppan[c] => h[c] + amp[c] + ppi[c] + 4ppcys[c]	0	BT_1362	0	1000	2	Cofactor and Prosthetic Group Biosynthesis			6.3.2.5
rxn01268	PPND	prephenate dehydrogenase	nad[c] + pphn[c] => co2[c] + nadh[c] + 34hpp[c]	0	BT_3933	0	1000	2	Tyrosine, Tryptophan, and Phenylalanine Metabolism			1.3.1.12
rxn01269	PPND2	PrephenateNADP+ oxidoreductase(decarboxylating)	nadp[c] + pphn[c] => nadph[c] + co2[c] + 34hpp[c]	0	BT_3933	0	1000	2	Tyrosine, Tryptophan, and Phenylalanine Metabolism			1.3.1.13
rxn01000	PPNDH	prephenate dehydratase	h[c] + pphn[c] => h2o[c] + co2[c] + phpyr[c]	0	BT_3936	0	1000	2	Tyrosine, Tryptophan, and Phenylalanine Metabolism			4.2.1.51

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn10199	PPTGS	Peptidoglycan subunit synthesis	uaagmda[c] => h[c] + peptido_EC[c] + udcpdp[c]	0	(BT_3453 or BT_0943 or BT_0162 or BT_2501)	0	1000	2	Cell Envelope Biosynthesis		Drawn from the E. coli iJR904 reconstruction for lack of better information.	
rxn03892	PPTT	trans-pentaprenyltranstransferase	ipdp[c] + pendp[c] => ppi[c] + hexdp[c]	0	(BT_3261 or BT_2058)	0	1000	2	Cofactor and Prosthetic Group Biosynthesis		Added manually to BIGG database based on SEED database	2.5.1.33
rxn02895	PRAGS	phosphoribosylglycinamide synthetase	atp[c] + gly[c] + pram[c] => h[c] + pi[c] + adp[c] + gar[c]	0	BT_3253	0	1000	2	Purine and Pyrimidine Biosynthesis			6.3.4.13
rxn02508	PRAI	phosphoribosylanthranilate isomerase	pran[c] <=> 2cpr5p[c]	1	BT_0528	-1000	1000	2	Purine and Pyrimidine Biosynthesis			5.3.1.24
rxn02937	PRAIS	phosphoribosylaminoimidazole synthase	atp[c] + fpram[c] => 2 h[c] + pi[c] + adp[c] + air[c]	0	BT_4211	0	1000	2	Purine and Pyrimidine Biosynthesis		Reversible reaction in Model SEED	6.3.3.1
rxn02835	PRAMPC	phosphoribosyl-AMP cyclohydrolase	h2o[c] + prbamp[c] => prfp[c]	0	BT_1377	0	1000	2	Histidine Metabolism		Reviewed bifunctional phosphoribosyl-AMP cyclohydrolase/phosphoribosyl-ATP pyrophosphatase (NCBI Gene). Reversible reaction in SEED.	3.5.4.19
rxn03147	PRASCSi	phosphoribosylaminoimidazolesuccinocarboxamide synthase	atp[c] + asp-L[c] + 5aizc[c] => h[c] + pi[c] + adp[c] + 25aics[c]	0	BT_4217	0	1000	2	Purine and Pyrimidine Biosynthesis			6.3.2.6
rxn02834	PRATPP	phosphoribosyl-ATP pyrophosphatase	h2o[c] + prbatp[c] => h[c] + ppi[c] + prbamp[c]	0	BT_1377	0	1000	2	Histidine Metabolism		Reviewed bifunctional phosphoribosyl-AMP cyclohydrolase/ phosphoribosyl-ATP-pyrophosphatase (NCBI Gene)	3.6.1.31
rxn03084	PRFGS	phosphoribosylformylglycinamidine synthase	h2o[c] + atp[c] + gln-L[c] + fgam[c] => h[c] + glu-L[c] + pi[c] + adp[c] + fpram[c]	0	BT_1733	0	1000	2	Purine and Pyrimidine Biosynthesis			6.3.5.3

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn03175	PRMICI	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) methylideneamino)imidazole-4-carboxamide isomerase	prfp[c] <=> prlp[c]	1	BT_1379	-1000	1000	2	Histidine Metabolism			5.3.1.16
rxn00929	PRO1x	L-ProlineNAD+ 5-oxidoreductase	nad[c] + pro-L[c] => 2 h[c] + nadh[c] + 1pyr5c[c]	0	(BT_1902 or BT_3757)	0	1000	2	Arginine and Proline Metabolism		Reversible reaction in Model SEED	1.5.1.2
rxn09188	PROD2	Proline dehydrogenase	pro-L[c] + fad[c] => h[c] + 1pyr5c[c] + fadh2[c]	0	BT_3115	0	1000	2	Arginine and Proline Metabolism	PMID: 18369526	Reversible reaction in Model SEED	1.5.99.8
rxn02359	PROD3	Proline dehydrogenase (trans-4-Hydroxy-L-proline)	fad[c] + 4hpro-LT[c] <=> h[c] + 1p3h5c[c] + fadh2[c]	1	BT_3115	-1000	1000	2	Arginine and Proline Metabolism	PMID:19140736	Ref. PMID:19140736 suggests FAD as cofactor. It is not known if the reaction is dependent on FAD in B. thetaiotaomicron.	1.5.99.8
	PROGLYt	L-prolylglycine transport via proton symport	h[e] + progly[e] => h[c] + progly[c]	0	(BT_0580 or BT_4385 or BT_1086)	0	1000	2	Transport, Extracellular		Genes added based on TransportDB (last consulted 06.06.12).	
rxn05221	PROt4r	proline transporter	na1[e] + pro-L[e] <=> na1[c] + pro-L[c]	1	BT_0182	-1000	1000	2	Transport, Extracellular			
rxn00770	PRPPS	phosphoribosylpyrophosphate synthetase	atp[c] + r5p[c] <=> h[c] + amp[c] + prpp[c]	1	BT_0748	-1000	1000	2	Pentose Phosphate Pathway			2.7.6.1
rxn02476	PSCVT	3-phosphoshikimate 1-carboxyvinyltransferase	pep[c] + skm5p[c] <=> pi[c] + 3psme[c]	1	BT_2186	-1000	1000	2	Tyrosine, Tryptophan, and Phenylalanine Metabolism			2.5.1.19
rxn09197	PSD120	Phosphatidylserine decarboxylase (n-C12:0)	h[c] + ps120[c] => co2[c] + pe120[c]	0	BT_2231	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Reversible reaction in Model SEED. The fatty acid composition of B. thetaiotaomicron was determined experimentally.	4.1.1.65

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn09198	PSD140	Phosphatidylserine decarboxylase (n-C14:0)	h[c] + ps140[c] => co2[c] + pe140[c]	0	BT_2231	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Reversible reaction in Model SEED. The fatty acid composition of B. thetaiotaomicron was determined experimentally.	4.1.1.65
rxn09200	PSD160	Phosphatidylserine decarboxylase (n-C16:0)	h[c] + ps160[c] => co2[c] + pe160[c]	0	BT_2231	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Reversible reaction in Model SEED. The fatty acid composition of B. thetaiotaomicron was determined experimentally.	4.1.1.65
rxn09202	PSD180	Phosphatidylserine decarboxylase (n-C18:0)	h[c] + ps180[c] => co2[c] + pe180[c]	0	BT_2231	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Reversible reaction in Model SEED. The fatty acid composition of B. thetaiotaomicron was determined experimentally.	4.1.1.65
rxn09203	PSD181	Phosphatidylserine decarboxylase (n-C18:1)	h[c] + ps181[c] => co2[c] + pe181[c]	0	BT_2231	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Reversible reaction in Model SEED. The fatty acid composition of B. thetaiotaomicron was determined experimentally.	4.1.1.65
rxn10236	PSDAI15	anteisopentadecanoyl-phosphatidylserine decarboxylase	h[c] + psai15[c] => co2[c] + peai15[c]	0	BT_2231	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	4.1.1.65

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn10233	PSDAI17	anteisoheptadecanoyl-phosphatidylserine decarboxylase	h[c] + psai17[c] => co2[c] + peai17[c]	0	BT_2231	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	4.1.1.65
rxn10234	PSDI14	isotetradecanoyl-phosphatidylserine decarboxylase	h[c] + psi14[c] => co2[c] + pei14[c]	0	BT_2231	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	4.1.1.65
rxn10235	PSDI15	isopentadecanoyl-phosphatidylserine decarboxylase	h[c] + psi15[c] => co2[c] + pei15[c]	0	BT_2231	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	4.1.1.65

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn10237	PSDI16	isohexadecanoyl-phosphatidylserine decarboxylase	h[c] + psi16[c] => co2[c] + pei16[c]	0	BT_2231	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	4.1.1.65
rxn10232	PSDI17	isoheptadecanoyl-phosphatidylserine decarboxylase	h[c] + psi17[c] => co2[c] + pei17[c]	0	BT_2231	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	4.1.1.65
rxn02914	PSERTr	3-Phosphoserine2-oxoglutarate aminotransferase	akg[c] + pser-L[c] <=> glu-L[c] + 3php[c]	1	BT_1153	-1000	1000	2	Glycine, Serine, and Threonine Metabolism			2.6.1.52
rxn00420	PSP_L	phosphoserine phosphatase (L-serine)	h2o[c] + pser-L[c] => pi[c] + ser-L[c]	0	BT_0832	0	1000	2	Glycine, Serine, and Threonine Metabolism		Putative annotation (NCBI)	3.1.3.3
rxn09205	PSSA120	Phosphatidylserine syntase (n-C12:0)	ser-L[c] + cdpdddecg[c] => h[c] + cmp[c] + ps120[c]	0	BT_2232	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	2.7.8.8
rxn09206	PSSA140	Phosphatidylserine syntase (n-C14:0)	ser-L[c] + cdpdtdecg[c] => h[c] + cmp[c] + ps140[c]	0	BT_2232	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	2.7.8.8

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn09208	PSSA160	Phosphatidylserine syntase (n-C16:0)	ser-L[c] + cdpdhdecg[c] => h[c] + cmp[c] + ps160[c]	0	BT_2232	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	2.7.8.8
rxn09210	PSSA180	Phosphatidylserine syntase (n-C18:0)	ser-L[c] + cdpdodecg[c] => h[c] + cmp[c] + ps180[c]	0	BT_2232	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	2.7.8.8
rxn09211	PSSA181	Phosphatidylserine syntase (n-C18:1)	ser-L[c] + cdpdodec11eg[c] => h[c] + cmp[c] + ps181[c]	0	BT_2232	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of B. thetaiotaomicron was determined experimentally.	2.7.8.8
rxn10230	PSSAAI15	anteisopentadecanoyl-CDPdiacylglycerol-serine O-phosphatidyltransferase	ser-L[c] + cdpdaipdecg[c] => h[c] + cmp[c] + psai15[c]	0	BT_2232	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.7.8.8
rxn10227	PSSAAI17	anteisoheptadecanoyl-CDPdiacylglycerol-serine O-phosphatidyltransferase	ser-L[c] + cdpdaihpdecg[c] => h[c] + cmp[c] + psai17[c]	0	BT_2232	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.7.8.8

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn10228	PSSAI14	isotetradecanoyl-CDPdiacylglycerol-serine O-phosphatidyltransferase	ser-L[c] + cdpditdecg[c] => h[c] + cmp[c] + psi14[c]	0	BT_2232	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.7.8.8
rxn10229	PSSAI15	isopentadecanoyl-CDPdiacylglycerol-serine O-phosphatidyltransferase	ser-L[c] + cdpdipdecg[c] => h[c] + cmp[c] + psi15[c]	0	BT_2232	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.7.8.8
rxn10231	PSSAI16	isohexadecanoyl-CDPdiacylglycerol-serine O-phosphatidyltransferase	ser-L[c] + cdpdihdecg[c] => h[c] + cmp[c] + psi16[c]	0	BT_2232	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.7.8.8

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn10226	PSSAI17	isoheptadecanoyl-CDPdiacylglycerol-serine O-phosphatidyltransferase	ser-L[c] + cdpdihpdecg[c] => h[c] + cmp[c] + psi17[c]	0	BT_2232	0	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.7.8.8
rxn00670	PTA2	Phosphate acetyltransferase	pi[c] + ppcoa[c] => coa[c] + ppap[c]	0	BT_3692	0	1000	2	Alternate Carbon Metabolism		Reversible reaction in Model SEED	2.3.1.8
rxn00173	PTAr	phosphotransacetylase	pi[c] + accoa[c] <=> coa[c] + actp[c]	1	BT_3692	-1000	1000	2	Central Metabolism			2.3.1.8
rxn02175	PTPAT	Phosphopantetheine adenylyltransferase (EC 2.7.7.3)	h[c] + atp[c] + pan4p[c] <=> ppi[c] + dpcoa[c]	1	BT_3034	-1000	1000	2	Cofactor and Prosthetic Group Biosynthesis			2.7.7.3
rxn05163	PTRCabc	Putrescine-ABC transport	h2o[c] + atp[c] + ptrc[e] => h[c] + pi[c] + adp[c] + ptrc[c]	0	(BT_1288 and BT_1289 and BT_1290 and BT_1291)	0	1000	2	Transport, Extracellular			TC 3.A.1.11.1
	PTRCtex2	putrescine excretion (cytosol to extracellular)	ptrc[c] => ptrc[e]	0		0	1000	2	Transport, Extracellular	PMID:10801923	B. thetaiotaomicron secretes putrescine and spermidine.	
	PULLe	pullulane hydrolysis by alpha-1,6 pullulanase and alpha-amylase	399 h2o[e] + pullulan1200[e] => 400 malttr[e]	0	((BT_3698 and BT_3701 and BT_3702) or (BT_3701 and BT_3702 and BT_4689) or (BT_1663 and BT_3701 and BT_3702))	0	1000	4	Plant Polysaccharide Degradation	PMID:10986238, PMID:2722747, PMID:8955399, PMID: 18981178, PMID:18611383	The starch utilization system of B. thetaiotaomicron is well characterized.	
rxn01138	PUNP1	purine-nucleoside phosphorylase (Adenosine)	pi[c] + adn[c] <=> ade[c] + r1p[c]	1	(BT_1881 or BT_4554)	-1000	1000	2	Nucleotide Salvage Pathway			3.4.2.1
rxn01859	PUNP2	purine-nucleoside phosphorylase (Deoxyadenosine)	pi[c] + dad-2[c] <=> ade[c] + 2dr1p[c]	1	(BT_1881 or BT_4554)	-1000	1000	2	Nucleotide Salvage Pathway			3.4.2.1

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn01548	PUNP3	purine-nucleoside phosphorylase (Guanosine)	pi[c] + gsn[c] <=> gua[c] + r1p[c]	1	(BT_1881 or BT_4554)	-1000	1000	2	Nucleotide Salvage Pathway			3.4.2.1
rxn01446	PUNP4	purine-nucleoside phosphorylase (Deoxyguanosine)	pi[c] + dgsn[c] <=> 2dr1p[c] + gua[c]	1	(BT_1881 or BT_4554)	-1000	1000	2	Nucleotide Salvage Pathway			3.4.2.1
rxn01358	PUNP5	purine-nucleoside phosphorylase (Inosine)	pi[c] + ins[c] <=> hxan[c] + r1p[c]	1	(BT_1881 or BT_4554)	-1000	1000	2	Nucleotide Salvage Pathway			3.4.2.1
rxn01985	PUNP6	purine-nucleoside phosphorylase (Deoxyinosine)	pi[c] + din[c] <=> 2dr1p[c] + hxan[c]	1	(BT_1881 or BT_4554)	-1000	1000	2	Nucleotide Salvage Pathway			3.4.2.1
rxn01649	PUNP7	purine-nucleoside phosphorylase (Xanthosine)	pi[c] + xtsn[c] <=> r1p[c] + xan[c]	1	(BT_1881 or BT_4554)	-1000	1000	2	Nucleotide Salvage Pathway			3.4.2.1
rxn00183	PUTA3	puta3	h2o[c] + nad[c] + glu5sa[c] => 2 h[c] + glu-L[c] + nadh[c]	0	BT_3115	0	1000	2	Glutamate Metabolism		Reversible reaction in Model SEED	1.5.1.12
rxn00208	PYAM5PO	pyridoxamine 5'-phosphate oxidase	h2o[c] + o2[c] + pyam5p[c] => nh4[c] + h2o2[c] + pydx5p[c]	0	BT_1577	0	1000	2	Cofactor and Prosthetic Group Biosynthesis			1.4.3.5
rxn01807	PYDAMK	pyridoxamine kinase	atp[c] + pydam[c] => h[c] + adp[c] + pyam5p[c]	0	BT_4458	0	1000	2	Vitamin B6 Metabolism		Reversible reaction in Model SEED	2.7.1.35
rxn00124	PYDXK	pyridoxal kinase	atp[c] + pydx[c] => h[c] + adp[c] + pydx5p[c]	0	BT_4458	0	1000	2	Vitamin B6 Metabolism		Reversible reaction in Model SEED	2.7.1.35
rxn01396	PYDXNK	pyridoxine kinase	atp[c] + pydxn[c] => h[c] + adp[c] + pdx5p[c]	0	BT_4458	0	1000	2	Vitamin B6 Metabolism		Reversible reaction in Model SEED	2.7.1.35
rxn01252	PYDXNO	pyridoxine oxidase	o2[c] + pydxn[c] <=> h2o2[c] + pydx[c]	1	BT_1577	-1000	1000	2	Vitamin B6 Metabolism			1.4.3.5

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	PYDXNtr	pyridoxine transport via diffusion	pydxn[e] <=> pydxn[c]	1		-1000	1000	2	Transport, Extracellular	PMID:894368, PMID:9167138, PMID:9562034	It is well established that the gut microbiota produces B vitamins in mammals. Germ-free rats fed a pyridoxine-free diet suffer far more severe deficiency symptoms than conventional rats (PMID:894368). Pyridoxine transport by B. thetaiotaomicron is therefore assumed to occur.	
	PYDXO	pyridoxal oxidase	2 h2o[c] + nh4[c] + 0.5 o2[c] + pydx[c] <=> 2 h2o2[c] + pydam[c]	1	BT_1577	-1000	1000	2	Vitamin B6 Metabolism			1.4.3.5
rxn00148	PYK	pyruvate kinase	h[c] + adp[c] + pep[c] => pyr[c] + atp[c]	0	BT_2841	0	1000	2	Glycolysis/Gluconeogenesis	PMID:148460	Reversible reaction in SEED. The enzyme was demonstrated by enzyme assay in the close relative B. fragilis.	2.7.1.40
	PYRt2r	pyruvate reversible transport via proton symport	h[e] + pyr[e] <=> h[c] + pyr[c]	1		-1000	1000	2	Transport, Extracellular	PMID:11260473	No gene found, but B. thetaiotaomicronwas shown to secrete pyruvate.	
	QMO3	quinol monooxygenase (menaquinol 8)	mql8[c] + 2 o2[c] => 2 h[c] + mqn8[c] + 2 o2s[c]	0	(BT_3054 and BT_3055)	0	1000	2	Central Metabolism	PMID:7649986, PMID:11260473	The reaction seems to be carried out by fumarate reductase. When it is exposed to air, fumarate reductase generates oxygen free radicals through autooxidation. The electrons seem to pass from reduced menaquinone via Fe-S clusters and a flavin to oxygen.	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn02988	QULNS	quinolinate synthase	dhap[c] + iasp[c] => 2 h2o[c] + pi[c] + quln[c]	0	BT_3164	0	1000	2	Cofactor and Prosthetic Group Biosynthesis			4.1.99.-
	RAFFabc	raffinose transport via ABC system (import)	h2o[c] + atp[c] + raffin[e] => h[c] + pi[c] + adp[c] + raffin[c]	0		0	1000	2	Transport, Extracellular	PMID:2557798	B. thetaiotaomicron can use raffinose as carbon source.	
rxn00818	RAFGH	Raffinose galactohydrolase	h2o[c] + raffin[c] => gal[c] + sucr[c]	0	(BT_1871 or BT_2851 or BT_3065 or BT_3131 or BT_3133 or BT_3410)	0	1000	4	Plant Polysaccharide Degradation	PMID:19646996, PMID:18848471, PMID:2557798	B. thetaiotaomicron can use raffinose as carbon source.	3.2.1.22
rxn01737	RAFH	raffinose hydrolyzing enzyme	h2o[c] + raffin[c] => fru[c] + melib[c]	0	BT_1765	0	1000	4	Plant Polysaccharide Degradation	PMID: 20603004, PMID:2557798	Reversible reaction in Model SEED. B. thetaiotaomicron can use raffinose as carbon source.	3.2.1.26
rxn00392	RBFK	riboflavin kinase	atp[c] + ribflv[c] => h[c] + adp[c] + fmn[c]	0	BT_2543	0	1000	2	Cofactor and Prosthetic Group Biosynthesis		Reversible reaction in Model SEED	2.7.1.26
rxn03080	RBFSa	riboflavin synthase	db4p[c] + 4r5au[c] => 2 h2o[c] + pi[c] + dmlz[c]	0	BT_4253	0	1000	3	Cofactor and Prosthetic Group Biosynthesis	PMID:4853401	B. thetaiotaomicron does not require riboflavin in medium, therefore presence of biosynthesis pathway is likely.	2.5.1.9
rxn00048	RBFSb	riboflavin synthase	2 dmlz[c] => ribflv[c] + 4r5au[c]	0	BT_1317	0	1000	3	Cofactor and Prosthetic Group Biosynthesis	PMID:4853401	B. thetaiotaomicron does not require riboflavin in medium, therefore presence of biosynthesis pathway is likely.	2.5.1.9
rxn00772	RBK	ribokinase	atp[c] + rib-D[c] => h[c] + adp[c] + r5p[c]	0	(BT_2799 or BT_3576 or (BT_2803 and BT_2804))	0	1000	2	Pentose Phosphate Pathway			2.7.1.15
rxn01114	RBK_D	D-ribulokinase	atp[c] + rbl-D[c] => h[c] + ru5p-D[c] + adp[c]	0	BT_0350	0	1000	2	Pentose and Glucuronate Interconversions			2.7.1.47

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn01763	RBK_L1	L-ribulokinase (L-ribulose)	atp[c] + rbl-L[c] => h[c] + adp[c] + ru5p-L[c]	0	BT_0350	0	1000	4	Alternate Carbon Metabolism	PMID:16887504	Needed for L-arabinose utilization, which can serve as sole carbon source for B. thetaiotaomicron.	2.7.1.16
rxn04082	RBP4E	L-ribulose-phosphate 4-epimerase	ru5p-L[c] <=> xu5p-D[c]	1	BT_0353	-1000	1000	2	Alternate Carbon Metabolism			5.1.3.4
	RFA_BT	Formation of lipidA and sugar core for LPS	adphep-DD[c] + adphep-LD[c] + kdolipid4L_bt[c] + 2 udpg[c] + udpgal[c] + adphep7p-LD[c] => 3 adp[c] + 3 udp[c] + core_lps_bt[c]	0		0	1000	2	Lipopolysaccharide Biosynthesis	PMID:18931137, PMID:19460428, PMID:20974832	Based on H. pylori LPS biosynthesis (BIGG database), as in the P. gingivalis reconstruction (PMID:18931137). P. gingivalis' LPS is similar in structure to the Bacteroides LPS. Based on structural information taken from (PMID:19460428, PMID:20974832).	
	RFAC_HP	RFAC HP	atp[c] + adphep-LD[c] => h[c] + adp[c] + adphep7p-LD[c]	0		0	1000	2	Lipopolysaccharide Biosynthesis	PMID:18931137, PMID:19460428, PMID:20974832	Based on H. pylori LPS biosynthesis (BIGG database), as in the P. gingivalis reconstruction (PMID:18931137). P. gingivalis' LPS is similar in structure to the Bacteroides LPS. Based on structural information taken from (PMID:19460428, PMID:20974832).	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	RHAMNOGALURASEe_I	Rhamnogalacturonan I degradation, extracellular	979 h2o[e] + rhamnogalurI[e] => 30 arab-L[e] + 120 gal[e] + 200 rmn[e] + 620 galur[e] + 10 xyl-D[e]	0	(BT_1021 and BT_3662 and (BT_4152 or BT_0983 or BT_0992 or BT_0993 or BT_0996) and (BT_1001 or BT_1013 or BT_1019) and (BT_4146 or BT_4149 or BT_4153 or BT_4155 or BT_4183 or BT_4115 or BT_4116 or BT_1011 or BT_1018) and (BT_4150 or BT_4173) and BT_4175 and (BT_4109 or BT_4110) and ((BT_4670 and BT_4671) or (BT_4164 and BT_4165) or (BT_4113 and BT_4114) or (BT_1028 and BT_1029) or (BT_1683 and BT_1683) or (BT_3670 and BT_3671)))	0	1000	4	Plant Polysaccharide Degradation	PMID: 22205877	B. thetaiotaomicron grows on rhamnogalacturonan I. The genes included in the GPR are upregulated during growth. Enzymes/ proteins assumed to be involved: arabinosidase, xylosidase, galactosidase, galacturonisidase, rhamnogalactorunan esterase, rhamnogalacturonan lyase, pectinesterase, susC/ SusD	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	RHAMNOGALURASEe_II	Rhamnogalacturonan II degradation, extracellular	52 h2o[e] + rhamnogalurII[e] => 2 fuc-L[e] + 6 arab-L[e] + 3 gal[e] + 8 rmn[e] + 19 galur[e] + 3 glcur[e] + 2 2omfuc[e] + 2 2omxyl[e] + 2 3ddlhept[e] + acerA[e] + 3 apio-D[e] + 2 kdo[e]	0	(BT_1021 or BT_0348) and (BT_3662 or BT_3663) and BT_1011 and BT_3664 and BT_3665 and (BT_4152 or BT_0983 or BT_0992 or BT_0993 or BT_0996) and (BT_1001 or BT_1013 or BT_1019) and (BT_4146 or BT_4149 or BT_4153 or BT_4155 or BT_4183 or BT_4115 or BT_4116 or BT_1018) and (BT_4150 or BT_4173) and BT_4175 and (BT_4109 or BT_4110) and ((BT_4670 and BT_4671) or (BT_4164 and BT_4165) or (BT_4113 and BT_4114) or (BT_1028 and BT_1029) or (BT_1683 and BT_1683) or (BT_3670 and BT_3671) or (BT_1024 and BT_1025))	0	1000	4	Plant Polysaccharide Degradation	PMID: 22205877	B. thetaiotaomicron grows on rhamnogalacturonan I. I'm not sure what happens to the rare sugars included in RGII. The genes included in the GPR are upregulated during growth. Enzymes/ proteins assumed to be involved: arabinosidase, xylosidase, galactosidase, fucosidase, beta-glucosidase, galacturonisidase, glucuronidase rhamnogalactorunan esterase, rhamnogalacturonan lyase, pectinesterase, susC/ SusD	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	RIBFLVt2r	riboflavin transport in via proton symport reversible	h[e] + ribflv[e] <=> h[c] + ribflv[c]	1		-1000	1000	2	Transport, Extracellular	PMID:9167138	Riboflavin is synthesized by the gut bacterial flora of the colon.	
	RIBt2r	ribose transport in via proton symporter, reversible	h[e] + rib-D[e] <=> h[c] + rib-D[c]	1		-1000	1000	2	Transport, Extracellular	PMID: 17579514	Bacteroides thetaiotaomicron grows on D-ribose.	
rxn01761	RMI	L-rhamnose isomerase	rmn[c] <=> rml[c]	1	BT_3764	-1000	1000	4	Alternate Carbon Metabolism	PMID: 18848625	The rhamnose utilization gene cluster was characterized.	5.3.1.14
rxn02161	RMK	rhamnulokinase	atp[c] + rml[c] => h[c] + adp[c] + rml1p[c]	0	BT_3763	0	1000	4	Alternate Carbon Metabolism	PMID: 18848625	Reversible reaction in Model SEED. The rhamnose utilization gene cluster was characterized.	2.7.1.5
rxn01390	RMK2	Rhamnulokinase	atp[c] + xylu-L[c] <=> h[c] + adp[c] + xu1p-L[c]	1	BT_3763	-1000	1000	4	Alternate Carbon Metabolism	PMID: 18848625	The rhamnose utilization gene cluster was characterized.	2.7.1.5
rxn05646	RMNt	L-rhamnose transport via proton symport	h[e] + rmn[e] => h[c] + rmn[c]	0	(BT_2953 or BT_3765)	0	1000	4	Alternate Carbon Metabolism	PMID: 18848625 (BT_3765)	B. thetaiotaomicron grows on L-rhamnose.	
rxn01621	RMPA	Rhamnulose-1-phosphate aldolase	rml1p[c] <=> dhap[c] + lald-L[c]	1	BT_3766	-1000	1000	4	Alternate Carbon Metabolism	PMID: 18848625	The rhamnose utilization gene cluster was characterized.	4.1.2.19
rxn05232	RNTR1	ribonucleoside-triphosphate reductase (ATP)	atp[c] + trdrd[c] => h2o[c] + trdox[c] + datp[c]	0	(BT_1998 and BT_1999)	0	1000	2	Nucleotide Salvage Pathway			1.17.4.2
rxn05234	RNTR2	ribonucleoside-triphosphate reductase (GTP)	gtp[c] + trdrd[c] => h2o[c] + trdox[c] + dgtp[c]	0	(BT_1998 and BT_1999)	0	1000	2	Nucleotide Salvage Pathway			1.17.4.2
rxn05235	RNTR3	ribonucleoside-triphosphate reductase (CTP)	trdrd[c] + ctp[c] => h2o[c] + trdox[c] + dctp[c]	0	(BT_1998 and BT_1999)	0	1000	2	Nucleotide Salvage Pathway			1.17.4.2
rxn05236	RNTR4	ribonucleoside-triphosphate reductase (UTP)	trdrd[c] + utp[c] => h2o[c] + trdox[c] + dutp[c]	0	(BT_1998 and BT_1999)	0	1000	2	Nucleotide Salvage Pathway			1.17.4.2
rxn01116	RPE	ribulose 5-phosphate 3-epimerase	ru5p-D[c] <=> xu5p-D[c]	1	BT_3946	-1000	1000	2	Pentose Phosphate Pathway			5.1.3.1

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rxn00777	RPI	ribose-5-phosphate isomerase	r5p[c] <=> ru5p-D[c]	1	(BT_0346 or BT_1986)	-1000	1000	2	Pentose Phosphate Pathway			5.3.1.6
rxn03917	S7PIr	sedoheptulose 7-phosphate isomerase (reversible)	s7p[c] <=> gmhep7p[c]	1	BT_0475	-1000	1000	2	Lipopolysaccharide Biosynthesis			5.3.1.-
rxn00379	SADT	sulfate adenylyltransferase	h[c] + atp[c] + so4[c] => ppi[c] + aps[c]	0	(BT_0414 and BT_0415)	0	1000	2	Cysteine Metabolism		Reversible reaction in Model SEED	2.7.7.4
rxn09240	SADT2	Sulfate adenyltransferase	h2o[c] + atp[c] + gtp[c] + so4[c] => pi[c] + ppi[c] + aps[c] + gdp[c]	0	(BT_0414 and BT_0415)	0	1000	2	Cysteine Metabolism		Reversible reaction in Model SEED	2.7.7.4
rxn11702	SEPHCHS	2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylic-acid synthase	h[c] + akg[c] + ichor[c] => co2[c] + 2s5epchc[c]	0	BT_4701	0	1000	2	Cofactor and Prosthetic Group Biosynthesis			2.2.1.9
rxn00423	SERATi	Serine acetyltransferase (EC 2.3.1.30)	accoa[c] + ser-L[c] => coa[c] + acser[c]	0	BT_3256	0	1000	2	Cysteine Metabolism			2.3.1.30
rxn00165	SERD_L	L-serine deaminase	ser-L[c] => pyr[c] + nh4[c]	0	BT_4678	0	1000	2	Glycine, Serine, and Threonine Metabolism			4.3.1.17

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	SERPT	serine C-palmitoyltransferase	h[c] + pmtcoa[c] + ser-L[c] => coa[c] + 3dsphgn[c] + co2[c]	0	BT_0870	0	1000	4	Sphingolipid Metabolism	PMID:16887518, PMID:20855611	Bacteroides are well established to produce sphingolipids. Homologs of human serine palmitoyl transferase were found in Bacteroides and related species. In B. thetaiotaomicron, BLASTP of human serine palmitoyl transferase subunit 1 returns BT_0870, 8-amino-7-oxononanoate synthase, as homolog. It is unclear if this gene really encodes SERPT. Presence of this enzyme is supported by inhibition of sphingolipid synthesis in B. fragilis if cultures are exposed to the SERPT inhibitor myriocin (PMID:20855611).	2.3.1.50
rxn05307	SERt2r	L-serine reversible transport via proton symport	h[e] + ser-L[e] <=> h[c] + ser-L[c]	1		-1000	1000	2	Transport, Extracellular	Dworkin, M. and S. Falkow (2006). The prokaryotes : a handbook on the biology of bacteria. New York ; [London], Springer	B. thetaiotaomicron is weakly proteolytic, so a transport reaction for all amino acids is assumed to be present.	
rxn11703	SHCHCS3	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase	2s5epchc[c] => pyr[c] + 2shchc[c]	0		0	1000	1	Cofactor and Prosthetic Group Biosynthesis		Added by Model SEED during auto-completion step in pipeline.	4.2.99.20

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn01740	SHK3Dr	shikimate dehydrogenase	h[c] + nadph[c] + 3dhsk[c] <=> nadp[c] + skm[c]	1	BT_4215	-1000	1000	2	Tyrosine, Tryptophan, and Phenylalanine Metabolism			1.1.1.25
rxn01739	SHKK	shikimate kinase	atp[c] + skm[c] => h[c] + adp[c] + skm5p[c]	0	BT_3393	0	1000	2	Tyrosine, Tryptophan, and Phenylalanine Metabolism		Reversible reaction in Model SEED	2.7.1.71
	SHSL2r	O-succinylhomoserine lyase (H2S)	h2s[c] + suchms[c] <=> h[c] + hcys-L[c] + succ[c]	1	(BT_1923 or BT_2387)	-1000	1000	2	Methionine Metabolism			4.2.99.9
	SIAASE_OGLYCAN1e	Sialidase, mucin-type O-glycans, extracellular	h2o[e] + sTn_antigen[e] => acnam[e] + Tn_antigen[e]	0	BT_0455 or BT_2194 or BT_2892	0	1000	4	O-Glycan Degradation	PMID: 18996345, PMID: 10430883, PMID: 848954	B. thetaiotaomicron is well known to degrade mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis.	
	SIAASE_OGLYCAN2e	Sialidase, mucin-type O-glycans, extracellular	h2o[e] + dsT_antigen[e] => acnam[e] + sT_antigen[e]	0	BT_0455 or BT_2194 or BT_2892	0	1000	4	O-Glycan Degradation	PMID: 18996345, PMID: 10430883, PMID: 848954	B. thetaiotaomicron is well known to degrade mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis.	
	SIAASE_OGLYCAN3e	Sialidase, mucin-type O-glycans, extracellular	h2o[e] + sT_antigen[e] => acnam[e] + T_antigen[e]	0	BT_0455 or BT_2194 or BT_2892	0	1000	4	O-Glycan Degradation	PMID: 18996345, PMID: 10430883, PMID: 848954	B. thetaiotaomicron is well known to degrade mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis.	
	SIAASEe	sialidase, extracellular	2 h2o[c] + s2l2n2m2mn[e] => 2 acnam[e] + l2n2m2mn[e]	0	BT_0455 or BT_2194 or BT_2892	0	1000	4	N-Glycan Degradation	PMID:7463468, PMID:15790854, PMID:19304853	B. thetaiotaomicron has sialidase activity. However, it does not grow on N-acetyl neuraminic acid as sole carbon source (PMID:19304853).	3.2.1.18
	sink_chols	sink_reaction_choline sulfate	chols[c] <=>	1		-1000	1000	0	exchange/demand reaction			
	sink_s	sink_reaction_sulfur[c]	s[c] <=>	1		-1000	1000	0	exchange/demand reaction			

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rxn05651	SO4t2	sulfate transport in via proton symport	h[e] + so4[e] <=> h[c] + so4[c]	1	(BT_0412 or BT_3181)	-1000	1000	2	Transport, Extracellular			
	SPHMYLN_BTt	Sphingomyelin (B.thetaiotaomicron specific) export	sphmyln_bt[c] <=> sphmyln_bt[e]	1		-1000	1000	2	Sphingolipid Metabolism	PMID:16887518, PMID:20855611, Anaerobe (2001) 07, 103?112 doi:10.1006/anae .2001.0376	Bacteroides species are well established to produce sphingolipids.	
rxn05175	SPMDabc	spermidine transport via ABC system	h2o[c] + atp[c] + spmd[e] => h[c] + pi[c] + adp[c] + spmd[c]	0	(BT_1288 or BT_1289 or BT_1290 or BT_1291)	0	1000	2	Transport, Extracellular			
rxn09264	SPMDAT1	Spermidine acetyltransferase	accoa[c] + spmd[c] => h[c] + coa[c] + N1aspmd[c]	0	BT_1079	0	1000	2	Spermidine and Putrescine Biosynthesis			2.3.1.57
rxn09265	SPMDAT2	Spermidine acetyltransferase (N8)	accoa[c] + spmd[c] => h[c] + coa[c] + n8aspmd[c]	0	BT_1079	0	1000	2	Spermidine and Putrescine Biosynthesis			2.3.1.57
	SPMDtex2	spermidine excretion (cytosol to extracellular)	spmd[c] => spmd[e]	0		0	1000	2	Transport, Extracellular	PMID:10801923	B. thetaiotaomicron secretes putrescine and spermidine.	
rxn00206	SPODM	superoxide dismutase	2 h[c] + 2 o2s[c] => o2[c] + h2o2[c]	0	BT_0655	0	1000	4	ROS Detoxification	PMID:3700336, PMID:18398604	Superoxide dismutase activity was demonstrated in B. thetaiotaomicron.	1.15.1.1
rxn05459	STCOATA	stearyl-ACP[acyl-carrier-protein] transferase	coa[c] + ocdcaACP[c] <=> ACP[c] + stcoa[c]	1	BT_0789	-1000	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.180
	STYSabc	stachyose transport via ABC system (import)	h2o[c] + atp[c] + stys[e] => h[c] + pi[c] + adp[c] + stys[c]	0		0	1000	2	Transport, Extracellular	PMID:2557798	B. thetaiotaomicron can utilize stachyose as carbon source.	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn02596	STYSGH	a-galactosidase (stachyose)	h2o[c] + stys[c] <=> gal[c] + raffin[c]	1	(BT_1871 or BT_2851 or BT_3065 or BT_3131 or BT_3133 or BT_3410)	-1000	1000	4	Plant Polysaccharide Degradation	PMID:19646996, PMID:18848471, PMID:2557798	B. thetaiotaomicron can utilize stachyose as carbon source.	3.2.1.22
rxn02831	SUCBZL	o-succinylbenzoate-CoA ligase	coa[c] + atp[c] + sucbz[c] => amp[c] + ppi[c] + sbzcoa[c]	0	BT_4704	0	1000	2	Cofactor and Prosthetic Group Biosynthesis			6.2.1.26
rxn02832	SUCBZS	O-succinylbenzoate-CoA synthase	2shchc[c] => h2o[c] + sucbz[c]	0	BT_4703	0	1000	2	Cofactor and Prosthetic Group Biosynthesis		Model SEED annotation, not confirmed by NCBI gene	4.2.1.-
	SUCCITRDSs	N-succinyl-L-citrulline desuccinylase (spontaneous)	h2o[c] + succitr-L[c] => h[c] + citr-L[c] + succ[c]	0		0	1000	1	Arginine and Proline Metabolism		Reaction for modeling purposes only, added manually to fill gap in arginine biosynthesis	
rxn05654	SUCCt2r	succinate transport via proton symport	h[e] + succ[e] <=> h[c] + succ[c]	1	BT_2756	-1000	1000	4	Transport, Extracellular	PMID:19321416, PMID:12740060, PMID:11880608	Bacteroides species are well established to produce succinate. Also, growth of B. fragilis is stimulated by uptake of succinate in heme-resitricted culture (PMID:11880608). Annotation based on NCBI Gene.	
rxn00288	SUCD1	succinate dehydrogenase	succ[c] + fad[c] <=> fum[c] + fadh2[c]	1	(BT_3054 and BT_3055)	-1000	1000	4	TCA Cycle	PMID:12777495, PMID:11260473	Bacteroides have both succinate dehydrogenase and fumarate reductase acitivity. Fumarate reductase is a key enzyme in central metabolism.	1.3.99.1
rxn09272	SUCDi	succinate dehydrogenase (irreversible)	succ[c] + q8[c] => fum[c] + q8h2[c]	0	(BT_3054 and BT_3055)	0	1000	4	TCA Cycle	PMID:12777495, PMID:11260473	Bacteroides have both succinate dehydrogenase and fumarate reductase acitivity. Fumarate reductase is a key enzyme in central metabolism.	1.3.99.1

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn00285	SUCOAS	succinyl-CoA synthetase (ADP-forming)	coa[c] + atp[c] + succ[c] <=> pi[c] + adp[c] + succoa[c]	1	(BT_0787 and BT_0788)	-1000	1000	2	TCA Cycle			6.2.1.5
	SUCORNTC	N-succinyl-L-ornithine transcarbamylase	cbp[c] + sucorn[c] => pi[c] + succitr-L[c]	0	BT_3717	0	1000	4	Arginine and Proline Metabolism	PMID:16704984	The reaction mechanism of this enzyme was demonstrated in Bacteroides fragilis.	2.1.3.11
rxn00577	SUCR	sucrose hydrolyzing enzyme	h2o[c] + sucr[c] => glc-D[c] + fru[c]	0	BT_1765	0	1000	4	Plant Polysaccharide Degradation	PMID:20603004	B. thetaiotaomicron can utilize sucrose as carbon source.	3.2.1.26
	SUCRt2	sucrose transport in via proton symport	h[e] + sucr[e] => h[c] + sucr[c]	0		0	1000	2	Transport, Extracellular	PMID:20603004	B. thetaiotaomicron can utilize sucrose as carbon source.	
	T2DECAI	trans-2-decenoyl-ACP isomerase	tdec2eACP[c] <=> cdec3eACP[c]	1		-1000	1000	2	Cell Envelope Biosynthesis	PMID:6102980	This reaction is carried out by FabA. B. thetaiotaomicron does not have this enzyme. However, production of monounsaturated fatty acids in B. thetaiotaomicron is confirmed.	
rxn01857	TAGURr	tagaturonate reductase	nad[c] + altrn[c] <=> h[c] + nadh[c] + tagur[c]	1	BT_0825	-1000	1000	2	Alternate Carbon Metabolism			1.1.1.58
rxn01333	TALA	transaldolase	g3p[c] + s7p[c] <=> e4p[c] + f6p[c]	1	BT_1658	-1000	1000	2	Pentose Phosphate Pathway			2.2.1.2
	TAURtex2	taurine transport via diffusion	taur[e] <=> taur[c]	1		-1000	1000	1	Transport, Extracellular	PMID: 14665678	Diffusion through a porine assumed due to metabolites small size.	
	TCHOLAH	Bile acid hydrolase (taurocholate)	h2o[c] + tchola[c] => h[c] + cholate[c] + taur[c]	0	(BT_1259 or BT_2086)	0	1000	4	Bile Acid Metabolism	PMID:10993, Dworkin, M. and S. Falkow (2006). The prokaryotes : a handbook on the biology of bacteria. New York ; [London], Springer	This enzyme was demonstrated in B. thetaiotaomicron (PMID:10993). Growth is stimulated by 20 % bile (textbook The Prokaryotes).	3.5.1.24

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	TCHOLAt2	taurocholate transport via sodium cotransport	2 na1[e] + tchola[e] => 2 na1[c] + tchola[c]	0		0	1000	2	Transport, Extracellular	PMID:10993	B. thetaiotaomicron metabolizes glycocholate and taurocholate. A bile acid/ sodium symporter is annotated for Bacteroides salanitronis (NCBI Gene, last updated 18.05.11).	
rxn05457	TDCOATA	tetradecanoyl-ACP[acyl-carrier-protein] transferase	coa[c] + myrsACP[c] <=> ACP[c] + tdcoa[c]	1	BT_0789	-1000	1000	3	Glycerophospholipid Metabolism	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added manually to BIGG database based on reaction mechanism proposed by Model SEED. This reaction is involved in fatty acid biosynthesis. B. thetaiotaomicron is well known to synthesize iso- and anteiso-branched fatty acids.	2.3.1.180
rxn02000	TDPDRE	dTDP-4-dehydrorhamnose 3,5-epimerase	dtdp4d6dg[c] => dtdp4d6dm[c]	0	(BT_0464 or BT_0828 or BT_1349 or BT_1338)	0	1000	2	Capsular Polysaccharide Biosynthesis		Reversible reaction in Model SEED	5.1.3.13
rxn02003	TDPDRR	dTDP-4-dehydrorhamnose reductase	h[c] + nadph[c] + dtdp4d6dm[c] => nadp[c] + dtdprmn[c]	0	(BT_0725 or BT_0465 or BT_1730)	0	1000	2	Capsular Polysaccharide Biosynthesis		Reversible reaction in Model SEED	1.1.1.133
rxn01997	TDPGDH	dTDPglucose 4,6-dehydratase	dtdpglu[c] => h2o[c] + dtdp4d6dg[c]	0	(BT_0466 or BT_1350 or BT_2016 or BT_2880)	0	1000	2	Capsular Polysaccharide Biosynthesis			4.2.1.46

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn03181	TDSK_BT	Tetraacyldisaccharide 4'kinase	atp[c] + lipidAds_bt[c] => h[c] + adp[c] + lipidA_bt[c]	0	BT_1880	0	1000	3	Lipopolysaccharide Biosynthesis	PMID:18931137, PMID:19460428, PMID:20974832	Based on H. pylori LPS biosynthesis (BIGG database), as in the P. gingivalis reconstruction (PMID:18931137). P. gingivalis' LPS is similar in structure to the Bacteroides LPS. Based on structural information taken from (PMID:19460428, PMID:20974832).	2.7.1.130
rxn00787	TGBPA	Tagatose-bisphosphate aldolase	tagdp-D[c] <=> dhap[c] + g3p[c]	1		-1000	1000	2	Alternate Carbon Metabolism	PMID:2845859, PMID:10931310	B. thetaiotaomicron grows on N-acetyl-galactosamine (PMID:2845859), but the utilization pathway is poorly studied. In E. coli, this enzyme is involved in GalNAc utilization (PMID:10931310).	4.1.2.40
rxn09296	THIORDXi	hydrogen peroxide reductase (thioredoxin)	trdrd[c] + h2o2[c] => 2 h2o[c] + trdox[c]	0	(BT_0218 or BT_0677 or BT_1456 or BT_1914 or BT_2229)	0	1000	2	ROS Detoxification			
	THMDP	thiamin diphosphatase	2 h2o[c] + thmpp[c] => h[c] + 2 pi[c] + thm[c]	0	BT_3017	0	1000	2	Thiamine Metabolism		The enzyme is an acid phosphatase with wide specifity. Added based on annotation from The SEED Viewer (last checked 01.07.11)	3.1.3.2
rxn05200	THMDt2	thymidine transport in via proton symport	h[e] + thymd[e] => h[c] + thymd[c]	0	BT_4330	0	1000	2	Transport, Extracellular		Reversible reaction in Model SEED	
rxn09657	THMt3	Thiamine transport in via proton antiport	h[c] + thm[e] <=> h[e] + thm[c]	1	BT_2396	-1000	1000	2	Transport, Extracellular			

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn00541	THRAr	Threonine Aldolase	thr-L[c] <=> acald[c] + gly[c]	1	BT_1815	-1000	1000	2	Glycine, Serine, and Threonine Metabolism			4.1.2.5
rxn01068	THRD	L-threonine dehydrogenase	nad[c] + thr-L[c] => h[c] + nadh[c] + 2aobut[c]	0	BT_1370	0	1000	2	Glycine, Serine, and Threonine Metabolism			1.1.1.103
rxn01069	THRS	threonine synthase	h2o[c] + phom[c] => pi[c] + thr-L[c]	0	BT_2401	0	1000	2	Glycine, Serine, and Threonine Metabolism			4.2.3.1
	THRt2r	L-threonine reversible transport via proton symport	h[e] + thr-L[e] <=> h[c] + thr-L[c]	1		-1000	1000	1	Transport, Extracellular	Dworkin, M. and S. Falkow (2006). The prokaryotes : a handbook on the biology of bacteria. New York ; [London], Springer	B. thetaiotaomicron is weakly proteolytic, so a transport reaction for all amino acids is assumed to be present.	
rxn09310	THZPSN	thiazole phosphate synthesis	atp[c] + cys-L[c] + tyr-L[c] + dxyl5p[c] => h2o[c] + h[c] + ala-L[c] + co2[c] + amp[c] + ppi[c] + 4hba[c] + 4mpetz[c]	0	((BT_0648 and BT_0651 and BT_0653 and BT_0649) or (BT_0648 and BT_0651 and BT_0653 and BT_1836))	0	1000	2	Cofactor and Prosthetic Group Biosynthesis			
rxn01200	TKT1	transketolase	r5p[c] + xu5p-D[c] <=> g3p[c] + s7p[c]	1	BT_0347	-1000	1000	2	Pentose Phosphate Pathway			2.2.1.1
rxn00785	TKT2	transketolase	e4p[c] + xu5p-D[c] <=> g3p[c] + f6p[c]	1	BT_0347	-1000	1000	2	Pentose Phosphate Pathway			2.2.1.1
rxn01143	TMDK1	thymidine kinase (ATP:thymidine)	atp[c] + thymd[c] => h[c] + adp[c] + dtmp[c]	0	BT_2275	0	1000	2	Nucleotide Salvage Pathway		Reversible reaction in Model SEED	2.7.1.21
rxn00440	TMDPK	Thiamin pyrophosphokinase (EC 2.7.6.2)	atp[c] + thm[c] => h[c] + amp[c] + thmpp[c]	0	BT_2397	0	1000	2	Thiamine Metabolism		Reversible reaction in Model SEED	2.7.6.2
rxn01520	TMDS	thymidylate synthase	dump[c] + mlthf[c] => dhf[c] + dtmp[c]	0	BT_2047	0	1000	2	Nucleotide Salvage Pathway			2.1.1.45

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn00438	TMPKr	thiamine-phosphate kinase	atp[c] + thmmp[c] <=> adp[c] + thmpp[c]	1	BT_1882	-1000	1000	2	Thiamine Metabolism			2.7.4.16
rxn02305	TMPPP	thiamine-phosphate diphosphorylase	h[c] + 2mahmp[c] + 4mpetz[c] => ppi[c] + thmmp[c]	0	(BT_0652 or BT_0647)	0	1000	2	Cofactor and Prosthetic Group Biosynthesis		BT_0647: evidence at protein level (PDB entry 3ceu)	2.5.1.3
rxn00747	TPI	triose-phosphate isomerase	dhap[c] <=> g3p[c]	1	BT_3929	-1000	1000	2	Glycolysis/Gluconeogenesis			5.3.1.1
rxn05289	TRDRr	Thioredoxin reductase	h[c] + nadph[c] + trdox[c] <=> nadp[c] + trdrd[c]	1	BT_4336	-1000	1000	2	Unassigned			1.8.1.9
	TREHe	alpha,alpha-trehalase	h2o[e] + tre[e] => 2 glc-D[e]	0		0	1000	2	Alternate Carbon Metabolism	PMID:10993, Dworkin, M. and S. Falkow (2006). The prokaryotes : a handbook on the biology of bacteria. New York ; [London], Springer	B. thetaiotaomicron grows on trehalose. The reaction may be carried out be another enzyme, no annotation available.	3.2.1.28
rxn00473	TRPAS2	Tryptophanase (L-tryptophan)	h2o[c] + trp-L[c] <=> pyr[c] + nh4[c] + indole[c]	1	BT_1492	-1000	1000	2	Tyrosine, Tryptophan, and Phenylalanine Metabolism		Irreversible in Model SEED	4.1.99.1
rxn01964	TRPS1	tryptophan synthase (indoleglycerol phosphate)	ser-L[c] + 3ig3p[c] => h2o[c] + trp-L[c] + g3p[c]	0	(BT_0527 and BT_0533)	0	1000	2	Tyrosine, Tryptophan, and Phenylalanine Metabolism			4.2.1.20
rxn00474	TRPS2	tryptophan synthase (indole)	ser-L[c] + indole[c] => h2o[c] + trp-L[c]	0	(BT_0533 and BT_0527)	0	1000	2	Tyrosine, Tryptophan, and Phenylalanine Metabolism			4.2.1.20
rxn01682	TRPS3r	(1S,2R)-1-C-(indol-3-yl)glycerol 3-phosphate	3ig3p[c] <=> g3p[c] + indole[c]	1	(BT_0527 and BT_0533)	-1000	1000	2	Tyrosine, Tryptophan, and Phenylalanine Metabolism			4.2.1.20

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05663	TRPt2r	L-tryptophan reversible transport via proton symport	h[e] + trp-L[e] <=> h[c] + trp-L[c]	1		-1000	1000	1	Transport, Extracellular	Dworkin, M. and S. Falkow (2006). The prokaryotes : a handbook on the biology of bacteria. New York ; [London], Springer	B. thetaiotaomicron is weakly proteolytic, so a transport reaction for all amino acid is assumed to be present.	
rxn05301	TYRt2r	L-tyrosine reversible transport via proton symport	h[e] + tyr-L[e] <=> h[c] + tyr-L[c]	1		-1000	1000	1	Transport, Extracellular	Dworkin, M. and S. Falkow (2006). The prokaryotes : a handbook on the biology of bacteria. New York ; [London], Springer	B. thetaiotaomicron is weakly proteolytic, so a transport reaction for all amino acids is assumed to be present.	
rxn00527	TYRTA	tyrosine transaminase	akg[c] + tyr-L[c] <=> glu-L[c] + 34hpp[c]	1	(BT_0202 or BT_3935)	-1000	1000	2	Tyrosine, Tryptophan, and Phenylalanine Metabolism			2.6.1.5
	U23GAAT_BT	UDP-3-O-(anteiso-C17)glycosamine acyltransferase	15m3hpalmACP[c] + u3hga_HP[c] => h[c] + ACP[c] + u23ga_bt[c]	0	BT_4207	0	1000	4	Lipopolysaccharide Biosynthesis	PMID:18931137, PMID:19460428, PMID:20974832	Based on H. pylori LPS biosynthesis (BIGG database), as in the P. gingivalis reconstruction (PMID:18931137). P. gingivalis' LPS is similar in structure to the Bacteroides LPS. Based on structural information taken from (PMID:19460428, PMID:20974832).	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	U2GAAT_BT	u2gaat	3hpalmACP[c] + ugam[c] => ACP[c] + u2hga_bt[c]	0		0	1000	2	Lipopolysaccharide Biosynthesis	PMID:18931137, PMID:19460428, PMID:20974832	Based on H. pylori LPS biosynthesis (BIGG database), as in the P. gingivalis reconstruction (PMID:18931137). P. gingivalis' LPS is similar in structure to the Bacteroides LPS. Based on structural information taken from (PMID:19460428, PMID:20974832).	
	U2GAAT2_BT	u2gaat2	15m3hpalmACP[c] + u2hga_bt[c] => ACP[c] + u2ga_bt[c]	0		0	1000	2	Lipopolysaccharide Biosynthesis	PMID:18931137, PMID:19460428, PMID:20974832	Based on H. pylori LPS biosynthesis (BIGG database), as in the P. gingivalis reconstruction (PMID:18931137). P. gingivalis' LPS is similar in structure to the Bacteroides LPS. Based on structural information taken from (PMID:19460428, PMID:20974832).	
rxn02011	UAAGDS	UDP-N-acetylmuramoyl-L-alanyl-D-glutamyl-meso-2,6-diaminopimelate synthetase	atp[c] + 26dap-M[c] + uamag[c] => h[c] + pi[c] + adp[c] + ugmd[c]	0	BT_3452	0	1000	2	Cell Envelope Biosynthesis			6.3.2.13
rxn02377	UACMAMO	UDP-N-acetyl-D-mannosamine oxidoreductase	h2o[c] + 2 nad[c] + uacmam[c] => 3 h[c] + 2 nadh[c] + uacmamu[c]	0	BT_0602	0	1000	2	Capsular Polysaccharide Biosynthesis	PMID:17579514	Annotation taken from PMID:17579514, Table S5	
rxn00297	UAG2E	UDP-N-acetylglucosamine 2-epimerase	uacgam[c] <=> uacmam[c]	1	(BT_0383 or BT_1203 or BT_0601 or BT_2944)	-1000	1000	2	Aminosugar Metabolism			5.1.3.14

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn00292	UAG2EMA	UDP-N-acetyl-D-glucosamine 2-epimerase (Hydrolysis)	h2o[c] + uacgam[c] <=> h[c] + acmana[c] + udp[c]	1	(BT_0383 or BT_1203 or BT_0601 or BT_2944)	-1000	1000	2	Aminosugar Metabolism			5.1.3.14
rxn00295	UAG4E	UDP-N-acetyl-D-glucosamine 4-epimerase	uacgam[c] <=> udpacgal[c]	1	(BT_0623 or BT_2887)	-1000	1000	2	Aminosugar Metabolism			5.1.3.7
	UAGAAT_HP	UDP-N-acetylglucosamine acyltransferase	3hpalmACP[c] + uacgam[c] <=> ACP[c] + u3aga_HP[c]	1	(BT_3336 or BT_4205)	-1000	1000	4	Lipopolysaccharide Biosynthesis	PMID:18931137, PMID:19460428, PMID:20974832	Based on H. pylori LPS biosynthesis (BIGG database), as in the P. gingivalis reconstruction (PMID:18931137). P. gingivalis LPS is similar in structure to the Bacteroides LPS. Based on structural information taken from (PMID:19460428, PMID:20974832).	
rxn00461	UAGCVT_r	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	uacgam[c] + pep[c] <=> pi[c] + uaccg[c]	1	BT_2005	-1000	1000	2	Aminosugar Metabolism			2.5.1.7
rxn00293	UAGDP	UDP-N-acetylglucosamine diphosphorylase	h[c] + acgam1p[c] + utp[c] => uacgam[c] + ppi[c]	0		0	1000	1	Aminosugar Metabolism	PMID:7240086	Manually filled in based on KEGG Pathway to to make N-acetylglucosamine, a substrate known to support growth, usable.	2.7.7.23
	UAGDP2	UDP-glucosamine diphosphorylase	h[c] + utp[c] + gam1p[c] => ppi[c] + ugam[c]	0		0	1000	2	Aminosugar Metabolism	PMID:18931137, PMID:19460428, PMID:20974832	Based on H. pylori LPS biosynthesis (BIGG database), as in the P. gingivalis reconstruction (PMID:18931137). P. gingivalis LPS is similar in structure to the Bacteroides LPS. Based on structural information taken from (PMID:19460428, PMID:20974832).	2.7.7.23

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn03933	UAGPT2	UDP-N-acetylglucosamine-N-acetylmuramyl-(pentapeptide)pyrophosphoryl-undecaprenol N-acetylglucosamine transferase	uacgam[c] + uaGgla[c] => h[c] + udp[c] + uaaGgla[c]	0	BT_3448	0	1000	2	Cell Envelope Biosynthesis		Reversible reaction in Model SEED	2.4.1.227
rxn03408	UAGPT3	UDP-N-acetylglucosamine-N-acetylmuramyl-(pentapeptide)pyrophosphoryl-undecaprenol N-acetylglucosamine transferase	uacgam[c] + uagmda[c] => h[c] + udp[c] + uaagmda[c]	0	BT_3448	0	1000	2	Cell Envelope Biosynthesis			2.4.1.227
rxn02008	UAMAGS	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	atp[c] + glu-D[c] + uama[c] => h[c] + pi[c] + adp[c] + uamag[c]	0	BT_3450	0	1000	2	Cell Envelope Biosynthesis			6.3.2.9
rxn02286	UAMAS	UDP-N-acetylmuramoyl-L-alanine synthetase	ala-L[c] + atp[c] + uamr[c] => h[c] + pi[c] + adp[c] + uama[c]	0	BT_3447	0	1000	2	Cell Envelope Biosynthesis			6.3.2.8
rxn02285	UAPGR	UDP-N-acetylenolpyruvoylglucosamine reductase	h[c] + nadph[c] + uaccg[c] => nadp[c] + uamr[c]	0	BT_1368	0	1000	2	Cell Envelope Biosynthesis			1.1.1.158
rxn03901	UDCPDP	undecaprenyl-diphosphatase	h2o[c] + udcpdp[c] => h[c] + pi[c] + udcpp[c]	0	BT_3212	0	1000	2	Cell Envelope Biosynthesis			3.6.1.27
rxn04308	UDCPDPS	Undecaprenyl diphosphate synthase	8 ipdp[c] + frdp[c] => 8 ppi[c] + udcpdp[c]	0	BT_3726	0	1000	2	Cofactor and Prosthetic Group Biosynthesis			2.5.1.31
rxn00214	UDPG4E	UDPglucose 4-epimerase	udpg[c] <=> udpgal[c]	1	(BT_0623 or BT_2887)	-1000	1000	2	Alternate Carbon Metabolism			5.1.3.2
rxn00211	UDPGDr	UDPglucoseNAD+ oxidoreductase	h2o[c] + 2 nad[c] + udpg[c] <=> 3 h[c] + 2 nadh[c] + udpglcur[c]	1	(BT_0379 or BT_0599 or BT_0829 or BT_1341)	-1000	1000	2	Pentose and Glucuronate Interconversions			1.1.1.22

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	UDPGLCURE	UDP-glucuronate 5'-epimerase	udpglcur[c] <=> udpidour[c]	1	(BT_0600 or BT_1342 or BT_0380)	-1000	1000	2	Pentose and Glucuronate Interconversions		Annotation taken from The SEED. This reaction is probably involved in chondroitin sulfate degradation, but the exact pathway is unknown.	5.1.3.12
	UDPGLDC	UDP-D-glucuronate decarboxylase	h[c] + udpglcur[c] => co2[c] + udpxyl[c]	0	BT_1059	0	1000	2	Capsular Polysaccharide Biosynthesis	PMID:21804000	The product is likely a precursor for capsule polysaccharide biosynthesis, but the exact function is unknown.	4.1.1.35
	UGLT	UDPglucose--hexose-1-phosphate uridylyltransferase	gal1p[c] + udpg[c] <=> g1p[c] + udpgal[c]	1		-1000	1000	2	Alternate Carbon Metabolism	PMID:16887504	The reaction is needed for galactose utilization.	2.7.7.12
rxn03164	UGMDDS	UDP-N-acetylmuramoyl-L-alanyl-D-glutamyl-meso-2,6-diaminopimeloyl-D-alanyl-D-alanine synthetase	atp[c] + alaala[c] + ugmd[c] => h[c] + pi[c] + adp[c] + ugmda[c]	0	(BT_3644 or BT_4101)	0	1000	2	Cell Envelope Biosynthesis			6.3.2.15
	UHGADA_HP	UDP-3-O-acetylglucosamine deacetylase	h2o[c] + u3aga_HP[c] => ac[c] + u3hga_HP[c]	0		0	1000	2	Lipopolysaccharide Biosynthesis	PMID:18931137, PMID:19460428, PMID:20974832	Based on H. pylori LPS biosynthesis (BIGG database), as in the P. gingivalis reconstruction (PMID:18931137). P. gingivalis LPS is similar in structure to the Bacteroides LPS. Based on structural information taken from (PMID:19460428, PMID:20974832).	
rxn00711	UPPRT	uracil phosphoribosyltransferase	prpp[c] + ura[c] => ump[c] + ppi[c]	0	BT_2791	0	1000	2	Nucleotide Salvage Pathway			2.4.2.9
rxn05197	URAt2r	uracil transport in via proton symport reversible	h[e] + ura[e] <=> h[c] + ura[c]	1	BT_0686	-1000	1000	2	Transport, Extracellular			

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn02085	URCN	urocanase	h2o[c] + urcan[c] => 4izp[c]	0	BT_2694	0	1000	2	Histidine Metabolism		Reversible reaction in Model SEED	4.2.1.49
rxn05667	UREAt	Urea transport via facilitate diffusion	urea[e] <=> urea[c]	1		-1000	1000	1	Transport, Extracellular			
rxn03397	URFGTT	UDP-L-rhamnose:flavonol-3-O-D-glucoside L-rhamnosyltransferase	amet[c] + 2ombz[c] => h[c] + ahcys[c] + 2ommb[c]	0	(BT_0853 or BT_4216)	0	1000	2	Unassigned	PMID: 893348	It is not clear whether only menaquinone or mq and ubiquinone are synthesized. PMID: 893348 states that only menaquinone is present, however ubiquinone-using enzymes are annotated in the genome.	2.1.1.-
rxn00119	URIDK1	uridylate kinase (UMP)	atp[c] + ump[c] => adp[c] + udp[c]	0	BT_2242	0	1000	2	Nucleotide Salvage Pathway		Reversible reaction in Model SEED	2.7.4.-
rxn01517	URIDK2r	uridylate kinase (dUMP)	atp[c] + dump[c] <=> adp[c] + dudp[c]	1	BT_2242	-1000	1000	2	Nucleotide Salvage Pathway			2.7.4.-
rxn00709	URIK1	uridine kinase (ATP:Uridine)	atp[c] + uri[c] => h[c] + adp[c] + ump[c]	0	(BT_0184 or BT_2527)	0	1000	2	Nucleotide Salvage Pathway		Reversible reaction in Model SEED	2.7.1.48
rxn00713	URIK2	uridine kinase (GTP:Uridine)	gtp[c] + uri[c] => h[c] + ump[c] + gdp[c]	0	(BT_0184 or BT_2527)	0	1000	2	Nucleotide Salvage Pathway		Reversible reaction in Model SEED	2.7.1.48
rxn00715	URIK3	uridine kinase (ITP:Uridine)	uri[c] + itp[c] => h[c] + ump[c] + idp[c]	0	(BT_0184 or BT_2527)	0	1000	2	Nucleotide Salvage Pathway		Reversible reaction in Model SEED	2.7.1.48
rxn05199	URIt2r	uridine transport in via proton symport reversible	h[e] + uri[e] <=> h[c] + uri[c]	1	BT_4330	-1000	1000	2	Transport, Extracellular			

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
	USHD_BT	UDP-sugar hydrolase	h2o[c] + u23ga_bt[c] => 2 h[c] + ump[c] + lipidX_bt[c]	0	BT_3697	0	1000	4	Lipopolysaccharide Biosynthesis	PMID:18931137, PMID:19460428, PMID:20974832	Based on H. pylori LPS biosynthesis (BIGG database), as in the P. gingivalis reconstruction (PMID:18931137). P. gingivalis LPS is similar in structure to the Bacteroides LPS. Based on structural information taken from (PMID:19460428, PMID:20974832).	
	VALO	Valine oxidation by gut bacteria	4 h2o[c] + 5 val-L[c] => h[c] + co2[c] + 5 nh4[c] + 6 isobut[c]	0		0	1000	2	Valine, Leucine, and Isoleucine Metabolism	PMID:3572204, PMID:16887608, Krieg, N. R. (2010). Bergey's manual of systematic bacteriology, 2nd ed., volume 4. New York, Springer.	Valine and leucine are oxidized by gut bacteria to BCFA (branched-chain fatty acids) with one less carbon atom (isobutyrate and isovalerate, respectively), CO2 and ammonia.This reaction formula is hypothetical, no information on exact pathway and involved enzymes is avaiable. KEGG does not provide any pathway information either.Isobutyrate and isovalerate are known secretion products of B. thetaiotaomicron.	

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05669	VALt2r	L-valine reversible transport via proton symport	h[e] + val-L[e] <=> h[c] + val-L[c]	1		-1000	1000	2	Transport, Extracellular	PMID:7462155	B. thetaiotaomicron incorporates leucine, valine and isoleucine into its phospholipids,which suggests the presence of a transporter for these amino acids. However, it is not known which gene encodes this transporter.	
rxn00903	VALTA	valine transaminase	akg[c] + val-L[c] <=> glu-L[c] + 3mob[c]	1	BT_3892	-1000	1000	2	Valine, Leucine, and Isoleucine Metabolism			2.6.1.42
rxn05202	XANt2r	xanthine transport in via proton symport	h[e] + xan[e] <=> h[c] + xan[c]	1	BT_4473	-1000	1000	2	Transport, Extracellular			
rxn01544	XPPT	xanthine phosphoribosyltransferase	prpp[c] + xan[c] => ppi[c] + xmp[c]	0	(BT_0427 or BT_4386)	0	1000	2	Nucleotide Salvage Pathway			2.4.2.22
rxn01545	XTSNH	Xanthosine hydrolase	h2o[c] + xtsn[c] => rib-D[c] + xan[c]	0	BT_2808	0	1000	2	Nucleotide Salvage Pathway		Reversible reaction in Model SEED	3.2.2.8
rxn01044	XYLI1	xylose isomerase	xyl-D[c] <=> xylu-D[c]	1	BT_0793	-1000	1000	3	Alternate Carbon Metabolism	PMID:16887504	B. thetaiotaomicron can use D-xylose as carbon source.	5.3.1.5
rxn00223	XYLI2	xylose isomerase	glc-D[c] <=> fru[c]	1	BT_0793	-1000	1000	3	Alternate Carbon Metabolism	PMID:16887504	B. thetaiotaomicron can use D-xylose as carbon source.	5.3.1.5
rxn01199	XYLKr	ATPD-xylulose 5-phosphotransferase	atp[c] + xylu-D[c] <=> h[c] + adp[c] + xu5p-D[c]	1	(BT_0792 or BT_4423)	-1000	1000	2	Pentose and Glucuronate Interconversions			2.7.1.17
rxn05671	XYLt2	D-xylose transport in via proton symport	h[e] + xyl-D[e] => h[c] + xyl-D[c]	0	BT_0794	0	1000	4	Transport, Extracellular	PMID: 16887504	B. thetaiotaomicron can use D-xylose as carbon source.	
rxn00776	YUMPS	yUMP synthetase	r5p[c] + ura[c] <=> h2o[c] + psd5p[c]	1	((BT_3872 and BT_4501) or (BT_3213 and BT_4237))	-1000	1000	2	Purine and Pyrimidine Biosynthesis			4.2.1.70
rxn05315	ZN2t4	ZN2t4	h[e] + zn2[c] + k[e] <=> h[c] + k[c] + zn2[e]	1	BT_0499	-1000	1000	2	Transport, Extracellular			

SEED Rxn ID	BIGG Rxn ID	Function	Formula	Rev	GA	LB	UB	CS	Subsystem	Reference	Notes	EC Number
rxn05150	ZNabc	zinc transport via ABC system	h2o[c] + atp[c] + zn2[e] => h[c] + pi[c] + adp[c] + zn2[c]	0	(BT_2206 and BT_3248 and BT_3249)	0	1000	2	Transport, Extracellular			

Table S10b: All metabolites included in iAH991.

SEED Met ID	BIGG Met ID	Name	Formula	Charge	KEGG ID
cpd00201	10fthf	10-Formyltetrahydrofolate	C20H21N7O7	-2	C00234
cpd03524	10fthf5glu	10-formyltetrahydrofolate-[Glu](5)	C40H45N11O19	-6	
cpd11509	10m3hddcaACP	10-methyl-3-hydroxy-dodecanoyl-ACP	C24H45N2O9PRS	-1	
cpd11559	10m3hundecACP	10-methyl-3-hydroxy-undecanoyl-ACP	C23H43N2O9PRS	-1	
cpd11508	10m3oddcaACP	10-methyl-3-oxo-dodecanoyl-ACP	C24H43N2O9PRS	-1	
cpd11558	10m3oundecACP	10-methyl-3-oxo-undecanoyl-ACP	C23H41N2O9PRS	-1	
cpd11511	10mddcaACP	10-methyl-dodecanoyl-ACP	C24H45N2O8PRS	-1	
cpd11510	10mtddec2eACP	10-methyl-trans-dodec-2-enoyl-ACP	C24H43N2O8PRS	-1	
cpd11560	10mtundec2eACP	10-methyl-trans-undec-2-enoyl-ACP	C23H41N2O8PRS	-1	
cpd11561	10mundecACP	10-methyl-undecanoyl-ACP	C23H43N2O8PRS	-1	
cpd11534	11m3hddcaACP	11-methyl-3-hydroxy-dodecanoyl-ACP	C24H45N2O9PRS	-1	
cpd11533	11m3oddcaACP	11-methyl-3-oxo-dodecanoyl-ACP	C24H43N2O9PRS	-1	
cpd11536	11mddcaACP	11-methyl-dodecanoyl-ACP	C24H45N2O8PRS	-1	
cpd11535	11mtddec2eACP	11-methyl-trans-dodec-2-enoyl-ACP	C24H43N2O8PRS	-1	
	12dgr160	1,2-Diacyl-sn-glycerol (dihexadecanoyl, n-C16:0)	C35H68O5	0	C00641
	12ethd	1,2-Ethanediol	C2H6O2	0	C01380
cpd11513	12m3hmyrsACP	12-methyl-3-hydroxy-tetra-decanoyl-ACP	C26H49N2O9PRS	-1	
cpd11563	12m3htridecACP	12-methyl-3-hydroxy-tridecanoyl-ACP	C25H47N2O9PRS	-1	
cpd11512	12m3omyrsACP	12-methyl-3-oxo-tetra-decanoyl-ACP	C26H47N2O9PRS	-1	
cpd11562	12m3otridecACP	12-methyl-3-oxo-tridecanoyl-ACP	C25H45N2O9PRS	-1	
cpd11515	12mmyrsACP	12-methyl-tetra-decanoyl-ACP	C26H49N2O8PRS	-1	
cpd11514	12mtmrs2eACP	12-methyl-trans-tetra-dec-2-enoyl-ACP	C26H47N2O8PRS	-1	

SEED Met ID	BIGG Met ID	Name	Formula	Charge	KEGG ID
cpd11565	12mtridecACP	12-methyl-tridecanoyl-ACP	C25H47N2O8PRS	-1	
cpd11564	12mttritec2eACP	12-methyl-trans-tridec-2-enoyl-ACP	C25H45N2O8PRS	-1	
	12ppd-R	(R)-Propane-1,2-diol	C3H8O2	0	C02912
cpd00453	12ppd-S	(S)-Propane-1,2-diol	C3H8O2	0	C02917
cpd00203	13dpg	3-Phospho-D-glyceroyl phosphate	C3H4O10P2	-4	C00236
cpd11538	13m3hmyrsACP	13-methyl-3-hydroxy-tetra-decanoyl-ACP	C26H49N2O9PRS	-1	
cpd11537	13m3omyrsACP	13-methyl-3-oxo-tetra-decanoyl-ACP	C26H47N2O9PRS	-1	
cpd11540	13mmyrsACP	13-methyl-tetra-decanoyl-ACP	C26H49N2O8PRS	-1	
cpd11539	13mtmrs2eACP	13-methyl-trans-tetra-dec-2-enoyl-ACP	C26H47N2O8PRS	-1	
cpd11517	14m3hpalmACP	14-methyl-3-hydroxy-hexa-decanoyl-ACP	C28H53N2O9PRS	-1	
cpd11567	14m3hpentdecACP	14-methyl-3-hydroxy-pentadecanoyl-ACP	C27H51N2O9PRS	-1	
cpd11516	14m3opalmACP	14-methyl-3-oxo-hexa-decanoyl-ACP	C28H51N2O9PRS	-1	
cpd11566	14m3opentdecACP	14-methyl-3-oxo-pentadecanoyl-ACP	C27H49N2O9PRS	-1	
cpd11519	14mpalmACP	14-methyl-hexa-decanoyl-ACP	C28H53N2O8PRS	-1	
cpd11569	14mpentdecACP	14-methyl-pentadecanoyl-ACP	C27H51N2O8PRS	-1	
cpd11518	14mtpalm2eACP	14-methyl-trans-hexa-dec-2-enoyl-ACP	C28H51N2O8PRS	-1	
cpd11568	14mtpentdec2eACP	14-methyl-trans-pentadec-2-enoyl-ACP	C27H49N2O8PRS	-1	
	15dap	1,5-Diaminopentane	C5H16N2	2	C01672
cpd11542	15m3hpalmACP	15-methyl-3-hydroxy-hexa-decanoyl-ACP	C28H53N2O9PRS	-1	
cpd11541	15m3opalmACP	15-methyl-3-oxo-hexa-decanoyl-ACP	C28H51N2O9PRS	-1	
cpd11544	15mpalmACP	15-methyl-hexa-decanoyl-ACP	C28H53N2O8PRS	-1	
cpd11543	15mtpalm2eACP	15-methyl-trans-hexa-dec-2-enoyl-ACP	C28H51N2O8PRS	-1	
cpd15672	1aihpdecg3p	1-anteisoheptadecanoyl-sn-glycerol 3-phosphate (14-methyl-hexadecanoyl, anteiso-C17)	C20H39O7P	-2	

SEED Met ID	BIGG Met ID	Name	Formula	Charge	KEGG ID
cpd15675	1aipdecg3p	1-anteisopentadecanoyl-sn-glycerol 3-phosphate (12-methyl-tetradecanoyl, anteiso-C15)	C18H36O7P	-1	
cpd15325	1ddecg3p	1-dodecanoyl-sn-glycerol 3-phosphate	C15H29O7P1	-2	C00681
cpd15327	1hdecg3p	1-hexadecanoyl-sn-glycerol 3-phosphate	C19H37O7P1	-2	C00681
cpd15676	1ihdecg3p	1-isohexadecanoyl-sn-glycerol 3-phosphate (14-methyl-pentadecanoyl, iso-C16)	C19H38O7P	-1	
cpd15671	1ihpdecg3p	1-isoheptadecanoyl-sn-glycerol 3-phosphate (15-methyl-hexadecanoyl, iso-C17)	C20H39O7P	-2	
cpd15674	1ipdecg3p	1-isopentadecanoyl-sn-glycerol 3-phosphate (13-methyl-tetradecanoyl, iso-C15)	C18H36O7P	-1	
cpd15673	1itdecg3p	1-isotetradecanoyl-sn-glycerol 3-phosphate (12-methyl-tridecanoyl, iso-C14)	C17H34O7P	-1	
cpd15328	1odec11eg3p	1-octadec-11-enoyl-sn-glycerol 3-phosphate	C21H39O7P1	-2	
cpd15329	1odecg3p	1-octadecanoyl-sn-glycerol 3-phosphate	C21H41O7P1	-2	C00681
cpd02625	1p3h5c	L-1-Pyrroline-3-hydroxy-5-carboxylate	C5H6NO3	-1	C04281
cpd02431	1pyr5c	1-Pyrroline-5-carboxylate	C5H6NO2	-1	C03912
cpd15331	1tdecg3p	1-tetradecanoyl-sn-glycerol 3-phosphate	C17H33O7P1	-2	C00681
cpd01570	23camp	2,3-Cyclic AMP	C10H11N5O6P	-1	C02353
cpd01571	23ccmp	2,3-Cyclic CMP	C9H11N3O7P	-1	C02354
cpd03702	23cgmp	2,3-Cyclic GMP	C10H11N5O7P	-1	C06194
cpd01572	23cump	2,3-Cyclic UMP	C9H10N2O8P	-1	C02355
cpd02120	23dhdp	2,3-Dihydrodipicolinate	C7H5NO4	-2	C03340
cpd02498	23dhmb	(R)-2,3-Dihydroxy-3-methylbutanoate	C5H9O4	-1	C04272
cpd02535	23dhmp	(R)-2,3-Dihydroxy-3-methylpentanoate	C6H11O4	-1	C06007
cpd02921	25aics	(S)-2-[5-Amino-1-(5-phospho-D-ribosyl)imidazole-4-carboxamido]succinate	C13H15N4O12P	-4	C04823
cpd00957	25dhpp	2,5-Diamino-6-hydroxy-4-(5-phosphoribosylamino)-pyrimidine	C9H14N5O8P	-2	C01304
cpd00504	26dap-LL	LL-2,6-Diaminoheptanedioate	C7H14N2O4	0	C00666
cpd00516	26dap-M	meso-2,6-Diaminoheptanedioate	C7H14N2O4	0	C00680

SEED Met ID	BIGG Met ID	Name	Formula	Charge	KEGG ID
cpd00498	2ahbut	(S)-2-Aceto-2-hydroxybutanoate	C6H9O4	-1	C06006
cpd02920	2ahhmd	2-Amino-4-hydroxy-6-hydroxymethyl-7,8-dihydropteridine diphosphate	C7H8N5O8P2	-3	C04807
cpd00954	2ahhmp	2-Amino-4-hydroxy-6-hydroxymethyl-7,8-dihydropteridine	C7H9N5O2	0	C01300
cpd02233	2ameph	(2-Aminoethyl)phosphonate	C2H7NO3P	-1	C03557
cpd02211	2aobut	L-2-Amino-3-oxobutanoate	C4H7NO3	0	C03508
cpd00938	2c25dho	2-Carboxy-2,5-dihydro-5-oxofuran-2-acetate	C7H6O6	0	C01278
cpd00956	2cpr5p	1-(2-Carboxyphenylamino)-1-deoxy-D-ribulose 5-phosphate	C12H13NO9P	-3	C01302
cpd02857	2dda7p	2-Dehydro-3-deoxy-D-arabino-heptonate 7-phosphate	C7H10O10P	-3	C04691
cpd02711	2ddg6p	2-Dehydro-3-deoxy-D-gluconate 6-phosphate	C6H8O9P	-3	C04442
cpd00176	2ddglcn	2-Dehydro-3-deoxy-D-gluconate	C6H9O6	-1	C00204
	2dglcn	2-Deoxy-D-gluconate	C6H11O6	-1	C02782
cpd00712	2dhp	2-Dehydropantoate	C6H9O4	-1	C00966
	2dmmq10	2-Demethylmenaquinone 10	C60H86O2	0	C05818
	2dmmq11	2-Demethylmenaquinone 11	C65H94O2	0	C05818
	2dmmq7	2-Demethylmenaquinone 7	C45H62O2	0	C05818
cpd15352	2dmmq8	2-Demethylmenaquinone 8	C50H70O2	0	C05818
	2dmmq9	2-Demethylmenaquinone 9	C55H78O2	0	C05818
cpd15353	2dmmql8	2-Demethylmenaquinol 8	C50H72O2	0	
cpd00509	2dr1p	2-Deoxy-D-ribose 1-phosphate	C5H9O7P	-2	C00672
cpd00510	2dr5p	2-Deoxy-D-ribose 5-phosphate	C5H9O7P	-2	C00673
	2fuclac	2-Fucosyllactose (HMO, PMID:11425797)	C18H32O15	0	G00268
cpd01710	2ippm	2-Isopropylmaleate	C7H8O4	-2	C02631
cpd02894	2mahmp	2-Methyl-4-amino-5-hydroxymethylpyrimidine diphosphate	C6H8N3O7P2	-3	C04752

SEED Met ID	BIGG Met ID	Name	Formula	Charge	KEGG ID
cpd00760	2mbcoa	2-Methylbutanoyl-CoA	C26H40N7O17P3S	-4	C01033
cpd11495	2mbutACP	2-methylbutanoyl-ACP,2-methylbutyryl-ACP	C16H29N2O8PRS	-1	
cpd08286	2me4p	2-C-methyl-D-erythritol 4-phosphate	C5H11O7P	-2	C11434
cpd08301	2mecdp	2-C-methyl-D-erythritol 2,4-cyclodiphosphate	C5H10O9P2	-2	C11453
	2mmal	(R)-2-Methylmalate	C5H6O5	-2	
	2mmale	2-Methylmaleate	C5H4O4	-2	
cpd11545	2mpropACP	2-methylpropionyl-ACP,isobutyryl-ACP	C15H27N2O8PRS	-1	
cpd00094	2obut	2-Oxobutanoate	C4H5O3	-1	C00109
cpd03445	2ohph	2-Octaprenyl-6-hydroxyphenol	C46H70O2	0	C05811
cpd03447	2ombz	2-Octaprenyl-6-methoxy-1,4-benzoquinone	C47H70O3	0	C05813
	2omfuc	2-o-methylfucose (rare sugar in rhamnogalacturonan II)	C7H14O5	0	
cpd03449	2omhmbl	2-Octaprenyl-3-methyl-5-hydroxy-6-methoxy-1,4-benzoquinol	C48H74O4	0	
cpd03448	2ommb	2-Octaprenyl-3-methyl-6-methoxy-1,4-benzoquinone	C48H72O3	0	C05814
cpd03446	2omph	2-Octaprenyl-6-methoxyphenol	C47H72O2	0	C05812
	2omxyl	2-O-methylxylose (rare sugar in rhamnogalacturonan II)	C6H12O5	0	560157
cpd08288	2p4c2me	2-phospho-4-(cytidine 5-diphospho)-2-C-methyl-D-erythritol	C14H22N3O17P3	-4	
cpd00482	2pg	D-Glycerate 2-phosphate	C3H4O7P	-3	C00631
cpd00727	2pglyc	2-Phosphoglycolate	C2H2O6P	-3	C00988
	2s5epchc	2-Succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate	C14H13O9	-3	C16519
cpd03451	2shchc	2-Succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate	C11H10O6	-2	C05817
cpd00868	34hpp	3-(4-Hydroxyphenyl)pyruvate	C9H7O4	-1	C01179
cpd00840	36dahx	(3S)-3,6-Diaminohexanoate	C6H15N2O2	1	C01142
cpd00988	3amp	3-AMP	C10H12N5O7P	-2	C01367

SEED Met ID	BIGG Met ID	Name	Formula	Charge	KEGG ID
cpd02693	3c2hmp	3-Carboxy-2-hydroxy-4-methylpentanoate	C7H10O5	-2	C04411
cpd01646	3c3hmp	3-Carboxy-3-hydroxy-4-methylpentanoate	C7H10O5	-2	C02504
cpd02605	3c4mop	3-Carboxy-4-methyl-2-oxopentanoate	C7H8O5	-2	C04236
cpd03454	3cmp	3-cmp	C9H12N3O8P	-2	C05822
	3ddgc	3-Dehydro-2-deoxy-D-gluconate	C6H9O6	-1	C03926
	3ddlhept	3-deoxy-d-lyxo-heptulosaric acid (rare sugar in rhamnogalacturonan II)	C7H9O8	-1	
cpd00699	3dhq	3-Dehydroquinate	C7H9O6	-1	C00944
cpd01716	3dhsk	3-Dehydroshikimate	C7H7O5	-1	C02637
	3dsphgn	(2S)-1-hydroxy-3-oxooctadecan-2-aminium	C18H38NO2	1	C02934
	3fuclac	3-Fucosyllactose (HMO, PMID:11425797)	C18H32O15	0	G00313
cpd03701	3gmp	3-GMP	C10H12N5O8P	-2	C06193
cpd11478	3haACP	(3R)-3-Hydroxyacyl-[acyl-carrier protein]	C15H27N2O9PRS	-1	C04618
	3hcddec5eACP	(R)-3-hydroxy-cis-dodec-5-enoyl-[acyl-carrier protein]	C23H41N2O9PRS	-1	
	3hcmrs7eACP	(R)-3-hydroxy-cis-myristol-7-eoyl-[acyl-carrier protein]	C25H45N2O9PRS	-1	
	3hcpalm9eACP	(R)-3-hydroxy-cis-palm-9-eoyl-[acyl-carrier protein]	C27H49N2O9PRS	-1	
	3hcvac11eACP	(R)-3-hydroxy-cis-vacc-11-enoyl-[acyl-carrier protein]	C29H53N2O9PRS	-1	
cpd11480	3hddecACP	(R)-3-Hydroxydodecanoyl-[acyl-carrier protein]	C23H43N2O9PRS	-1	C05757
cpd11482	3hdecACP	(R)-3-Hydroxydecanoyl-[acyl-carrier protein]	C21H39N2O9PRS	-1	C04619
	3hgACPm	3-hydroxyglutaryl-ACP methyl ester	C17H29N2O11PRS	-1	
cpd11479	3hhexACP	(R)-3-Hydroxyhexanoyl-[acyl-carrier protein]	C17H31N2O9PRS	-1	C05747
cpd11484	3hmrsACP	(R)-3-Hydroxytetradecanoyl-[acyl-carrier protein]	C25H47N2O9PRS	-1	C04688
cpd11571	3hoctaACP	(R)-3-Hydroxyoctadecanoyl-[acyl-carrier protein]	C29H55N2O9PRS	-1	
cpd11483	3hoctACP	(R)-3-Hydroxyoctanoyl-[acyl-carrier protein]	C19H35N2O9PRS	-1	C04620

SEED Met ID	BIGG Met ID	Name	Formula	Charge	KEGG ID
	3hpACPm	3-hydroxypimeloyl-ACP methyl ester	C19H33N2O11PRS	-1	
cpd11481	3hpalmACP	R-3-hydroxypalmitoyl-[acyl-carrier protein]	C27H51N2O9PRS	-1	C04633
cpd02210	3ig3p	C-(3-Indolyl)-glycerol 3-phosphate	C11H12NO6P	-2	C03506
cpd11520	3mbutACP	3-methylbutanoyl-ACP,isovaleryl-ACP	C16H29N2O8PRS	-1	
cpd00123	3mob	3-Methyl-2-oxobutanoate	C5H7O3	-1	C00141
cpd00508	3mop	(S)-3-Methyl-2-oxopentanoate	C6H9O3	-1	C00671
	3ocddec5eACP	3-oxo-cis-dodec-5-enoyl-[acyl-carrier protein]	C23H39N2O9PRS	-1	
	3ocmrs7eACP	3-oxo-cis-myristol-7-eoyl-[acyl-carrier protein]	C25H43N2O9PRS	-1	
	3ocpalm9eACP	3-oxo-cis-palm-9-eoyl-[acyl-carrier protein]	C27H47N2O9PRS	-1	
	3ocvac11eACP	3-oxo-cis-vacc-11-enoyl-[acyl-carrier protein]	C29H51N2O9PRS	-1	
cpd11489	3oddecACP	3-Oxododecanoyl-[acyl-carrier protein]	C23H41N2O9PRS	-1	C05756
cpd11487	3odecACP	3-Oxodecanoyl-[acyl-carrier protein]	C21H37N2O9PRS	-1	C05753
	3ogACPm	3-ketoglutaryl-ACP methyl ester	C17H27N2O11PRS	-1	
cpd11486	3ohexACP	3-Oxohexanoyl-[acyl-carrier protein]	C17H29N2O9PRS	-1	C05746
cpd11491	3omrsACP	3-Oxotetradecanoyl-[acyl-carrier protein]	C25H45N2O9PRS	-1	C05759
cpd11490	3ooctACP	3-Oxooctanoyl-[acyl-carrier protein]	C19H33N2O9PRS	-1	C05750
cpd11570	3ooctdACP	3-Oxooctadecanoyl-[acyl-carrier protein]	C29H53N2O9PRS	-1	
	3opACPm	3-ketopimeloyl-ACP methyl ester	C19H31N2O11PRS	-1	
cpd11485	3opalmACP	3-Oxohexadecanoyl-[acyl-carrier protein]	C27H49N2O9PRS	-1	C05762
cpd00169	3pg	3-Phospho-D-glycerate	C3H4O7P	-3	C00197
cpd02069	3php	3-Phosphohydroxypyruvate	C3H2O7P	-3	C03232
	3pop	3-Phosphonopyruvate	C3H2O6P	-3	C02798
cpd00932	3psme	5-O-(1-Carboxyvinyl)-3-phosphoshikimate	C10H9O10P	-4	C01269

SEED Met ID	BIGG Met ID	Name	Formula	Charge	KEGG ID
cpd00989	3ump	3-UMP	C9H11N2O9P	-2	C01368
cpd00281	4abut	4-Aminobutanoate	C4H9NO2	0	C00334
cpd00443	4abz	4-Aminobenzoate	C7H6NO2	-1	C00568
cpd08210	4adcho	4-amino-4-deoxychorismate	C10H10NO5	-1	C11355
cpd00939	4ahmmp	4-Amino-5-hydroxymethyl-2-methylpyrimidine	C6H9N3O	0	C01279
cpd02775	4ampm	4-Amino-2-methyl-5-phosphomethylpyrimidine	C6H8N3O4P	-2	C04556
cpd08287	4c2me	4-(cytidine 5-diphospho)-2-C-methyl-D-erythritol	C14H23N3O14P2	-2	C11435
cpd00830	4h2oglt	4-Hydroxy-2-oxoglutarate	C5H4O6	-2	C01127
cpd15378	4hba	4-Hydroxy-benzyl alcohol	C7H8O2	0	
	4hglusa	L-4-hydroxyglutamic semialdehyde	C5H9NO4	0	C05938
cpd00851	4hpro-LT	trans-4-Hydroxy-L-proline	C5H9NO3	0	C01157
cpd03608	4hthr	4-Hydroxy-L-threonine	C4H9NO4	0	C06056
cpd02311	4izp	4-Imidazolone-5-propanoate	C6H7N2O3	-1	C03680
cpd11497	4m3hhexACP	4-methyl-3-hydroxy-hexanoyl-ACP	C18H33N2O9PRS	-1	
cpd11547	4m3hpentACP	4-methyl-3-hydroxy-pentanoyl-ACP	C17H31N2O9PRS	-1	
cpd11496	4m3ohexACP	4-methyl-3-oxo-hexanoyl-ACP	C18H31N2O9PRS	-1	
cpd11546	4m3opentACP	4-methyl-3-oxo-pentanoyl-ACP	C17H29N2O9PRS	-1	
cpd11499	4mhexACP	4-methyl-hexanoyl-ACP	C18H33N2O8PRS	-1	
cpd00200	4mop	4-Methyl-2-oxopentanoate	C6H9O3	-1	C00233
cpd11549	4mpentACP	4-methyl-pentanoyl-ACP	C17H31N2O8PRS	-1	
cpd02654	4mpetz	4-Methyl-5-(2-phosphoethyl)-thiazole	C6H8NO4PS	-2	C04327
cpd11498	4mthex2eACP	4-methyl-trans-hex-2-enoyl-ACP	C18H31N2O8PRS	-1	
cpd11548	4mtpent2eACP	4-methyl-trans-pent-2-enoyl-ACP	C17H29N2O8PRS	-1	

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cpd01977	4pasp	4-Phospho-L-aspartate	C4H6NO7P	-2	C03082
cpd02147	4per	4-Phospho-D-erythronate	C4H6O8P	-3	C03393
cpd02201	4ppan	D-4-Phosphopantothenate	C9H15NO8P	-3	C03492
cpd02666	4ppcys	N-((R)-4-Phosphopantothenoyl)-L-cysteine	C12H20N2O9PS	-3	C04352
cpd02882	4r5au	4-(1-D-Ribitylamino)-5-aminouracil	C9H16N4O6	0	C04732
cpd02893	5aizc	5-amino-1-(5-phospho-D-ribosyl)imidazole-4-carboxylate	C9H11N3O9P	-3	C04751
cpd02720	5aprbu	5-Amino-6-(5-phosphoribitylamino)uracil	C9H15N4O9P	-2	C04454
cpd00931	5apru	5-Amino-6-(5-phosphoribosylamino)uracil	C9H13N4O9P	-2	C01268
	5caiz	5-phosphoribosyl-5-carboxyaminoimidazole	C9H11N3O9P	-3	
	5drib	5-deoxyribose	C5H10O4	0	
cpd00502	5forthf	5-Formiminotetrahydrofolate	C20H22N8O6	-2	C00664
cpd02197	5fthf	5-Formyltetrahydrofolate	C20H21N7O7	-2	C03479
cpd11522	5m3hhexACP	5-methyl-3-hydroxy-hexanoyl-ACP	C18H33N2O9PRS	-1	
cpd11521	5m3ohexACP	5-methyl-3-oxo-hexanoyl-ACP	C18H31N2O9PRS	-1	
cpd11524	5mhexACP	5-methyl-hexanoyl-ACP	C18H33N2O8PRS	-1	
cpd00147	5mta	5-Methylthioadenosine	C11H15N5O3S	0	C00170
cpd11523	5mthex2eACP	5-methyl-trans-hex-2-enoyl-ACP	C18H31N2O8PRS	-1	
cpd00345	5mthf	5-Methyltetrahydrofolate	C20H24N7O6	-1	C00440
cpd01981	5mtr	5-Methylthio-D-ribose	C6H12O4S	0	C03089
cpd02255	5odhf2a	5-Oxo-4,5-dihydrofuran-2-acetate	C6H5O4	-1	C03586
	6hmhptpp	6-hydroxymethyl-dihydropterin pyrophosphate	C7H8N5O8P2	-3	
cpd11551	6m3hheptACP	6-methyl-3-hydroxy-heptanoyl-ACP	C19H35N2O9PRS	-1	
cpd11501	6m3hocACP	6-methyl-3-hydroxy-octanoyl-ACP	C20H37N2O9PRS	-1	

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cpd11550	6m3oheptACP	6-methyl-3-oxo-heptanoyl-ACP	C19H33N2O9PRS	-1	
cpd11500	6m3oocACP	6-methyl-3-oxo-octanoyl-ACP	C20H35N2O9PRS	-1	
cpd11553	6mheptACP	6-methyl-heptanoyl-ACP	C19H35N2O8PRS	-1	
cpd11503	6mocACP	6-methyl-octanoyl-ACP	C20H37N2O8PRS	-1	
cpd11552	6mthept2eACP	6-methyl-trans-hept-2-enoyl-ACP	C19H33N2O8PRS	-1	
cpd11502	6mtoct2eACP	6-methyl-trans-oct-2-enoyl-ACP	C20H35N2O8PRS	-1	
cpd00284	6pgc	6-Phospho-D-gluconate	C6H10O10P	-3	C00345
cpd00911	6pgl	6-phospho-D-glucono-1,5-lactone	C6H9O9P	-2	C01236
cpd11526	7m3hocACP	7-methyl-3-hydroxy-octanoyl-ACP	C20H37N2O9PRS	-1	
cpd11525	7m3oocACP	7-methyl-3-oxo-octanoyl-ACP	C20H35N2O9PRS	-1	
cpd11528	7mocACP	7-methyl-octanoyl-ACP	C20H37N2O8PRS	-1	
cpd11527	7mtoct2eACP	7-methyl-trans-oct-2-enoyl-ACP	C20H35N2O8PRS	-1	
	7ocholate	3alpha,12alpha-Dihydroxy-7-oxo-5beta-cholanate	C24H37O5	-1	C04643
cpd00800	8aonn	8-Amino-7-oxononanoate	C9H17NO3	0	C01092
cpd11505	8m3hdcaACP	8-methyl-3-hydroxy-decanoyl-ACP	C22H41N2O9PRS	-1	
cpd11555	8m3hnonACP	8-methyl-3-hydroxy-nonanoyl-ACP	C21H39N2O9PRS	-1	
cpd11504	8m3odcaACP	8-methyl-3-oxo-decanoyl-ACP	C22H39N2O9PRS	-1	
cpd11554	8m3ononACP	8-methyl-3-oxo-nonanoyl-ACP	C21H37N2O9PRS	-1	
cpd11507	8mdcaACP	8-methyl-decanoyl-ACP	C22H41N2O8PRS	-1	
cpd11557	8mnonACP	8-methyl-nonanoyl-ACP	C21H39N2O8PRS	-1	
cpd11506	8mtdec2eACP	8-methyl-trans-dec-2-enoyl-ACP	C22H39N2O8PRS	-1	
cpd11556	8mtnon2eACP	8-methyl-trans-non-2-enoyl-ACP	C21H37N2O8PRS	-1	
cpd11530	9m3hdcaACP	9-methyl-3-hydroxy-decanoyl-ACP	C22H41N2O9PRS	-1	

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cpd11529	9m3odcaACP	9-methyl-3-oxo-decanoyl-ACP	C22H39N2O9PRS	-1	
cpd11532	9mdcaACP	9-methyl-decanoyl-ACP	C22H41N2O8PRS	-1	
cpd11531	9mtdec2eACP	9-methyl-trans-dec-2-enoyl-ACP	C22H39N2O8PRS	-1	
cpd01298	aact	Aminoacetone	C3H8NO	1	C01888
cpd00029	ac	Acetate	C2H3O2	-1	C00033
cpd11494	acACP	Acetyl-ACP	C13H23N2O8PRS	-1	
cpd00071	acald	Acetaldehyde	C2H4O	0	C00084
cpd00022	accoa	Acetyl-CoA	C23H34N7O17P3S	-4	C00024
	acerA	Aceric acid (3-C-carboxy-5-deoxy-l-xylose) (rare sugar in rhamnogalacturonan II)	C6H9O6	-1	
	acetol	Acetol	C3H6O2	0	C05235
cpd02552	acg5p	N-Acetyl-L-glutamyl 5-phosphate	C7H9NO8P	-3	C04133
cpd00918	acg5sa	N-Acetyl-L-glutamate 5-semialdehyde	C7H10NO4	-1	C01250
	acgal	N-Acetyl-D-galactosamine	C8H15NO6	0	C01132
	acgal6p	N-Acetyl-D-galactosamine 6-phosphate	C8H14NO9P	-2	
	acgalglcur	Dimer GalNAc-GlcA	C14H22NO12	-1	
	acgalidour	Dimer GalNAc-IdoA	C14H22NO12	-1	
	acgalidour2s	Dimer GalNAc-IdoA2S	C14H21NO15S	-2	
cpd00122	acgam	N-Acetyl-D-glucosamine	C8H15NO6	0	C00140
	acgam1p	N-Acetyl-D-glucosamine 1-phosphate	C8H14NO9P	-2	C04256
cpd00293	acgam6p	N-Acetyl-D-glucosamine 6-phosphate	C8H14NO9P	-2	C00357
cpd00477	acglu	N-Acetyl-L-glutamate	C7H9NO5	-2	C00624
cpd00790	achms	O-Acetyl-L-homoserine	C6H11NO4	0	C01077
	acmam	N-Acetyl-D-muramoate	C11H18NO8	-1	C05887

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cpd01923	acmama	N-Acetyl-D-muramoyl-L-alanine	C14H23N2O9	-1	C02999
cpd00492	acmana	N-Acetyl-D-mannosamine	C8H15NO6	0	C00645
cpd00232	acnam	N-Acetylneuraminate	C11H18NO9	-1	C00270
cpd00331	acon-C	cis-Aconitate	C6H3O6	-3	C00417
cpd00342	acorn	N2-Acetyl-L-ornithine	C7H14N2O3	0	C00437
cpd11493	ACP	acyl carrier protein	C11H21N2O7PRS	-1	C00229
cpd00722	acser	O-Acetyl-L-serine	C5H9NO4	0	C00979
cpd11488	actACP	Acetoacetyl-ACP	C15H25N2O9PRS	-1	C05744
cpd00361	actn-R	(R)-Acetoin	C4H8O2	0	C00810
cpd00196	actp	Acetyl phosphate	C2H3O5P	-2	C00227
cpd00128	ade	Adenine	C5H5N5	0	C00147
cpd00836	adhlam	S-Acetyldihydrolipoamide	C10H19NO2S2	0	C01136
cpd00182	adn	Adenosine	C10H13N5O4	0	C00212
cpd00166	adocbl	Adenosylcobalamin	C72H100CoN18O17P	0	C00194
cpd00008	adp	ADP	C10H12N5O10P2	-3	C00008
	adphep7p-LD	ADP-L-glycero-D-manno-heptose-7-phosphate	C17H24N5O19P3	-4	
	adphep-DD	ADP-D-glycero-D-manno-heptose	C17H25N5O16P2	-2	C06397
	adphep-LD	ADP-L-glycero-D-manno-heptose	C17H25N5O16P2	-2	C06398
cpd00152	agm	Agmatine	C5H16N4	2	C00179
cpd00019	ahcys	S-Adenosyl-L-homocysteine	C14H20N6O5S	0	C00021
cpd02978	ahdt	2-Amino-4-hydroxy-6-(erythro-1,2,3-trihydroxypropyl)dihydropteridine triphosphate	C9H12N5O13P3	-4	C04895
cpd02851	aicar	5-Amino-1-(5-Phospho-D-ribosyl)imidazole-4-carboxamide	C9H13N4O8P	-2	C04677
cpd11434	aihpdcoa	fa12coa,Anteiso-C17:0 CoA Anteisoheptadecanoyl-CoA	C38H64N7O17P3S	-4	

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cpd11439	aipdcoa	fa4coa,Anteiso-C15:0 CoA Anteisopentadecanoyl-CoA	C36H60N7O17P3S	-4	
cpd02140	air	5-amino-1-(5-phospho-D-ribosyl)imidazole	C8H12N3O7P	-2	C03373
cpd00024	akg	2-Oxoglutarate	C5H4O5	-2	C00026
cpd00731	alaala	D-Alanyl-D-alanine	C6H12N2O3	0	C00993
	alaasp	L-alanyl-L-aspartate	C7H11N2O5	-1	
cpd00085	ala-B	beta-Alanine	C3H7NO2	0	C00099
cpd00668	alac-S	(S)-2-Acetolactate	C5H7O4	-1	C06010
cpd00117	ala-D	D-Alanine	C3H7NO2	0	C00133
	alagln	L-alanyl-L-glutamine	C8H15N3O4	0	
	alaglu	L-alanyl-L-glutamate	C8H13N2O5	-1	
	alagly	L-alanylglycine	C5H10N2O3	0	
	alahis	L-alanyl-L-histidine	C9H14N4O3	1	
cpd00035	ala-L	L-Alanine	C3H7NO2	0	C00041
	alaleu	L-alanyl-L-leucine	C9H18N2O3	0	
	alathr	L-alanyl-L-threonine	C7H14N2O4	0	
cpd11830	alpro	S-Aminomethyldihydrolipoylprotein	CH6NS2X	1	C01242
cpd00608	altrn	D-Altronate	C6H11O7	-1	C00817
	amannan140	Alpha-mannan, yeast, has a MW of about 25000 (PMID: 5461381), equals ~ 140 mannose units.	C840H1402O701	0	
cpd00017	amet	S-Adenosyl-L-methionine	C15H23N6O5S	1	C00019
cpd02701	amob	S-Adenosyl-4-methylthio-2-oxobutanoate	C15H19N5O6S	0	C04425
cpd00018	amp	AMP	C10H12N5O7P	-2	C00020
	amylose300	amylose (n=300 repeat units, alpha-1,4-glc)	C1800H3002O1501	0	C00718
cpd00093	anth	Anthranilate	C7H6NO2	-1	C00108

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	apio-D	D-Apiose (rare sugar in rhamnogalacturonan II)	C5H10O5	0	C01488
cpd12370	apoACP	apoprotein [acyl carrier protein]	RHO	0	
cpd12543	apoC_Lys	Apocarboxylase (Lys residue)	C6H13N2OX	0	C04419
cpd12848	apoC_Lys_btn	Holocarboxylase (biotin covalent bound to Lys residue of apoC)	C16H27N4O3SX	0	C06250
cpd00193	aps	Adenosine 5-phosphosulfate	C10H12N5O10PS	-2	C00224
cpd00817	ara5p	D-Arabinose 5-phosphate	C5H9O8P	-2	C01112
	arabinan101	Arabinan, polymer of 1,5-a-L-linked arabinofuranose units substituted by 1,3 or 1,2 linked branches, MW ~ 15000 Da (REF: www.megazyme.com). Contains Arabinose: Galactose: Rhamnose: Galacturonic acid = 97: 0.4: 0.1: 2.1. -> 97 arab-L, 1 gal, 1 rmn, 2 galur	C509H812O410	-2	C02474
	arabinogal	Larch arabinogalactan, gal/ara 6:1, small amount of glcur, MW ~ 116000	C3862H6376O3218	0	C00569
cpd00224	arab-L	L-Arabinose	C5H10O5	0	C00259
cpd12115	arabttr	Arabinotriose	C15H26O13	0	C02474
	argarg	L-argininyl-L-arginine	C12H28N8O3	2	
cpd00051	arg-L	L-Arginine	C6H15N4O2	1	C00062
cpd02152	argsuc	N(omega)-(L-Arginino)succinate	C10H17N4O6	-1	C03406
cpd00132	asn-L	L-Asparagine	C4H8N2O3	0	C00152
cpd00041	asp-L	L-Aspartate	C4H6NO4	-1	C00049
cpd00346	aspsa	L-Aspartate 4-semialdehyde	C4H7NO3	0	C00441
cpd00002	atp	ATP(4-)	C10H12N5O13P3	-4	C00002
	Brfap	4-(B-D-ribofuranosyl)aminobenzene 5-phosphate	C11H14NO7P	-2	
cpd03517	btamp	Biotinyl-5-AMP	C20H27N7O9PS	-1	C05921
cpd00120	btcoa	Butanoyl-CoA	C25H38N7O17P3S	-4	C00136
cpd00104	btn	Biotin	C10H15N2O3S	-1	C00120
cpd00211	but	Butyrate (n-C4:0)	C4H7O2	-1	C00246

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cpd11465	but2eACP	But-2-enoyl-[acyl-carrier protein]	C15H25N2O8PRS	-1	C04246
cpd11464	butACP	Butyryl-ACP (n-C4:0ACP)	C15H27N2O8PRS	-1	C05745
cpd01662	butpi	Butanoyl phosphate	C4H7O5P	-2	C02527
cpd00063	ca2	Calcium	Ca	2	C00076
	carn	carnosine	C9H14N4O3	0	C00386
cpd00343	cbasp	N-Carbamoyl-L-aspartate	C5H6N2O5	-2	C00438
cpd00635	cbl1	Cob(I)alamin	C62H88CoN13O14P	-1	C00853
cpd00146	cbp	Carbamoyl phosphate	CH2NO5P	-2	C00169
cpd01012	cd2	Cadmium	Cd	2	C01413
	cddec5eACP	cis-dodec-5-enoyl-[acyl-carrier protein] (n-C12:1)	C23H41N2O8PRS	-1	
	cdec3eACP	cis-dec-3-enoyl-[acyl-carrier protein] (n-C10:1)	C21H37N2O8PRS	-1	
cpd00096	cdp	CDP	C9H12N3O11P2	-3	C00112
	cdpchol	CDPcholine	C14H25N4O11P2	-1	C00307
cpd15684	cdpdaihpdecg	CDP-1,2-dianteisoheptadecanoylglycerol (14-methyl-hexadecanoyl, anteiso-C17)	C46H83N3O15P2	-2	
cpd15687	cdpdaipdecg	CDP-1,2-dianteisopentadecanoylglycerol (12-methyl-tetradecanoyl, anteiso-C15)	C42H75N3O15P2	-2	
cpd15417	cdpdddecg	CDP-1,2-didodecanoylglycerol	C36H63N3O15P2	-2	C00269
	cdpddg	CDP-4-dehydro-6-deoxy-D-glucose	C15H21N3O15P2	-2	C01219
cpd15419	cdpdhdecg	CDP-1,2-dihexadecanoylglycerol	C44H79N3O15P2	-2	C00269
cpd15688	cdpdihdecg	CDP-1,2-diisohexadecanoylglycerol (14-methyl-pentadecanoyl, iso-C16)	C44H79N3O15P2	-2	
cpd15683	cdpdihpdecg	CDP-1,2-diisoheptadecanoylglycerol (15-methyl-hexadecanoyl, iso-C17)	C46H83N3O15P2	-2	
cpd15686	cdpdipdecg	CDP-1,2-diisopentadecanoylglycerol (13-methyl-tetradecanoyl, iso-C15)	C42H75N3O15P2	-2	
cpd15685	cdpditdecg	CDP-1,2-diisotetradecanoylglycerol (12-methyl-tridecanoyl, iso-C14)	C40H71N3O15P2	-2	
cpd15420	cdpdodec11eg	CDP-1,2-dioctadec-11-enoylglycerol	C48H83N3O15P2	-2	C00269

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cpd15421	cdpdodecg	CDP-1,2-dioctadecanoylglycerol	C48H87N3O15P2	-2	C00269
cpd15423	cdpdtdecg	CDP-1,2-ditetradecanoylglycerol	C40H71N3O15P2	-2	C00269
	cdpea	CDP-ethanolamine(1-)	C11H19N4O11P2	-1	C00570
cpd00390	cdpglc	CDPglucose	C15H23N3O16P2	-2	C00501
cpd00158	cellb	cellobiose	C12H22O11	0	C00185
	cer1_bt	Ceramide-1 (Sphinganine:C15:0 anteiso)(B. thetaiotaomicron specific)	C35H71NO3	0	
cpd01017	cgly	Cys-Gly	C5H10N2O3S	0	C01419
cpd00098	chol	Choline	C5H14NO	1	C00114
	cholate	Cholate	C24H39O5	-1	C00695
	cholp	choline phosphate(1-)	C5H13NO4P	-1	C00588
cpd00681	chols	Choline sulfate	C5H13NO4S	0	C00919
cpd00216	chor	chorismate	C10H8O6	-2	C00251
cpd01157	chtbs	N,N-diacetylchitobiose	C16H28N2O11	0	C01674
cpd00137	cit	Citrate	C6H5O7	-3	C00158
cpd00274	citr-L	L-Citrulline	C6H13N3O3	0	C00327
	ckdn	CMP-3-deoxy-D-glycero-D-galacto-nonulosonic acid	C18H26N3O16P	-2	
cpd02546	ckdo	CMP-3-deoxy-D-manno-octulosonate	C17H24N3O15P	-2	
cpd00099	cl	Chloride	Cl	-1	C00115
cpd15792	clpn140	cardiolipin (tetratetradecanoyl, n-C14:0)	C65H124O17P2	-2	C05980
cpd15791	clpn160	cardiolipin (tetrahexadecanoyl, n-C16:0)	C73H140O17P2	-2	C05980
cpd15793	clpn180	cardiolipin (tetraoctadecanoyl, n-C18:0)	C81H156O17P2	-2	C05980
cpd15798	clpnai15	cardiolipin (12-methyl-tetradecanoyl, anteiso-C15)	C69H132O17P2	-2	
cpd15795	clpnai17	cardiolipin (14-methyl-hexadecanoyl, anteiso-C17)	C77H148O17P2	-2	

SEED Met ID	BIGG Met ID	Name	Formula	Charge	KEGG ID
cpd15796	clpni14	cardiolipin (12-methyl-tridecanoyl, iso-C14)	C65H124O17P2	-2	
cpd15797	clpni15	cardiolipin (13-methyl-tetradecanoyl, iso-C15)	C69H132O17P2	-2	
cpd15799	clpni16	cardiolipin (14-methyl-pentadecanoyl, iso-C16)	C73H140O17P2	-2	
cpd15794	clpni17	cardiolipin (15-methyl-hexadecanoyl, iso-C17)	C77H148O17P2	-2	
cpd00046	cmp	CMP	C9H12N3O8P	-2	C00055
cpd00011	co2	CO2	CO2	0	C00011
cpd00010	coa	Coenzyme A	C21H32N7O16P3S	-4	C00010
cpd00149	cobalt2	Co2+	Co	2	C00175
	core_lps_bt	core_lps_bt	C139H253N2O66P3	-1	
	core2	Core 2	C22H37N2O15X	0	
	core3	Core 3	C16H27N2O10X	0	
	core4	Core 4	C24H40N3O15X	0	
	core5	Core 5	C16H27N2O10X	0	
	core6	Core 6	C16H27N2O10X	0	
	core7	Core 7	C16H27N2O10X	0	
	core8	Core 8	C14H24NO10X	0	
	cps_bt	Capsule polysaccharide (B.thetaiotaomicron specific)	C69H102O67P8N14	-10	
	cspg_a	chondroitin sulfate A (GalNAc4S-GlcA) proteoglycan	C45H66N2O45S3X	-5	
	cspg_a_degr	Dimer GalNAc4S-GlcA	C14H21NO15S	-2	
	cspg_ab_rest	Not degradable product CSABCPASE_A/B, Gal4S-Gal-Xyl-L-Ser-protein	C17H28O17SX	-1	
	cspg_b	chondroitin sulfate B / dermatan sulfate (IdoA2S-GalNAc4S) proteoglycan	C45H65N2O48S4X	-6	
	cspg_b_degr	Dimer GalNAc4S-IdoA2S	C14H20NO18S2	-3	
	cspg_c	chondroitin sulfate C (GalNAc6S-GlcA) proteoglycan	C45H66N2O45S3X	-5	

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	cspg_c_degr	Dimer GalNAc6S-GlcA	C14H21NO15S	-2	
	cspg_c_rest	Not degradable product CSABCPASE_C, Gal6S-Gal-Xyl-L-Ser-protein	C17H28O17SX	-1	
	cspmd	Carboxyspermidine	C8H20N3O2	1	C18172
cpd08305	ctbt	crotonobetaine	C7H13NO2	0	C04114
cpd00052	ctp	CTP	C9H12N3O14P3	-4	C00063
cpd00058	cu2	Cu2+	Cu	2	C00070
cpd00084	cys-L	L-Cysteine	C3H7NO2S	0	C00097
cpd00367	cytd	Cytidine	C9H13N3O5	0	C00475
cpd00438	dad-2	Deoxyadenosine	C10H13N5O3	0	C00559
cpd03091	dad-5	5-Deoxyadenosine	C10H13N5O3	0	C05198
cpd00177	dadp	dADP	C10H12N5O9P2	-3	C00206
cpd00294	damp	dAMP	C10H12N5O6P	-2	C00360
cpd00764	dann	7,8-Diaminononanoate	C9H21N2O2	1	C01037
cpd00115	datp	dATP	C10H12N5O12P3	-4	C00131
cpd11225	db4p	3,4-dihydroxy-2-butanone 4-phosphate	C4H7O6P	-2	C15556
cpd11474	dcaACP	Decanoyl-ACP (n-C10:0ACP)	C21H39N2O8PRS	-1	C05755
cpd02375	dcamp	N6-(1,2-Dicarboxyethyl)-AMP	C14H14N5O11P	-4	C03794
cpd00533	dcdp	dCDP	C9H12N3O10P2	-3	C00705
cpd00206	dcmp	dCMP	C9H12N3O7P	-2	C00239
cpd00356	dctp	dCTP	C9H12N3O13P3	-4	C00458
cpd00654	dcyt	Deoxycytidine	C9H13N3O4	0	C00881
cpd11468	ddcaACP	Dodecanoyl-ACP (n-C12:0ACP)	C23H43N2O8PRS	-1	C05223
	dextran40	Dextran 40, 1,6-alpha-D-Glucan	C480H800O400	0	C00372

SEED Met ID	BIGG Met ID	Name	Formula	Charge	KEGG ID
cpd00295	dgdp	dGDP	C10H12N5O10P2	-3	C00361
cpd00296	dgmp	dGMP	C10H12N5O7P	-2	C00362
cpd00277	dgsn	Deoxyguanosine	C10H13N5O4	0	C00330
cpd00241	dgtp	dGTP	C10H12N5O13P3	-4	C00286
cpd00157	dha	Dihydroxyacetone	C3H6O3	0	C00184
cpd00095	dhap	Dihydroxyacetone phosphate	C3H5O6P	-2	C00111
cpd00330	dhf	7,8-Dihydrofolate	C19H19N7O6	-2	C00415
cpd00449	dhlam	Dihydrolipoamide	C8H17NOS2	0	C00579
cpd12225	dhlpro	Dihydrolipolprotein	H2S2X	0	C02972
cpd02295	dhna	1,4-Dihydroxy-2-naphthoate	C11H7O4	-1	C03657
cpd02961	dhnpt	Dihydroneopterin	C9H13N5O4	0	C04874
cpd00282	dhor-S	(S)-Dihydroorotate	C5H5N2O4	-1	C00337
cpd00683	dhpt	Dihydropteroate	C14H13N6O3	-1	C00921
	dhrfap	7,8-dihydropterin-6-ylmethyl-4-(B-D-ribofuranosyl) aminobenzene 5-phosphate	C18H21N6O8P	-2	
cpd03704	dimp	dIMP	C10H11N4O7P	-2	C06196
cpd03279	din	Deoxyinosine	C10H12N4O4	0	C05512
cpd00977	ditp	dITP	C10H11N4O13P3	-4	C01345
	dkdglcn	2,5-Diketo-3-deoxy-D-gluconate	C6H7O6	-1	C04349
cpd02656	dmlz	6,7-Dimethyl-8-(1-D-ribityl)lumazine	C13H18N4O6	0	C04332
cpd00202	dmpp	Dimethylallyl diphosphate	C5H9O7P2	-3	C00235
cpd00638	dnad	Deamino-NAD+	C21H24N6O15P2	-2	C00857
cpd00655	dpcoa	Dephospho-CoA	C21H33N7O13P2S	-2	C00882
cpd01242	drib	Deoxyribose	C5H10O4	0	C01801

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	dsT_antigen	disialyl-T antigen	C36H56N3O26X	-2	
	dt5hsu	4-Deoxy-L-threo-5-hexosulose uronate	C6H7O6	-1	C04053
cpd01311	dtbt	Dethiobiotin	C10H17N2O3	-1	C01909
cpd00297	dtdp	dTDP	C10H13N2O11P2	-3	C00363
cpd00521	dtdp4d6dg	dTDP-4-dehydro-6-deoxy-D-glucose	C16H22N2O15P2	-2	C11907
cpd00522	dtdp4d6dm	dTDP-4-dehydro-6-deoxy-L-mannose	C16H22N2O15P2	-2	C00688
cpd00626	dtdpglu	dTDPglucose	C16H24N2O16P2	-2	C00842
cpd02113	dtdprmn	dTDP-L-rhamnose	C16H24N2O15P2	-2	C03319
cpd00298	dtmp	dTMP	C10H13N2O8P	-2	C00364
cpd00357	dttp	dTTP	C10H13N2O14P3	-4	C00459
cpd00978	dudp	dUDP	C9H11N2O11P2	-3	C01346
cpd00299	dump	dUMP	C9H11N2O8P	-2	C00365
cpd00412	duri	Deoxyuridine	C9H12N2O5	0	C00526
cpd00358	dutp	dUTP	C9H11N2O14P3	-4	C00460
cpd08289	dxyl5p	1-deoxy-D-xylulose 5-phosphate	C5H9O7P	-2	C11437
	e3mmal	D-erythro-3-Methylmalate	C5H6O5	-2	
cpd01974	e4hglu	L-erythro-4-Hydroxyglutamate	C5H8NO5	-1	C05947
cpd00236	e4p	D-Erythrose 4-phosphate	C4H7O7P	-2	C00279
	egACPm	Enoylglutaryl-ACP methyl ester	C17H27N2O10PRS	-1	
cpd02843	eig3p	D-erythro-1-(Imidazol-4-yl)glycerol 3-phosphate	C6H9N2O6P	-2	C04666
	epACPm	Enoylpimeloyl-ACP methyl ester	C19H31N2O10PRS	-1	
cpd00162	etha	Ethanolamine	C2H8NO	1	C00189
cpd00363	etoh	Ethanol	C2H6O	0	C00469

SEED Met ID	BIGG Met ID	Name	Formula	Charge	KEGG ID
	f1a	F1alpha	C22H37N2O15X	0	
cpd00802	f1p	D-Fructose 1-phosphate	C6H11O9P	-2	C02976
cpd00072	f6p	D-Fructose 6-phosphate	C6H11O9P	-2	C00085
cpd11430	fa1	Fatty acid (Iso-C14:0)	C14H27O2	-1	
cpd11431	fa11	Fatty acid (Iso-C17:0)	C17H33O2	-1	
cpd11433	fa12	Fatty acid (Anteiso-C17:0)	C17H33O2	-1	
cpd11436	fa3	Fatty acid (Iso-C15:0)	C15H29O2	-1	
cpd11438	fa4	Fatty acid (Anteiso-C15:0)	C15H29O2	-1	
cpd11440	fa6	Fatty acid (iso-C16:0)	C16H31O2	-1	
cpd00015	fad	Flavin adenine dinucleotide oxidized	C27H31N9O15P2	-2	C00016
cpd00982	fadh2	Flavin adenine dinucleotide reduced	C27H33N9O15P2	-2	C01352
cpd00806	fc1p	L-Fuculose 1-phosphate	C6H11O8P	-2	C01099
cpd01186	fcl-L	L-fuculose	C6H12O5	0	C01721
	fdox	ferredoxin (oxidized) 2[4Fe-4S]	Fe8S8X	3	
cpd00290	fdp	D-Fructose 1,6-bisphosphate	C6H10O12P2	-4	C00354
	fdred	ferredoxin (reduced) 2[4Fe-4S]	Fe8S8X	2	
cpd11621	fdxox	Oxidized ferredoxin	X	0	C00139
cpd11620	fdxrd	Reduced ferredoxin	XH2	0	C00138
cpd10515	fe2	Fe2+	Fe	2	C00023
cpd10516	fe3	Fe3+	Fe	3	
cpd03725	fe3dcit	Fe(III)dicitrate	C12H10FeO14	-3	C06229
cpd02678	fgam	N2-Formyl-N1-(5-phospho-D-ribosyl)glycinamide	C8H13N2O9P	-2	C04376
cpd00109	ficytcc553	Ferricytochrome c-553	C42H54FeN8O6S2	3	

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cpd00050	fmn	FMN	C17H19N4O9P	-2	C00061
cpd00110	focytcc553	Ferrocytochrome c-553	C42H54FeN8O6S2	2	C01071
cpd00393	fol	Folate	C19H18N7O6	-1	C00504
cpd00047	for	Formate	CH1O2	-1	C00058
cpd00344	forglu	N-Formimidoyl-L-glutamate	C6H8N2O4	-2	C00439
cpd02826	fpram	2-(Formamido)-N1-(5-phospho-D-ribosyl)acetamidine	C8H15N3O8P	-1	C04640
cpd02884	fprica	5-Formamido-1-(5-phospho-D-ribosyl)imidazole-4-carboxamide	C10H13N4O9P	-2	C04734
cpd00350	frdp	Farnesyl diphosphate	C15H25O7P2	-3	C00448
cpd00082	fru	D-Fructose	C6H12O6	0	C00095
cpd00672	fruur	D-Fructuronate	C6H9O7	-1	C00905
	fuc1p-L	L-Fucose 1-phosphate	C6H11O8P	-2	C02985
cpd00751	fuc-L	L-Fucose	C6H12O5	0	C01019
	fucneulacnhx	monofucosyl-monosialyl-lacto-N-hexaose (HMO, PMID: 17002410)	C57H94N3O43	-1	
cpd00106	fum	Fumarate	C4H2O4	-2	C00122
cpd00089	g1p	D-Glucose 1-phosphate	C6H11O9P	-2	C00103
cpd00501	g1p-B	beta D-Glucose 1-phosphate	C6H11O9P	-2	C00663
cpd00102	g3p	Glyceraldehyde 3-phosphate	C3H5O6P	-2	C00661
cpd00507	g3pc	sn-Glycero-3-phosphocholine	C8H20NO6P	0	C00670
cpd00908	g3pe	sn-Glycero-3-phosphoethanolamine	C5H14NO6P	0	C01233
cpd02090	g3pg	Glycerophosphoglycerol	C6H14O8P	-1	C03274
cpd00079	g6p	D-Glucose 6-phosphate	C6H11O9P	-2	C00092
cpd00863	g6p-B	beta-D-glucose 6-phosphate	C6H11O9P	-2	C01172
	gACPm	Glutaryl-ACP methyl ester	C17H29N2O10PRS	-1	

SEED Met ID	BIGG Met ID	Name	Formula	Charge	KEGG ID
cpd00108	gal	D-Galactose	C6H12O6	0	C00124
cpd00348	gal1p	alpha-D-Galactose 1-phosphate	C6H11O9P	-2	C00446
	galam	D-Galactosamine	C6H13NO5	0	C02262
	galam6p	D-galactosamine-6-phosphate	C6H13NO8P	-1	
	galctn-D	D-Galactonate	C6H11O7	-1	
cpd00280	galur	D-Galacturonate	C6H9O7	-1	C00333
	gam	D-Glucosamine	C6H14NO5	1	C00329
	gam1p	D-Glucosamine 1-phosphate	C6H13NO8P	-1	C06156
	gam26s	Glucosamine 2,6-sulfate	C6H11NO11S2	-2	
cpd00288	gam6p	D-Glucosamine 6-phosphate	C6H13NO8P	-1	C00352
cpd02394	gar	N1-(5-Phospho-D-ribosyl)glycinamide	C7H14N2O8P	-1	C03838
cpd00229	gcald	Glycolaldehyde	C2H4O2	0	C00266
	gchola	glycocholate	C26H43NO6	0	C01921
cpd00031	gdp	GDP	C10H12N5O11P2	-3	C00035
cpd00900	gdpddman	GDP-4-dehydro-6-deoxy-D-mannose	C16H21N5O15P2	-2	C01222
cpd00272	gdpfuc	GDP-L-fucose	C16H23N5O15P2	-2	C00325
cpd00083	gdpmann	GDP-D-mannose	C16H23N5O16P2	-2	C00096
cpd02740	gdptp	Guanosine 3-diphosphate 5-triphosphate	C10H11N5O20P5	-7	C04494
cpd00289	ggdp	Geranylgeranyl diphosphate	C20H33O7P2	-3	C00353
cpd00190	glc-bD	beta D-glucose	C6H12O6	0	
cpd00027	glc-D	D-Glucose	C6H12O6	0	C00031
cpd00164	glcur	D-Glucuronate	C6H9O7	-1	C00191
cpd00053	gln-L	L-Glutamine	C5H10N2O3	0	C00064

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cpd02097	glu5p	L-Glutamate 5-phosphate	C5H8NO7P	-2	C03287
cpd00858	glu5sa	L-Glutamate 5-semialdehyde	C5H9NO3	0	C01165
cpd00186	glu-D	D-Glutamate	C5H8NO4	-1	C00217
cpd00023	glu-L	L-Glutamate	C5H8NO4	-1	C00025
cpd00040	glx	Glyoxylate	C2H1O3	-1	C00048
cpd00033	gly	Glycine	C2H5NO2	0	C00037
cpd00448	glyald	D-Glyceraldehyde	C3H6O3	0	C00577
	glyasn	Glycyl-L-asparagine	C6H11N3O4	0	
	glyasp	Glycyl-L-aspartate	C6H9N2O5	-1	
cpd00540	glyb	Glycine betaine	C5H11NO2	0	C00719
cpd00100	glyc	Glycerol	C3H8O3	0	C00116
cpd00080	glyc3p	Glycerol 3-phosphate	C3H7O6P	-2	C00093
cpd00139	glyclt	Glycolate	C2H3O3	-1	C00160
cpd00155	glycogen	glycogen	C6H10O5	0	C00182
	glycogen1500	glycogen (n=1500 repeat units) (glc alpha 1,4/6 glc)	C9000H15002O7501	0	
cpd00223	glyc-R	(R)-Glycerate	C3H5O4	-1	C00258
	glygln	Glycyl-L-glutamine	C7H13N3O4	0	
	glyglu	Glycyl-L-glutamate	C7H11N2O5	-1	
	glygly	Glycyl-glycine	C4H8N2O3	0	C02037
cpd15604	glyleu	Glycylleucine	C8H16N2O3	0	C02155
	glymet	Glycyl-L-methionine	C7H14N2O3S	0	
	glyphe	Glycylphenylalanine	C11H14N2O3	0	
cpd11588	glypro	Glycylproline	C7H12N2O3	0	

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	glytyr	Glycyl-L-tyrosine	C11H14N2O4	0	
	gmhep17bp	D-Glycero-D-manno-heptose 1,7-bisphosphate	C7H12O13P2	-4	C11472
	gmhep1p	D-Glycero-D-manno-heptose 1-phosphate	C7H13O10P	-2	C07838
cpd04918	gmhep7p	D-Glycero-D-manno-heptose 7-phosphate	C7H13O10P	-2	C07836
cpd00126	gmp	GMP	C10H12N5O8P	-2	C00144
	gncore1	GlcNAc-alpha-1,4-Core 1	C22H37N2O15X	0	
	gncore2	GlcNAc-alpha-1,4-Core 2	C30H50N3O20X	0	
cpd00283	grdp	Geranyl diphosphate	C10H17O7P2	-3	C00341
cpd00311	gsn	Guanosine	C10H13N5O5	0	C00387
cpd00042	gthrd	Reduced glutathione	C10H16N3O6S	-1	C00051
cpd00038	gtp	GTP	C10H12N5O14P3	-4	C00044
cpd00207	gua	Guanine	C5H5N5O	0	C00242
cpd00067	h	proton	H	1	C00080
cpd11640	h2	H2	H2	0	C00282
cpd08615	h2mb4p	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate	C5H9O8P2	-3	C11811
cpd00001	h2o	H2O	H2O	0	C00001
cpd00025	h2o2	Hydrogen peroxide	H2O2	0	C00027
cpd00239	h2s	Hydrogen sulfide	H2S	0	C00283
	ha	hyaluronan	C28H40N2O22	0	C00518
	ha_deg1	hyaluronan degradation product 1	C22H33N2O16	-1	
	ha_pre1	hyaluronan biosynthesis, precursor 1	C14H20NO11	-1	
cpd00242	hco3	Bicarbonate	CHO3	-1	C00288
cpd00135	hcys-L	L-Homocysteine	C4H9NO2S	0	C00155

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cpd00214	hdca	Hexadecanoate (n-C16:0)	C16H31O2	-1	C00249
cpd15237	hdcea	Hexadecenoate (n-C16:1)	C16H29O2	-1	
cpd15238	hdcoa	Hexadecenoyl-CoA (n-C16:1CoA)	C37H60N7O17P3S	-4	
cpd15239	hdeACP	cis-hexadec-9-enoyl-[acyl-carrier protein] (n-C16:1)	C27H49N2O8PRS	-1	
cpd02590	hepdp	all-trans-Heptaprenyl diphosphate	C35H57O7P2	-3	C04216
cpd11472	hexACP	Hexanoyl-ACP (n-C6:0ACP)	C17H31N2O8PRS	-1	C05749
cpd00906	hexdp	all-trans-Hexaprenyl diphosphate	C30H49O7P2	-3	C01230
cpd00531	hg2	Hg2+	Hg	2	C00703
cpd00119	his-L	L-Histidine	C6H9N3O2	0	C00135
cpd00807	hisp	L-Histidinol phosphate	C6H11N3O4P	-1	C01100
cpd00641	histd	L-Histidinol	C6H12N3O	1	C00860
cpd00227	hom-L	L-Homoserine	C4H9NO3	0	C00263
	homogal	Homogalacturonan, 100 galacturonate residues. Assumed to be methylated/ acetylated in every 5th residue. Citrus HG consists of 72-100 galacturonate residues and has a methylesterification degree of 22,9% (PMID: 11278866).	C660H840O660	-120	
	hpyr	Hydroxypyruvate	C3H3O4	-1	C00168
	hspg	heparan sulfate proteoglycan	C79H113N5O101S12X	-13	
	hspg_degr_1	Product 1 HEPARL1_e, IdoA-GlcN2,6diS-GlcA-GlcN2,3,6triS	C24H33O36N2S5	-7	
	hspg_degr_10	Product AS3TASE_HS2, GlcN2S-IdoA-GlcNAc-GlcA-Gal-Gal-Xyl-L-Ser (protein)	C43H66N2O38SX	-3	
	hspg_degr_11	Product GAM2STASE_HS3, GlcN-IdoA-GlcNAc-GlcA-Gal-Gal-Xyl-L-Ser (protein)	C43H67N2O35X	-2	
	hspg_degr_12	Product GLCNACASE_HS2, GlcA-GlcNAc-IdoA-Gal-Gal-Xyl-L-Ser (protein)	C37H56NO31X	-2	
	hspg_degr_13	Product GLCAASE_HS, GlcNAc-IdoA-Gal-Gal-Xyl-L-Ser (protein)	C31H49NO25X	-1	
	hspg_degr_14	Product GLCNACASE_HS3, IdoA-Gal-Gal-Xyl-L-Ser (protein)	C23H36O20X	-1	
	hspg_degr_15	Product IDOURASE_HS3, Gal-Gal-Xyl-L-Ser (protein)	C17H29O14X	0	

SEED Met ID	BIGG Met ID	Name	Formula	Charge	KEGG ID
	hspg_degr_2	Product 2 HEPARL1_e, IdoA2S-GlcN2,6diS-IdoA2S-GlcNAc3S-GlcA-Gal-Gal-Xyl-L-Ser (protein)	C49H71N2O56S5X	-6	
	hspg_degr_3	Product IDOURASE_HS1, GlcN2,6diS-GlcA-GlcN2,3,6triS	C18H26O30N2S5	-6	
	hspg_degr_4	Product AS6TASE_HS1, GlcN2S-GlcA-GlcN2,3diS	C18H28O24N2S3	-4	
	hspg_degr_5	Product AS3TASE_HS1, GlcN2S-GlcA-GlcN2S	C18H29O21N2S2	-3	
	hspg_degr_6	Product GAM2STASE_HS2, GlcN-GlcA-GlcN	C18H31O15N2	-1	
	hspg_degr_7	Product IS2TASE_HS1, IdoA-GlcN2,6diS-IdoA-GlcNAc3S-GlcA-Gal-Gal-Xyl-L-Ser (protein)	C49H71N2O50S3X	-6	
	hspg_degr_8	Product IDOURASE_HS2, GlcN2,6diS-IdoA-GlcNAc3S-GlcA-Gal-Gal-Xyl-L-Ser (protein)	C43H64N2O44S3X	-5	
	hspg_degr_9	Product AS6TASE_HS2, GlcN2S-IdoA-GlcNAc3S-GlcA-Gal-Gal-Xyl-L-Ser (protein)	C43H65N2O41S2X	-4	
	hspg_rest	Undegradable product GALASE_HS, Xyl-L-Ser (protein)	C5H9O4X	0	
cpd00226	hxan	Hypoxanthine	C5H4N4O	0	C00262
cpd03470	iasp	Iminoaspartate	C4H3NO4	-2	C05840
cpd00481	ibcoa	Isobutyryl-CoA	C25H38N7O17P3S	-4	C00630
cpd00658	ichor	Isochorismate	C10H8O6	-2	C00885
cpd00260	icit	Isocitrate	C6H5O7	-3	C00311
	idour	L-Iduronate	C6H9O7	-1	C06472
cpd00090	idp	IDP	C10H11N4O11P2	-3	C00104
cpd11441	ihdcoa	fa6coa,Iso-C16:0 CoA Isohexadecanoyl-CoA	C37H62N7O17P3S	-4	
cpd11432	ihpdcoa	fa11coa, Iso-C17:0 CoA Isoheptadecanoyl-CoA	C38H64N7O17P3S	-4	
cpd00322	ile-L	L-Isoleucine	C6H13NO2	0	C00407
cpd00930	imacp	3-(Imidazol-4-yl)-2-oxopropyl phosphate	C6H7N2O5P	-2	C01267
cpd00114	imp	IMP	C10H11N4O8P	-2	C00130
cpd00359	indole	Indole	C8H7N	0	C00463
cpd00121	inost	myo-Inositol	C6H12O6	0	C00137

SEED Met ID	BIGG Met ID	Name	Formula	Charge	KEGG ID
cpd00246	ins	Inosine	C10H12N4O5	0	C00294
	inulin	Chicory inulin, 30 monosaccharide units (29 fru, 1 glc) on average	C180H302O151	0	C03323
cpd11437	ipdcoa	fa3coa,Iso-C15:0 CoA Isopentadecanoyl-CoA	C36H60N7O17P3S	-4	
cpd00113	ipdp	Isopentenyl diphosphate	C5H9O7P2	-3	C00129
	isobut	Isobutyrate, 2-Methylpropanoate	C4H7O2	-1	C02632
	isocapr	Isocaproate	C6H11O2	-1	
	isoval	Isovalerate, 3-Methylbutanoate	C5H9O2	-1	C08262
cpd11435	itdcoa	fa1coa,Iso-C14:0 CoA Isotetradecanoyl-CoA	C35H58N7O17P3S	-4	
cpd00068	itp	ITP	C10H11N4O14P3	-4	C00081
cpd01882	ivcoa	Isovaleryl-CoA	C26H40N7O17P3S	-4	C02939
cpd00205	k	potassium	K	1	C00238
	kdn	2-keto-3-deoxy-D-glycero-D-galactononic acid	C9H15O9	-1	
	kdnp	2-keto-3-deoxy-D-glycero-D-galactononic acid 9-phosphate	C9H14O12P	-3	
cpd00875	kdo	3-Deoxy-D-manno-2-octulosonate	C8H13O8	-1	C01187
cpd02730	kdo8p	3-Deoxy-D-manno-octulosonate 8-phosphate	C8H12O11P	-3	C04478
	kdolipid4_bt	KDO-lipid IV(A)_BT	C88H160N2O29P2	-5	
	kdolipid4L_bt	KDO-lipid IV(A)_BT	C100H182N2O30P2	-5	
	kesto	Kestose (2 fru, 1 glc inulin-type fructo-oligosaccharide)	C18H32O16	0	
	kestopt	Kestopentaose (4 fru, 1 glc inulin-type fructo-oligosaccharide)	C30H52O26	0	
	kestottr	Kestotetraose (3 fru, 1 glc inulin-type fructo-oligosaccharide)	C24H42O21	0	
cpd02414	l2a6o	L-2-Amino-6-oxopimelate	C7H10NO5	-1	C03871
	l2n2m2mn	de-Fuc, reducing GlcNAc removed, de-Sia form of PA6 (w/o peptide linkage)	C54H91N3O41	0	
cpd00221	lac-D	D-Lactate	C3H5O3	-1	C00256

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	lacdfucttr	Lactodifucotetraose (HMO, PMID:11425797)	C24H42O19	0	G00335
cpd00159	lac-L	L-Lactate	C3H5O3	-1	C00186
	lacndfuchx	Lacto-N-difucohexaose (HMO, PMID:11425797)	C38H65NO29	0	G00891
	lacnfucpt	Lacto-N-fucopentaose (HMO, PMID:11425797)	C32H55NO25	0	G00557
	lacnnttr	Lacto-N-neotetraose (HMO, PMID:11425797)	C26H45NO21	0	G00536
	lacnttr	Lacto-N-tetraose (HMO, PMID:11425797)	C26H45NO21	0	C06371
cpd00334	lald-L	L-Lactaldehyde	C3H6O2	0	C00424
cpd00616	Largn	L-Arogenate	C10H13NO5	0	C00826
cpd00208	lcts	Lactose	C12H22O11	0	C00243
	leugly	Leucylglycine	C8H16N2O3	0	
cpd00107	leu-L	L-Leucine	C6H13NO2	0	C00123
	leuleu	Leucylleucine	C12H24N2O3	0	
	levan1000	Levan, 1000 fructose units	C6000H10002O5001	0	
	levanb	Levanbiose	C12H22O11	0	
	levanttr	Levantriose	C18H32O16	0	
	levantttr	Levantetraose	C24H42O21	0	
cpd02182	lgt-S	(R)-S-Lactoylglutathione	C13H20N3O8S	-1	C03451
	lipidA_bt	lipidA_BT	C78H146N2O23P2	-4	
	lipidAds_bt	lipidAds_BT	C78H147N2O20P	-2	
	lipidX_bt	lipidX_BT	C39H74NO12P	-2	
	lmn2	Laminaribiose	C12H22O11	0	
	lmn30	laminarin (n=30 repeat units, beta -1,3 glc)	C180H302O151	0	
cpd00213	lpam	Lipoamide	C8H15NOS2	0	C00248

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cpd12005	lpro	Lipoylprotein	S2X	0	C02051
	lps_bt	Lipopolysacharide (B. thetaiotaomicron specific)	C198H360N4O109P3	8	
cpd00039	lys-L	L-Lysine	C6H15N2O2	1	C00047
	m2mn	(alpha-D-mannosyl)2-beta-D-mannosyl-N-acetylglucosamine	C26H45NO21	0	
cpd11492	malACP	Malonyl-[acyl-carrier protein]	C14H22N2O10PRS	-2	C01209
cpd00070	malcoa	Malonyl-CoA	C24H33N7O19P3S	-5	C00083
	malcoam	Malonyl-CoA methyl ester	C25H36N7O19P3S	-4	
cpd00130	mal-L	L-Malate	C4H4O5	-2	C00149
cpd00179	malt	Maltose	C12H22O11	0	C00208
cpd15494	malthp	Maltoheptaose	C42H72O36	0	
cpd01329	malthx	Maltohexaose	C36H62O31	0	C01936
cpd15495	maltpt	Maltopentaose	C30H52O26	0	
cpd01262	malttr	Maltotriose	C18H32O16	0	C01835
cpd01399	maltttr	Maltotetraose	C24H42O21	0	C02052
	man	D-Mannose	C6H12O6	0	C00159
cpd00485	man1p	D-Mannose 1-phosphate	C6H11O9P	-2	C03812
cpd00235	man6p	D-Mannose 6-phosphate	C6H11O9P	-2	C00275
cpd00403	mana	D-Mannonate	C6H11O7	-1	C00514
	manb	Mannobiose (beta-1,4)	C12H22O11	0	
	manpt	mannopentaose	C30H52O26	0	
cpd03200	mantr	mannotriose (beta-1,4)	C18H32O16	0	C05404
	manttr	mannotetraose	C24H42O21	0	
cpd03198	melib	Melibiose	C12H22O11	0	C05402

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cpd00116	meoh	Methanol	CH4O1	0	C00132
	metala	L-methionyl-L-alanine	C8H15N2O3S	0	
cpd00347	methf	5,10-Methenyltetrahydrofolate	C20H20N7O6	-1	C00445
cpd00060	met-L	L-Methionine	C5H11NO2S	0	C00073
cpd01914	metsox-S-L	L-Methionine Sulfoxide	C5H11NO3S	0	C02989
cpd00254	mg2	magnesium	Mg	2	C00305
cpd00867	mi1p-D	1D-myo-Inositol 1-phosphate	C6H11O9P	-2	C01177
cpd02484	mi3p-D	1D-myo-Inositol 3-phosphate	C6H11O9P	-2	C04006
cpd02230	mi4p-D	1D-myo-Inositol 4-phosphate	C6H11O9P	-2	C03546
cpd00125	mlthf	5,10-Methylenetetrahydrofolate	C20H21N7O6	-2	C00143
cpd00891	mmcoa-R	(R)-Methylmalonyl-CoA	C25H35N7O19P3S	-5	C01213
cpd00519	mmcoa-S	(S)-Methylmalonyl-CoA	C25H35N7O19P3S	-5	C00683
	mn	beta-1,4-mannose-N-acetylglucosamine	C14H25NO11	0	
cpd00030	mn2	Mn2+	Mn	2	C00034
	mql10	Menaquinol 10	C61H90O2	0	C05819
	mql11	Menaquinol 11	C66H98O2	0	C05819
	mql7	Menaquinol 7	C46H66O2	0	C05819
cpd15499	mql8	Menaquinol 8	C51H74O2	0	C05819
	mql9	Menaquinol 9	C56H82O2	0	C05819
	mqn10	Menaquinone 10	C61H88O2	0	C00828
	mqn11	Menaquinone 11	C66H96O2	0	C00828
	mqn7	Menaquinone 7	C46H64O2	0	C00828
cpd15500	mqn8	Menaquinone 8	C51H72O2	0	C00828

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	mqn9	Menaquinone 9	C56H80O2	0	C00828
cpd00428	mthgxl	Methylglyoxal	C3H4O2	0	C00546
cpd11466	myrsACP	Myristoyl-ACP (n-C14:0ACP)	C25H47N2O8PRS	-1	C05761
cpd00470	N1aspmd	N1-Acetylspermidine	C9H23N3O	2	C00612
	n2m2mn	de-Fuc, reducing GlcNAc removed, de-Sia, de-Gal form of PA6 (w/o peptide linkage)	C42H71N3O31	0	
cpd00758	n8aspmd	N8-Acetylspermidine	C9H23N3O	2	C01029
cpd00971	na1	Sodium	Na	1	C01330
cpd00218	nac	Nicotinate	C6H4NO2	-1	C00253
cpd00003	nad	Nicotinamide adenine dinucleotide	C21H26N7O14P2	-1	C00003
cpd00004	nadh	Nicotinamide adenine dinucleotide - reduced	C21H27N7O14P2	-2	C00004
cpd00006	nadp	Nicotinamide adenine dinucleotide phosphate	C21H25N7O17P3	-3	C00006
cpd00005	nadph	Nicotinamide adenine dinucleotide phosphate - reduced	C21H26N7O17P3	-4	C00005
cpd00133	ncam	Nicotinamide	C6H6N2O	0	C00153
cpd00341	ncptrc	N-Carbamoylputrescine	C5H14N3O	1	C00436
	neulacnttr	Sialyllacto-N-tetraose (HMO, PMID: 17002410)	C37H61N2O29	-1	
cpd00013	nh4	Ammonium	H4N	1	C01342
cpd03471	nicrns	Nicotinate D-ribonucleoside	C11H13NO6	0	C05841
cpd00873	nicrnt	Nicotinate D-ribonucleotide	C11H12NO9P	-2	C01185
cpd00355	nmn	NMN	C11H14N2O8P	-1	C00455
cpd00075	no2	Nitrite	NO2	-1	C00088
cpd00007	o2	O2	O2	0	C00007
cpd00532	o2s	Superoxide anion	O2	-1	C00704
cpd00032	oaa	Oxaloacetate	C4H2O5	-2	C00036

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cpd11470	ocACP	Octanoyl-ACP (n-C8:0ACP)	C19H35N2O8PRS	-1	C05752
cpd01080	ocdca	octadecanoate (n-C18:0)	C18H35O2	-1	C01530
cpd11573	ocdcaACP	Octadecanoyl-ACP (n-C18:0ACP)	C29H55N2O8PRS	-1	
cpd15269	ocdcea	octadecenoate (n-C18:1)	C18H33O2	-1	
cpd02557	octdp	all-trans-Octaprenyl diphosphate	C40H65O7P2	-3	C04146
cpd11825	octeACP	cis-octadec-11-enoyl-[acyl-carrier protein] (n-C18:1)	C29H53N2O8PRS	-1	
cpd15274	odecoa	Octadecenoyl-CoA (n-C18:1CoA)	C39H64N7O17P3S	-4	
cpd03606	ohpb	2-Oxo-3-hydroxy-4-phosphobutanoate	C4H4O8P	-3	C06054
	oligofru4	Oligofructose, polymerization average 4 units of beta-2,1-fructose per chain	C24H40O20	0	
cpd00064	orn	Ornithine	C5H13N2O2	1	C01602
cpd00247	orot	Orotate	C5H3N2O4	-1	C00295
cpd00810	orot5p	Orotidine 5-phosphate	C10H10N2O11P	-3	C01103
cpd15521	pa120	1,2-didodecanoyl-sn-glycerol 3-phosphate	C27H51O8P1	-2	C00416
cpd15522	pa140	1,2-ditetradecanoyl-sn-glycerol 3-phosphate	C31H59O8P1	-2	C00416
cpd15524	pa160	1,2-dihexadecanoyl-sn-glycerol 3-phosphate	C35H67O8P1	-2	C00416
cpd15526	pa180	1,2-dioctadecanoyl-sn-glycerol 3-phosphate	C39H75O8P1	-2	C00416
cpd15527	pa181	1,2-dioctadec-11-enoyl-sn-glycerol 3-phosphate	C39H71O8P1	-2	C00416
cpd15681	paai15	1,2-dianteisopentadecanoyl-sn-glycerol 3-phosphate (12-methyl-tetradecanoyl, anteiso-C15)	C33H63O8P	-2	C00416
cpd15678	paai17	1,2-dianteisoheptadecanoyl-sn-glycerol 3-phosphate (14-methyl-hexadecanoyl, anteiso-C17)	C37H71O8P	-2	C00416
	pac	Phenylacetic acid	C8H7O2	-1	C07086
cpd15679	pai14	1,2-diisotetradecanoyl-sn-glycerol 3-phosphate (12-methyl-tridecanoyl, iso-C14)	C31H59O8P	-2	C00416
cpd15680	pai15	1,2-diisopentadecanoyl-sn-glycerol 3-phosphate (13-methyl-tetradecanoyl, iso-C15)	C33H63O8P	-2	C00416
cpd15682	pai16	1,2-diisohexadecanoyl-sn-glycerol 3-phosphate (14-methyl-pentadecanoyl, iso-C16)	C35H67O8P	-2	C00416

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cpd15677	pai17	1,2-diisoheptadecanoyl-sn-glycerol 3-phosphate (15-methyl-hexadecanoyl, iso-C17)	C37H71O8P	-2	C00416
cpd02024	pald	phosphonoacetaldehyde	C2H3O4P	-2	C03167
cpd11476	palmACP	Palmitoyl-ACP (n-C16:0ACP)	C27H51N2O8PRS	-1	C05764
cpd00834	pan4p	Pantetheine 4-phosphate	C11H21N2O7PS	-2	C01134
cpd00408	pant-R	(R)-Pantoate	C6H11O4	-1	C00522
cpd00045	pap	Adenosine 3,5-bisphosphate	C10H11N5O10P2	-4	C00054
cpd00044	paps	3-Phosphoadenylyl sulfate	C10H11N5O13P2S	-4	C00053
cpd04097	pb	Lead	Pb	2	
cpd00478	pdx5p	Pyridoxine 5-phosphate	C8H10NO6P	-2	C00627
	pe_cer1_bt	Ceramide phosphoethanolamine (B. thetaiotaomicron specific)	C37H77N2O6P	0	
cpd15528	pe120	phosphatidylethanolamine (didodecanoyl, n-C12:0)	C29H58N1O8P1	0	C00350
cpd15529	pe140	phosphatidylethanolamine (ditetradecanoyl, n-C14:0)	C33H66N1O8P1	0	C00350
cpd15531	pe160	phosphatidylethanolamine (dihexadecanoyl, n-C16:0)	C37H74N1O8P1	0	C00350
cpd15533	pe180	phosphatidylethanolamine (dioctadecanoyl, n-C18:0)	C41H82N1O8P1	0	C00350
cpd15534	pe181	phosphatidylethanolamine (dioctadec-11-enoyl, n-C18:1)	C41H78N1O8P1	0	C00350
cpd15699	peai15	Phosphatidylethanolamine (12-methyl-tetradecanoyl, anteiso-C15)	C35H70NO8P	0	
cpd15696	peai17	Phosphatidylethanolamine (14-methyl-hexadecanoyl, anteiso-C17)	C39H78NO8P	0	
	pect	pectins	C2535H3509O2535	-1	
	pecticgal	Pectic galactan (potato), gal: arab-L: rmn: galur = 78: 9: 4: 9 (www.megazyme.com). Assumed to consist of 100 sugars per macromolecule (I could not find information).	C597H971O503	-11	
	pectin	Pectin	C6H7O6	-1	C00714
cpd15697	pei14	Phosphatidylethanolamine (12-methyl-tridecanoyl, iso-C14)	C33H66NO8P	0	
cpd15698	pei15	Phosphatidylethanolamine (13-methyl-tetradecanoyl, iso-C15)	C35H70NO8P	0	

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cpd15700	pei16	Phosphatidylethanolamine (14-methyl-pentadecanoyl, iso-C16)	C37H74NO8P	0	
cpd15695	pei17	Phosphatidylethanolamine (15-methyl-hexadecanoyl, iso-C17)	C39H78NO8P	0	
cpd02591	pendp	all-trans-Pentaprenyl diphosphate	C25H41O7P2	-3	C04217
cpd00061	pep	Phosphoenolpyruvate	C3H2O6P	-3	C00074
	peptido_EC	Peptidoglycan subunit of Escherichia coli	C40H62N8O21	-2	
cpd15535	pg120	Phosphatidylglycerol (didodecanoyl, n-C12:0)	C30H58O10P1	-1	C00344
cpd15536	pg140	Phosphatidylglycerol (ditetradecanoyl, n-C14:0)	C34H66O10P1	-1	C00344
cpd15538	pg160	Phosphatidylglycerol (dihexadecanoyl, n-C16:0)	C38H74O10P1	-1	C00344
cpd15540	pg180	Phosphatidylglycerol (dioctadecanoyl, n-C18:0)	C42H82O10P1	-1	C00344
cpd15541	pg181	Phosphatidylglycerol (dioctadec-11-enoyl, n-C18:1)	C42H78O10P1	-1	C00344
cpd15726	pgai15	Phosphatidylglycerol (12-methyl-tetradecanoyl, anteiso-C15)	C36H70O10P	-1	
cpd15723	pgai17	Phosphatidylglycerol (14-methyl-hexadecanoyl, anteiso-C17)	C40H78O10P	-1	
cpd15724	pgi14	Phosphatidylglycerol (12-methyltridecanoyl, iso-C14)	C34H66O10P	-1	
cpd15725	pgi15	Phosphatidylglycerol (13-methyltetradecanoyl, iso-C15)	C36H70O10P	-1	
cpd15727	pgi16	Phosphatidylglycerol (14-methylpentadecanoyl, iso-C16)	C38H74O10P	-1	
cpd15722	pgi17	Phosphatidylglycerol (15-methyl-hexadecanoyl, iso-C17)	C40H78O10P	-1	
cpd15542	pgp120	Phosphatidylglycerophosphate (didodecanoyl, n-C12:0)	C30H57O13P2	-3	C03892
cpd15543	pgp140	Phosphatidylglycerophosphate (ditetradecanoyl, n-C14:0)	C34H65O13P2	-3	C03892
cpd15545	pgp160	Phosphatidylglycerophosphate (dihexadecanoyl, n-C16:0)	C38H73O13P2	-3	C03892
cpd15547	pgp180	Phosphatidylglycerophosphate (dioctadecanoyl, n-C18:0)	C42H81O13P2	-3	C03892
cpd15548	pgp181	Phosphatidylglycerophosphate (dioctadec-11-enoyl, n-C18:1)	C42H77O13P2	-3	C03892
cpd15720	pgpai15	Phosphatidylglycerophosphate (12-methyl-tetradecanoyl, anteiso-C15)	C36H69O13P2	-3	
cpd15717	pgpai17	Phosphatidylglycerophosphate (14-methyl-hexadecanoyl, anteiso-C17)	C40H77O13P2	-3	

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cpd15718	pgpi14	Phosphatidylglycerophosphate (12-methyltridecanoyl, iso-C14)	C34H65O13P2	-3	
cpd15719	pgpi15	Phosphatidylglycerophosphate (13-methyltetradecanoyl, iso-C15)	C36H69O13P2	-3	
cpd15721	pgpi16	Phosphatidylglycerophosphate (14-methylpentadecanoyl, iso-C16)	C38H73O13P2	-3	
cpd15716	pgpi17	Phosphatidylglycerophosphate (15-methyl-hexadecanoyl, iso-C17)	C40H77O13P2	-3	
	phaccoa	Phenylacetyl-CoA	C29H38N7O17P3S	-4	C00582
	phearg	L-phenylalanyl-L-arginine	C15H24N5O3	1	
cpd00066	phe-L	L-Phenylalanine	C9H11NO2	0	C00079
	pheme	Protoheme	C34H30FeN4O4	-2	C00032
cpd00809	phom	O-Phospho-L-homoserine	C4H8NO6P	-2	C01102
cpd00143	phpyr	Phenylpyruvate	C9H7O3	-1	C00166
cpd03607	phthr	O-Phospho-4-hydroxy-L-threonine	C4H8NO7P	-2	C06055
cpd00009	pi	hydrogenphosphate	HO4P	-2	C00009
	pmACP	Pimeloyl-ACP	C18H30N2O10PRS	-2	
	pmACPm	Pimeloyl-ACP methyl ester	C19H33N2O10PRS	-1	
cpd00782	pmcoa	Pimeloyl-CoA	C28H41N7O19P3S	-5	C01063
cpd00134	pmtcoa	Palmitoyl-CoA (n-C16:0CoA)	C37H62N7O17P3S	-4	C00154
cpd00644	pnto-R	(R)-Pantothenate	C9H16NO5	-1	C00864
cpd00141	ppa	Propionate (n-C3:0)	C3H5O2	-1	C00163
cpd01844	ppap	Propanoyl phosphate	C3H5O5P	-2	C02876
cpd00086	ppcoa	Propanoyl-CoA	C24H36N7O17P3S	-4	C00100
cpd00905	ppgpp	Guanosine 3,5-bis(diphosphate)	C10H11N5O17P4	-6	C01228
cpd00219	pphn	Prephenate	C10H8O6	-2	C00254
cpd00012	ppi	Diphosphate	HO7P2	-3	C00013

SEED Met ID	BIGG Met ID	Name	Formula	Charge	KEGG ID
cpd00421	pppi	Inorganic triphosphate	HO10P3	-4	C03279
cpd01982	pram	5-Phospho-beta-D-ribosylamine	C5H11NO7P	-1	C03090
cpd02642	pran	N-(5-Phospho-D-ribosyl)anthranilate	C12H13NO9P	-3	C04302
cpd01777	prbamp	1-(5-Phosphoribosyl)-AMP	C15H19N5O14P2	-4	C02741
cpd01775	prbatp	1-(5-Phosphoribosyl)-ATP	C15H19N5O20P4	-6	C02739
cpd02979	prfp	1-(5-Phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide	C15H21N5O15P2	-4	C04896
cpd02991	prlp	5-[(5-phospho-1-deoxyribulos-1-ylamino)methylideneamino]-1-(5-phosphoribosyl)imidazole-4-carboxamide	C15H21N5O15P2	-4	C04916
	progly	L-Prolinylglycine	C7H12N2O3	0	
cpd00129	pro-L	L-Proline	C5H9NO2	0	C00148
cpd00103	prpp	5-Phospho-alpha-D-ribose 1-diphosphate	C5H8O14P3	-5	C00119
cpd15552	ps120	phosphatidylserine (didodecanoyl, n-C12:0)	C30H57N1O10P1	-1	C02737
cpd15553	ps140	phosphatidylserine (ditetradecanoyl, n-C14:0)	C34H65N1O10P1	-1	C02737
cpd15555	ps160	phosphatidylserine (dihexadecanoyl, n-C16:0)	C38H73N1O10P1	-1	C02737
cpd15557	ps180	phosphatidylserine (dioctadecanoyl, n-C18:0)	C42H81N1O10P1	-1	C02737
cpd15558	ps181	phosphatidylserine (dioctadec-11-enoyl, n-C18:1)	C42H77N1O10P1	-1	C02737
cpd15693	psai15	Phosphatidylserine (12-methyl-tetradecanoyl, anteiso-C15)	C36H69NO10P	-1	
cpd15690	psai17	Phosphatidylserine (14-methyl-hexadecanoyl, anteiso-C17)	C40H77NO10P	-1	
cpd00859	psd5p	Pseudouridine 5-phosphate	C9H11N2O9P	-2	C01168
cpd00738	pser-L	O-Phospho-L-serine	C3H6NO6P	-2	C01005
cpd15691	psi14	Phosphatidylserine (12-methyl-tridecanoyl, iso-C14)	C34H65NO10P	-1	
cpd15692	psi15	Phosphatidylserine (13-methyl-tetradecanoyl, iso-C15)	C36H69NO10P	-1	
cpd15694	psi16	Phosphatidylserine (14-methyl-pentadecanoyl, iso-C16)	C38H73NO10P	-1	
cpd15689	psi17	Phosphatidylserine (15-methyl-hexadecanoyl, iso-C17)	C40H77NO10P	-1	

SEED Met ID	BIGG Met ID	Name	Formula	Charge	KEGG ID
cpd00118	ptrc	Putrescine	C4H14N2	2	C00134
	pullulan1200	pullulan (n=1200 repeat units, alpha-1,4 and alph-1,6 bounds)	C7200H12002O6001	0	
cpd00493	pyam5p	Pyridoxamine 5-phosphate	C8H12N2O5P	-1	C00647
cpd00419	pydam	Pyridoxamine	C8H13N2O2	1	C00534
cpd00215	pydx	Pyridoxal	C8H9NO3	0	C00250
cpd00016	pydx5p	Pyridoxal 5-phosphate	C8H8NO6P	-2	C00018
cpd00263	pydxn	Pyridoxine	C8H11NO3	0	C00314
cpd00020	pyr	pyruvate	C3H3O3	-1	C00022
cpd15560	q8	Ubiquinone-8	C49H74O4	0	C00399
cpd15561	q8h2	Ubiquinol-8	C49H76O4	0	C00390
cpd02333	quln	Quinolinate	C7H3NO4	-2	C03722
cpd00475	r1p	alpha-D-Ribose 1-phosphate	C5H9O8P	-2	C00620
cpd00101	r5p	alpha-D-Ribose 5-phosphate	C5H9O8P	-2	C00117
cpd00382	raffin	Raffinose	C18H32O16	0	C00492
cpd00258	rbl-D	D-Ribulose	C5H10O5	0	C00309
cpd00397	rbl-L	L-Ribulose	C5H10O5	0	C00508
	rhamnogalurI	Potato rhamnogalacturonan I, MW assumed ~200000, 62 galur, 20 rmn, 12 gal, 3 arab-L, 1 xyl-D (www.megazyme.com, PMID: 16661590)	C5840H7862O5281	-620	G09800
	rhamnogalurII	Wine rhamnogalacturonan II, MW ~ 5-10 kDa, 37% galur, 16% rmn, 3% fuc-L, 11% arab-L, 6% gal, 5% glcur, 4% 2omfuc, 3% 2omxyl, 6% apio-D, 2% acerA, 4% kdo, 3% 3ddlhept, 53 sugars in total (http://www.ccrc.uga.edu/~mao/rg2/intro.htm, doi:10.1155/2011/964521)	C317H445O273	-27	G06506
cpd02227	rhcys	S-Ribosyl-L-homocysteine	C9H17NO6S	0	C03539
cpd00105	rib-D	D-Ribose	C5H10O5	0	C00121
cpd00220	ribflv	Riboflavin	C17H20N4O6	0	C00255
cpd00642	rml	L-Rhamnulose	C6H12O5	0	C00861

SEED Met ID	BIGG Met ID	Name	Formula	Charge	KEGG ID
cpd00831	rml1p	L-Rhamnulose 1-phosphate	C6H11O8P	-2	C01131
cpd00396	rmn	L-Rhamnose	C6H12O5	0	C00507
cpd02016	rnam	N-Ribosylnicotinamide	C11H15N2O5	1	C03150
cpd00171	ru5p-D	D-Ribulose 5-phosphate	C5H9O8P	-2	C00199
cpd00808	ru5p-L	L-Ribulose 5-phosphate	C5H9O8P	-2	C01101
cpd00074	s	Sulfur	S	0	
cpd00349	s17bp	Sedoheptulose 1,7-bisphosphate	C7H12O13P2	-4	C00447
	s2l2fn2m2masn	PA6	C90H145N6O65X	-2	
	s2l2n2m2m	de-Fuc form of PA6 (w/o peptide linkage)	C84H136N6O62	-2	
	s2l2n2m2masn	de-Fuc form of PA6	C84H135N6O61X	-2	
	s2l2n2m2mn	de-Fuc, reducing GlcNAc removed form of PA6 (w/o peptide linkage)	C76H123N5O57	-2	
cpd00238	s7p	Sedoheptulose 7-phosphate	C7H13O10P	-2	C00281
cpd02021	sbzcoa	O-Succinylbenzoyl-CoA	C32H39N7O20P3S	-5	C03160
	Ser_Thr	protein-linked serine or threonine residue (O-glycosylation site)	XH	0	
cpd00054	ser-L	L-Serine	C3H7NO3	0	C00065
cpd00383	skm	Shikimate	C7H9O5	-1	C00493
cpd02030	skm5p	Shikimate 5-phosphate	C7H8O8P	-3	C03175
cpd00081	so3	Sulfite	O3S	-2	C00094
cpd00048	so4	Sulfate	O4S	-2	C00059
	sphgn	sphinganine(1+)	C18H40NO2	1	C00836
	sphmyln_bt	Sphingomyelin (B. thetaiotaomicron specific)	C40H83N2O6P	0	
cpd00264	spmd	Spermidine	C7H22N3	3	C00315
	sT_antigen	sialyl-T antigen	C25H40N2O18X	-1	

SEED Met ID	BIGG Met ID	Name	Formula	Charge	KEGG ID
	starch1200	starch n=1200 repeat units (300 repeat units amylose, 900 repeat units amylopectin, corresponds to potatoe starch)	C7200H12002O6001	0	
cpd00327	stcoa	Stearoyl-CoA (n-C18:0CoA)	C39H66N7O17P3S	-4	C00412
	sTn_antigen	sialyl-Tn antigen	C19H30N2O13X	-1	
	strch1	starch, structure 1 (1,6-{7[1,4-Glc], 4[1,4-Glc]})	C66H112O56	0	
	strch2	starch, structure 2 (1,6-{2[1,4-Glc], [1,4-Glc]})	C18H32O16	0	
cpd01133	stys	Stachyose	C24H42O21	0	C01613
cpd01772	sucbz	o-Succinylbenzoate	C11H8O5	-2	C02730
cpd00036	succ	Succinate	C4H4O4	-2	C00042
	succitr-L	N-succinyl-L-citrulline	C10H16N3O6	-1	
cpd00078	succoa	Succinyl-CoA	C25H35N7O19P3S	-5	C00091
cpd00822	suchms	O-Succinyl-L-homoserine	C8H12NO6	-1	C01118
	sucorn	N2-Succinyl-L-ornithine	C9H15N2O5	-1	C03415
cpd00076	sucr	Sucrose	C12H22O11	0	C00089
	T_antigen	T antigen (core 1)	C14H24NO10X	0	
	t3c11vaceACP	trans-3-cis-11-vacceoyl-[acyl-carrier protein]	C29H51N2O8PRS	-1	
	t3c5ddeceACP	trans-3-cis-5-dodecenoyl-[acyl-carrier protein]	C23H39N2O8PRS	-1	
	t3c7mrseACP	trans-3-cis-7-myristoleoyl-[acyl-carrier protein]	C25H43N2O8PRS	-1	
	t3c9palmeACP	trans-3-cis-9-palmitoleoyl-[acyl-carrier protein]	C27H47N2O8PRS	-1	
cpd00805	tag6p-D	D-Tagatose 6-phosphate	C6H11O9P	-2	C01097
cpd02371	tagdp-D	D-Tagatose 1,6-biphosphate	C6H10O12P2	-4	C03785
cpd00437	tagur	D-Tagaturonate	C6H9O7	-1	C00558
	taur	Taurine	C2H7NO3S	0	C00245
	tchola	taurocholic acid	C26H45NO7S	0	C05122

SEED Met ID	BIGG Met ID	Name	Formula	Charge	KEGG ID
cpd01695	tdcoa	Tetradecanoyl-CoA (n-C14:0CoA)	C35H58N7O17P3S	-4	C02593
cpd11469	tddec2eACP	trans-Dodec-2-enoyl-[acyl-carrier protein]	C23H41N2O8PRS	-1	C05758
cpd15294	tdeACP	cis-tetradec-7-enoyl-[acyl-carrier protein] (n-C14:1)	C25H45N2O8PRS	-1	
cpd11475	tdec2eACP	trans-Dec-2-enoyl-[acyl-carrier protein]	C21H37N2O8PRS	-1	C05754
cpd02465	thdp	2,3,4,5-Tetrahydrodipicolinate	C7H7NO4	-2	C03972
cpd11473	thex2eACP	trans-Hex-2-enoyl-[acyl-carrier protein]	C17H29N2O8PRS	-1	C05748
cpd00087	thf	5,6,7,8-Tetrahydrofolate	C19H21N7O6	-2	C00101
cpd06227	thfglu	Tetrahydrofolyl-[Glu](2)	C24H27N8O9	-3	C09332
cpd00305	thm	Thiamin	C12H17N4OS	1	C00378
cpd00793	thmmp	Thiamin monophosphate	C12H16N4O4PS	-1	C01081
cpd00056	thmpp	Thiamine diphosphate	C12H16N4O7P2S	-2	C00068
cpd00161	thr-L	L-Threonine	C4H9NO3	0	C00188
cpd00184	thymd	Thymidine	C10H14N2O5	0	C00214
cpd11467	tmrs2eACP	trans-Tetradec-2-enoyl-[acyl-carrier protein]	C25H45N2O8PRS	-1	C05760
	Tn_antigen	Tn antigen	C8H14NO5X	0	C04383
cpd11471	toct2eACP	trans-Oct-2-enoyl-[acyl-carrier protein]	C19H33N2O8PRS	-1	C05751
cpd11572	toctd2eACP	trans-octadec-2-enoyl-[acyl-carrier protein]	C29H53N2O8PRS	-1	
cpd11477	tpalm2eACP	trans-Hexadec-2-enoyl-[acyl-carrier protein]	C27H49N2O8PRS	-1	C05763
cpd11420	trdox	Oxidized thioredoxin	X	0	C00343
cpd11421	trdrd	Reduced thioredoxin	XH2	0	C00342
	tre	Trehalose	C12H22O11	0	C01083
cpd00065	trp-L	L-Tryptophan	C11H12N2O2	0	C00078
cpd00268	tsul	Thiosulfate	O3S2	-2	C00320

SEED Met ID	BIGG Met ID	Name	Formula	Charge	KEGG ID
cpd03847	ttdca	tetradecanoate (n-C14:0)	C14H27O2	-1	C06424
cpd00069	tyr-L	L-Tyrosine	C9H11NO3	0	C00082
	u23ga_bt	UDP-2(3-hydroxypalmitoyl)-3(anteiso-C17)glucosamine	C48H85N3O20P2	-2	
	u2ga_bt	u2ga_bt	C48H86N3O20P2	-1	
	u2hga_bt	UDP-2-hydroxyoctadecanoyl-D-glucosamine	C31H54N3O18P2	-1	
	u3aga_HP	UDP-3-O-(3-hydroxypalmetoyl)-N-acetylglucosamine	C33H55N3O19P2	-2	
	u3hga_HP	UDP-3-O(3-hydroxypalmetoyl)-D-glucosamine	C31H54N3O18P2	-1	
cpd03491	uaaGgla	Undecaprenyl-diphospho-N-acetylmuramoyl-(N-acetylglucosamine)-L-alanyl-gamma-D-glutamyl-L-lysyl-D-alanyl-D-alanine	C94H153N8O26P2	-3	C05893
cpd03495	uaagmda	Undecaprenyl-diphospho-N-acetylmuramoyl-(N-acetylglucosamine)-L-ala-D-glu-meso-2,6-diaminopimeloyl-D-ala-D-ala	C95H152N8O28P2	-4	C05898
cpd02820	uaccg	UDP-N-acetyl-3-O-(1-carboxyvinyl)-D-glucosamine	C20H26N3O19P2	-3	C04631
cpd00037	uacgam	UDP-N-acetyl-D-glucosamine	C17H25N3O17P2	-2	C00043
cpd00861	uacmam	UDP-N-acetyl-D-mannosamine	C17H25N3O17P2	-2	C01170
	uacmamu	UDP-N-acetyl-D-mannosaminouronate	C17H22N3O18P2	-3	C06240
cpd02948	uaGgla	Undecaprenyl-diphospho-N-acetylmuramoyl-L-alanyl-gamma-D-glutamyl-L-lysyl-D-alanyl-D-alanine	C86H140N7O21P2	-3	C04851
cpd03494	uagmda	Undecaprenyl-diphospho-N-acetylmuramoyl-L-alanyl-D-glutamyl-meso-2,6-diaminopimeloyl-D-alanyl-D-alanine	C87H139N7O23P2	-4	C05897
cpd00890	uama	UDP-N-acetylmuramoyl-L-alanine	C23H33N4O20P2	-3	C01212
cpd00525	uamag	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate	C28H39N5O23P2	-4	C00692
cpd00773	uamr	UDP-N-acetylmuramate	C20H28N3O19P2	-3	C01050
cpd02229	udcpdp	Undecaprenyl diphosphate	C55H89O7P2	-3	C03543
cpd00286	udcpp	Undecaprenyl phosphate	C55H89O4P	-2	C00348
cpd00014	udp	UDP	C9H11N2O12P2	-3	C00015
cpd00175	udpacgal	UDP-N-acetyl-D-galactosamine	C17H25N3O17P2	-2	C00203
cpd00026	udpg	UDPglucose	C15H22N2O17P2	-2	C00029

SEED Met ID	BIGG Met ID	Name	Formula	Charge	KEGG ID
cpd00043	udpgal	UDPgalactose	C15H22N2O17P2	-2	C00052
cpd00144	udpglcur	UDP-D-glucuronate	C15H19N2O18P2	-3	C00167
	udpidour	UDP-L-iduronate	C15H19N2O18P2	-3	C02330
	udpxyl	UDP-alpha-D-xylose(2-)	C14H20N2O16P2	-2	C00190
	ugam	UDP-glucosamine	C15H24N3O16P2	-1	C02200
cpd02862	uGgla	UDP-N-acetylmuramoyl-L-alanyl-gamma-D-glutamyl-L-lysyl-D-alanyl-D-alanine	C40H62N9O26P2	-3	C04702
cpd02964	ugmd	UDP-N-acetylmuramoyl-L-alanyl-D-gamma-glutamyl-meso-2,6-diaminopimelate	C35H51N7O26P2	-4	C04877
cpd02968	ugmda	UDP-N-acetylmuramoyl-L-alanyl-D-glutamyl-meso-2,6-diaminopimeloyl-D-alanyl-D-alanine	C41H61N9O28P2	-4	C04882
cpd00091	ump	UMP	C9H11N2O9P	-2	C00105
cpd00946	unaga	Undecaprenyl diphospho N-acetyl-glucosamine	C63H103NO12P2	-2	
	unsdigalur	4-(4-Deoxy-alpha-D-gluc-4-enuronosyl)-D-galacturonate, Unsaturated digalacturonate	C12H14O12	-2	C06118
cpd00092	ura	Uracil	C4H4N2O2	0	C00106
cpd00581	urcan	Urocanate	C6H5N2O2	-1	C00785
cpd00073	urea	Urea	CH4N2O	0	C00086
cpd00249	uri	Uridine	C9H12N2O6	0	C00299
cpd00062	utp	UTP	C9H11N2O15P3	-4	C00075
cpd00156	val-L	L-Valine	C5H11NO2	0	C00183
cpd00309	xan	Xanthine	C5H4N4O2	0	C00385
cpd00497	xmp	Xanthosine 5-phosphate	C10H11N4O9P	-2	C00655
cpd00530	xtp	XTP	C10H11N4O15P3	-4	C00700
cpd01217	xtsn	Xanthosine	C10H12N4O6	0	C01762
cpd03861	xu1p-L	L-Xylulose 1-phosphate	C5H9O8P	-2	
cpd00198	xu5p-D	D-Xylulose 5-phosphate	C5H9O8P	-2	C00231

SEED Met ID	BIGG Met ID	Name	Formula	Charge	KEGG ID
cpd00154	xyl-D	D-Xylose	C5H10O5	0	C00181
cpd00259	xylu-D	D-Xylulose	C5H10O5	0	C00310
cpd00261	xylu-L	L-Xylulose	C5H10O5	0	C00312
cpd00034	zn2	Zinc	Zn	2	C00038

Table S10c: Reactions included in the automated Model SEED reconstruction *BΘ_Seed_v1* that were rejected based on manual inspection and replaced with similar reactions.

SEED Rxn ID	BIGG Rxn ID	Function	EC Number	Subsystem	GPR	Replaced with	Reason for Replacement	Reference
bio01632	Not in BIGG DB	Biomass reaction Bacteroides thetaiotaomicron	Unassigned			Biomass_BT_v2		The biomass reaction was modified based on literature.
rxn00001	PPA	Inorganic pyrophospatase PpaX	None	BT_4315		PPA_1	Manual inspection of gene annotation revealed that this enzyme carries out a different reaction (generation of a proton motive force when PMF is sufficient).	NCBI Gene (last updated 28.05.11)
rxn00011	ACLS_a	pyruvatethiamin diphosphate acetaldehydetransferase	2.2.1.6	Branched-Chain Amino Acid Biosynthesis; Acetoin, butanediol metabolism	(BT_2076 and BT_2077)	ACLS	Two BIGG reactions sum up three SEED reactions (performed by same enzyme)	BIGG Database
rxn00016	AHEXASE3	Hexosaminidase	3.2.1.52	Chitin and N-acetylglucosamine utilization	(BT_4394 or BT_4395 or BT_4337 or BT_3598 or BT_1627 or BT_3868 or BT_0459 or BT_0460 or BT_0506 or BT_4681 or BT_1621 or BT_3178 or BT_0456 or BT_1051 or BT_2459)	AHEXASE3e	The saccharolytic enzymes of *B. thetaiotaomicron* are located mostly in periplasm (extracellular for modelling purposes).	PMID:12663928
rxn00199	Not in BIGG DB	Isocitrate dehydrogenase [NADP] (EC 1.1.1.42)	1.1.1.42	TCA Cycle	BT_2071	ICDHyr	One BIGG reaction sums up two SEED reactions (performed by same enzyme)	BIGG Database
rxn00302	Not in BIGG DB	GTP cyclohydrolase I type 1	3.5.4.16	Folate Biosynthesis; Queuosine-Archaeosine Biosynthesis	BT_3931	GTPCI	One BIGG reaction sums up four SEED reactions (performed by same enzyme)	BIGG Database

SEED Rxn ID	BIGG Rxn ID	Function	EC Number	Subsystem	GPR	Replaced with	Reason for Replacement	Reference
rxn00816	LACZ	Lactose galactohydrolase	3.2.1.108	Lactose and Galactose Uptake and Utilization; Lactose utilization; Galactosylceramide and Sulfatide metabolism	BT_1626 or BT_4050	LACZe	The saccharolytic enzymes of *B. thetaiotaomicron* are located mostly in periplasm (extracellular for modelling purposes).	PMID:12663928
rxn00863	Not in BIGG DB	Histidinol dehydrogenase	1.1.1.23	Histidine Biosynthesis	BT_0201	HISTD	One BIGG reaction sums up two SEED reactions (performed by same enzyme)	BIGG Database
rxn01316	ACNAMS	N-acetylneuraminate synthase	2.5.1.56	CMP-N-acetylneuraminate Biosynthesis	BT_1714	ACNAM9PL2	BT_1714 gene product was experimentally characterized and shown to carry out a different reaction (KDN-9-P-synthase).	PMID:18804026
rxn01387	Not in BIGG DB	Isocitrate dehydrogenase [NADP] (EC 1.1.1.42)	1.1.1.42	TCA Cycle	BT_2071	ICDHyr	One BIGG reaction sums up two SEED reactions (performed by same enzyme)	BIGG Database
rxn02159	Not in BIGG DB	Histidinol dehydrogenase	1.1.1.23	Histidine Biosynthesis	BT_0201	HISTD	One BIGG reaction sums up two SEED reactions (performed by same enzyme)	BIGG Database
rxn02185	ACLS_b	2-Acetolactate pyruvate-lyase (carboxylating)	2.2.1.6	Branched-Chain Amino Acid Biosynthesis; Acetoin, butanediol metabolism	(BT_2076 and BT_2077)	ACLS	Two BIGG reactions sum up three SEED reactions (performed by same enzyme)	BIGG Database
rxn02186	Not in BIGG DB	Ketol-acid reductoisomerase (EC 1.1.1.86)	1.1.1.86	Coenzyme A Biosynthesis; Branched-Chain Amino Acid Biosynthesis	BT_2074	KARA1	One BIGG reaction sums up three SEED reactions (performed by same enzyme)	BIGG Database
rxn02187	Not in BIGG DB	Ketol-acid reductoisomerase (EC 1.1.1.86)	1.1.1.86	Coenzyme A Biosynthesis; Branched-Chain Amino Acid Biosynthesis	BT_2074	KARA1	One BIGG reaction sums up three SEED reactions (performed by same enzyme)	BIGG Database

SEED Rxn ID	BIGG Rxn ID	Function	EC Number	Subsystem	GPR	Replaced with	Reason for Replacement	Reference
rxn03068	Not in BIGG DB	Ketol-acid reductoisomerase (EC 1.1.1.86)	1.1.1.86	Coenzyme A Biosynthesis; Branched-Chain Amino Acid Biosynthesis	BT_2074	KARA1	One BIGG reaction sums up three SEED reactions (performed by same enzyme)	BIGG Database
rxn03130	USHD	UDP-2,3-diacylglucosamine hydrolase	3.6.1.-	KDO2-Lipid A biosynthesis	BT_3697	USHD_BT	Replaced with *B. thetaiotaomicron*-specific reaction	PMID:19460428.; PMID:20974832; PMID:18931137
rxn03159	LPADSS	Lipid-A-disaccharide synthase	2.4.1.182	KDO2-Lipid A biosynthesis	BT_4004	LPADSS_BT	Replaced with *B. thetaiotaomicron*-specific reaction	PMID:19460428.; PMID:20974832; PMID:18931137
rxn03174	Not in BIGG DB	2-Amino-4-hydroxy-6-(erythro-1,2,3-trihydroxypropyl)	3.5.4.16	Folate Biosynthesis; Queuosine-Archaeosine Biosynthesis	BT_3931	GTPCI	One BIGG reaction sums up four SEED reactions (performed by same enzyme)	BIGG Database
rxn03181	TDSK	Tetraacyldisaccharide 4'-kinase	2.7.1.130	KDO2-Lipid A biosynthesis	BT_1880	TTDSK_BT	Replaced with *B. thetaiotaomicron*-specific reaction	PMID:19460428.; PMID:20974832; PMID:18931137
rxn03182	MOAT	3-deoxy-D-manno-octulosonic-acid transferase	2.-.-.-	KDO2-Lipid A biosynthesis	BT_2747	MOAT_BT	Replaced with *B. thetaiotaomicron*-specific reaction	PMID:19460428.; PMID:20974832; PMID:18931137
rxn03194	ilvg	(S)-2-Aceto-2-hydroxybutanoate pyruvate-lyase (carboxylating)	2.2.1.6	Branched-Chain Amino Acid Biosynthesis; Acetoin, butanediol metabolism	(BT_2076 and BT_2077)	ACHBS	Two BIGG reactions sum up three SEED reactions (performed by same enzyme)	BIGG Database
rxn03419	Not in BIGG DB	GTP cyclohydrolase I type 1	3.5.4.16	Folate Biosynthesis; Queuosine-Archaeosine Biosynthesis	BT_3931	GTPCI	One BIGG reaction sums up four SEED reactions (performed by same enzyme)	BIGG Database
rxn03421	Not in BIGG DB	GTP cyclohydrolase I type 1	3.5.4.16	Folate Biosynthesis; Queuosine-Archaeosine Biosynthesis	BT_3931	GTPCI	One BIGG reaction sums up four SEED reactions (performed by same enzyme)	BIGG Database
rxn03435	Not in BIGG DB	Ketol-acid reductoisomerase (EC 1.1.1.86)	1.1.1.86	Coenzyme A Biosynthesis; Branched-Chain Amino Acid Biosynthesis	BT_2074	KARA2	One BIGG reaction sums up two SEED reactions (performed by same enzyme)	BIGG Database
rxn03436	Not in BIGG DB	Ketol-acid reductoisomerase (EC 1.1.1.86)	1.1.1.86	Coenzyme A Biosynthesis; Branched-Chain Amino Acid Biosynthesis	BT_2074	KARA2	One BIGG reaction sums up two SEED reactions (performed by same enzyme)	BIGG Database

SEED Rxn ID	BIGG Rxn ID	Function	EC Number	Subsystem	GPR	Replaced with	Reason for Replacement	Reference
rxn03439	MOAT2	3-deoxy-D-manno-octulosonic-acid transferase	2.-.-.-	KDO2-Lipid A biosynthesis	BT_2747	MOAT_BT	Replaced with *B. thetaiotaomicron*-specific reaction	PMID:19460428.; PMID:20974832; PMID:18931137
rxn03951	Not in BIGG DB	4-hydroxythreonine-4-phosphate dehydrogenase	1.1.1.262	ECSIG4-SIG7; Pyridoxin (Vitamin B6) Biosynthesis	BT_4374	PDX5PS	One BIGG reaction sums up two SEED reactions and one spontaneous reaction. GPR changed to (BT_3918 and BT_4374).	BIGG Database
rxn04070	Not in BIGG DB	Pyridoxine 5'-phosphate synthase	2.6.99.2	Pyridoxin (Vitamin B6) Biosynthesis	BT_3918	PDX5PS	One BIGG reaction sums up two SEED reactions and one spontaneous reaction. GPR changed to (BT_3918 and BT_4374).	BIGG Database
rxn05012	Not in BIGG DB	N-acetylornithine carbamoyltransferase	2.1.3.9	Arginine Biosynthesis extended	BT_3717	SUCORNTC	It was shown experimentally that this enzyme carries out a different reaction in *Bacteroides* species.	PMID:16704984
rxn05024	Not in BIGG DB	Naphthoate synthase	4.1.3.36	Menaquinone and Phylloquinone Biosynthesis	BT_4702	NPHS	SEED reaction is incomplete. Complete reaction was drawn from BIGG database.	BIGG Database
rxn05116	Not in BIGG DB	rxn05116	Undetermined	None	Spontaneous	PDX5PS	One BIGG reaction sums up two SEED reactions and one spontaneous reaction. GPR changed to (BT_3918 and BT_4374).	BIGG Database
rxn06723	U23GAAT	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	2.3.1.-	KDO2-Lipid A biosynthesis	BT_4207	U23GAAT_BT	Replaced with *B. thetaiotaomicron*-specific reaction	PMID:19460428.; PMID:20974832; PMID:18931137
rxn06729	UAGAAT	(R)-3-Hydroxytetradecanoly-[acyl-carrier-protein]UDP-N-acetyl-	2.3.1.129	KDO2-Lipid A biosynthesis	(BT_3336 or BT_4205)	UAGAAT_HP	Drawn from *H. pylori* LPS biosynthesis pathway (BIGG), following protocol by Mazumdar et al. 2009	PMID:18931137
rxn06865	EDTXS1	Lipid A biosynthesis lauroyl acyltransferase	2.3.1.-	KDO2-Lipid A biosynthesis	BT_2152	EDTXS1_BT	Replaced with *B. thetaiotaomicron*-specific reaction	PMID:19460428.; PMID:20974832; PMID:18931137

SEED Rxn ID	BIGG Rxn ID	Function	EC Number	Subsystem	GPR	Replaced with	Reason for Replacement	Reference
rxn08335	DHORD5	Dihydroorotate dehydrogenase (quinone)	1.3.3.1	De Novo Pyrimidine Synthesis	false annotation (BT_0891 and BT_0892)	DHORDfum	*B. thetaiotaomicron* has a fumarate-dependent, not a quinone-dependent dihydroorotate dehydrogenase.	KEGG database
rxn08336	DHORD2	Dihydroorotate dehydrogenase (quinone)	1.3.3.1	De Novo Pyrimidine Synthesis	false annotation (BT_0891 and BT_0892)	DHORDfum	*B. thetaiotaomicron* has a fumarate-dependent, not a quinone-dependent dihydroorotate dehydrogenase.	KEGG database
rxn09988	ARABASE	alpha-N-arabinofuranosidase	3.2.1.55	L-Arabinose utilization; COG3533	(BT_0348 or BT_3096 or BT_3657)	ARABASE3e	The saccharolytic enzymes of *B. thetaiotaomicron* are located mostly in periplasm (extracellular for modelling purposes).	PMID:12663928
rxn10122	NADH6	NADH dehydrogenase (ubiquinone-8 3.5 protons)		Respiratory Complex I	(BT_4058 and BT_4059 and BT_4060 and BT_4061 and BT_4062 and BT_4063 and BT_4064 and BT_4065 and BT_4066 and BT_4067)	NADH17	It is unclear if *B. thetaiotaomicron* utilizes ubiquinone. Therefore, a menaquinone-dependent reaction was drawn from the E. coli reconstruction iAF1260 (BIGG).	PMID:6102980

Table S10d: Reactions included in the automated Model SEED reconstruction BΘ_Seed_v1 that were rejected based on manual inspection.

SEED Rxn ID	BIGG Rxn ID	Function	EC Number	Subsystem	Gene Associated	Reason for Removal	Reference
rxn00146	Not in BIGG DB	D-lactate dehydrogenase (ferricytochrome)	1.1.1.28	Fermentations: Lactate; Fermentations: Mixed acid	false annotation BT_1575	Only NADH use reported for biochemically characterized lactate dehydrogenase. This reaction is catalyzed by a different enzyme (EC 1.1.2.4) which is not known to be present in *B. thetaiotaomicron*.	PMID:19525515
rxn00222	Not in BIGG DB	beta-D-Glucoside glucohydrolase		Beta-glucosidase (EC 3.2.1.21)	(BT_3300) or (BT_1778 and BT_1780) or (BT_3009) or (BT_3314) or (BT_2854) or (BT_4714)	This reaction produces α-glucose. Only β-glucose-producing reaction (BGLA) is included in the BIGG database and will be added.	
rxn00350	GTHRDH	glutathione hydralase	2.3.2.2,3.4.11.4	Utilization_of_glutathione_as_a_sulphur_source|Glutathione:_Biosynthesis_and_gamma-glutamyl_cycle|Glutathione:_gamma-glutamyl_cycle|Poly-gamma-glutamate_biosynthesis|Ammonium_metabolism_H._pylori	No	*Bacteroides fragilis* does not have a pathway for glutathione synthesis. In *B. thetaiotaomicron*, genes required for glutathione synthesis are absent as well. All reactions involving glutathione were added during auto-completion, there is no evidence for their presence.	PMID:17873045
rxn00351	GTHS	glutathione synthetase	6.3.2.3	CBSS-320372.3.peg.6046|Glutathione:_Biosynthesis_and_gamma-glutamyl_cycle|Heat_shock_dnaK_gene_cluster_extended|Glutathione:_gamma-glutamyl_cycle|Glutathione_synthesis|Glutaredoxins|Heme_temp_review|Glutathione:_Non-redox_reactions	No	*Bacteroides fragilis* does not have a pathway for glutathione synthesis. In *B. thetaiotaomicron*, genes required for glutathione synthesis are absent as well. All reactions involving glutathione were added during auto-completion, there is no evidence for their presence.	PMID:17873045
rxn00396	Not in BIGG DB	ATPL-arginine N-phosphotransferase	2.7.3.3	None	No	This reaction was added in to allow arginine production from arginine phosphate. Arginine is not essential, so the gaps in arginine biosynthesis were filled. Since arginine synthesis by *Bacteroides* is only partly known, a sink reaction was necessary.	PMID:4853401 PMID:16704984
rxn00612	G3PD2	Glycerol-3-phosphate dehydrogenase [NADP+]	1.1.1.94	Glycerolipid and Glycerophospholipid Metabolism in Bacteria	BT_2123	According to UniProt, this enzyme only uses NAD as ligand.	UniProt

rxn00973	ACONT	Aconitase, complete reaction	4.2.1.3	Biogenesis of c-type cytochromes; Serine-glyoxylate cycle; TCA Cycle	BT_2072	The model originally included ACONT, ACONTa and ACONTb, which caused a flux loop. Removing ACONT solves this problem while still allowing the complete reaction to take place.	
rxn01602	FOLR2	DihydrofolateNADP+ oxidoreductase	1.5.1.3	Folate Biosynthesis; 5-FCL-like protein	(BT_0106 or BT_2048)	Reaction causes balanced cycles and infeasible ATP production and was therefore removed. Removing this reaction does not affect model performance.	
rxn01664	AADSACYCL	(S)-2-Amino-6-oxohexanoate hydro-lyase (spontaneous)	Undetermined	None	No	This spontaneous reaction both produces and consumes metabolites that are not included in the reconstruction.	
rxn01981	Not in BIGG DB	(5-L-Glutamyl)-L-amino-acid 5-glutamyltransferase (cyclizing)	2.3.2.4	Glutathione:_Biosynthesis_ and_gamma-glutamyl_cycle|Glutathione: _gamma-glutamyl_cycle	No	*Bacteroides fragili*s does not have a pathway for glutathione synthesis. In *B. thetaiotaomicro*n, genes required for glutathione synthesis are absent as well. All reactions involving glutathione were added during auto-completion, there is no evidence for their presence.	PMID:17873045
rxn02166	Not in BIGG DB	4-Nitrophenyl phosphate phosphohydrolase	3.1.3.1	Phosphate metabolism	(BT_3708) or (BT_4363) or (BT_0028)	This reaction consumes a metabolite not included in the reconstruction. This reaction is not included in the BIGG database.	
rxn02760	FFSDr	Sucrose phosphatase	3.2.1.26	Sucrose utilization	(BT_1765) or (BT_1759)	These enzymes are levanases. Itis not likely that they catalyze this reaction.	PMID:20603004
rxn02916	AOXHEXCYCL	6-Amino-2-oxohexanoate cyclation (spontaneous)	Undetermined	None	No	This spontaneous reaction both produces and consumes metabolites that are not included in the reconstruction.	
rxn03012	Not in BIGG DB	rxn03012	Undetermined	None	No	This spontaneous reaction both produces and consumes metabolites that are not included in the reconstruction.	
rxn03406	GLNSP1	Glutamine synthetase (uaaAgld)	6.3.1.2	Peptidoglycan biosynthesis	BT_0785	There is no evidence that this enzyme performs any reaction other than glutamine synthetase in *B. thetaiotaomicron*.	
rxn03407	GLNSP2	Glutamine synthetase (uaaGgla)	6.3.1.2	Peptidoglycan biosynthesis	BT_0785	There is no evidence that this enzyme performs any reaction other than glutamine synthetase in *B. thetaiotaomicron*.	

rxn03409	GLNSP3	Glutamine synthetase (uaagmda)	6.3.1.2	Peptidoglycan biosynthesis	BT_0785	There is no evidence that this enzyme performs any reaction other than glutamine synthetase in *B. thetaiotaomicron*.	
rxn03535	Not in BIGG DB	ATPcob(I)yrinic acid-a,c-diamide Cobeta-adenosyltransferase	2.5.1.17	G3E family of P-loop GTPases (metallocenter biosynthesis)	BT_2760	This enzyme catalyzes several reactions. Since *B. thetaiotaomicron* does not have a vitamin B12 synthesis pathway, the one most likely to take place in the cell is conversion of uptaken cob(I)alamin to adenosylcobalamin (active vitamin B12 coenzyme) (CBLAT in BIGG). Vitamin B12 is required for methylmalonyl-CoA mutase.	PMID:148460
rxn03843	FT	farnesyltranstransferase (trans,trans,cis-geranylgeranyl diphosphate-generating)	2.5.1.31	Isoprenoid Biosynthesis; Polyprenyl Diphosphate Biosynthesis	BT_3726	BIGG database suggests that this reaction only takes place in humans.	BIGG database
rxn03975	FMNRx2	FMN reductase	1.-.-.-	None	BT_2144	Produces a dead-end metabolite; annotation is weak (NCBI Gene: putative oxidoreductase).	NCBI Gene
rxn04132	Not in BIGG DB	5-hydroxyisourate spontaneous conversion to R-allantoin	Undetermined	None	No	This spontaneous reaction both produces and consumes metabolites that are not included in the reconstruction.	
rxn04133	Not in BIGG DB	5-hydroxyisourate spontaneous conversion to S-allantoin	Undetermined	None	No	This spontaneous reaction both produces and consumes metabolites that are not included in the reconstruction.	
rxn04456	Not in BIGG DB	5-Hydroxy-2-oxo-4-ureido-2,5-dihydro-1H-imidazole-5-carboxylate spontaneous conversion to R-allantoin	Undetermined	None	No	This spontaneous reaction both produces and consumes metabolites that are not included in the reconstruction.	
rxn04457	Not in BIGG DB	5-Hydroxy-2-oxo-4-ureido-2,5-dihydro-1H-imidazole-5-carboxylate spontaneous conversion to S-allantoin	Undetermined	None	No	This spontaneous reaction both produces and consumes metabolites that are not included in the reconstruction.	
rxn04673	Not in BIGG DB	1,4-dihydroxy-2-naphthoate octaprenyltransferase	EC 2.5.1.-	Menaquinone and Phylloquinone Biosynthesis	BT_2015	This reaction is necessary for phylloquinone biosynthesis. Phylloquinone is only present in photosynthetic organisms. The gene product of BT_2015 is involved in menaquinone biosynthesis.	PMID:20599680

rxn04674	Not in BIGG DB	rxn04674	EC 2.1.1.-	Menaquinone and Phylloquinone Biosynthesis	(BT_4216) or (BT_0853)	This reaction synthesizes phylloquinone. It is only present in photosynthetic organisms. The gene products of BT_4216 and BT_0853 are involved in menaquinone biosynthesis.	PMID:20599680
rxn05029	CBIAT	ATPcobinamide Cobeta-adenosyltransferase	2.5.1.17	G3E family of P-loop GTPases (metallocenter biosynthesis)	BT_2760	This enzyme catalyzes several reactions. Since *B. thetaiotaomicron* does not have a vitamin B12 synthesis pathway, the one most likely to take place in the cell is conversion of uptaken cob(I)alamin to adenosylcobalamin (active vitamin B12 coenzyme) (CBLAT in BIGG). Vitamin B12 is required for methylmalonyl-CoA mutase.	PMID:148460
rxn05064	Not in BIGG DB	carbamate hydro-lyase	4.2.1.104	None	No	This reaction occurs spontaneously from the product of cyanate lyase (EC 4.2.1.104). No evidence for the presence of this enzyme in *B. thetaiotaomicron* is available.	KEGG database
rxn05193	Not in BIGG DB	Butyro-betaine ABC transport	3.6.3.32	Choline and Betaine Uptake and Betaine Biosynthesis	(BT_1749 and BT_1750 and BT_1751)	This reaction is not included in the BIGG database and not connected to any pathway.	
rxn05502	Not in BIGG DB	L-arginine phosphate transport in/out via proton symport	Undetermined	None	No	This reaction was added in to allow arginine production from arginine phosphate. Arginine is not essential, so the gaps in arginine biosynthesis were filled. Since arginine synthesis by *Bacteroides* is only partly known, a sink reaction was necessary.	PMID:4853401 PMID:16704984
rxn05504	Not in BIGG DB	arsenobetaine transport in via ABC system	3.6.3.32	Choline and Betaine Uptake and Betaine Biosynthesis	(BT_1749 and BT_1750 and BT_1751)	This reaction is not included in the BIGG database and not connected to any pathway.	
rxn05517	Cobalt-zinc-cadmium resistance protein CzcD					Causes balanced cycles, therefore removed.	
rxn05526	Not in BIGG DB	chromate transport out via proton antiport	TC-2.A.51	None	(BT_2788 and BT_2789) or (BT_1735 and BT_1736)	This reaction is not included in the BIGG database and not connected to any pathway.	
rxn05567	GALTpts	Galactitol transport via PEPPyr PTS (phosphoenolpyruvate: phosphotransferase)	2.7.1.69	None	BT_4107	*B. thetaiotaomicron* does not possess a PTS system.	PMID:16887504

rxn05613	METSOX1abc	L-methionine S-oxide transport via ABC system		No		No evidence for the presence of this transport reaction in B. *thetaiotaomicron*. BIGG suggests that methionine oxidation to methionine-S-oxide occurs spontaneously (METOX1s).	
rxn05613	METSOX1abc	L-methionine S-oxide transport via ABC system	Undetermined	Transporters_In_Models|Staphylococcal_pathogenicity_islands_SaPI|Methionine_Biosynthesis|Methionine_Degradation	No	No evidence for the presence of this transport reaction in B. *thetaiotaomicron*.	
rxn05952	GTMLT	gamma-glutamyltransferase	2.3.2.2	None	No	*Bacteroides fragili*s does not have a pathway for glutathione synthesis. In *B. thetaiotaomicro*n, genes required for glutathione synthesis are absent as well. All reactions involving glutathione were added during auto-completion, there is no evidence for their presence.	PMID:17873045
rxn06472	GGLUCT2	(5-L-Glutamyl)-L-amino-acid 5-glutamyltransferase (cyclizing)	2.3.2.4	None	No	*Bacteroides fragili*s does not have a pathway for glutathione synthesis. In *B. thetaiotaomicro*n, genes required for glutathione synthesis are absent as well. All reactions involving glutathione were added during auto-completion, there is no evidence for their presence.	PMID:17873045
rxn06526		Cytochrome c-type biogenesis protein DsbD, protein-disulfide reductase (EC 1.8.1.8)				A generic reaction from KEGG that will not be added.	
rxn06672		biotin-carboxyl-carrier-proteincarbon-dioxide ligase (ADP-forming)				Represented by reaction BTNPL.	
rxn07438	Not in BIGG DB	peptide-methioninethioredoxin-disulfide S-oxidoreductase	1.8.4.12	Peptide methionine sulfoxide reductase	BT_2499	A generic reaction from KEGG that will not be added. BIGG uses METSOXR1 for this enzyme, which is already present in model.	
rxn07584	Lipoate-protein ligase A					This subsystem is not included in the BIGG database.	
rxn08085	AGPAT141	Membrane lipid synthesis 14:1/ 16:1	2.3.1.51	Glycerolipid and Glycerophospholipid Metabolism in Bacteria; Phosphate metabolism	(BT_0243 or BT_4462)	It is unclear whether *B. thetaiotaomicron* possesses these membrane lipids. Studies did not detect them.	PMID:7204330; PMID:6102980; PMID:7440508

rxn08087	AGPAT161	Membrane lipid synthesis 14:1/ 16:1	2.3.1.51	Glycerolipid and Glycerophospholipid Metabolism in Bacteria; Phosphate metabolism	(BT_0243 or BT_4462)	It is unclear whether *B. thetaiotaomicron* possesses these membrane lipids. Studies did not detect them.	PMID:7204330; PMID:6102980; PMID:7440508
rxn08308	DASYN141	Membrane lipid synthesis 14:1/ 16:1	2.7.7.41	Glycerolipid and Glycerophospholipid Metabolism in Bacteria; Iojap	(BT_4006 or BT_4463)	It is unclear whether *B. thetaiotaomicron* possesses these membrane lipids. Studies did not detect them.	PMID:7204330; PMID:6102980; PMID:7440508
rxn08310	DASYN161	Membrane lipid synthesis 14:1/ 16:1	2.7.7.41	Glycerolipid and Glycerophospholipid Metabolism in Bacteria; Iojap	(BT_4006 or BT_4463)	It is unclear whether *B. thetaiotaomicron* possesses these membrane lipids. Studies did not detect them.	PMID:7204330; PMID:6102980; PMID:7440508
rxn08783	LDH_D2	D-lactate dehydrogenase (ubiquinone)	1.1.2.4	Fermentations: Lactate; Fermentations: Mixed acid	false annotation BT_1575	Only NADH use reported for biochemically characterized lactate dehydrogenase. This reaction is catalyzed by a different enzyme (EC 1.1.2.4) which is not known to be present in *B. thetaiotaomicron*.	PMID:19525515
rxn09103	PGPP141	Membrane lipid synthesis 14:1/ 16:1	3.1.3.27	Competence or DNA damage-inducible protein CinA and related protein families; Glycerolipid and Glycerophospholipid Metabolism in Bacteria	BT_1525	It is unclear whether *B. thetaiotaomicron* possesses these membrane lipids. Studies did not detect them.	PMID:7204330; PMID:6102980; PMID:7440508
rxn09105	PGPP161	Membrane lipid synthesis 14:1/ 16:1	3.1.3.27	Competence or DNA damage-inducible protein CinA and related protein families; Glycerolipid and Glycerophospholipid Metabolism in Bacteria	BT_1525	It is unclear whether *B. thetaiotaomicron* possesses these membrane lipids. Studies did not detect them.	PMID:7204330; PMID:6102980; PMID:7440508
rxn09110	PGSA141	Membrane lipid synthesis 14:1/ 16:1	2.7.8.5	Competence or DNA damage-inducible protein CinA and related protein families; Glycerolipid and Glycerophospholipid Metabolism in Bacteria	(BT_1523 or BT_4464)	It is unclear whether *B. thetaiotaomicron* possesses these membrane lipids. Studies did not detect them.	PMID:7204330; PMID:6102980; PMID:7440508
rxn09112	PGSA161	Membrane lipid synthesis 14:1/ 16:1	2.7.8.5	Competence or DNA damage-inducible protein CinA and related protein families; Glycerolipid and Glycerophospholipid Metabolism in Bacteria	(BT_1523 or BT_4464)	It is unclear whether *B. thetaiotaomicron* possesses these membrane lipids. Studies did not detect them.	PMID:7204330; PMID:6102980; PMID:7440508
rxn09199	PSD141	Membrane lipid synthesis 14:1/ 16:1	4.1.1.65	Glycerolipid and Glycerophospholipid Metabolism in Bacteria	BT_2231	It is unclear whether *B. thetaiotaomicron* possesses these membrane lipids. Studies did not detect them.	PMID:7204330; PMID:6102980; PMID:7440508

rxn09201	PSD161	Membrane lipid synthesis 14:1/ 16:1	4.1.1.65	Glycerolipid and Glycerophospholipid Metabolism in Bacteria	BT_2231	It is unclear whether *B. thetaiotaomicron* possesses these membrane lipids. Studies did not detect them.	PMID:7204330; PMID:6102980; PMID:7440508
rxn09207	PSSA141	Membrane lipid synthesis 14:1/ 16:1	2.7.8.8	Glycerolipid and Glycerophospholipid Metabolism in Bacteria	BT_2232	It is unclear whether *B. thetaiotaomicron* possesses these membrane lipids. Studies did not detect them.	PMID:7204330; PMID:6102980; PMID:7440508
rxn09209	PSSA161	Membrane lipid synthesis 14:1/ 16:1	2.7.8.8	Glycerolipid and Glycerophospholipid Metabolism in Bacteria	BT_2232	It is unclear whether *B. thetaiotaomicron* possesses these membrane lipids. Studies did not detect them.	PMID:7204330; PMID:6102980; PMID:7440508
rxn09978	Not in BIGG DB	beta-glucosidase (methyl-alpha-D-glucoside)	3.2.1.21	Beta-glucosidase (EC 3.2.1.21)	(BT_3300) or (BT_1778 and BT_1780) or (BT_3009) or (BT_3314) or (BT_2854) or (BT_4714)	This reaction is not included in the BIGG database and not connected to any pathway.	
rxn09979	Not in BIGG DB	beta-glucosidase	3.2.1.21	Beta-glucosidase (EC 3.2.1.21)	(BT_3300) or (BT_1778 and BT_1780) or (BT_3009) or (BT_3314) or (BT_2854) or (BT_4714)	This reaction is not included in the BIGG database and not connected to any pathway.	
rxn09996		Teichuronic acid biosynthesis protein TuaE, putative secreted polysaccharide polymerase		- none -	BT_1165	NCBI Gene does not agree with this annotation. Furthermore, teichuronic acid hass only been found in gram-positive cell walls yet.	
rxn10120	NO3R1	periplasmic nitrate reductase		Nitrate reductase (Ubiquinol-8)	BT_0963	*Bacteroides* do not reduce nitrate to nitrite. Annotation is weak (NCBI Gene: putative ferredoxin-type protein).	Krieg NR (2010) Bergey's manual of systematic bacteriology, 2nd ed., volume 4 (Springer, New York)., NCBI Gene, last updated 08.01.11
rxn10126	SUCD4	succinate dehydrogenase		Succinate dehydrogenase; Serine-glyoxylate cycle; TCA Cycle	(BT_3054 and BT_3055)	The enzyme is present in *B. thetaiotaomicron*, but the evidence for this subreaction is weak.	
rxn10180	PNTOt4	Pantothenate transport	Undetermined	Coenzyme_A_Biosynthesis	No	Pantothenate is not an essential nutrient for *B. thetaiotaomicron*. The gap in pantothenate biosynthesis was filled by adding pantothenate synthetase (PANTS) based on gene annotation from KEGG.	PMID:4853401

rxn10192	Not in BIGG DB	CDP-glycerolpoly(glycerophosphate) glycerophosphotransferase	2.7.8.12	Teichoic and lipoteichoic acids biosynthesis	(BT_1650) or (BT_1716)	*Bacteroides thetaiotaomicron* is a gram-negative bacterium. Only gram-positive bacteria produce lipoteichoic acids. BT_1339 and BT_2888 are annotated as undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase and glycosyltransferase, respectively. They may have a role in lipolysaccharide synthesis, but their role is unclear.	PMID:20452953, NCBI Gene, last updates 04.03.11
rxn10289	TECA1S160	palmitoyl-lipoteichoic acid synthesis (n=24), linked, unsubstituted	2.7.8.12	Teichoic and lipoteichoic acids biosynthesis	(BT_1650) or (BT_1716)	*Bacteroides thetaiotaomicron* is a gram-negative bacterium. Only gram-positive bacteria produce lipoteichoic acids. BT_1339 and BT_2888 are annotated as undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase and glycosyltransferase, respectively. They may have a role in lipolysaccharide synthesis, but their role is unclear.	PMID:20452953, NCBI Gene, last updates 04.03.11
rxn10290	TECA1S140	myristoyl-lipoteichoic acid synthesis (n=24), linked, unsubstituted	2.7.8.12	Teichoic and lipoteichoic acids biosynthesis	(BT_1650) or (BT_1716)	*Bacteroides thetaiotaomicron* is a gram-negative bacterium. Only gram-positive bacteria produce lipoteichoic acids. BT_1339 and BT_2888 are annotated as undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase and glycosyltransferase, respectively. They may have a role in lipolysaccharide synthesis, but their role is unclear.	PMID:20452953, NCBI Gene, last updates 04.03.11
rxn10291	TECA1S180	stearoyl-lipoteichoic acid synthesis (n=24), linked, unsubstituted	2.7.8.12	Teichoic and lipoteichoic acids biosynthesis	(BT_1650) or (BT_1716)	*Bacteroides thetaiotaomicron* is a gram-negative bacterium. Only gram-positive bacteria produce lipoteichoic acids. BT_1339 and BT_2888 are annotated as undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase and glycosyltransferase, respectively. They may have a role in lipolysaccharide synthesis, but their role is unclear.	PMID:20452953, NCBI Gene, last updates 04.03.11

rxn10292	TECA1SI17	isoheptadecanoyl-lipoteichoic acid synthesis (n=24), linked, unsubstituted	2.7.8.12	Teichoic and lipoteichoic acids biosynthesis	(BT_1650) or (BT_1716)	*Bacteroides thetaiotaomicron* is a gram-negative bacterium. Only gram-positive bacteria produce lipoteichoic acids. BT_1339 and BT_2888 are annotated as undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase and glycosyltransferase, respectively. They may have a role in lipolysaccharide synthesis, but their role is unclear.	PMID:20452953, NCBI Gene, last updates 04.03.11
rxn10293	TECA1SAI17	anteisoheptadecanoyl-lipoteichoic acid synthesis (n=24), linked, unsubstituted	2.7.8.12	Teichoic and lipoteichoic acids biosynthesis	(BT_1650) or (BT_1716)	*Bacteroides thetaiotaomicron* is a gram-negative bacterium. Only gram-positive bacteria produce lipoteichoic acids. BT_1339 and BT_2888 are annotated as undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase and glycosyltransferase, respectively. They may have a role in lipolysaccharide synthesis, but their role is unclear.	PMID:20452953, NCBI Gene, last updates 04.03.11
rxn10294	TECA1SI14	isotetradecanoyl-lipoteichoic acid synthesis (n=24), linked, unsubstituted	2.7.8.12	Teichoic and lipoteichoic acids biosynthesis	(BT_1650) or (BT_1716)	*Bacteroides thetaiotaomicron* is a gram-negative bacterium. Only gram-positive bacteria produce lipoteichoic acids. BT_1339 and BT_2888 are annotated as undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase and glycosyltransferase, respectively. They may have a role in lipolysaccharide synthesis, but their role is unclear.	PMID:20452953, NCBI Gene, last updates 04.03.11
rxn10295	TECA1SI15	isopentadecanoyl-lipoteichoic acid synthesis (n=24), linked, unsubstituted	2.7.8.12	Teichoic and lipoteichoic acids biosynthesis	(BT_1650) or (BT_1716)	*Bacteroides thetaiotaomicron* is a gram-negative bacterium. Only gram-positive bacteria produce lipoteichoic acids. BT_1339 and BT_2888 are annotated as undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase and glycosyltransferase, respectively. They may have a role in lipolysaccharide synthesis, but their role is unclear.	PMID:20452953, NCBI Gene, last updates 04.03.11

rxn10296	TECA1SAI15	anteisopentadecanoyl-lipoteichoic acid synthesis (n=24), linked, unsubstituted	2.7.8.12	Teichoic and lipoteichoic acids biosynthesis	(BT_1650) or (BT_1716)	*Bacteroides thetaiotaomicron* is a gram-negative bacterium. Only gram-positive bacteria produce lipoteichoic acids. BT_1339 and BT_2888 are annotated as undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase and glycosyltransferase, respectively. They may have a role in lipolysaccharide synthesis, but their role is unclear.	PMID:20452953, NCBI Gene, last updates 04.03.11
rxn10297	TECA1SI16	isohexadecanoyl-lipoteichoic acid synthesis (n=24), linked, unsubstituted	2.7.8.12	Teichoic and lipoteichoic acids biosynthesis	(BT_1650) or (BT_1716)	*Bacteroides thetaiotaomicron* is a gram-negative bacterium. Only gram-positive bacteria produce lipoteichoic acids. BT_1339 and BT_2888 are annotated as undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase and glycosyltransferase, respectively. They may have a role in lipolysaccharide synthesis, but their role is unclear.	PMID:20452953, NCBI Gene, last updates 04.03.11
rxn10307	TECA5S160	palmitoyl-lipoteichoic acid synthesis (n=24), linked, N-acetylglucosamine substituted	2.7.8.12	Teichoic and lipoteichoic acids biosynthesis	(BT_1339) or (BT_2888)	*Bacteroides thetaiotaomicron* is a gram-negative bacterium. Only gram-positive bacteria produce lipoteichoic acids. BT_1339 and BT_2888 are annotated as undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase and glycosyltransferase, respectively. They may have a role in lipolysaccharide synthesis, but their role is unclear.	PMID:20452953, NCBI Gene, last updates 04.03.11
rxn10308	TECA5S140	myristoyl-lipoteichoic acid synthesis (n=24), linked, N-acetylglucosamine substituted	2.7.8.12	Teichoic and lipoteichoic acids biosynthesis	(BT_1339) or (BT_2888)	*Bacteroides thetaiotaomicron* is a gram-negative bacterium. Only gram-positive bacteria produce lipoteichoic acids. BT_1339 and BT_2888 are annotated as undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase and glycosyltransferase, respectively. They may have a role in lipolysaccharide synthesis, but their role is unclear.	PMID:20452953, NCBI Gene, last updates 04.03.11

rxn10309	TECA5S180	stearoyl-lipoteichoic acid synthesis (n=24), linked, N-acetylglucosamine substituted	2.7.8.12	Teichoic and lipoteichoic acids biosynthesis	(BT_1339) or (BT_2888)	*Bacteroides thetaiotaomicron* is a gram-negative bacterium. Only gram-positive bacteria produce lipoteichoic acids. BT_1339 and BT_2888 are annotated as undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase and glycosyltransferase, respectively. They may have a role in lipolysaccharide synthesis, but their role is unclear.	PMID:20452953, NCBI Gene, last updates 04.03.11
rxn10310	TECA5SI17	isoheptadecanoyl-lipoteichoic acid synthesis (n=24), linked, N-acetylglucosamine substituted	2.7.8.12	Teichoic and lipoteichoic acids biosynthesis	(BT_1339) or (BT_2888)	*Bacteroides thetaiotaomicron* is a gram-negative bacterium. Only gram-positive bacteria produce lipoteichoic acids. BT_1339 and BT_2888 are annotated as undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase and glycosyltransferase, respectively. They may have a role in lipolysaccharide synthesis, but their role is unclear.	PMID:20452953, NCBI Gene, last updates 04.03.11
rxn10311	TECA5SAI17	anteisoheptadecanoyl-lipoteichoic acid synthesis (n=24), linked, N-acetylglucosamine substituted	2.7.8.12	Teichoic and lipoteichoic acids biosynthesis	(BT_1339) or (BT_2888)	*Bacteroides thetaiotaomicron* is a gram-negative bacterium. Only gram-positive bacteria produce lipoteichoic acids. BT_1339 and BT_2888 are annotated as undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase and glycosyltransferase, respectively. They may have a role in lipolysaccharide synthesis, but their role is unclear.	PMID:20452953, NCBI Gene, last updates 04.03.11
rxn10312	TECA5SI14	isotetradecanoyl-lipoteichoic acid synthesis (n=24), linked, N-acetylglucosamine substituted	2.7.8.12	Teichoic and lipoteichoic acids biosynthesis	(BT_1339) or (BT_2888)	*Bacteroides thetaiotaomicron* is a gram-negative bacterium. Only gram-positive bacteria produce lipoteichoic acids. BT_1339 and BT_2888 are annotated as undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase and glycosyltransferase, respectively. They may have a role in lipolysaccharide synthesis, but their role is unclear.	PMID:20452953, NCBI Gene, last updates 04.03.11

rxn10313	TECA5SI15	isopentadecanoyl-lipoteichoic acid synthesis (n=24), linked, N-acetylglucosamine substituted	2.7.8.12	Teichoic and lipoteichoic acids biosynthesis	(BT_1339) or (BT_2888)	*Bacteroides thetaiotaomicron* is a gram-negative bacterium. Only gram-positive bacteria produce lipoteichoic acids. BT_1339 and BT_2888 are annotated as undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase and glycosyltransferase, respectively. They may have a role in lipolysaccharide synthesis, but their role is unclear.	PMID:20452953, NCBI Gene, last updates 04.03.11
rxn10314	TECA5SAI15	anteisopentadecanoyl-lipoteichoic acid synthesis (n=24), linked, N-acetylglucosamine substituted	2.7.8.12	Teichoic and lipoteichoic acids biosynthesis	(BT_1339) or (BT_2888)	*Bacteroides thetaiotaomicron* is a gram-negative bacterium. Only gram-positive bacteria produce lipoteichoic acids. BT_1339 and BT_2888 are annotated as undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase and glycosyltransferase, respectively. They may have a role in lipolysaccharide synthesis, but their role is unclear.	PMID:20452953, NCBI Gene, last updates 04.03.11
rxn10315	TECA5SI16	isohexadecanoyl-lipoteichoic acid synthesis (n=24), linked, N-acetylglucosamine substituted	2.7.8.12	Teichoic and lipoteichoic acids biosynthesis	(BT_1339) or (BT_2888)	*Bacteroides thetaiotaomicron* is a gram-negative bacterium. Only gram-positive bacteria produce lipoteichoic acids. BT_1339 and BT_2888 are annotated as undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase and glycosyltransferase, respectively. They may have a role in lipolysaccharide synthesis, but their role is unclear.	PMID:20452953, NCBI Gene, last updates 04.03.11
rxn10829	GTHRDt2	glutathione transport	Undetermined	None	No	*Bacteroides fragilis* does not have a pathway for glutathione synthesis. In *B. thetaiotaomicron*, genes required for glutathione synthesis are absent as well. All reactions involving glutathione were added during auto-completion, there is no evidence for their presence.	PMID:17873045
rxn11268	PPIt2r	Probable low-affinity inorganic phosphate transporter		Phosphate metabolism	BT_4637	A pyrophosphate transporter is not included in the BIGG database. Only phosphate transport (PIt6) will be added to the reconstruction.	

rxn12666	PYDXtr	Pyridoxal transport	Undetermined	None	No	Pyridoxal is not an essential nutrient for *B. thetaiotaomicron*. Therefore, vitamin B6 biosynthesis needs to be possible without uptake of any precursors.	PMID:4853401
rxn12844	Not in BIGG DB	Gly-Cys aminopeptidase	E3.4.11.2	Dipeptidases (EC 3.4.13.-); Recycling of Peptidoglycan Amino Acids	((BT_2706) or (BT_0638) or (BT_1615) or (BT_4045))	Replaced with AMPTASECG	
rxn13782	Not in BIGG DB	Protein biosynthesis	Undetermined		No	A generic reaction that will not be included.	
rxn13783	Not in BIGG DB	DNA replication	Undetermined		No	A generic reaction that will not be included.	
rxn13784	Not in BIGG DB	RNA transcription	Undetermined		No	A generic reaction that will not be included.	

Table S10e: Reactions added to the automated reconstruction based on evidence literature and for gapfilling.

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
12ETHDt	1,2-Ethanediol facilitated transport		Transport, Extracellular	Evidence from KEGG database		KEGG Pathway suggests that this metabolite is formed.	
12PPDRt	R-Propane-1,2-diol facilitated transport		Transport, Extracellular	Evidence from literature	PMID:18848625, PMID:8370454	Fermentation of rhamnose leads to secretion of propane-1,2-diol as end product. R-propane-1,2-diol is formed via methylglyoxal (PMID:8370454). Gene is unknown.	
12PPDt	S-Propane-1,2-diol facilitated transport		Transport, Extracellular	Evidence from literature	PMID:17448155, PMID:18848625	Fermentation of fucose and rhamnose leads to secretion of propane-1,2-diol as end product. Gene is unknown.	
2FUCLAC_FUCASEe	alpha-fucosidase, 2-fucosyllactose (extracellular)	((BT_1625 or BT_4136) and ((BT_4134 and BT_4135) or (BT_1630 and BT_1631)))	HMO Degradation	Evidence from literature	PMID: 22036470	B. thetaiotaomicron grows on human milk oligosaccharides (HMOs); numerous glycosidase hydrolases are upregulated during growth on HMOs. Involves alpha-fucosidase and susC/ SusD (binding proteins).	
2MMALD	(R)-2-methylmalate dehydratase	(BT_1859 and BT_1860)	Valine, Leucine, and Isoleucine Metabolism	Manually added gene annotation from databases		Added based on annotation from KEGG	4.2.1.35
2MMALD2	3-isopropylmalate/(R)-2-methylmalate dehydratase	(BT_1859 and BT_1860)	Valine, Leucine, and Isoleucine Metabolism	Manually added gene annotation from databases		Added based on annotation from KEGG	4.2.1.35
3DSPHR	3-Dehydrosphinganine reductase		Sphingolipid Metabolism	Evidence from literature	PMID:16887518, PMID:20855611	*Bacteroides* are well established to produce sphingolipids. However, no homolog of human 3DSPHR was found in *Bacteroides* species. Either *Bacteroides* have structural homologs of this enzyme, which are not revealed by BLASTP search, or sphingolipids are synthesized by another mechanism.	1.1.1.102
3FUCLAC_FUCASEe	alpha-fucosidase, 3-fucosyllactose (extracellular)	((BT_1625 or BT_4136) and ((BT_4134 and BT_4135) or (BT_1630 and BT_1631)))	HMO Degradation	Evidence from literature	PMID: 22036470	B. thetaiotaomicron grows on human milk oligosaccharides (HMOs); numerous glycosidase hydrolases are upregulated during growth on HMOs. Involves alpha-fucosidase and susC/ SusD (binding proteins).	

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
3HACPR1	3-hydroxyacyl-ACP-dehydratase (FabZ)	BT_4206	Biotin Metabolism	Evidence from literature	PMID:20693992	Based on biotin synthesis described in PMID:20693992 for *E. coli*.	
3HACPR2	3-hydroxyacyl-ACP-dehydratase (FabZ)	BT_4206	Biotin Metabolism	Evidence from literature	PMID:20693992	Based on biotin synthesis described in PMID:20693992 for *E. coli*	
3HAD121	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C12:1)	BT_4206	Cell Envelope Biosynthesis	Evidence from literature	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of *B. thetaiotaomicron* was determined experimentally.	4.2.1.61
3HAD141	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C14:1)	BT_4206	Cell Envelope Biosynthesis	Evidence from literature	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of *B. thetaiotaomicron* was determined experimentally.	4.2.1.61
3HAD161	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C16:1)	BT_4206	Cell Envelope Biosynthesis	Evidence from literature	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of *B. thetaiotaomicron* was determined experimentally.	4.2.1.61
3HAD181	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C18:1)	BT_4206	Cell Envelope Biosynthesis	Evidence from literature	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of *B. thetaiotaomicron* was determined experimentally.	4.2.1.61
3OAACPR1	3-ketoacyl-ACP-reductase (FabG)	BT_0409	Biotin Metabolism	Evidence from literature	PMID:20693992	Based on biotin synthesis described in PMID:20693992 for *E. coli*. BT_0409 was considered the most likely putatively annotated gene for FabG	
3OAACPR2	3-ketoacyl-ACP-reductase (FabG)	BT_0409	Biotin Metabolism	Evidence from literature	PMID:20693992	Based on biotin synthesis described in PMID:20693992 for *E. coli*. BT_0409 was considered the most likely putatively annotated gene for FabG	
3OAR121	3-oxoacyl-[acyl-carrier-protein] reductase (n-C12:1)	(BT_0972 or BT_2380)	Cell Envelope Biosynthesis	Evidence from literature	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of *B. thetaiotaomicron* was determined experimentally.	1.1.1.100
3OAR141	3-oxoacyl-[acyl-carrier-protein] reductase (n-C14:1)	(BT_0972 or BT_2380)	Cell Envelope Biosynthesis	Evidence from literature	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of *B. thetaiotaomicron* was determined experimentally.	1.1.1.100
3OAR161	3-oxoacyl-[acyl-carrier-protein] reductase (n-C16:1)	(BT_0972 or BT_2380)	Cell Envelope Biosynthesis	Evidence from literature	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of *B. thetaiotaomicron* was determined experimentally.	1.1.1.100
3OAR181	3-oxoacyl-[acyl-carrier-protein] reductase (n-C18:1)	(BT_0972 or BT_2380)	Cell Envelope Biosynthesis	Evidence from literature	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of *B. thetaiotaomicron* was determined experimentally.	1.1.1.100
3OAS121	3-oxoacyl-[acyl-carrier-protein] synthase (n-C12:1)	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	Cell Envelope Biosynthesis	Evidence from literature	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of *B. thetaiotaomicron* was determined experimentally.	2.3.1.41

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
3OAS141	3-oxoacyl-[acyl-carrier-protein] synthase (n-C14:1)	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	Cell Envelope Biosynthesis	Evidence from literature	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of *B. thetaiotaomicron* was determined experimentally.	2.3.1.41
3OAS161	3-oxoacyl-[acyl-carrier-protein] synthase (n-C16:1)	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	Cell Envelope Biosynthesis	Evidence from literature	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of *B. thetaiotaomicron* was determined experimentally.	2.3.1.41
3OAS181	3-oxoacyl-[acyl-carrier-protein] synthase (n-C18:1)	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	Cell Envelope Biosynthesis	Evidence from literature	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of *B. thetaiotaomicron* was determined experimentally.	2.3.1.41
3POPDC	phosphonopyruvate decarboxylase	BT_1719	Capsular Polysaccharide Biosynthesis	Evidence from literature	PMID:12904299	The enzyme catalyses a step in the biosynthetic pathway of 2-aminoethylphosphonate, a component of the capsular polysaccharide complex of *Bacteroides fragilis* and most likely other *Bacteroides* species. Requires thiamine diphosphate and Mg2+ as cofactors. The enzyme is activated by the divalent cations Mg2+, Ca2+ and Mn2+. Pyruvate and sulfopyruvate can also act as substrates, but more slowly. This enzyme drives the reaction catalysed by EC 5.4.2.9, phosphoenolpyruvate mutase, in the thermodynamically unfavourable direction of 3-phosphonopyruvate formation.	4.1.1.82
5DOAN	5'-deoxyadenosine nuclosidase	BT_4451	Cofactor and Prosthetic Group Biosynthesis	Evidence from literature	PMID:21166890	This reaction is catalyzed by Methylthioadenosine/S-adenosylhomocysteine nucleosidase.	
7AHSDH	7-alpha-hydroxysteroid dehydrogenase	BT_1911	Bile Acid Metabolism	Evidence from literature	PMID:189820	Partly purified and characterized (PMID:189820) and annotated in *B. thetaiotaomicron* genome	1.1.1.159

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
7OCHOLATEt2	3alpha,12alpha-Dihydroxy-7-oxo-5beta-cholanate transport out via sodium cotransport		Transport, Extracellular	Evidence from literature	PMID:16299351	*B. thetaiotaomicron* cannot completely epimerize bile acids. Further biotransformation of bile acid is performed by other gut bacteria (reviewed in PMID:16299351). Therefore, secretion of metabolized bile acid assumed.	
A_MANASEe	alpha-mannosidase, extracellular	(BT_3774 or BT_3990 or BT_3991 or BT_2199 or BT_2105 or BT_4072 or BT_4092 or BT_3994 or BT_3784 or BT_3527 or BT_3530 or BT_2629)	N-Glycan Degradation	Evidence from literature	PMID:18996345	*B. thetaiotaomicron* is known to degrade host N-glycans.	3.2.1.24
ACETOLt	Acetol facilitated transport		Transport, Extracellular	Evidence from literature	PMID:11260473	B. thetaiotaomicron produces acetol.	
ACGALK3	N-acetylgalactosamine kinase (6-phosphate)		Aminosugar Metabolism	Evidence from literature	PMID:2845859	*B. thetaiotaomicron* grows on N-acetylgalactosamine: PMID:2845859. However, the utilization pathway is poorly understood.	
ACGALr	N-acetylgalactosamine reversible transport via proton symport		Transport, Extracellular	Evidence from literature	PMID:2845859	*B. thetaiotaomicron* grows on N-acetylgalactosamine: PMID:2845859. However, the utilization pathway is poorly understood.	
ACGAMPM	phosphoacetylglucosamine mutase		Aminosugar Metabolism	Manual gapfilling	PMID:7240086	Manually filled in based on KEGG Pathway to to make N-acetylglucosamine, a substrate known to support growth, usable.	5.4.2.3
ACGAMtr	Na-acetylglucosamine transport in via proton symport, reversible	(BT_3180 or BT_3619)	Transport, Extracellular	Evidence from literature	PMID:7240086	*B. thetaiotaomicron* grows on N-acetylglucosamine as sole carbon source. Gene annotation taken from The SEED Viewer (last checked 01.07.11).	
ACGS	N-acetylglutamate synthase		Arginine and Proline Metabolism	Manual gapfilling		No GPR association available, but all reaction following up from this reaction to acetylornithine deacetylase are present, so a complete pathway was assumed.	2.3.1.1

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
ACNAM9PL2	2-keto-3-deoxy-d-glycero-d-galacto-9-phosphonononic acid (KDN-9-P) synthase	BT_1714	Capsular Polysaccharide Biosynthesis	Evidence from literature	PMID: 18804026	*B. thetaiotaomicron* forms and cytidylates 2-keto-3-deoxy-D-glycero-D-galacto-nononic acid (KDN), most likely for inclusion in its capsular polysaccharides.	2.5.1.56
ACS	acetyl-CoA synthetase	BT_2924	Glycolysis/Gluconeogenesis	Manually added gene annotation from databases		Annotation from NCBI Gene, last updated 21.05.11	6.2.1.1
ACS2	acetyl-CoA synthase (propionate)	BT_2924	Glycolysis/Gluconeogenesis	Manually added gene annotation from databases		Annotation from NCBI Gene, last updated 21.05.11	6.2.1.1
ACtr	acetate transporter		Transport, Extracellular	Evidence from literature	PMID:19321416, PMID:12740060	*Bacteroides* species are well established to produce short-chain fatty acids (SCFAs).	
AGDC2	N-acetylgalactosamine-6-phosphate amidohydrolase	(BT_0675 or BT_0676 or BT_3588)	Aminosugar Metabolism	Evidence from literature	PMID:2845859	*B. thetaiotaomicron* grows on N-acetylgalactosamine. Utilization pathway is based on assumption.	3.5.1.25
AGMHE	ADP-D-glycero-D-manno-heptose epimerase		Lipopolysaccharide Biosynthesis	Evidence from literature	PMID:20974832	No gene found, but this reaction is required for lipopolysaccharide synthesis. The structure of *B. thetaiotaomicron* LPS has been studied.	5.1.3.20
AHEXASE2e	N-acetylglucosaminidase, N-glycans, extracellular	(BT_4394 or BT_4395 or BT_4337 or BT_3598 or BT_1627 or BT_3868 or BT_0459 or BT_0460 or BT_0506 or BT_4681 or BT_1621 or BT_3178 or BT_0456 or BT_1051 or BT_2459)	N-Glycan Degradation	Evidence from literature	PMID:16565725, PMID: 20689974	BT_4395 gene product was purified and characterized.	

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
AHEXASE3e	beta-N-acetylhexosaminidase, extracellular	(BT_4394 or BT_4395 or BT_4337 or BT_3598 or BT_1627 or BT_3868 or BT_0459 or BT_0460 or BT_0506 or BT_4681 or BT_1621 or BT_3178 or BT_0456 or BT_1051 or BT_2459)	N-Glycan Degradation	Evidence from literature	PMID:16565725, PMID: 20689974	BT_4395 gene product was purified and characterized.	3.2.1.52
AHEXASEe	beta-N-acetylhexosaminidase, extracellular	(BT_4394 or BT_4395 or BT_4337 or BT_3598 or BT_1627 or BT_3868 or BT_0459 or BT_0460 or BT_0506 or BT_4681 or BT_1621 or BT_3178 or BT_0456 or BT_1051 or BT_2459)	N-Glycan Degradation	Evidence from literature	PMID:16565725, PMID: 20689974	BT_4395 gene product was purified and characterized.	3.2.1.52
AIRC3	phosphoribosylaminoimidazole carboxylase (mutase rxn)	BT_2518	Purine and Pyrimidine Biosynthesis	Based on BIGG database		According to KEGG and BIGG databases, phosphoribosylaminoimidazole carboxylase also catalyzes NCAIR mutase reaction.	4.1.1.21
ALAALADe	D-alanine-D-alanine dipeptidase, extracellular	(BT_3007 or BT_3187)	Peptide Degradation	Evidence from literature	PMID:12663928	Predicted non-cytosolic in PMID:12663928. Assumed to be extracellular for modeling purposes.	3.4.17.14
ALAASPt	L-alanyl-L-aspartate transport via proton symport	(BT_0580 or BT_4385 or BT_1086)	Transport, Extracellular	Manually added gene annotation from databases		Genes added based on TransportDB (last consulted 06.06.12).	
ALAGLNt	L-alanyl-L-glutamine transport via proton symport	(BT_0580 or BT_4385 or BT_1086)	Transport, Extracellular	Manually added gene annotation from databases		Genes added based on TransportDB (last consulted 06.06.12).	

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
ALAGLUt	L-alanyl-L-glutamate transport via proton symport	(BT_0580 or BT_4385 or BT_1086)	Transport, Extracellular	Manually added gene annotation from databases		Genes added based on TransportDB (last consulted 06.06.12).	
ALAGLYt	L-alanylglycine transport via proton symport	(BT_0580 or BT_4385 or BT_1086)	Transport, Extracellular	Manually added gene annotation from databases		Genes added based on TransportDB (last consulted 06.06.12).	
ALAHISt	L-alanyl-L-histidine transport via proton symport	(BT_0580 or BT_4385 or BT_1086)	Transport, Extracellular	Manually added gene annotation from databases		Genes added based on TransportDB (last consulted 06.06.12).	
ALALEUt	L-alanyl-L-leucine transport via proton symport	(BT_0580 or BT_4385 or BT_1086)	Transport, Extracellular	Manually added gene annotation from databases		Genes added based on TransportDB (last consulted 06.06.12).	
ALAR	alanine racemase	BT_4101	Alanine and Aspartate Metabolism	Manually added gene annotation from databases		Annotation from KEGG and NCBI Gene (last updated 01.01.11)	5.1.1.1
ALAt4r	Alanine-Sodium symporter	BT_4476	Transport, Extracellular	Manually added gene annotation from databases		Annotation from TransportDB (www.membranetransport.org).	
ALATHRt	L-alanyl-L-threonine transport via proton symport	(BT_0580 or BT_4385 or BT_1086)	Transport, Extracellular	Manually added gene annotation from databases		Genes added based on TransportDB (last consulted 06.06.12).	
ALR2	aldose reductase (methylglyoxal)		Central Metabolism	Evidence from literature	PMID:18848625, PMID:8370454, PMID:11260473	No GPR is known. The reaction is putatively added to reconcile the results by PMID:18848625, which suggest the presence of a second pathway for 1,2-propanediol formation in *B. thetaiotaomicron*. Also based on pathways described by PMID:8370454. There is evidence for acetol production in *B. thetaiotaomicron* (PMID:11260473).	1.1.1.21
ALR4x	aldose reductase (acetol)	(BT_3617 or BT_4424)	Glycerophospholipid Metabolism	Evidence from literature	PMID:18848625, PMID:8370454	The reaction is carried out by sorbitol dehydrogenase. Added to reconcile the results by PMID:18848625, which suggest the presence of a second pathway for 1,2-propanediol formation in *B. thetaiotaomicron*. Also based on pathways described by PMID:8370454.	

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
AMANNANASEe	Alpha-mannan degradation, extracellular	((BT_3990 or BT_2629 or BT_2199 or BT_3784 or BT_3962 or BT_4092) and (BT_3991 or BT_3858 or BT_1769 or BT_1878 or BT_3130 or BT_3773) and (BT_3994 or BT_3792 or BT_2623 or BT_2949 or BT_3501 or BT_1883 or BT_3524 or BT_3301 or BT_3521) and ((BT_2625 and BT_2626) or (BT_3788 and BT_3789) or (BT_3854 and BT_3855)))	N-Glycan Degradation	Evidence from literature	PMID: 22205877, PMID: 20081828	B. thetaiotaomicron grows on yeast alpha-mannan.The enzymes carrying out the reaction are assumed to be secreted. The reaction involves cleaving of alpha-1,2, -1,3 and -1,6 bonds. Several susC and susD are upregulated during growth on alpha-mannan (included in the GPR).	
AMMQLT8	S-adenosylmethione:2-demthylmenaquinole methyltransferase (menaquinone 8)	(BT_0853 or BT_4216)	Cofactor and Prosthetic Group Biosynthesis	Evidence from literature	PMID:6102980	*B. thetaiotaomicron* produces menaquinone 8.	2.1.1.-
AMMQT10	S-adenosylmethione:2-demthylmenaquinone methyltransferase (menaquinone 10)	(BT_0853 or BT_4216)	Cofactor and Prosthetic Group Biosynthesis	Evidence from literature	PMID:6102980	B. thetaiotaomicron produces menaquinone 7,8,9,10 and 11. MK-10 and MK-11 are the main components. Reaction is not charge balanced. Needs to be fixed. AH	
AMMQT11	S-adenosylmethione:2-demthylmenaquinone methyltransferase (menaquinone 11)	(BT_0853 or BT_4216)	Cofactor and Prosthetic Group Biosynthesis	Evidence from literature	PMID:6102980	B. thetaiotaomicron produces menaquinone 7,8,9,10 and 11. MK-10 and MK-11 are the main components. Reaction is not charge balanced. Needs to be fixed. AH	2.7.7.38

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
AMMQT7	S-adenosylmethione:2-demthylmenaquinone methyltransferase (menaquinone 7)	(BT_0853 or BT_4216)	Cofactor and Prosthetic Group Biosynthesis	Evidence from literature	PMID:6102980	B. thetaiotaomicron produces menaquinone 7,8,9,10 and 11. MK-10 and MK-11 are the main components. Reaction is not charge balanced. Needs to be fixed. AH	3.2.1.65
AMMQT9	S-adenosylmethione:2-demthylmenaquinone methyltransferase (menaquinone 9)	(BT_0853 or BT_4216)	Cofactor and Prosthetic Group Biosynthesis	Evidence from literature	PMID:6102980	B. thetaiotaomicron produces menaquinone 7,8,9,10 and 11. MK-10 and MK-11 are the main components. Reaction is not charge balanced. Needs to be fixed. AH	3.2.1.65
AMPTASEPG	aminopeptidase (pro-gly)	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314)	Peptide Degradation	Manually added gene annotation from databases			
AMPTASEPGe	hydrolysis of Prolylglycine by predicted non-cytosolic proline peptidase	BT_0587	Peptide Degradation	Evidence from literature	PMID:12663928	Predicted non-cytosolic in PMID:12663928. Assumed to be extracellular for modeling purposes.	3.4.13.9
AMY1e	alpha-amylase, extracellular (strch1 -> strch2)	((BT_3698 and BT_3701 and BT_3702) or (BT_0773 and BT_3701 and BT_3702) or (BT_4305 and BT_3701 and BT_3702))	Plant Polysaccharide Degradation	Evidence from literature	PMID:10986238, PMID:2722747, PMID:8955399, PMID: 18981178, PMID:18611383	Starch utilization by B. thetaiotaomicron as sole carbon source is well established.	3.2.1.1
AMYe	starch hydrolysis by alpha-1,4-amylase and alpha-1,6 pullulanase	((BT_3698 and BT_3701 and BT_3702) or (BT_0773 and BT_3701 and BT_3702) or (BT_4305 and BT_3701 and BT_3702))	Plant Polysaccharide Degradation	Evidence from literature	PMID:10986238, PMID:2722747, PMID:8955399, PMID: 18981178, PMID:18611383	Starch utilization by B. thetaiotaomicron as sole carbon source is well established.	3.2.1.1

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
AMYLe	amylose hydrolysis by alpha-1,4-amylase	((BT_3698 and BT_3701 and BT_3702) or (BT_0773 and BT_3701 and BT_3702) or (BT_4305 and BT_3701 and BT_3702))	Plant Polysaccharide Degradation	Evidence from literature	PMID:10986238, PMID:2722747, PMID:8955399, PMID: 18981178, PMID:18611383	Starch utilization by B. thetaiotaomicron as sole carbon source is well established.	3.2.1.1
AOXSr2	8-amino-7-oxononanoate synthase (pimeloyl-ACP)	(BT_0870 or BT_1443)	Biotin Metabolism	Evidence from literature	PMID:20693992	This enzyme is generally believed to utilize pimeloyl-CoA. Use of pimeloyl-ACP was recently shown.	2.3.1.47
ARABASE3e	arabinotriose arabinosidase	(BT_0348 or BT_3096 or BT_3657)	Plant Polysaccharide Degradation	Evidence from literature	PMID: 21339299	Takes place in periplasm. Extracellular for modelling purposes.	3.2.1.55
ARABINANASEe	Arabinan degradation, extracellular	((BT_0360 or BT_0367 or BT_0368 or BT_0369) and (BT_4152 or BT_4667 or BT_4668) and (BT_4153 or BT_4170) and (BT_4175 or BT_4176) and ((BT_0361 and BT_0362) or (BT_4164 and BT_4165) or (BT_0363 and BT_0364) or (BT_4670 and BT_4671) or (BT_3680 and BT_3681)))	Plant Polysaccharide Degradation	Evidence from literature	PMID: 22205877, PMID: 21339299	B. thetaiotaomicron grows on arabinan. BT_0360, BT_0367 and BT_0369 are active against sugar beet arabinan. susC/ susD homologs and enzymes for galactose, galacturonate and L-rhamnose degradation (included in GPR) are upregulated during growth on arabinan.	

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
ARABINOGALASEe	Arabinogalactan degradation by beta-galactosidase, endo-arabinofuranosidase and beta-glucuronidase, extracellular/periplasmatic	((BT_0348 or BT_0265 or BT_3675 or BT_3685) and BT_0290 and BT_3687 and ((BT_3045 and BT_3046) or (BT_0268 and BT_0269) or (BT_0272 and BT_0273) or (BT_3680 and BT_3681)))	Plant Polysaccharide Degradation	Evidence from literature	PMID:848954, PMID:7251978, PMID:16887514 PMID:10820072, PMID: 22205877	B. thetaiotaomicron degrades larch arabinogalactan, which consists of galactose/arabinose (6:1) and small amounts of glucuronic acid. Larch AG is likely degraded via beta-galactosidase, Arabinan endo-1,5-alpha-L-arabinosidase (EC 3.2.1.99) and Alpha-N-arabinofuranosidase (EC 3.2.1.55) and involves susC/ susD. The genes included in the GPR are upregulated during growth on arabinogalactan.	
ARGabc	L-arginine transport via ABC system	BT_4049	Transport, Extracellular	Manually added gene annotation from databases		Annotation from NCBI Gene (last updated 01.01.11)	
ARGARG1c	Hydrolysis of L-argininyl-L-arginine	BT_1846	Peptide Degradation	Evidence from literature	PMID: 22628297	B. thetaiotaomicron peptidase M49 was characterized and shown to hydrolyze Arg-Arg and Phe-Arg specifically.	1.1.3.9
ARGARGt	L-argininyl-L-arginine transport via proton symport	(BT_0580 or BT_4385 or BT_1086)	Transport, Extracellular	Evidence from literature	PMID: 22628297	B. thetaiotaomicron peptidase M49 was characterized and shown to hydrolyze Arg-Arg and Phe-Arg specifically.	3.2.1.31
AROH	L-Arogenate hydro-lyase	BT_3936	Tyrosine, Tryptophan, and Phenylalanine Metabolism	Manually added gene annotation from databases		Added based on KEGG Pathway	4.2.1.51
AS3TASE_HS1	N-acetylglucosamine-3-sulfatase, heparin degradation		Glycosaminoglycan Degradation	Evidence from literature	PMID:19801541, PMID:7574611	*B.thetaiotaomicron* specific putative heparin sulfate degradation pathway. It is unknown which sulfatase catalyzes this reaction.	3.1.6.14
AS3TASE_HS2	N-acetylglucosamine-3-sulfatase, heparin degradation		Glycosaminoglycan Degradation	Evidence from literature	PMID:19801541, PMID:7574611	*B.thetaiotaomicron* specific putative heparin sulfate degradation pathway. It is unknown which sulfatase catalyzes this reaction.	3.1.6.14
AS6TASE_HS1	N-acetylglucosamine-6-sulfatase, heparin degradation	(BT_4656 and BT_0238)	Glycosaminoglycan Degradation	Evidence from literature	PMID:19801541, PMID:7574611, PMID:21507958	*B. thetaiotaomicron* specific putative heparin sulfate degradation pathway. Requires sulfatase-maturing enzyme (BT_0238) to be functional.	3.1.6.14

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
AS6TASE_HS2	N-acetylglucosamine-6-sulfatase, heparin degradation	(BT_4656 and BT_0238)	Glycosaminoglycan Degradation	Evidence from literature	PMID:19801541, PMID:7574611, PMID:21507958	*B. thetaiotaomicron* specific putative heparin sulfate degradation pathway. Requires sulfatase-maturing enzyme (BT_0238) to be functional.	3.1.6.14
ASNt2r	L-asparagine reversible transport via proton symport		Transport, Extracellular	Evidence from literature	Dworkin, M. and S. Falkow (2006). The prokaryotes : a handbook on the biology of bacteria. New York ; [London], Springer	B. thetaiotaomicron is weakly proteolytic, so a transport reaction for all amino acids is assumed.	
ASPO5	L-aspartate oxidase	BT_3184	Cofactor and Prosthetic Group Biosynthesis	Evidence from literature	PMID:11863440	O2 can be replaced by fumarate as electron acceptor, yielding succinate. The ability of the enzyme to use both O2 and fumarate in cofactor reoxidation enables it to function under both aerobic and anaerobic conditions.	1.4.3.16
ASPt2r	L-aspartate reversible transport via proton symport		Transport, Extracellular	Evidence from literature	Dworkin, M. and S. Falkow (2006). The prokaryotes : a handbook on the biology of bacteria. New York ; [London], Springer	B. thetaiotaomicron is weakly proteolytic, so a transport reaction for all amino acids is assumed.	3.2.1.51
ATPM	ATP maintenance requirement		Unassigned	Based on existing metabolic reconstruction		Added based on published reconstructions in BIGG database	
B_MANNASEe	beta-mannosidase, extracellular	(BT_0458 or BT_2855 or BT_4074 or BT_2432 or BT_3599)	N-Glycan Degradation	Evidence from literature	PMID:17287210, PMID:18996345	BT_0458 gene product was purified and characterized. Shown to have beta-mannosidase activity on human N-glycans.	3.2.1.25
BGLAe	beta-glucosidase, extracellular	(BT_1780 or BT_1872 or BT_3567 or BT_2854 or BT_4714)	Alternate Carbon Metabolism	Evidence from literature	PMID:879772	Beta-glucosidase activity and cellobiose degradation was shown experimentally in *B. thetaiotaomicron*.	3.2.1.21
BTNt2	Biotin reversible transport via proton symport		Transport, Extracellular	Evidence from literature	PMID: 19748469	B. thetaiotaomicron mutants in biotin biosynthesis are not essential in vitro on tryptone-yeast extract-glucose medium, suggesting that B. thetaiotaomicron can uptake biotin from yeast extract.	

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
CARNCNc	hydrolysis of L-Carnosine for uptake	(BT_4045 or BT_1615)	Histidine Metabolism	Evidence from literature	PMID:3543210, PMID:12663928	B. thetaiotaomicron is weakly proteolytic. Has a predicted cytosolic Nalpha-(beta-alanyl)-L-histidine hydrolase.	
CARPEPT1tr	Reversible transport of L-Carnosine by Di-/tripeptide transporter	(BT_4385 or BT_0580)	Transport, Extracellular	Evidence from literature	PMID:3543210, PMID:12663928	*B. thetaiotaomicron* is weakly proteolytic. Has a predicted cytosolic Nalpha-(beta-alanyl)-L-histidine hydrolase.	
CAt7r	calcium / sodium antiporter (1:3), reversible	BT_3019	Transport, Extracellular	Evidence from literature	PMID: 19748469	BT_2541 KO appears to be viable in vitro, which suggest that another calcium transporter exists.	
CBL1abc	Cob(1)alamin transport via ABC system	(BT_1799 or BT_1489)	Transport, Extracellular	Evidence from literature	PMID:4853401	*B. thetaiotaomicron* requires cobalamin (vitamin B12) for growth. Gene annotation is putatively based on NCBI Gene.	
CCP	Cytochrome c peroxidase	BT_1606	ROS Detoxification	Manually added gene annotation from databases		Added based on annotation from NCBI Gene.	1.11.1.5
CDPGHL	CDPglucose 4,6-hydro-lyase	BT_1350	Alternate Carbon Metabolism	Manually added gene annotation from databases		Added based on KEGG Pathway. The products function and further metabolic fate seems to be unknown.	4.2.1.45
CELLBabc	Cellobiose transport via ATP transporter		Transport, Extracellular	Evidence from literature	PMID:869524, PMID:879772	*B. thetaiotaomicron* can utilize cellobiose as carbon source.	
CEPTC_BT	choline phosphotransferase		Sphingolipid Metabolism	Evidence from literature	PMID:6102980, PMID:16887518, PMID:20855611, Anaerobe (2001) 07, 103–112 doi:10.1006/anae.2001.0376	*Bacteroides* are well established to produce sphingolipids. Pathway added manually to BIGG database to represent known structural differences between eukaryotic and bacterial sphingolipids. The main sphingolipid types in *B. thetaiotaomicron* are ceramide-1-phosphoethanolamine and ceramide-1-phosphocholine. The fatty acid is usually branched. In *B. thetaiotaomicron*, the main FA is iso-branched C17. However, no homolog of human ceramide synthase was found in *Bacteroides* species. Either *Bacteroides* have structural homologs of this enzyme, which are not revealed by BLASTP search, or sphingolipids are synthesized by another mechanism.	2.7.8.3

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
CEPTE_BT	ethanolamine phosphotransferase (B.thetaiotaomicron specific)		Sphingolipid Metabolism	Evidence from literature	PMID:6102980, PMID:16887518, PMID:20855611, Anaerobe (2001) 07, 103–112 doi:10.1006/anae.2001.0376	*Bacteroides* are well established to produce sphingolipids. Pathway added manually to BIGG database to represent known structural differences between eukaryotic and bacterial sphingolipids. The main sphingolipid types in *B. thetaiotaomicron* are ceramide-1-phosphoethanolamine and ceramide-1-phosphocholine. The fatty acid is usually branched. In *B. thetaiotaomicron*, the main FA is iso-branched C17. However, no homolog of human ceramide synthase was found in *Bacteroides* species. Either *Bacteroides* have structural homologs of this enzyme, which are not revealed by BLASTP search, or sphingolipids are synthesized by another mechanism.	2.7.8.1
CERS_BT	Ceramide-1 synthase (B.thetaioataomicron specific)		Sphingolipid Metabolism	Evidence from literature	PMID:6102980, PMID:16887518, PMID:20855611, Anaerobe (2001) 07, 103–112 doi:10.1006/anae.2001.0376	*Bacteroides* are well established to produce sphingolipids. Pathway added manually to BIGG database to represent known structural differences between eukaryotic and bacterial sphingolipids. The main sphingolipid types in *B. thetaiotaomicron* are ceramide-1-phosphoethanolamine and ceramide-1-phosphocholine. The fatty acid is usually branched. In *B. thetaiotaomicron*, the main FA is iso-branched C17. However, no homolog of human ceramide synthase was found in *Bacteroides* species. Either *Bacteroides* have structural homologs of this enzyme, which are not revealed by BLASTP search, or sphingolipids are synthesized by another mechanism.	
CGLYt3_2_	Cys-Gly transport in via proton symport	(BT_0580 or BT_4385)	Transport, Extracellular	Manually added gene annotation from databases		Genes added based on TransportDB (last consulted 19.07.11).	

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
CHLPCTD	choline phosphate cytididyltransferase	BT_1721	Sphingolipid Metabolism	Evidence from literature	PMID:6102980, PMID:16887518, PMID:20855611, Anaerobe (2001) 07, 103–112 doi:10.1006/anae.2001.0376	May also be glucose-1-phosphate-cytidylyltransferase (NCBI Gene, last updated 04.03.10). This reaction is needed for sphingolipid synthesis. Sphingolipids are known to be synthesized in *B. thetaiotaomicron*.	
CHOLK	Choline kinase		Sphingolipid Metabolism	Evidence from literature	PMID:6102980, PMID:16887518, PMID:20855611, Anaerobe (2001) 07, 103–112 doi:10.1006/anae.2001.0376	No gene is known. Added to allow sphingolipid synthesis.	2.7.1.32
CITRAMALS	citramalate synthase	BT_1858	Valine, Leucine, and Isoleucine Metabolism	Manually added gene annotation from databases		One of the enzymes involved in a novel pyruvate pathway for isoleucine biosynthesis that is found in some, mainly archaeal, bacteria (KEGG). It is also annotated in *B. thetaiotaomicron*'s genome.	2.3.1.182
CKDNS	CMP-3-deoxy-D-glycero-D-galacto-nonulosonic acid (CMP-KDN) synthetase	BT_1715	Capsular Polysaccharide Biosynthesis	Evidence from literature	PMID:18804026	*B. thetaiotaomicron* forms and cytidylates 2-keto-3-deoxy-D-glycero-D-galacto-nononic acid (KDN), most likely for inclusion in its capsular polysaccharides.	
CPS_BT_ABC	Capsule polysaccharide (B.thetaiotaomicron specific) export	(BT_0057 and BT_0398 and BT_0481 and BT_0613 and BT_1356 and BT_2863)	Capsular Polysaccharide Biosynthesis	Evidence from literature	PMID:17579514	Not sure if ABC transporter is correct. See comments for reaction CPSS_BT for more details on B. thetaiotaomicron CPS. Genes taken from Table S5 in PMID:17579514.	

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
CPSS_BT	Capsular polysaccharide synthesis (B. thetaiotaomicron specific)	(BT_0033 and BT_0378 and BT_0381 and BT_0382 and BT_0391 and BT_0394 and BT_0598 and BT_1343 and BT_1346 and BT_1355 and BT_1644 and BT_1653 and BT_1708 and BT_1722 and BT_2872)	Capsular Polysaccharide Biosynthesis	Evidence from literature	PMID:12904299, PMID:18804026, PMID:15774760, PMID:17579514, PMID:18263721 PMID:19403529	Putative reaction and product formula, no information about exact reaction stochiometry and structure of *B. thetaiotaomicron* CPS found. *B. thetaiotaomicron* most likely synthesizes 2-aminoethylphosphonate (PMID:12904299) and CMP-KDN (PMID:18804026) for inclusion into CPS. Annotation is based on Table S5 in PMID:17579514. Boolean rules may be incorrect. There are eight CPS biosynthesis loci in the *B. thetaiotaomicron* genome. dTDP-L-rhamnose is also generally involved in capsule polysaccharide synthesis. The capsules of gram-negative bacteria also include N-acetylmannosaminuronate (ManNAcA) (PMID:18263721). *Bacteroides* also incorporate GDP-fucose synthesized from host-derived fucose into their capsular polysaccharides (PMID:15774760).	
CS4TASE	chondro-4-sulfatase	((BT_0238 and BT_3095) or (BT_0238 and BT_3051) or (BT_0238 and BT_3177))	Glycosaminoglycan Degradation	Evidence from literature	PMID:21507958	BT_0238 encodes anSME (anaerobic Sulfatase-Maturing Enzyme).	3.1.6.9
CS4TASE2	chondro-4-sulfatase	((BT_0238 and BT_3095) or (BT_0238 and BT_3051) or (BT_0238 and BT_3177))	Glycosaminoglycan Degradation	Evidence from literature	PMID:21507958	BT_0238 encodes anSME (anaerobic Sulfatase-Maturing Enzyme).	3.1.6.9

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
CS6TASE	chondro-6-sulfatase	((BT_0238 and BT_1622) or (BT_3057 and BT_0238) or (BT_4656 and BT_0238) or (BT_3486 and BT_0238))	Glycosaminoglycan Degradation	Evidence from literature	PMID:21507958	BT_0238 encodes anSME (anaerobic Sulfatase-Maturing Enzyme).	3.1.6.4
CSABCASE_A_e	Chondroitin sulfate lyase ABC, CS_A	(BT_3331 and BT_3332 and BT_3348)	Glycosaminoglycan Degradation	Evidence from literature	PMID:6782076, PMID:7574611, PMID:18512954, PMID:18992215, PMID:18996345	*B. thetaiotaomicron* ferments chondroitin sulfate. The polysaccharide utilization locus (PUL) BT3324 - BT3350 is upregulated in its presence. BT_3348 degrades chondroitin sulfate to oligosaccharides, which requires BT_3331 (sus C homolog) and BT_3332 (csuF). BT_3324 and BT_3350 degrade the desulfated oligosaccharides to monosaccharides. Based on Figure 3, PMID:18996345. It is assumed that the proteoglycan rest is undegradable for B. thetaiotaomicron.	4.2.2.20
CSABCASE_B_e	Chondroitin sulfate lyase ABC, CS_B	(BT_3331 and BT_3332 and BT_3348)	Glycosaminoglycan Degradation	Evidence from literature	PMID:6782076, PMID:7574611, PMID:18512954, PMID:18992215, PMID:18996345	*B. thetaiotaomicron* ferments chondroitin sulfate. The polysaccharide utilization locus (PUL) BT3324 - BT3350 is upregulated in its presence. BT_3348 degrades chondroitin sulfate to oligosaccharides, which requires BT_3331 (sus C homolog) and BT_3332 (csuF). BT_3324 and BT_3350 degrade the desulfated oligosaccharides to monosaccharides. Based on Figure 3, PMID:18996345. It is assumed that the proteoglycan rest is undegradable for B. thetaiotaomicron.	4.2.2.20

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
CSABCASE_C_e	Chondroitin sulfate lyase ABC, CS_C	(BT_3331 and BT_3332 and BT_3348)	Glycosaminoglycan Degradation	Evidence from literature	PMID:6782076, PMID:7574611, PMID:18512954, PMID:18992215, PMID:18996345	*B. thetaiotaomicron* ferments chondroitin sulfate. The polysaccharide utilization locus (PUL) BT3324 - BT3350 is upregulated in its presence. BT_3348 degrades chondroitin sulfate to oligosaccharides, which requires BT_3331 (sus C homolog) and BT_3332 (csuF). BT_3324 and BT_3350 degrade the desulfated oligosaccharides to monosaccharides. Based on Figure 3, PMID:18996345. It is assumed that the proteoglycan rest is undegradable for B. thetaiotaomicron.	4.2.2.20
CSPMDDC	carboxyspermidine decarboxylase	BT_0674	Spermidine and Putrescine Biosynthesis	Evidence from literature	PMID:10801923	Annotation from NCBI Gene, last updated 02.04.11	4.1.1.-
CSPMDDH	carboxyspermidine:NADP+ oxidoreductase		Spermidine and Putrescine Biosynthesis	Evidence from literature	PMID:10801923	Added to allow *B. thetaiotaomicron* to secrete putrescine (shown in vivo). Annotated for *Bacteroides helcogenes* (Bache_1714).	4.1.1.-
CYSDS	Cysteine Desulfhydrase	(BT_1923 or BT_2387)	Cysteine Metabolism	Evidence from literature	PMID:4853401	Added to allow *B. thetaiotaomicron* to use cysteine as sulfur source.	4.1.99.1
CYSt2r	L-cysteine reversible transport via proton symport		Transport, Extracellular	Evidence from literature	PMID:4853401	Cysteine is required as sulfur source if sulfide is not available.	
D_LACt2	D-lactate transport via proton symport		Transport, Extracellular	Evidence from literature	PMID:438119, PMID:148460, PMID:12740060, PMID:11260473	*Bacteroides* produce lactate under certain circumstances.	
DAGK160	diacylglycerol kinase (n-C16:0)		Sphingolipid Metabolism	Manual gapfilling		Not sure if this enzyme is present. It is annotated for most *Bacteroides* species except *B. thetaiotaomicron*. Needed for degradation of diacylglycerol and sphingolipid synthesis.	

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
DALAt2r	D-alanine transport via proton symport		Transport, Extracellular	Evidence from literature	PMID:12663928	Added by Model SEED during auto-completion. No gene annotation for ala-D transport available, but B. thetaiotaomicron is believed to possess a non-cytosolic D-alanine-D-alanine dipeptidase.	
DEXTRAN40e	alpha-dextrin endo-1,6-alpha-glucosidase/ pullulanase	(BT_1663 or BT_4689)	Plant Polysaccharide Degradation	Evidence from literature	PMID:848954	Assumed to perform dextran (alpha-1,6-glucan) degradation. Maltose is the smallest sugar that it can release from an alpha-(1->6)-linkage (KEGG Enzyme). *B. thetaiotaomicron* ferments dextran.	3.2.1.41
DGC3D	2-deoxy-D-gluconate 3-dehydrogenase	(BT_3232 or BT_1015)	Pentose and Glucuronate Interconversions	Manually added gene annotation from databases		Gene annotation was drawn from The SEED.	1.1.1.125
DGC3D2	2-deoxy-D-gluconate 3-dehydrogenase	(BT_3232 or BT_1015)	Pentose and Glucuronate Interconversions	Manually added gene annotation from databases		Gene annotation was drawn from The SEED.	1.1.1.125
DHNAOT10	1,4-dihydroxy-2-naphthoate octaprenyltransferase (demethylmenaquinone 10)		Cofactor and Prosthetic Group Biosynthesis	Evidence from literature	PMID:6102980	B. thetaiotaomicron produces menaquinone 7,8,9,10 and 11. MK-10 and MK-11 are the main components.Note: Reaction is unbalanced, but I don't know to fix this. KEGG doesn't have any information. AH	3.2.1.65
DHNAOT11	1,4-dihydroxy-2-naphthoate octaprenyltransferase (demethylmenaquinone 11)		Cofactor and Prosthetic Group Biosynthesis	Evidence from literature	PMID:6102980	B. thetaiotaomicron produces menaquinone 7,8,9,10 and 11. MK-10 and MK-11 are the main components.Note: Reaction is unbalanced, but I don't know to fix this. KEGG doesn't have any information. AH	3.2.1.51
DHNAOT7	1,4-dihydroxy-2-naphthoate octaprenyltransferase (demethylmenaquinone 7)	(BT_2014 or BT_2015)	Cofactor and Prosthetic Group Biosynthesis	Evidence from literature	PMID:6102980	B. thetaiotaomicron produces menaquinone 7,8,9,10 and 11. MK-10 and MK-11 are the main components.Note: Reaction is unbalanced, but I don't know to fix this. KEGG doesn't have any information. AH	3.2.1.51

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
DHNAOT9	1,4-dihydroxy-2-naphthoate octaprenyltransferase (demethylmenaquinone 9)	(BT_2014 or BT_2015)	Cofactor and Prosthetic Group Biosynthesis	Evidence from literature	PMID:6102980	B. thetaiotaomicron produces menaquinone 7,8,9,10 and 11. MK-10 and MK-11 are the main components.Note: Reaction is unbalanced, but I don't know to fix this. KEGG doesn't have any information. AH	3.2.1.51
DHORDfum	Fumarate dependent DHORD	(BT_1009 or (BT_0891 and BT_0892))	Purine and Pyrimidine Biosynthesis	Curation of incorrect annotation in Model SEED		Gene was incorrectly annotated by Model SEED, correct: dihydroorotate dehydrogenase (fumarate)	1.3.98.1
DHPS3	7,8 dihydropteroate synthase (methanopterin)	BT_1410	Cofactor and Prosthetic Group Biosynthesis	Manually added gene annotation from databases		Gene annotation was drawn from The SEED.	2.5.1.15
DM_4HBA	Sink needed to allow 4-hydroxy-benzoate to leave system		exchange/demand reaction	Manual gapfilling			
DM_5DRIB	Sink needed to allow 5-deoxyribose to leave system		exchange/demand reaction	Manual gapfilling			
DM_AMOB	Sink needed to allow S-Adenosyl-4-methylthio-2-oxobutanoate to leave the system		exchange/demand reaction	Manual gapfilling			
DT5HSUt2r	5-Dehydro-4-deoxy-D-glucuronate transport in via proton symport, reversible	BT_4105	Transport, Extracellular	Evidence from literature	PMID:3968032	Added to allow complete degradation of pectin, not sure if this degradation product is generated in periplasm or cytosol. Degradation pathway may be slightly different. Added based on NCBI Gene (annotation: hexouronate transporter).	
EACPR1	Enoyl-ACP-reductase (FabI)	BT_4188	Biotin Metabolism	Evidence from literature	PMID:20693992	Based on biotin synthesis described in PMID:20693992 for *E. coli*	
EACPR2	Enoyl-ACP-reductase (FabI)	BT_4188	Biotin Metabolism	Evidence from literature	PMID:20693992	Based on biotin synthesis described in PMID:20693992 for *E. coli*	
EAR121x	enoyl-[acyl-carrier-protein] reductase (NADH) (n-C12:1)	BT_4188	Cell Envelope Biosynthesis	Evidence from literature	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of *B. thetaiotaomicron* was determined experimentally.	1.3.1.9
EAR141x	enoyl-[acyl-carrier-protein] reductase (NADH) (n-C14:1)	BT_4188	Cell Envelope Biosynthesis	Evidence from literature	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of *B. thetaiotaomicron* was determined experimentally.	1.3.1.9

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
EAR161x	enoyl-[acyl-carrier-protein] reductase (NADH) (n-C16:1)	BT_4188	Cell Envelope Biosynthesis	Evidence from literature	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of *B. thetaiotaomicron* was determined experimentally.	1.3.1.9
EAR181x	enoyl-[acyl-carrier-protein] reductase (NADH) (n-C18:1)	BT_4188	Cell Envelope Biosynthesis	Evidence from literature	PMID: 6102980, PMID: 7440508, PMID: 7204330	The fatty acid composition of *B. thetaiotaomicron* was determined experimentally.	1.3.1.9
EDTXS1_BT	Endotoxin Synthesis (lauroyl transferase)	BT_2152	Lipopolysaccharide Biosynthesis	Evidence from literature	PMID:18931137, PMID:19460428, PMID:20974832	LPS biosynthesis partly based on reconstruction of the related microbe *P. gingivalis* (PMID:18931137). Based on structural information taken from (PMID:19460428, PMID:20974832). Could not find information, though, if laurate is really added to kdolipid IV in *B. thetaiotaomicron*.	
EPGALURSe	Endopolygalacturonase (extracellular)	(BT_1018 or BT_2378 or BT_4123 or BT_4155 or BT_4187)	Alternate Carbon Metabolism	Evidence from literature	PMID:3968032	Purified and characterized by enzyme assay. Genome annotation from NCBI Gene. Appears to be located in periplasm (extracellular for modeling purposes).	3.2.1.15
ETOHt	ethanol reversible transport		Transport, Extracellular	Evidence from literature	PMID:438119, PMID:17563350	*Bacteroides* produce weak amounts of ethanol under certain circumstances.	
F1PGT	fucose-1-phosphate guanylyltransferase	BT_2128	Alternate Carbon Metabolism	Evidence from literature	PMID:15774760, PMID:19379697	*Bacteroides* use host-derived fucose for cell surface decoration.	2.7.7.30
FCLK	L-fuculokinase	BT_1275	Alternate Carbon Metabolism	Evidence from literature	PMID:10449780	The L-fucose utilization operon was characterized experimentally.	

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
FDNADOX	ferredoxin:NAD+ oxidoreductase		Unassigned	Evidence from literature	PMID:760499, PMID:12740060, PMID:20444704	In the gut, this reaction allows primary fermenters, such as *B. thetaiotaomicron*, to regenerate NAD+. Also involves a ferredoxin-dependent hydrogenase (HYD4). The pathway only takes place if the end product hydrogen is removed from the environment because the equilibrium of the reaction favors the formation of NADH. *B. thetaiotaomicron* generates hydrogen as one of its fermentation end products; accumulation of hydrogen inhibits reoxidation of NADH. It is therefore assumed that it regenerates NAD+ via this pathway, which leads to increased hydrogen partial pressure. Removal of hydrogen allows *B. thetaiotaomicron* to regenerate NAD+. No gene is known, reaction was added during manual gapfilling.	1.18.1.3
FK	Fucokinase	BT_2128	Alternate Carbon Metabolism	Evidence from literature	PMID:15774760	The pathway was demonstrated experimentally in *Bacteroides fragilis*.	2.7.1.52
FOLR	tetrahydrofolate NADP oxidoreductase	(BT_0106 or BT_2048)	Folate Metabolism	Evidence from literature	PMID:4853401, PMID:9167138	Added to allow folate biosynthesis. *B. thetaiotaomicron* does not require folate in medium.	1.5.1.3
FOMETR	aminomethyltransferase	BT_4584	Cofactor and Prosthetic Group Biosynthesis	Evidence from KEGG Database		One of several reactions catalyzed by aminomethyltransferase (EC 2.1.2.10). Added based on KEGG Pathway.	2.1.2.10
FORt	formate transport via diffusion		Transport, Extracellular	Evidence from literature	PMID:9178362	*B. thetaiotaomicron* produces formate under certain circumstances.	
FRD10	fumarate reductase	(BT_3054 and BT_3055)	TCA Cycle	Evidence from literature	PMID:12777495, PMID:11260473	Bacteroides have both succinate dehydrogenase and fumarate reductase acitivity. Fumarate reductase is a key enzyme in central metabolism. AH	

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
FRD11	fumarate reductase	(BT_3054 and BT_3055)	TCA Cycle	Evidence from literature	PMID:12777495, PMID:11260473	Bacteroides have both succinate dehydrogenase and fumarate reductase acitivity. Fumarate reductase is a key enzyme in central metabolism. AH	
FRD8	fumarate reductase	(BT_3054 and BT_3055)	TCA Cycle	Evidence from literature	PMID:12777495, PMID:11260473	Bacteroides have both succinate dehydrogenase and fumarate reductase acitivity. Fumarate reductase is a key enzyme in central metabolism. AH	
FRD9	fumarate reductase	(BT_3054 and BT_3055)	TCA Cycle	Evidence from literature	PMID:12777495, PMID:11260473	Bacteroides have both succinate dehydrogenase and fumarate reductase acitivity. Fumarate reductase is a key enzyme in central metabolism. AH	
FRUASE3	Intracellular endofructanase	BT_1765	Plant Polysaccharide Degradation	Evidence from literature	PMID:20603004	Intracellular fructanase acitivity was demonstrated in *B. thetaiotaomicron*.	3.2.1.65
FRUt2r	D-fructose transport in via proton symport reversible	BT_1758	Transport, Extracellular	Evidence from literature	PMID: 20603004	*B. thetaiotaomicron* grows on D-fructose.	
FUCASEe	alpha-fucosidase, extracellular	(BT_1842 or BT_2970 or BT_3665)	N-Glycan Degradation	Evidence from literature	PMID:15774760, PMID:19379697	*Bacteroides* use host-derived fucose for cell surface decoration.	3.2.1.51

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
FUCNEULACNHX_DEGe	monofucosyl-monosialyl-lacto-N-hexaose degradation by alpha-fucosidase, sialidase, N-acetylglutaminidase and beta-galactosidase (extracellular)	((BT_1625 or BT_4136) and (BT_0455 or BT_2194 or BT_2892) and (BT_1626 or BT_0461) and (BT_1627 or BT_1632 or BT_4132 or BT_0459 or BT_0460 or BT_1038 or BT_1044 or BT_1048 or BT_1051 or BT_4295 or BT_2825) and ((BT_1630 and BT_1631) or (BT_4134 and BT_4135) or (BT_1039 and BT_1040) or (BT_1042 and BT_1043) or (BT_1046 and BT_1047) or (BT_4297 and BT_4298) or (BT_2818 and BT_2819) or (BT_2820 and BT_2821)))	HMO Degradation	Evidence from literature	PMID: 22036470, PMID: 20679197	B. thetaiotaomicron grows on human milk oligosaccharides (HMOs); numerous glycosidase hydrolases are upregulated during growth on HMOs. Lacto-N-tetraose and Lacto-N-neotetraose are poorly metabolized and accumulate if BT is grown on HMOs. Putative reaction. Structure based on PMID: 20679197. Involves beta-galactosidase, alpha-fucosidase, sialidase, N-acetylglucosaminidase, susC, susD (binding proteins).	
FUCt	L-fucose transport via proton symport	(BT_1277 or BT_3616)	Transport, Extracellular	Evidence from literature	PMID:10449780	*B. thetaiotaomicron* can use L-fucose as carbon source.	
FUMt2r	fumarate reversible transport via symport	BT_2756	Transport, Extracellular	Manually added gene annotation from databases		Annotation from NCBI Gene.	

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
G1PACT	glucosamine-1-phosphate N-acetyltransferase		Cell Envelope Biosynthesis	Manual gapfilling		This enzyme was added to allow synthesis of N-acetylglucosamine from glucose . This role might also be fulfilled by glucosamine-6-phosphate-acetyltransferase (EC 2.3.1.4), it is unclear which pathway is used by *B. thetaiotaomicron*.	2.3.1.157
G3PAT120	glycerol-3-phosphate acyltransferase (C12:0)		Glycerophospholipid Metabolism	Evidence from literature	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added during manual gapfilling to allow lipid biosynthesis to take place. GPR is unknown.	2.3.1.15
G3PAT140	glycerol-3-phosphate acyltransferase (C14:0)		Glycerophospholipid Metabolism	Evidence from literature	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added during manual gapfilling to allow lipid biosynthesis to take place. GPR is unknown.	2.3.1.15
G3PAT160	glycerol-3-phosphate acyltransferase (C16:0)		Glycerophospholipid Metabolism	Evidence from literature	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added during manual gapfilling to allow lipid biosynthesis to take place. GPR is unknown.	2.3.1.15
G3PAT181	glycerol-3-phosphate acyltransferase (C18:1)		Glycerophospholipid Metabolism	Evidence from literature	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added during manual gapfilling to allow lipid biosynthesis to take place. GPR is unknown.	2.3.1.15
G3PATAI15	anteisopentadecanoyl-glycerol-3-phosphate O-acyltransferase		Glycerophospholipid Metabolism	Evidence from literature	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added during manual gapfilling to allow lipid biosynthesis to take place. GPR is unknown.	2.3.1.15
G3PATI14	isotetradecanoyl-glycerol-3-phosphate O-acyltransferase		Glycerophospholipid Metabolism	Evidence from literature	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added during manual gapfilling to allow lipid biosynthesis to take place. GPR is unknown.	2.3.1.15
G3PATI15	isopentadecanoyl-glycerol-3-phosphate O-acyltransferase		Glycerophospholipid Metabolism	Evidence from literature	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added during manual gapfilling to allow lipid biosynthesis to take place. GPR is unknown.	2.3.1.15
G3PATI16	isohexadecanoyl-glycerol-3-phosphate O-acyltransferase		Glycerophospholipid Metabolism	Evidence from literature	PMID: 6102980, PMID: 7440508, PMID: 7204330	Added during manual gapfilling to allow lipid biosynthesis to take place. GPR is unknown.	2.3.1.15
GACPCD	Glutaryl-ACP condensation catalyzed by FabB or FabF	BT_3358	Biotin Metabolism	Evidence from literature	PMID:20693992	Based on biotin synthesis described in PMID:20693992 for *E. coli*. The authors are unsure if this reaction is carried out by FabB or FabF. Here, FabF is assumed to carry out the reaction.	
GALAM6PDA	Galactosamine-6-phosphate deaminase		Aminosugar Metabolism	Evidence from literature	PMID:2845859	*B. thetaiotaomicron* grows on N-acetylgalactosamine: PMID:2845859. However, the utilization pathway is poorly understood.	

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
GALAMt2r	galactosamine transport (proton symport)		Transport, Extracellular	Evidence from literature	PMID: 6367911	B. thetaiotaomicron metabolizes galactosamine to some extent (though the compound does not support growth in vivo).	
GALASE_HSe	Extracellular beta-galactosidase, heparin degradation	(BT_0290 or BT_0461 or BT_0757 or BT_0983 or BT_0992 or BT_0993 or BT_0996 or BT_1626 or BT_2190 or BT_2680 or BT_2922 or BT_2969 or BT_3092 or BT_3114 or BT_3179 or BT_3293 or BT_3340 or BT_3513 or BT_3654 or BT_4050 or BT_4152 or BT_4156 or BT_4160 or BT_4181 or BT_4241 or BT_4667 or BT_4684)	Glycosaminoglycan Degradation	Evidence from literature	PMID:19801541, PMID:7574611	*B. thetaiotaomicron* specific putative heparin sulfate degradation pathway.	3.2.1.23
GALASE_OGLYCAN1e	Beta-galactosidase, mucin-type O-glycans, extracellular	BT_4241 and BT_4246 and BT_4247	O-Glycan Degradation	Evidence from literature	PMID: 18996345, PMID: 10430883, PMID: 848954	B. thetaiotaomicron is well known to degrade mucin, the genes included in the GPR are upregulated during growth on mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis. Involves beta-galactosidase, susC, susD (binding proteins).	

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
GALASE_OGLYCAN2e	Beta-galactosidase, mucin-type O-glycans, extracellular	BT_4241 and BT_4246 and BT_4247	O-Glycan Degradation	Evidence from literature	PMID: 18996345, PMID: 10430883, PMID: 848954	B. thetaiotaomicron is well known to degrade mucin, the genes included in the GPR are upregulated during growth on mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis. Involves beta-galactosidase, susC, susD (binding proteins).	
GALASE_OGLYCAN3e	Beta-galactosidase, mucin-type O-glycans, extracellular	BT_4241 and BT_4246 and BT_4247	O-Glycan Degradation	Evidence from literature	PMID: 18996345, PMID: 10430883, PMID: 848954	B. thetaiotaomicron is well known to degrade mucin, the genes included in the GPR are upregulated during growth on mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis. Involves beta-galactosidase, susC, susD (binding proteins).	
GALASE1e	beta-galactosidase, extracellular	(BT_0290 or BT_0461 or BT_0757 or BT_0983 or BT_0992 or BT_0993 or BT_0996 or BT_1626 or BT_2190 or BT_2680 or BT_2922 or BT_2969 or BT_3092 or BT_3114 or BT_3179 or BT_3293 or BT_3340 or BT_3513 or BT_3654 or BT_4050 or BT_4152 or BT_4156 or BT_4160 or BT_4181 or BT_4241 or BT_4667 or BT_4684)	N-Glycan Degradation	Evidence from literature	PMID:16968696, PMID:17132046	*B. thetaiotaomicron* ferments host-derived N-glycans.	3.2.1.23

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
GALNACASE_OGLYCAN1e	N-acetylgalactosaminidase, mucin-type O-glycans, extracellular	BT_0065	O-Glycan Degradation	Evidence from literature	PMID: 19403529, PMID: 18996345, PMID: 10430883, PMID: 848954	B. thetaiotaomicron is well known to degrade mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis. BT_0065 is N-acetylgalactosaminidase according to PMID: 19403529. There may be other enzymes performing this function.	
GALNACASE_OGLYCAN2e	N-acetylgalactosaminidase, mucin-type O-glycans, extracellular	BT_0065	O-Glycan Degradation	Evidence from literature	PMID: 19403529, PMID: 18996345, PMID: 10430883, PMID: 848954	B. thetaiotaomicron is well known to degrade mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis. BT_0065 is N-acetylgalactosaminidase according to PMID: 19403529. There may be other enzymes performing this function.	3.4.13.20 or 3.4.13.18
GALNACASE_OGLYCAN3e	N-acetylgalactosaminidase, mucin-type O-glycans, extracellular	BT_0065	O-Glycan Degradation	Evidence from literature	PMID: 19403529, PMID: 18996345, PMID: 10430883, PMID: 848954	B. thetaiotaomicron is well known to degrade mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis. BT_0065 is N-acetylgalactosaminidase according to PMID: 19403529. There may be other enzymes performing this function.	
GALOX	Galactose oxidase	BT_4040 or BT_4632	Alternate Carbon Metabolism	Evidence from literature	PMID: 22036470	Reaction R01098 in KEGG. The gene may be wrongly annotated and have a different function (upregulated during growth on human milk oligosaccharides).	2.7.1.51
GALUi	UTP-glucose-1-phosphate uridylyltransferase (irreversible)		Cell Envelope Biosynthesis	Evidence from literature	PMID:19460428	This reaction is neccessary to produce UDP-glucose for lipopolysaccharide biosynthesis. No gene annotation is available, however. The structure of *B. thetaiotaomicron* LPS is described in PMID:19460428.	2.7.7.9
GAM2STASE_HS1	N-sulfoglucosamine sulfohydrolase, heparin degradation	((BT_1624 and BT_0238) or (BT_3796 and BT_0238))	Glycosaminoglycan Degradation	Evidence from literature	PMID:21507958, PMID:19801541, PMID:7574611	*B. thetaiotaomicron* specific putative heparin sulfate degradation pathway. Requires sulfatase-maturing enzyme (BT_0238) to be functional. Not sure if annotation (putative secreted sulfatase) is correct.	3.10.1.1

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
GAM2STASE_HS2	N-sulfoglucosamine sulfohydrolase, heparin degradation	((BT_1624 and BT_0238) or (BT_3796 and BT_0238))	Glycosaminoglycan Degradation	Evidence from literature	PMID:19801541, PMID:7574611	*B. thetaiotaomicron* specific putative heparin sulfate degradation pathway. Not sure if annotation (putative secreted sulfatase) is correct.	3.10.1.1
GAM2STASE_HS3	N-sulfoglucosamine sulfohydrolase, heparin degradation	((BT_1624 and BT_0238) or (BT_3796 and BT_0238))	Glycosaminoglycan Degradation	Evidence from literature	PMID:19801541, PMID:7574611	*B. thetaiotaomicron* specific putative heparin sulfate degradation pathway. Not sure if annotation (putative secreted sulfatase) is correct.	3.10.1.1
GAMt2r	glucosamine transport (proton symport)		Transport, Extracellular	Evidence from literature	PMID:7240086	*B. thetaiotaomicron* metabolizes glucosamine.	
GCHOLAH	Bile acid hydrolase (glycocholate)	(BT_1259 or BT_2086)	Bile Acid Metabolism	Evidence from literature	PMID:10993, Dworkin, M. and S. Falkow (2006). The prokaryotes : a handbook on the biology of bacteria. New York ; [London], Springer	Enzyme was demonstrated experimentally (PMID:10993). Growth of *B. thetaiotaomicron* is stimulated by 20% bile.	3.5.1.24
GCHOLAt2	glycocholate transport via sodium cotransport		Transport, Extracellular	Evidence from literature	PMID:10993	*B. thetaiotaomicron* metabolizes glycocholate and taurocholate. A bile acid/ sodium symporter is annotated for *Bacteroides salanitronis.*	
GLCAASE	beta-glucuronidase/ chondroitinase	(BT_3292 or BT_4151 or BT_3324 or BT_3350)	Glycosaminoglycan Degradation	Evidence from literature	PMID:6782076, PMID:7574611, PMID:848954, PMID:18996345	*B. thetaiotaomicron* ferments chondroitin sulfate. The polysaccharide utilization locus (PUL) BT3324 - BT3350 is upregulated in its presence. BT_3348 degrades chondroitin sulfate to oligosaccharides, which requires BT_3331 (sus C homolog) and BT_3332 (csuF). BT_3324 and BT_3350 degrade the desulfated oligosaccharides to monosaccharides. Based on Figure 3, PMID:18996345. BT_3292 and BT_4151 were added based on gene annotation, not sure they perform this role. Reaction takes place in periplasm (extracellular for modeling purposes).	3.2.1.31
GLCAASE_HS	Beta-glucuronidase, heparin degradation	(BT_3292 or BT_4151)	Glycosaminoglycan Degradation	Evidence from literature	PMID:19801541, PMID:7574611	*B. thetaiotaomicron* specific putative heparin sulfate degradation pathway.	3.2.1.31

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
GLCAASE_HSe	Beta-glucuronidase, heparin degradation	(BT_3292 or BT_4151)	Glycosaminoglycan Degradation	Evidence from literature	PMID:19801541, PMID:7574611	B. thetaiotaomicron specific putative heparin sulfate degradation pathway.	
GLCAASE8e	beta-glucuronidase, hyaluronan degradation	(BT_3292 or BT_4151)	Glycosaminoglycan Degradation	Evidence from literature	PMID:848954, PMID:18996345	*B. thetaiotaomicron* ferments hyaluronan. The polysaccharide utilization locus (PUL) BT3324 - BT3350 is upregulated in its presence.	3.2.1.31
GLCAASE9e	beta-glucuronidase, hyaluronan degradation	(BT_3292 or BT_4151)	Glycosaminoglycan Degradation	Evidence from literature	PMID:848954, PMID:18996345	*B. thetaiotaomicron* ferments hyaluronan. The polysaccharide utilization locus (PUL) BT3324 - BT3350 is upregulated in its presence.	3.2.1.31
GLCAASEe	beta-glucuronidase/ chondroitinase	(BT_3292 or BT_4151 or BT_3324 or BT_3350)	Glycosaminoglycan Degradation	Evidence from literature	PMID:6782076, PMID:7574611, PMID:848954, PMID:18996345	B. thetaiotaomicron ferments chondroitin sulfate. The polysaccharide utilization locus (PUL) BT3324 - BT3350 is upregulated in its presence. BT_3348 degrades chondroitin sulfate to oligosaccharides, which requires BT_3331 (sus C homolog) and BT_3332 (csuF). BT_3324 and BT_3350 degrade the desulfated oligosaccharides to monosaccharides. Based on Figure 3, PMID:18996345. BT_3292 and BT_4151 were added based on gene annotation, not sure they perform this role. Reaction takes place in periplasm (extracellular for modeling purposes).	
GLCNACASE_HS1	Alpha-N-acetylglucosaminidase, heparin degradation	(BT_0438 or BT_3590 or BT_4359)	Glycosaminoglycan Degradation	Evidence from literature	PMID:19801541, PMID:7574611	*B. thetaiotaomicron* specific putative heparin sulfate degradation pathway.	3.2.1.50
GLCNACASE_HS2	Alpha-N-acetylglucosaminidase, heparin degradation	(BT_0438 or BT_3590 or BT_4359)	Glycosaminoglycan Degradation	Evidence from literature	PMID:19801541, PMID:7574611	*B. thetaiotaomicron* specific putative heparin sulfate degradation pathway.	3.2.1.50
GLCNACASE_HS3	Alpha-N-acetylglucosaminidase, heparin degradation	(BT_0438 or BT_3590 or BT_4359)	Glycosaminoglycan Degradation	Evidence from literature	PMID:19801541, PMID:7574611	*B. thetaiotaomicron* specific putative heparin sulfate degradation pathway.	3.2.1.50

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
GLCNACASE_OGLYCAN1e	N-acetylglucosaminidase, mucin-type O-glycans, extracellular	(BT_2825 or BT_1038 or BT_1044 or BT_1048 or BT_0865 or BT_1282 or BT_3753 or BT_4132 or BT_4406 or BT_3985 or BT_3987) and ((BT_1039 and BT_1040) or (BT_1042 and BT_1043) or (BT_1046 and BT_1047) or (BT_4134 and BT_4135) or (BT_4404 and BT_4405) or (BT_3983 and BT_3984) or (BT_0866 and BT_0867) or (BT_3751 and BT_3752) or (BT_1280 and BT_1281) or (BT_3958 and BT_3959) or (BT_4633 and BT_4634) or (BT_2818 and BT_2819) or (BT_2820 and BT_2821))	O-Glycan Degradation	Evidence from literature	PMID: 18996345, PMID: 10430883, PMID: 848954	B. thetaiotaomicron is well known to degrade mucin, the genes included in the GPR are upregulated during growth on mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis. Involves N-acetylglucosaminidase, susC, susD (binding proteins).	

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
GLCNACASE_OGLYCAN2e	N-acetylglucosaminidase, mucin-type O-glycans, extracellular	(BT_2825 or BT_1038 or BT_1044 or BT_1048 or BT_0865 or BT_1282 or BT_3753 or BT_4132 or BT_4406 or BT_3985 or BT_3987) and ((BT_1039 and BT_1040) or (BT_1042 and BT_1043) or (BT_1046 and BT_1047) or (BT_4134 and BT_4135) or (BT_4404 and BT_4405) or (BT_3983 and BT_3984) or (BT_0866 and BT_0867) or (BT_3751 and BT_3752) or (BT_1280 and BT_1281) or (BT_3958 and BT_3959) or (BT_4633 and BT_4634) or (BT_2818 and BT_2819) or (BT_2820 and BT_2821))	O-Glycan Degradation	Evidence from literature	PMID: 18996345, PMID: 10430883, PMID: 848954	B. thetaiotaomicron is well known to degrade mucin, the genes included in the GPR are upregulated during growth on mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis. Involves N-acetylglucosaminidase, susC, susD (binding proteins).	

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
GLCNACASE_OGLYCAN3e	N-acetylglucosaminidase, mucin-type O-glycans, extracellular	(BT_2825 or BT_1038 or BT_1044 or BT_1048 or BT_0865 or BT_1282 or BT_3753 or BT_4132 or BT_4406 or BT_3985 or BT_3987) and ((BT_1039 and BT_1040) or (BT_1042 and BT_1043) or (BT_1046 and BT_1047) or (BT_4134 and BT_4135) or (BT_4404 and BT_4405) or (BT_3983 and BT_3984) or (BT_0866 and BT_0867) or (BT_3751 and BT_3752) or (BT_1280 and BT_1281) or (BT_3958 and BT_3959) or (BT_4633 and BT_4634) or (BT_2818 and BT_2819) or (BT_2820 and BT_2821))	O-Glycan Degradation	Evidence from literature	PMID: 18996345, PMID: 10430883, PMID: 848954	B. thetaiotaomicron is well known to degrade mucin, the genes included in the GPR are upregulated during growth on mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis. Involves N-acetylglucosaminidase, susC, susD (binding proteins).	

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
GLCNACASE_OGLYCAN4e	N-acetylglucosaminidase, mucin-type O-glycans, extracellular	(BT_2825 or BT_1038 or BT_1044 or BT_1048 or BT_0865 or BT_1282 or BT_3753 or BT_4132 or BT_4406 or BT_3985 or BT_3987) and ((BT_1039 and BT_1040) or (BT_1042 and BT_1043) or (BT_1046 and BT_1047) or (BT_4134 and BT_4135) or (BT_4404 and BT_4405) or (BT_3983 and BT_3984) or (BT_0866 and BT_0867) or (BT_3751 and BT_3752) or (BT_1280 and BT_1281) or (BT_3958 and BT_3959) or (BT_4633 and BT_4634) or (BT_2818 and BT_2819) or (BT_2820 and BT_2821))	O-Glycan Degradation	Evidence from literature	PMID: 18996345, PMID: 10430883, PMID: 848954	B. thetaiotaomicron is well known to degrade mucin, the genes included in the GPR are upregulated during growth on mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis. Involves N-acetylglucosaminidase, susC, susD (binding proteins).	

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
GLCNACASE_OGLYCAN5e	N-acetylglucosaminidase, mucin-type O-glycans, extracellular	(BT_2825 or BT_1038 or BT_1044 or BT_1048 or BT_0865 or BT_1282 or BT_3753 or BT_4132 or BT_4406 or BT_3985 or BT_3987) and ((BT_1039 and BT_1040) or (BT_1042 and BT_1043) or (BT_1046 and BT_1047) or (BT_4134 and BT_4135) or (BT_4404 and BT_4405) or (BT_3983 and BT_3984) or (BT_0866 and BT_0867) or (BT_3751 and BT_3752) or (BT_1280 and BT_1281) or (BT_3958 and BT_3959) or (BT_4633 and BT_4634) or (BT_2818 and BT_2819) or (BT_2820 and BT_2821))	O-Glycan Degradation	Evidence from literature	PMID: 18996345, PMID: 10430883, PMID: 848954	B. thetaiotaomicron is well known to degrade mucin, the genes included in the GPR are upregulated during growth on mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis. Involves N-acetylglucosaminidase, susC, susD (binding proteins).	

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
GLCNACASE_OGLYCAN6e	N-acetylglucosaminidase, mucin-type O-glycans, extracellular	(BT_2825 or BT_1038 or BT_1044 or BT_1048 or BT_0865 or BT_1282 or BT_3753 or BT_4132 or BT_4406 or BT_3985 or BT_3987) and ((BT_1039 and BT_1040) or (BT_1042 and BT_1043) or (BT_1046 and BT_1047) or (BT_4134 and BT_4135) or (BT_4404 and BT_4405) or (BT_3983 and BT_3984) or (BT_0866 and BT_0867) or (BT_3751 and BT_3752) or (BT_1280 and BT_1281) or (BT_3958 and BT_3959) or (BT_4633 and BT_4634) or (BT_2818 and BT_2819) or (BT_2820 and BT_2821))	O-Glycan Degradation	Evidence from literature	PMID: 18996345, PMID: 10430883, PMID: 848954	B. thetaiotaomicron is well known to degrade mucin, the genes included in the GPR are upregulated during growth on mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis. Involves N-acetylglucosaminidase, susC, susD (binding proteins).	
GLCS2	glycogen synthase (UDPGlc)	(BT_1294 or BT_4307)	Alternate Carbon Metabolism	Evidence from literature	PMID:37285	Gene annotation from NCBI Gene (last updated 01.01.11). It was demonstrated that *B. thetaiotaomicron* produces a glycogen.	2.4.1.11

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
GLCt2r	GLCt2r	(BT_3589 or BT_1758 or BT_0371 or BT_4311 or BT_4653)	Transport, Extracellular	Evidence from literature	PMID: 16887504	*B. thetaiotaomicron* grows on glucose, does not utilize a phosphotransferase system for uptake. Annotation from KEGG.	
GLCt4	glucose transport via sodium symport	BT_0355	Transport, Extracellular	Evidence from literature	PMID: 4853401	B. thetaiotaomicron uses glucose as sole carbon source.	
GLNt2r	L-glutamine reversible transport via proton symport		Transport, Extracellular	Evidence from literature	Dworkin, M. and S. Falkow (2006). The prokaryotes : a handbook on the biology of bacteria. New York ; [London], Springer	B. thetaiotaomicron is weakly proteolytic, so a transport reaction for all amino acids is assumed to be present.	
GLUABUTt7	4-aminobutyrate/glutamate antiport	BT_2573	Transport, Extracellular	Manually added gene annotation from databases		Annotation from TransportDB (www.membranetransport.org).	
GLYASNt	Glycyl-L-asparagine transport via proton symport	(BT_0580 or BT_4385 or BT_1086)	Transport, Extracellular	Manually added gene annotation from databases		Genes added based on TransportDB (last consulted 06.06.12).	
GLYASPt	Glycyl-L-aspartate transport via proton symport	(BT_0580 or BT_4385 or BT_1086)	Transport, Extracellular	Manually added gene annotation from databases		Genes added based on TransportDB (last consulted 06.06.12).	
GLYCOe	glycogen hydrolysis by samylases	(BT_3698 and BT_3701 and BT_3702)	Alternate Carbon Metabolism	Evidence from literature	Dworkin, M. and S. Falkow (2006). The prokaryotes : a handbook on the biology of bacteria. New York ; [London], Springer, PMID:16788175	*B. thetaiotaomicron* ferments glycogen. In *B. fragilis*, glycogen utilization seems to be performed by the starch utilization operon. It is assumed this is also the case in *B. thetaiotaomicron*.	
GLYD	glycerate dehydrogenase	BT_1207	Glycine, Serine, and Threonine Metabolism	Curation of incorrect annotation in Model SEED		Gene was annotated by Model SEED as phosphoglycerate oxidoreductase (EC 1.1.1.95). NCBI Gene (last updated 21.05.11) confirms annotation as glycerate dehydrogenase.	1.1.1.29
GLYGLNt	Glycyl-L-glutamine transport via proton symport	(BT_0580 or BT_4385 or BT_1086)	Transport, Extracellular	Manually added gene annotation from databases		Genes added based on TransportDB (last consulted 06.06.12).	
GLYGLUt	Glycyl-L-glutamate transport via proton symport	(BT_0580 or BT_4385 or BT_1086)	Transport, Extracellular	Manually added gene annotation from databases		Genes added based on TransportDB (last consulted 06.06.12).	3.2.1.18

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
GLYGLYHyi	hydrolysis of glycylycine, irreversible	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314)	Peptide Degradation	Manually added gene annotation from databases			2.6.1.85
GLYGLYt	Glycylglycine transport	(BT_0580 or BT_4385 or BT_1086)	Transport, Extracellular	Manually added gene annotation from databases		Genes added based on TransportDB (last consulted 06.06.12).	
GLYLEUHYDROe	hydrolysis of Glycylleucine by predicted non-cytosolic leucine peptidase	BT_2548	Peptide Degradation	Evidence from literature	PMID:12663928	Predicted non-cytosolic in PMID:12663928. Assumed to be extracellular for modeling purposes.	3.4.11.15
GLYMETt	Glycyl-L-methionine transport via proton symport	(BT_0580 or BT_4385 or BT_1086)	Transport, Extracellular	Manually added gene annotation from databases		Genes added based on TransportDB (last consulted 06.06.12).	
GLYPHEHYi	hydrolysis of glycylphenylalanine, irreversible	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314)	Peptide Degradation	Manually added gene annotation from databases			
GLYPHEt	Glycylphenylalanine transport	(BT_0580 or BT_4385 or BT_1086)	Transport, Extracellular	Manually added gene annotation from databases		Genes added based on TransportDB (last consulted 06.06.12).	
GLYPROPRO1e	hydrolysis of Glycylproline by predicted non-cytosolic proline peptidase	BT_0587	Peptide Degradation	Evidence from literature	PMID:12663928	Predicted non-cytosolic in PMID:12663928. Assumed to be extracellular for modeling purposes.	3.4.13.9
GLYPROt	Glycyl-L-proline transport via proton symport	(BT_0580 or BT_4385 or BT_1086)	Transport, Extracellular	Manually added gene annotation from databases		Genes added based on TransportDB (last consulted 06.06.12).	
GLYt2r	glycine reversible transport via proton symport		Transport, Extracellular	Manual gapfilling			
GLYTYRt	Glycyl-L-tyrosine transport via proton symport	(BT_0580 or BT_4385 or BT_1086)	Transport, Extracellular	Manually added gene annotation from databases		Genes added based on TransportDB (last consulted 06.06.12).	
GMAND	GDP-D-mannose dehydratase	BT_1224	Alternate Carbon Metabolism	Evidence from literature	DOI: 10.1007/s10068-010-0120-0	Gene was cloned and gene product was characterized.	4.2.1.47

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
GMHEPAT	D-glycero-D-manno-hepose 1-phosphate adenyltransferase		Lipopolysaccharide Biosynthesis	Evidence from literature	PMID:20974832, PMID:19460428	The structure of *B. thetaiotaomicron* LPS was studied, but the exact LPS synthesis pathway is unknown.	
GMHEPK	D-glycero-D-manno-heptose 7-phosphate kinase		Lipopolysaccharide Biosynthesis	Evidence from literature	PMID:20974832, PMID:19460428	The structure of *B. thetaiotaomicron* LPS was studied, but the exact LPS synthesis pathway is unknown.	
GMHEPPA	D-glycero-D-manno-heptose 1,7-bisphosphate phosphatase	BT_0477	Lipopolysaccharide Biosynthesis	Evidence from literature	PMID:20050615	The enzyme was purified and enzyme kinetics were studied.	
GTPDPDP	guanosine-5-triphosphate,3-diphosphate diphosphatase	BT_0540	Cofactor and Prosthetic Group Biosynthesis	Manually added gene annotation from databases		Included based on KEGG and NCBI putative gene annotation.	3.6.1.40
H2St	h2s transport (diffusion)		Transport, Extracellular	Evidence from literature	PMID:4853401	Sulfide (alternatively cysteine) is required as sulfur source.	
H2td	hydrogen transport		Transport, Extracellular	Evidence from literature	PMID:20444704	*B. thetaiotaomicron* produces hydrogen.	
HCYSMT	homocysteine S-methyltransferase	BT_0180	Methionine Metabolism	Manually added gene annotation from databases			
HEMEti	Heme transport via ABC system	(BT_0491 and BT_0492 and BT_0493 and BT_0494 and BT_0495 and BT_0496 and BT_0497 and BT_0498 and BT_0499)	Transport, Extracellular	Evidence from literature	PMID:4853401, PMID:17074906	*B. thetaiotaomicron* requires heme for growth. Lewis et al. (2006) characterized the putative heme uptake operon in the related species *Porphyromonas gingivalis* (*Bacteroidales* order) and located the genes in *B. thetaiotaomicron* by using BLAST search.	
HEPARL1_e	Heparin Lyase I, extracellular	BT_4675	Glycosaminoglycan Degradation	Evidence from literature	PMID:19801541, PMID:7574611	Heparin Lyase I cleaves the glycosidic linkage to the nonreducing end of iduronate. *B. thetaiotaomicron* specific putative pathway.	4.2.2.7
HEX10	hexokinase (D-glucosamine:ATP)	BT_2430	Aminosugar Metabolism	Evidence from literature	PMID:7240086	*B. thetaiotaomicron* is able to ferment glucosamine. Proposed pathway, not sure if glucosamine is utilized in this way.	2.7.1.1
HEX11	hexokinase (D-galactosamine:ATP)		Aminosugar Metabolism	Evidence from literature	PMID: 6367911	Galactosamine is metabolized by B. thetaiotaomicron to some extent and appears to be phosphorylated (though the compound does not support growth in vivo).	

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
HEX4	hexokinase (D-mannose:ATP)	(BT_2430 or BT_2493 or BT_4654)	Alternate Carbon Metabolism	Evidence from literature	PMID:15659667	Reversible reaction in SEED. Enzyme was characterized experimentally for *B. fragilis*.	2.7.1.7
HISt2r	L-histidine reversible transport via proton symport		Transport, Extracellular	Evidence from literature	Dworkin, M. and S. Falkow (2006). The prokaryotes : a handbook on the biology of bacteria. New York ; [London], Springer.	B. thetaiotaomicron is weakly proteolytic, so a transport reaction for all amino acids is assumed to be present.	4.1.3.18
HOMOGALASEe	Homogalacturonan degradation (citrus HG, 100 residues)	((BT_4146 or BT_4149 or BT_4153 or BT_4155 or BT_4170 or BT_4183 or BT_4115 or BT_4116 or BT_4119 or BT_4123) and BT_4150 and BT_4175 and (BT_4109 or BT_4110) and ((BT_4670 and BT_4671) or (BT_4164 and BT_4165) or (BT_4113 and BT_4114) or (BT_4121 and BT_4122) or (BT_3680 and BT_3681)))	Plant Polysaccharide Degradation	Evidence from literature	PMID: 22205877, PMID: 12913136	Bacteroides thetaiotaomicron grows on citrus homogalacturonan. The genes included in the GPR are upregulated during growth. Enzymes/ proteins assumed to be involved: galacturonisidase, rhamnogalactorunan esterase, rhamnogalacturonan lyase, pectinesterase, susC/ SusD	

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
HYD4	hydrogen:ferredoxin oxidoreductase	(BT_1210 or BT_0124 or BT_1834)	Central Metabolism	Evidence from literature	PMID:893348, PMID:760499, PMID:12740060, PMID:11260473, PMID:12777495, PMID:20444704	In the gut, this reaction regenerates NAD+ via NADH:ferredoxin oxidoreductase (FDNADOX). *B. thetaiotaomicron* generates hydrogen as one of its fermentation end products; accumulation of hydrogen inhibits reoxidation of NADH. It is therefore assumed that it regenerates NAD+ via this pathway, which leads to increased hydrogen partial pressure. Removal of hydrogen allows *B. thetaiotaomicron* to regenerate NAD+. The reaction can also be linked to pyruvate:ferredoxin oxidoreductase (PMID:11260473). Hydrogen also serves as an alternate electron donor for fumarate reduction via fumarate reductase (PMID:12777495). Gene annotation was proposed by the SEED Viewer, however, the reaction was not included in the draft model generated by Model SEED. NCBI Gene proposes NADH: ubiquinone oxidoreductase for BT_0124. According to KEGG, this reaction and ubiquinone-dependent hydrogenase (HYD1) are carried out by the same enzyme.	1.12.7.2
HYPSUCORNS	putative succinylornithine synthesis (hypothetical reaction)		exchange/demand reaction	Manual gapfilling	PMID:16704984	The metabolite is used for arginine biosynthesis, but its synthesis pathway is unknown.	
ICDHyr	isocitrate dehydrogenase (NADP)	BT_2071	TCA Cycle	Evidence from literature	PMID:11880608	Enzyme was characterized experimentally for *B. fragilis*.	1.1.1.42
IDOURASE	L-iduronidase		Glycosaminoglycan Degradation	Evidence from literature	PMID:18227125	Assumed to be present since *B. thetaiotaomicron* can degrade dermatan, which contains iduronate .	3.2.1.76

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
IDOURASE_HS1	Iduronidase, heparin degradation		Glycosaminoglycan Degradation	Evidence from literature	PMID:19801541, PMID:7574611	*B. thetaiotaomicron* specific putative heparin sulfate degradation pathway. It is not known which enzyme performs this step.	3.2.1.76
IDOURASE_HS2	Iduronidase, heparin degradation		Glycosaminoglycan Degradation	Evidence from literature	PMID:19801541, PMID:7574611	*B. thetaiotaomicron* specific putative heparin sulfate degradation pathway. It is not known which enzyme performs this step.	3.2.1.76
IDOURASE_HS3	Iduronidase, heparin degradation		Glycosaminoglycan Degradation	Evidence from literature	PMID:19801541, PMID:7574611	*B. thetaiotaomicron* specific putative heparin sulfate degradation pathway. It is not known which enzyme performs this step.	3.2.1.76
ILEt2r	L-isoleucine reversible transport via proton symport		Transport, Extracellular	Evidence from literature	PMID:7462155	*B. thetaiotaomicron* incorporates leucine, valine and isoleucine into its phospholipids,which suggests the presence of a transporter for these amino acids. However, it is not known which gene encodes this transporter.	
INULINASEe	Inulin degradation, extracellular	(BT_1759 or BT_3082)	Plant Polysaccharide Degradation	Evidence from literature	PMID: 19251883, PMID: 19321416, PMID:20603004	B. thetaiotaomicron grows on inulin (though slowly and less efficient than on levan).	
IOR2	indolepyruvate ferredoxin oxidoreductase (phenylpyvurate)	(BT_0429 and BT_0430)	Tyrosine, Tryptophan, and Phenylalanine Metabolism	Evidence from literature	PMID:18396344, PMID:16887608	Added based on annotation from NCBI Gene. *B. thetaiotaomicron* produces phenylacetate as a minor fermentation product (PMID:18396344). The indolepyruvate-dependent reaction of this enzyme may not take place since indoleacetate (a product of this pathway) was not found in *B. thetaiotaomicron*. Phenylacetate is also formed in the gut from aromatic acid metabolism (PMID:16887608).	1.2.7.8
IPMD2	(2R,3S)-3-methylmalate:NAD+ oxidoreductase	BT_1857	Valine, Leucine, and Isoleucine Metabolism	Manually added gene annotation from databases		Added based on annotation from KEGG Pathway	1.1.1.85
IS2TASE	Iduronate 2-sulfatase	((BT_0238 and BT_0756) or (BT_0238 and BT_2914))	Glycosaminoglycan Degradation	Evidence from literature	PMID:21507958	BT_0238 encodes anSME (anaerobic Sulfatase-Maturing Enzyme).	3.1.6.13

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
IS2TASE_HS1	Iduronate 2-sulfatase, heparin degradation	((BT_0238 and BT_0756) or (BT_0238 and BT_2914))	Glycosaminoglycan Degradation	Evidence from literature	PMID:21507958, PMID:19801541, PMID:7574611	*B. thetaiotaomicron* specific putative heparin sulfate degradation pathway. Requires sulfatase-maturing enzyme (BT_0238) to be functional.	3.1.6.13
ISOBUTt2r	Isobutyrate transport via proton symport		Transport, Extracellular	Evidence from literature	Krieg, N. R. (2010). Bergeys manual of systematic bacteriology, 2nd ed., volume 4. New York, Springer.	Isobutyrate and isovalerate are known secretion products of *B. thetaiotaomicron*.It is not known if transport of these metabolites consumes energy, and which transporter carries out this function.	
ISOCAPRt2r	Isocaproate transport via proton symport		Transport, Extracellular	Evidence from literature	PMID:1541601, PMID:16887608	Isocaproate is a minor product in the large intestine from leucine reduction. It is not known if this metabolite is produced in *B. thetaiotaomicron*. Needed for reaction LEUO to be element and charge balanced.	
ISOVALt2r	Isovalerate transport via proton symport		Transport, Extracellular	Evidence from literature	Krieg, N. R. (2010). Bergeys manual of systematic bacteriology, 2nd ed., volume 4. New York, Springer.	Isobutyrate and isovalerate are known secretion products of *B. thetaiotaomicron*.It is not known if transport of these metabolites consumes energy, and which transporter carries out this function.	
KAS1	b-ketoacyl synthetase (Iso-C14:0)	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	Glycerophospholipid Metabolism	Evidence from literature	PMID:6102980, PMID:7440508, PMID: 7204330, PMID:19460428	*B. thetaiotaomicron* is well known to produce iso- and anteiso-branched fatty acids besides straight-chain fatty acids.	2.3.1.41
KAS11	b-ketoacyl synthetase (Iso-C17:0)	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	Glycerophospholipid Metabolism	Evidence from literature	PMID:6102980, PMID:7440508, PMID: 7204330, PMID:19460428	*B. thetaiotaomicron* is well known to produce iso- and anteiso-branched fatty acids besides straight-chain fatty acids.	2.3.1.41
KAS12	b-ketoacyl synthetase (Anteiso-C17:0)	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	Glycerophospholipid Metabolism	Evidence from literature	PMID:6102980, PMID:7440508, PMID: 7204330, PMID:19460428	*B. thetaiotaomicron* is well known to produce iso- and anteiso-branched fatty acids besides straight-chain fatty acids.	2.3.1.41
KAS13	b-ketoacyl synthetase (octadecanoate)	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	Glycerophospholipid Metabolism	Evidence from literature	PMID:6102980, PMID:7440508, PMID: 7204330, PMID:19460428	*B. thetaiotaomicron* is well known to produce iso- and anteiso-branched fatty acids besides straight-chain fatty acids.	2.3.1.41
KAS2	b-ketoacyl synthetase (n-C14:0)	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	Glycerophospholipid Metabolism	Evidence from literature	PMID:6102980, PMID:7440508, PMID: 7204330, PMID:19460428	*B. thetaiotaomicron* is well known to produce iso- and anteiso-branched fatty acids besides straight-chain fatty acids.	2.3.1.41

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
KAS3	b-ketoacyl synthetase (Iso-C15:0)	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	Glycerophospholipid Metabolism	Evidence from literature	PMID:6102980, PMID:7440508, PMID: 7204330, PMID:19460428	*B. thetaiotaomicron* is well known to produce iso- and anteiso-branched fatty acids besides straight-chain fatty acids.	2.3.1.41
KAS4	b-ketoacyl synthetase (Anteiso-C15:0)	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	Glycerophospholipid Metabolism	Evidence from literature	PMID:6102980, PMID:7440508, PMID: 7204330, PMID:19460428	*B. thetaiotaomicron* is well known to produce iso- and anteiso-branched fatty acids besides straight-chain fatty acids.	2.3.1.41
KAS6	b-ketoacyl synthetase (Iso-C16:0)	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	Glycerophospholipid Metabolism	Evidence from literature	PMID:6102980, PMID:7440508, PMID: 7204330, PMID:19460428	*B. thetaiotaomicron* is well known to produce iso- and anteiso-branched fatty acids besides straight-chain fatty acids.	2.3.1.41
KAS8	b-ketoacyl synthetase (palmitate, n-C16:0)	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	Glycerophospholipid Metabolism	Evidence from literature	PMID:6102980, PMID:7440508, PMID: 7204330, PMID:19460428	*B. thetaiotaomicron* is well known to produce iso- and anteiso-branched fatty acids besides straight-chain fatty acids.	2.3.1.41
KDNH	2-keto-3deoxy-D-glycero-D-galactononic acid phosphohydrolase	BT_1713	Capsular Polysaccharide Biosynthesis	Evidence from literature	PMID:18804026	*B. thetaiotaomicron* forms and cytidylates 2-keto-3-deoxy-D-glycero-D-galacto-nononic acid (KDN), most likely for inclusion in its capsular polysaccharides.	
KDOCT2	3-deoxy-manno-octulosonate cytidylyltransferase	BT_0745	Lipopolysaccharide Biosynthesis	Manually added gene annotation from databases			3.6.1.1, T3.A.10
KDUI	5-keto-4-deoxyuronate isomerase	(BT_3231 or BT_4106)	Pentose and Glucuronate Interconversions	Manually added gene annotation from databases		Added based on annotation from KEGG Pathway	5.3.1.17
KESTOASEe	Beta-2-1 fructan degradation, extracellular	(BT_1759 or BT_3082)	Plant Polysaccharide Degradation	Evidence from literature	PMID:20603004	B. thetaiotaomicron grows well on short chain beta-2-1 fructans.	
KESTOPTASEe	Beta-2-1 fructan degradation, extracellular	(BT_1759 or BT_3082)	Plant Polysaccharide Degradation	Evidence from literature	PMID:20603004	B. thetaiotaomicron grows well on short chain beta-2-1 fructans.	
KESTOTTRASEe	Beta-2-1 fructan degradation, extracellular	(BT_1759 or BT_3082)	Plant Polysaccharide Degradation	Evidence from literature	PMID:20603004	B. thetaiotaomicron grows well on short chain beta-2-1 fructans.	
LACDFUCTTR_FUCASEe	alpha-fucosidase, Lactodifucotetraose (extracellular)	((BT_1625 or BT_4136) and ((BT_4134 and BT_4135) or (BT_1630 and BT_1631)))	HMO Degradation	Evidence from literature	PMID: 22036470	B. thetaiotaomicron grows on human milk oligosaccharides (HMOs); numerous glycosidase hydrolases are upregulated during growth on HMOs. Involves alpha-fucosidase and susC/ SusD (binding proteins).	

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
LACNDFUCHX_FUCASEe	alpha-fucosidase, Lacto-N-difucohexaose (extracellular)	((BT_1625 or BT_4136) and ((BT_4134 and BT_4135) or (BT_1630 and BT_1631)))	HMO Degradation	Evidence from literature	PMID: 22036470	B. thetaiotaomicron grows on human milk oligosaccharides (HMOs); numerous glycosidase hydrolases are upregulated during growth on HMOs. Involves alpha-fucosidase and susC/ SusD (binding proteins).	
LACNFUCPT_FUCASEe	alpha-fucosidase, Lacto-N-fucopentaose (extracellular)	((BT_1625 or BT_4136) and ((BT_4134 and BT_4135) or (BT_1630 and BT_1631)))	HMO Degradation	Evidence from literature	PMID: 22036470	B. thetaiotaomicron grows on human milk oligosaccharides (HMOs); numerous glycosidase hydrolases are upregulated during growth on HMOs. Involves alpha-fucosidase and susC/ SusD (binding proteins).	
LACNTTR_DEGe	Lacto-N-tetraose degradation by beta-galactosidase and N-acetylglucosaminidase, extracellular	((BT_1626 or BT_0461) and (BT_1627 or BT_1632 or BT_4132 or BT_0459 or BT_0460 or BT_1038 or BT_1044 or BT_1048 or BT_1051 or BT_4295 or BT_2825) and ((BT_1630 and BT_1631) or (BT_4134 and BT_4135) or (BT_1039 and BT_1040) or (BT_1042 and BT_1043) or (BT_1046 and BT_1047) or (BT_4297 and BT_4298) or (BT_2818 and BT_2819) or (BT_2820 and BT_2821)))	HMO Degradation	Evidence from literature	MID: 22036470	Growth on this human milk oligosaccharide is very slow and inefficient, but detectable. No information on growth on Lacto-N-neotetraose is available. Involves beta-galactosidase, N-acetylglucosaminidase, susC, susD (binding proteins).	
LACZe	b-galactosidase, extracellular	(BT_1626 or BT_4050)	Alternate Carbon Metabolism	Evidence from literature	PMID:16968696	Genes are upregulated in the presence of lactose from mothers milk.	3.2.1.23

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
LCAR2	Lactaldehyde reductase (glycolaldehyde)	BT_3767	Alternate Carbon Metabolism	Evidence from literature	PMID:3308886	Lactaldehyde dehydrogenase accepts glycolaldehyde as substrate (also shown in KEGG Pathway).	1.1.1.77
LDH_L	L-lactate dehydrogenase	(BT_4455 and BT_4456 and BT_4457)	Central Metabolism	Evidence from literature	PMID:148460	Gene annotation was proposed by The SEED Viewer, however, the reaction was not included in the draft model generated by Model SEED. No other genome database confirms this annotation. However, L-lactate dehydrogenase was demonstrated in the closely related organism *Bacteroides fragilis*.	1.1.1.27
LEUGLY1c	Hydrolysis of L-Leucylglycine	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314)	Peptide Degradation	Manually added gene annotation from databases			
LEUGLYLAPe	hydrolysis of Leucylglycine by predicted non-cytosolic leucine peptidase	BT_2548	Peptide Degradation	Evidence from literature	PMID:12663928	Predicted non-cytosolic by Xu et al. (2003): "A Genomic View of the Human-B. thetaiotaomicron Symbiosis.". Assumed to be extracellular for modeling purposes.	
LEUGLYt	L-Leucylglycine transport via proton symport	(BT_0580 or BT_4385 or BT_1086)	Transport, Extracellular	Manually added gene annotation from databases		Genes added based on TransportDB (last consulted 06.06.12).	
LEULEU1c	Hydrolysis of L-leucyl-L-leucine	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314)	Peptide Degradation	Manually added gene annotation from databases			

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
LEULEULAPe	hydrolysis of Leucylleucine by predicted non-cytosolic leucine peptidase	BT_2548	Peptide Degradation	Evidence from literature	PMID:12663928	Predicted non-cytosolic by Xu et al. (2003): "A Genomic View of the Human-*B. thetaiotaomicron* Symbiosis.". Assumed to be extracellular for modeling purposes.	3.4.11.15
LEULEUt	L-leucyl-L-leucine transport via proton symport	(BT_0580 or BT_4385 or BT_1086)	Transport, Extracellular	Manually added gene annotation from databases		Genes added based on TransportDB (last consulted 06.06.12).	
LEUO	Leucine oxidation by gut bacteria		Valine, Leucine, and Isoleucine Metabolism	Evidence from literature	PMID:1541601, PMID:3572204, PMID:16887608, Krieg, N. R. (2010). Bergey's manual of systematic bacteriology, 2nd ed., volume 4. New York, Springer.	Valine and leucine are oxidized by gut bacteria to BCFA (branched-chain fatty acids) with one less carbon atom (isobutyrate and isovalerate, respectively), CO2 and ammonia.Isocaproate is also formed in the large intestine by reduction of leucine. This reaction formula is hypothetical,no information on exact pathway and involved enzymes is avaiable. KEGG does not provide any pathway information either.Isobutyrate and isovalerate are known secretion products of *B. thetaiotaomicron*.	
LEUt2r	L-leucine reversible transport via proton symport		Transport, Extracellular	Evidence from literature	PMID:7462155	*B. thetaiotaomicron* incorporates leucine, valine and isoleucine into its phospholipids,which suggests the presence of a transporter.	
LEVANASE_1e	Extracellular levanase	BT_1760	Plant Polysaccharide Degradation	Evidence from literature	PMID:20603004	*B. thetaiotaomicron* utilizes levan from hosts diet as carbon source.	3.2.1.65
LEVANASE_2e	Extracellular levanase	(BT_1759 or BT_3082 or BT_1760)	Plant Polysaccharide Degradation	Evidence from literature	PMID:20603004	*B. thetaiotaomicron* utilizes levanoligosaccharides.	3.2.1.65
LEVANASE_3e	Extracellular levanase	(BT_1759 or BT_3082 or BT_1760)	Plant Polysaccharide Degradation	Evidence from literature	PMID:20603004	*B. thetaiotaomicron* utilizes levanoligosaccharides.	3.2.1.65
LEVANASE_4e	Extracellular levanase	(BT_1759 or BT_3082 or BT_1760)	Plant Polysaccharide Degradation	Evidence from literature	PMID:20603004	*B. thetaiotaomicron* utilizes levanoligosaccharides.	3.2.1.65
LEVANB_ABC	levanbiose transport		Plant Polysaccharide Degradation	Evidence from literature	PMID:20603004	*B. thetaiotaomicron* has an intracellular leavanbiose-degrading fructanase, therefore presence of a transport reaction is assumed.	

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
LMN2e	laminaribiase (extracellular)	(BT_2550 or BT_2824 or BT_3683)	Plant Polysaccharide Degradation	Evidence from literature	PMID:879772, PMID:9178362	*B. thetaiotaomicron* grows on laminaran, products are laminaribiose and glucose.	3.2.1.6
LMNe	Laminarinase (extracellular)	(BT_2550 or BT_2824 or BT_3683)	Plant Polysaccharide Degradation	Evidence from literature	PMID:879772, PMID:9178362	*B. thetaiotaomicron* grows on laminaran, products are laminaribiose and glucose.	3.2.1.6
LPADSS_BT	lipidA_bt disaccaride synthase	BT_4004	Lipopolysaccharide Biosynthesis	Evidence from literature	PMID:18931137, PMID:19460428, PMID:20974832	Based on *H. pylori* LPS biosynthesis (BIGG database), as in the *P. gingivalis* reconstruction (PMID:18931137). *P. gingivalis* LPS is similar in structure to the *Bacteroides* LPS. Based on structural information taken from (PMID:19460428, PMID:20974832).	2.4.1.182
LPS_BTabc	Lipopolysaccharide transport out via ABC system		Transport, Extracellular	Evidence from literature	PMID:18931137, PMID:19460428, PMID:20974832	Based on *H. pylori* LPS biosynthesis (BIGG database), as in the *P. gingivalis* reconstruction (PMID:18931137). *P. gingivalis* LPS is similar in structure to the *Bacteroides* LPS.	
LPSSYN_BT	Formation for LPS from Core oligosaccharide-Lipid A and O-chain		Lipopolysaccharide Biosynthesis	Evidence from literature	PMID:18931137, PMID:19460428, PMID:20974832. See also PMID:15774760	Based on *H. pylori* LPS biosynthesis (BIGG database), as in the *P. gingivalis* reconstruction (PMID:18931137). *P. gingivalis* LPS is similar in structure to the *Bacteroides* LPS. Based on structural information taken from (PMID:19460428, PMID:20974832).	
LYSDC	lysine decarboxylase	BT_3307	Threonine and Lysine Metabolism	Manually added gene annotation from databases		Added based on annotation from KEGG Pathway	4.1.1.18
MALCOACD	Malonyl-CoA condensation catalyzed by FabH	(BT_0122 or BT_3834)	Biotin Metabolism	Evidence from literature	PMID:20693992	Based on biotin synthesis described in PMID:20693992 for *E. coli*.	
MALCOAMT	Malonyl-CoA methyltransferase BioC	BT_1445	Biotin Metabolism	Evidence from literature	PMID:20693992	Based on biotin synthesis described in PMID:20693992 for *E. coli*. Malonyl-CoA is considered the most likely substrate.	
MALTe	alpha-glucosidase, extracellular	(BT_3704 or BT_3703)	Plant Polysaccharide Degradation	Evidence from literature	PMID:18981178, PMID:18611383, PMID:10986238	The starch and maltooligosaccharide utilization system of *B. thetaiotaomicron* is well characterized.	3.2.1.20

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
MALTt2r	maltose transport in via proton symport reversible		Transport, Extracellular	Evidence from literature	PMID: 10986238	*B. thetaiotaomicron* grows on maltose.	
MANA1e	beta-mannosidase, mannobiose degradation	(BT_0458 or BT_2855 or BT_4074 or BT_2432 or BT_3599)	Plant Polysaccharide Degradation	Evidence from literature	PMID:17287210	BT_0458 gene product was purifed and characterized. Shown to have high activity on mannobiose and especially mannotriose,mannotetraose and mannopentaose.	3.2.1.25
MANA2e	beta-mannosidase, mannotriose degradation	(BT_0458 or BT_2855 or BT_4074 or BT_2432 or BT_3599)	Plant Polysaccharide Degradation	Evidence from literature	PMID:17287210	BT_0458 gene product was purifed and characterized. Shown to have high activity on mannobiose and especially mannotriose,mannotetraose and mannopentaose.	3.2.1.25
MANA3e	beta-mannosidase, mannotetraose degradation	(BT_0458 or BT_2855 or BT_4074 or BT_2432 or BT_3599)	Plant Polysaccharide Degradation	Evidence from literature	PMID:17287210	BT_0458 gene product was purifed and characterized. Shown to have high activity on mannobiose and especially mannotriose,mannotetraose and mannopentaose.	3.2.1.25
MANA4e	beta-mannosidase, mannopentaose degradation	(BT_0458 or BT_2855 or BT_4074 or BT_2432 or BT_3599)	Plant Polysaccharide Degradation	Evidence from literature	PMID:17287210	BT_0458 gene product was purifed and characterized. Shown to have high activity on mannobiose and especially mannotriose,mannotetraose and mannopentaose.	3.2.1.25
MANabc	mannose transport via ABC transporter	BT_1536	Transport, Extracellular	Evidence from literature	PMID: 22205877	B. thetaiotaomicron grows on mannose and alpha-mannan. The ABC transporter BT_1536 is upregulated during growth on alpha-mannan.	
MANt2r	D-mannose transport in via proton symport reversible		Transport, Extracellular	Evidence from literature	PMID: 16887504	GPR is not not known, but *B. thetaiotaomicron* was demonstrated to grow on mannose as sole carbon source.	
MANTRabc	mannotriose transport via ABC transporter		Transport, Extracellular	Evidence from literature	PMID:17287210	*B. thetaiotaomicro*n grows on mannotriose.	
MELIBabc	melibiose transport via ABC system (import)		Transport, Extracellular	Evidence from literature	PMID:2557798	*B. thetaiotaomicron* grows on melibiose.	
MEOHt2	Methanol diffusion		Transport, Extracellular	Evidence from literature	PMID:20693992	Biotin synthesis pathway as proposed by PMID:20693992 produces methanol.	
METALAt	L-methionyl-L-alanine transport via proton symport	(BT_0580 or BT_4385 or BT_1086)	Transport, Extracellular	Manually added gene annotation from databases		Genes added based on TransportDB (last consulted 06.06.12).	4.2.99.9

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
METOX1s	methionine oxidation (spontaneous)		Methionine Metabolism	Based on BIGG database			
METt2r	L-methionine reversible transport via proton symport	BT_1270	Transport, Extracellular	Evidence from literature	PMID:10867063	Gut microbiota contribute to host amino acid homeostasis. Methionine is an essential amino acid for humans. This annotation (Methionine transporter MetT) is only supported by The SEED.	
MK10t	Menaquinone secretion/ uptake (menaquinone 10)		Transport, Extracellular	Evidence from literature	PMID: 18841274	Gut microbiota, in particular Bacteroides, produce menaquinone, which contributes to host vitamin K homeostasis. AH	
MK11t	Menaquinone secretion/ uptake (menaquinone 11)		Transport, Extracellular	Evidence from literature	PMID: 18841274	Gut microbiota, in particular Bacteroides, produce menaquinone, which contributes to host vitamin K homeostasis. AH	
MK7t	Menaquinone secretion/ uptake (menaquinone 7)		Transport, Extracellular	Evidence from literature	PMID: 18841274	Gut microbiota, in particular Bacteroides, produce menaquinone, which contributes to host vitamin K homeostasis. AH	
MK8t	Menaquinone secretion/ uptake (menaquinone 8)		Transport, Extracellular	Evidence from literature	PMID: 18841274	Gut microbiota, in particular Bacteroides, produce menaquinone, which contributes to host vitamin K homeostasis. AH	
MK9t	Menaquinone secretion/ uptake (menaquinone 9)		Transport, Extracellular	Evidence from literature	PMID: 18841274	Gut microbiota, in particular Bacteroides, produce menaquinone, which contributes to host vitamin K homeostasis. AH	
MLTG1	Maltodextrin glucosidase (maltotriose)	BT_4690	Plant Polysaccharide Degradation	Evidence from literature	PMID:848954	Added based on annotation from NCBI Gene. There may also be other cytoplasmatic enzymes carrying out this reaction. The starch and maltooligosaccharide utilization system of *B. thetaiotaomicron* is well characterized.	3.2.1.1
MLTG1e	Maltodextrin glucosidase (maltotriose), extracellular	(BT_3703 or BT_3704)	Plant Polysaccharide Degradation	Evidence from literature	PMID:10986238, PMID:2722747, PMID: 18981178, PMID:18611383	The starch and maltooligosaccharide utilization system of *B. thetaiotaomicron* is well characterized.	3.2.1.1

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
MLTG2	Maltodextrin glucosidase (maltotetraose)	BT_4690	Plant Polysaccharide Degradation	Evidence from literature	PMID:848954	Added based on annotation from NCBI Gene. There may also be other cytoplasmatic enzymes carrying out this reaction. The starch and maltooligosaccharide utilization system of *B. thetaiotaomicron* is well characterized.	3.2.1.1
MLTG2e	Maltodextrin glucosidase (maltotetraose), extracellular	(BT_3703 or BT_3704)	Plant Polysaccharide Degradation	Evidence from literature	PMID: 18981178, PMID:18611383	The starch and maltooligosaccharide utilization system of *B. thetaiotaomicron* is well characterized.	3.2.1.1
MLTG3	Maltodextrin glucosidase (maltopentaose)	BT_4690	Plant Polysaccharide Degradation	Evidence from literature	PMID:848954	Added based on annotation from NCBI Gene. There may also be other cytoplasmatic enzymes carrying out this reaction. The starch and maltooligosaccharide utilization system of *B. thetaiotaomicron* is well characterized.	3.2.1.1
MLTG3e	Maltodextrin glucosidase (maltopentaose), extracellular	(BT_3703 or BT_3704)	Plant Polysaccharide Degradation	Evidence from literature	PMID: 18981178, PMID:18611383	The starch and maltooligosaccharide utilization system of *B. thetaiotaomicron* is well characterized.	3.2.1.1
MLTG4	Maltodextrin glucosidase (maltohexaose)	BT_4690	Plant Polysaccharide Degradation	Evidence from literature	PMID:848954	Added based on annotation from NCBI Gene. There may also be other cytoplasmatic enzymes carrying out this reaction. The starch and maltooligosaccharide utilization system of *B. thetaiotaomicron* is well characterized.	3.2.1.1
MLTG4e	Maltodextrin glucosidase (maltohexaose), extracellular	((BT_3698 and BT_3701 and BT_3702) or (BT_0773 and BT_3701 and BT_3702) or (BT_4305 and BT_3701 and BT_3702))	Plant Polysaccharide Degradation	Evidence from literature	PMID:10986238, PMID:2722747, PMID:8955399, PMID: 18981178, PMID:18611383	The starch and maltooligosaccharide utilization system of *B. thetaiotaomicron* is well characterized.	3.2.1.1

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
MLTG5	Maltodextrin glucosidase (maltoheptaose)	BT_4690	Plant Polysaccharide Degradation	Evidence from literature	PMID:848954	Added based on annotation from NCBI Gene. There may also be other cytoplasmatic enzymes carrying out this reaction. The starch and maltooligosaccharide utilization system of *B. thetaiotaomicron* is well characterized.	3.2.1.1
MLTG5e	Maltodextrin glucosidase (maltoheptaose), extracellular	((BT_3698 and BT_3701 and BT_3702) or (BT_0773 and BT_3701 and BT_3702) or (BT_4305 and BT_3701 and BT_3702))	Plant Polysaccharide Degradation	Evidence from literature	PMID:10986238, PMID:2722747, PMID:8955399, PMID: 18981178, PMID:18611383	The starch and maltooligosaccharide utilization system of *B. thetaiotaomicron* is well characterized.	3.2.1.1
MOAT_BT	3-deoxy-D-manno-octulosonic acid transferase	BT_2747	Lipopolysaccharide Biosynthesis	Evidence from literature	PMID:18931137, PMID:19460428, PMID:20974832	Based on *H. pylori* LPS biosynthesis (BIGG database), as in the *P. gingivalis* reconstruction (PMID:18931137). *P. gingivalis* LPS is similar in structure to the *Bacteroides* LPS. Based on structural information taken from (PMID:19460428, PMID:20974832).	2.4.99.12
MTHGXLt	Methylglyoxal transport (cytosol to extracellular)		Transport, Extracellular	Evidence from literature	PMID:11260473	*B. thetaiotaomicron* produces weak amounts of methylglyoxal.	
NACHEX27e	beta-N-acetylhexosaminidase, hyaluronan degradation	(BT_4394 or BT_4395 or BT_4337 or BT_3598 or BT_1627 or BT_3868 or BT_0459 or BT_0460 or BT_0506 or BT_4681 or BT_1621 or BT_3178 or BT_0456 or BT_1051 or BT_2459)	Glycosaminoglycan Degradation	Evidence from literature	PMID:16565725, PMID: 20689974, PMID:848954	BT_4395 gene product was purified and characterized. *B. thetaiotaomicron* ferments hyaluronan.	3.2.1.52

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
NACt	Nicotinate secretion/ uptake		Transport, Extracellular	Evidence from literature	PMID: 19748469	B. thetaiotaomicron mutants in NAD biosynthesis are not essential in vitro on tryptone-yeast extract-glucose medium, suggesting that B. thetaiotaomicron can uptake nicotinate from yeast extract.	
NADDP	NAD diphosphatase	BT_1544	Cofactor and Prosthetic Group Biosynthesis	Manually added gene annotation from databases		Added based on KEGG Pathway	3.6.1.22
NADH17	NADH dehydrogenase (menaquinone-8 & 3 protons)	(BT_4058 and BT_4059 and BT_4060 and BT_4061 and BT_4062 and BT_4063 and BT_4064 and BT_4065 and BT_4066 and BT_4067)	Central Metabolism	Evidence from literature, based on existing metabolic reconstruction	PMID:12777495	The reaction is linked to fumarate reductase. The exact stochiometry is unkown, formula was putatively added based on *E. coli* iAF1260.	1.6.5.3
NARK	Nitrite transport in		ROS Detoxification	Evidence from literature	Dworkin, M. and S. Falkow (2006). The prokaryotes : a handbook on the biology of bacteria. New York ; [London], Springer, PMID:14665678, PMID:16183308	Nitrite appears to be produced from NH4 by nitrite reductase (the reaction does not seem to go the other way since nitrite does not serve as nitrogen source). Nitrite does not react further to nitric oxide (or only in very slight amounts) (PMID:16183308). It is assumed that nitrite is transported out via diffusion through porin (PMID:14665678).	
NBAHH_ir	Nalpha-(beta-alanyl)-L-histidine hydrolase IR	(BT_4045 or BT_1615)	Histidine Metabolism	Evidence from literature	PMID:3543210	Added based on KEGG Pathway. *B. thetaitaomicron* has weak proteolytic activity (cell-bound). The enzyme is possibly involved in degrading host-derived peptides.	3.4.13.3
NEULACNTTR_SIASEe	sialidase, Sialyllacto-N-tetraose	BT_0455 or BT_2194 or BT_2892	HMO Degradation	Evidence from literature	PMID: 22036470	B. thetaiomicron liberates sialic acid from human milk oligosaccharides, though it cannot use it. Lacto-N-tetraose is poorly metabolized and accumulates if BT is grown on HMOs.	
NMNt2r	NMN transport via proton symport reversible	BT_2396	Transport, Extracellular	Manually added gene annotation from databases		Annotation from NCBI Gene (last updated 01.01.11)	

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
O16G2e	oligo-1,6-glucosidase (strch2 ->strch3), extracellular	BT_3299	Plant Polysaccharide Degradation	Evidence from literature	PMID:10986238, PMID:2722747, PMID:8955399, PMID: 18981178, PMID:18611383	Starch utilization by *B. thetaiotaomicron* as sole carbon source is well established.	3.2.1.10
OGALURLe	Oligogalacturonate lyase (extracellular)	(BT_4115 or BT_4116)	Plant Polysaccharide Degradation	Manual gapfilling	PMID:3968032	Oligogalacturonate lyase is not annotated in the *B. thetaiotaomicron* genome. Is assumed to also by carried out by pectate lyase to allow complete degradation of pectin.	4.2.2.6
OIVD2	2-oxoisovalerate dehydrogenase (acylating; 3-methyl-2-oxobutanoate)		Valine, Leucine, and Isoleucine Metabolism	Manual gapfilling		Manual_Gapfilling based on reactions OIVD1r and OIVD3 added by Model SEED. Required for lipid metabolism.	1.2.1.25
OLIGOFRUASEe	Oligofructose degradation by extracellular fructanase	(BT_1759 or BT_3082)	Plant Polysaccharide Degradation	Evidence from literature	PMID:16461642, PMID:20603004	*B. thetaiotaomicron* grows on the prebiotic oligofructose. Degradation is carried out by exo-acting periplasmatic fructosidases (extracellular for modeling purposes).	
OORr	2-oxoglutarate synthase (reversible)	((BT_0329 and BT_0330 and BT_0331 and BT_0333) or (BT_2836 and BT_2837))	TCA Cycle	Manual gapfilling	PMID: 533772, PMID:11880608	Demonstrated for several *Bacteroides* species. Neccessary for heme-dependent 2-oxoglutarate synthesis from oxaloacetate. OORr is an additional reaction catalyzed by 2-oxoglutarate synthase apart from OOR2r. Necessary to allow IOR2 to run. Not sure which form of ferredoxin is used.	1.2.7.3
ORNabc	ornithine transport via ABC system	BT_4049	Transport, Extracellular	Manually added gene annotation from databases		Annotation from NCBI Gene (last updated 01.01.11)	
ORNTA	ornithine transaminase	BT_3758	Arginine and Proline Metabolism	Evidence from literature	PMID:238949	Acetylornithine transaminase catalyzes the transamination of N-2-acetyl-L-ornithine (ACOTA) as well as of L-ornithine (this reaction) with 2-oxoglutarate.	2.6.1.13
PACCOALr	phenylacetate-CoA ligase	(BT_0428 or BT_0571)	Tyrosine, Tryptophan, and Phenylalanine Metabolism	Evidence from literature	PMID:18396344, PMID:16887608	*B. thetaiotaomicron* produces phenylacetate as a minor fermentation product (PMID:18396344). Phenylacetate is also formed in the gut from aromatic acid metabolism (PMID:16887608).	6.2.1.30

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
PACt2r	phenylacetate transport in via proton symporter		Transport, Extracellular	Evidence from literature	PMID:18396344	*B. thetaiotaomicron* produces phenylacetate as a minor fermentation product during growth on carbohydrates.	
PANTS	pantothenate synthase	BT_4308	Cofactor and Prosthetic Group Biosynthesis	Evidence from literature	PMID:4853401	Annotation from KEGG Pathway. *B. thetaiotaomicron* does not require patothenate.	6.3.2.1
PDHa	pyruvate dehydrogenase (lipoamide)	BT_0311	Glycolysis/Gluconeogenesis	Manually added gene annotation from databases			
PE_CER1_BTt	Ceramide phosphoethanolamine (B.thetaiotaomicron specific) export		Sphingolipid Metabolism	Evidence from literature	PMID:16887518, PMID:20855611, Anaerobe (2001) 07, 103–112 doi:10.1006/anae.2001.0376	*Bacteroides* species are well established to produce sphingolipids.	

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
PECTICGALASEe	Pectic galactan (potato) degradation, extracellular	((BT_0348 or BT_0360 or BT_0367 or BT_0368 or BT_0369) and (BT_4667 or BT_4668 or BT_4152) and (BT_4146 or BT_4149 or BT_4153 or BT_4155 or BT_4160 or BT_4170 or BT_4183 or BT_4115 or BT_4116 or BT_4119 or BT_4123) and (BT_4150 or BT_4173) and BT_4175 and (BT_4109 or BT_4110) and ((BT_0361 and BT_0362) or (BT_0363 and BT_0364) or (BT_4670 and BT_4671) or (BT_4164 and BT_4165) or (BT_4113 and BT_4114) or (BT_4121 and BT_4122)))	Plant Polysaccharide Degradation	Evidence from literature	PMID: 22205877	B. thetaiotaomicron grows on pectic galactan. The genes included in the GPR are upregulated during growth. Enzymes/ proteins assumed to be involved: arabinosidase, galactosidase, galacturonisidase, rhamnogalactorunan esterase, rhamnogalacturonan lyase, pectinesterase, susC/ SusD	
PECTIN_DEG2e	Pectin degradation by extracellular pectate lyase and pectinesterase, gut microbiota specific	((BT_4115 or BT_4116) and BT_4110)	Plant Polysaccharide Degradation	Evidence from literature	PMID:3968032	Purified and characterized by enzyme assay in B. thetaiotaomicron. Genome annotation from NCBI Gene. Appears to be located in periplasm (extracellular for modeling purposes).	

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
PECTIN_DEGe	Pectin degradation by extracellular endopolygalacturonase and pectinesterase, gut microbiota specific	((BT_1018 or BT_2378 or BT_4123 or BT_4155 or BT_4187) and BT_4110)	Plant Polysaccharide Degradation	Evidence from literature	PMID:3968032	Purified and characterized by enzyme assay. Genome annotation from NCBI Gene. Appears to be located in periplasm (extracellular for modeling purposes).	
PECTLe	Pectate lyase (extracellular)	(BT_4115 or BT_4116)	Plant Polysaccharide Degradation	Evidence from literature	PMID:3968032	Purified and characterized by enzyme assay. Genome annotation from NCBI Gene. Appears to be located in periplasm (extracellular for modeling purposes).	4.2.2.2
PEPM	phosphoenolpyruvate mutase	BT_1720	Capsular Polysaccharide Biosynthesis	Evidence from literature	PMID:12904299	PEPM, 3OPDC and 2AMEPHPAT form the biosynthetic pathway of 2-aminoethylphosphonate, a component of the capsular polysaccharide complex of *Bacteroides fragilis*, and most likely other *Bacteroides* species.	5.4.2.9
PEPT160	ethanolamine phosphotransferase (n-C16:0)		Sphingolipid Metabolism	Manual gapfilling	PMID:16887518, PMID:20855611, Anaerobe (2001) 07, 103–112 doi:10.1006/anae.2001.0376	Reaction required for sphingolipid synthesis. The pathway mechanism may be different.	
PGAMT	phosphoglucosamine mutase	BT_3950	Cell Envelope Biosynthesis	Evidence from literature	PMID:18931137, PMID:19460428, PMID:20974832.	Reaction is needed for LPS biosynthesis, based on *H. pylori* LPS biosynthesis (BIGG database). Annotation from The SEED.	5.4.2.10
PHCHGS	L-1-Pyrroline-3-hydroxy-5-carboxylate spontaneous conversion to L-4-Hydroxyglutamate semialdehyde		Arginine and Proline Metabolism	Based on BIGG database		BIGG database suggests that this reaction occurs spontaneously.	
PHEARG1c	Hydrolysis of L-phenylalanyl-L-arginine	BT_1846	Peptide Degradation	Evidence from literature	PMID: 22628297	B. thetaiotaomicron peptidase M49 was characterized and shown to hydrolyze Arg-Arg and Phe-Arg specifically.	3.2.1.31
PHEARGt	L-phenylalanyl-L-arginine transport via proton symport	(BT_0580 or BT_4385 or BT_1086)	Transport, Extracellular	Evidence from literature	PMID: 22628297	B. thetaiotaomicron peptidase M49 was characterized and shown to hydrolyze Arg-Arg and Phe-Arg specifically.	

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
PMACPME	Cleavage of ester from pimeloyl-ACP methyl ester (BioH)		Biotin Metabolism	Evidence from literature	PMID:20693992, PMID:4853401	Based on biotin synthesis described in PMID:20693992 for E. coli. Gene is not known, but the gap was filled to complete biotin synthesis pathway (biotin is not required by *B. thetaiotaomicron*, see PMID:4853401).	
PMANM	phosphomannomutase	(BT_3950 or BT_1548)	Alternate Carbon Metabolism	Manually added gene annotation from databases		Based on annotation from NCBI Gene (last updated 21.05.11)	5.4.2.8
PNTOt2	Pantothenate reversible transport via proton symport		Transport, Extracellular	Evidence from literature	PMID: 19748469	B. thetaiotaomicron mutants in panthotenate biosynthesis are not essential in vitro on tryptone-yeast extract-glucose medium, suggesting that B. thetaiotaomicron can uptake panthotenate from yeast extract.	
PPAtr	Propionate transport, diffusion		Transport, Extracellular	Evidence from literature	PMID:19321416, PMID:12740060	*Bacteroides* species are well established to produce short-chain fatty acids (SCFAs).	
PPK2	polyphosphate kinase	(BT_0541 or BT_2019)	Central Metabolism	Manually added gene annotation from databases		Added based on annotation from NCBI Gene.	2.7.4.1
PROGLYt	L-prolylglycine transport via proton symport	(BT_0580 or BT_4385 or BT_1086)	Transport, Extracellular	Manually added gene annotation from databases		Genes added based on TransportDB (last consulted 06.06.12).	2.1.3.11
PTRCtex2	putrescine excretion (cytosol to extracellular)		Transport, Extracellular	Evidence from literature	PMID:10801923	B. thetaiotaomicron secretes putrescine and spermidine.	
PULLe	pullulane hydrolysis by alpha-1,6 pullulanase and alpha-amylase	((BT_3698 and BT_3701 and BT_3702) or (BT_3701 and BT_3702 and BT_4689) or (BT_1663 and BT_3701 and BT_3702))	Plant Polysaccharide Degradation	Evidence from literature	PMID:10986238, PMID:2722747, PMID:8955399, PMID: 18981178, PMID:18611383	The starch utilization system of *B. thetaiotaomicron* is well characterized.	
PYDXNO	pyridoxine oxidase	BT_1577	Vitamin B6 Metabolism	Manually added gene annotation from databases			1.4.3.5

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
PYDXNtr	pyridoxine transport via diffusion		Transport, Extracellular	Evidence from literature	PMID:894368, PMID:9167138, PMID:9562034	It is well established that the gut microbiota produces B vitamins in mammals. Germ-free rats fed a pyridoxine-free diet suffer far more severe deficiency symptoms than conventional rats (PMID:894368). Pyridoxine transport by *B. thetaiotaomicron* is therefore assumed to occur.	
PYDXO	pyridoxal oxidase	BT_1577	Vitamin B6 Metabolism	Manually added gene annotation from databases			1.4.3.5
PYRt2r	pyruvate reversible transport via proton symport		Transport, Extracellular	Evidence from literature	PMID:11260473	No gene found, but *B. thetaiotaomicron*was shown to secrete pyruvate.	
QMO3	quinol monooxygenase (menaquinol 8)	(BT_3054 and BT_3055)	Central Metabolism	Evidence from literature	PMID:7649986, PMID:11260473	The reaction seems to be carried out by fumarate reductase. When it is exposed to air, fumarate reductase generates oxygen free radicals through autooxidation. The electrons seem to pass from reduced menaquinone via Fe-S clusters and a flavin to oxygen.	
RAFFabc	raffinose transport via ABC system (import)		Transport, Extracellular	Evidence from literature	PMID:2557798	*B. thetaiotaomicron* can use raffinose as carbon source.	
RFA_BT	Formation of lipidA and sugar core for LPS		Lipopolysaccharide Biosynthesis	Evidence from literature	PMID:18931137, PMID:19460428, PMID:20974832	Based on *H. pylori* LPS biosynthesis (BIGG database), as in the *P. gingivalis* reconstruction (PMID:18931137). *P. gingivalis* LPS is similar in structure to the *Bacteroides* LPS. Based on structural information taken from (PMID:19460428, PMID:20974832).	
RFAC_HP	RFAC HP		Lipopolysaccharide Biosynthesis	Based on existing metabolic reconstruction	PMID:18931137, PMID:19460428, PMID:20974832	Based on *H. pylori* LPS biosynthesis (BIGG database), as in the *P. gingivalis* reconstruction (PMID:18931137). *P. gingivalis* LPS is similar in structure to the *Bacteroides* LPS. Based on structural information taken from (PMID:19460428, PMID:20974832).	

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
RHAMNOGALURASEe_I	Rhamnogalacturonan I degradation, extracellular	(BT_1021 and BT_3662 and (BT_4152 or BT_0983 or BT_0992 or BT_0993 or BT_0996) and (BT_1001 or BT_1013 or BT_1019) and (BT_4146 or BT_4149 or BT_4153 or BT_4155 or BT_4183 or BT_4115 or BT_4116 or BT_1011 or BT_1018) and (BT_4150 or BT_4173) and BT_4175 and (BT_4109 or BT_4110) and ((BT_4670 and BT_4671) or (BT_4164 and BT_4165) or (BT_4113 and BT_4114) or (BT_1028 and BT_1029) or (BT_1683 and BT_1683) or (BT_3670 and BT_3671)))	Plant Polysaccharide Degradation	Evidence from literature	PMID: 22205877	B. thetaiotaomicron grows on rhamnogalacturonan I. The genes included in the GPR are upregulated during growth. Enzymes/ proteins assumed to be involved: arabinosidase, xylosidase, galactosidase, galacturonisidase, rhamnogalactorunan esterase, rhamnogalacturonan lyase, pectinesterase, susC/ SusD	

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
RHAMNOGALURASEe_II	Rhamnogalacturonan II degradation, extracellular	(BT_1021 or BT_0348) and (BT_3662 or BT_3663) and BT_1011 and BT_3664 and BT_3665 and (BT_4152 or BT_0983 or BT_0992 or BT_0993 or BT_0996) and (BT_1001 or BT_1013 or BT_1019) and (BT_4146 or BT_4149 or BT_4153 or BT_4155 or BT_4183 or BT_4115 or BT_4116 or BT_1018) and (BT_4150 or BT_4173) and BT_4175 and (BT_4109 or BT_4110) and ((BT_4670 and BT_4671) or (BT_4164 and BT_4165) or (BT_4113 and BT_4114) or (BT_1028 and BT_1029) or (BT_1683 and BT_1683) or (BT_3670 and BT_3671) or (BT_1024 and BT_1025))	Plant Polysaccharide Degradation	Evidence from literature	PMID: 22205877	B. thetaiotaomicron grows on rhamnogalacturonan I. I'm not sure what happens to the rare sugars included in RGII. The genes included in the GPR are upregulated during growth. Enzymes/ proteins assumed to be involved: arabinosidase, xylosidase, galactosidase, fucosidase, beta-glucosidase, galacturonisidase, glucuronidase rhamnogalactorunan esterase, rhamnogalacturonan lyase, pectinesterase, susC/ SusD	
RIBFLVt2r	riboflavin transport in via proton symport reversible		Transport, Extracellular	Evidence from literature	PMID:9167138	Riboflavin is synthesized by the gut bacterial flora of the colon.	

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
RIBt2r	ribose transport in via proton symporter, reversible		Transport, Extracellular	Evidence from literature	PMID: 17579514	Bacteroides thetaiotaomicron grows on D-ribose.	
SERPT	serine C-palmitoyltransferase	BT_0870	Sphingolipid Metabolism	Evidence from literature	PMID:16887518, PMID:20855611	*Bacteroides* are well established to produce sphingolipids. Homologs of human serine palmitoyl transferase were found in *Bacteroides* and related species. In B. thetaiotaomicron, BLASTP of human serine palmitoyl transferase subunit 1 returns BT_0870, 8-amino-7-oxononanoate synthase, as homolog. It is unclear if this gene really encodes SERPT. Presence of this enzyme is supported by inhibition of sphingolipid synthesis in B. fragilis if cultures are exposed to the SERPT inhibitor myriocin (PMID:20855611).	2.3.1.50
SHSL2r	O-succinylhomoserine lyase (H2S)	(BT_1923 or BT_2387)	Methionine Metabolism	Manually added gene annotation from databases			
SIAASE_OGLYCAN1e	Sialidase, mucin-type O-glycans, extracellular	BT_0455 or BT_2194 or BT_2892	O-Glycan Degradation	Evidence from literature	PMID: 18996345, PMID: 10430883, PMID: 848954	B. thetaiotaomicron is well known to degrade mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis.	
SIAASE_OGLYCAN2e	Sialidase, mucin-type O-glycans, extracellular	BT_0455 or BT_2194 or BT_2892	O-Glycan Degradation	Evidence from literature	PMID: 18996345, PMID: 10430883, PMID: 848954	B. thetaiotaomicron is well known to degrade mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis.	
SIAASE_OGLYCAN3e	Sialidase, mucin-type O-glycans, extracellular	BT_0455 or BT_2194 or BT_2892	O-Glycan Degradation	Evidence from literature	PMID: 18996345, PMID: 10430883, PMID: 848954	B. thetaiotaomicron is well known to degrade mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis.	
SIAASEe	sialidase, extracellular	BT_0455	N-Glycan Degradation	Evidence from literature	PMID:7463468, PMID:15790854, PMID:19304853	*B. thetaiotaomicron* has sialidase activity. However, it does not grow on N-acetyl neuraminic acid as sole carbon source (PMID:19304853).	3.2.1.18
sink_chols	sink_reaction_choline sulfate		exchange/demand reaction	Manual gapfilling			

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
sink_s	sink_reaction_sulfur[c]		exchange/demand reaction	Manual gapfilling			
SPHMYLN_BTt	Sphingomyelin (B.thetaiotaomicron specific) export		Sphingolipid Metabolism	Evidence from literature	PMID:16887518, PMID:20855611, Anaerobe (2001) 07, 103–112 doi:10.1006/anae.2001.0376	*Bacteroides* species are well established to produce sphingolipids.	
SPMDtex2	spermidine excretion (cytosol to extracellular)		Transport, Extracellular	Evidence from literature	PMID:10801923	*B. thetaiotaomicron* secretes putrescine and spermidine.	
STYSabc	stachyose transport via ABC system (import)		Transport, Extracellular	Evidence from literature	PMID:2557798	*B. thetaiotaomicron* can utilize stachyose as carbon source.	
SUCCITRDSs	N-succinyl-L-citrulline desuccinylase (spontaneous)		Arginine and Proline Metabolism	Manual gapfilling	PMID:16704984	The product of this reaction is used for arginine biosynthesis by *B. thetaiotaomicron*. It is not known if this reaction happens spontaneously or enzymatically.	
SUCCt2r	succinate transport via proton symport	BT_2756	Transport, Extracellular	Evidence from literature	PMID:19321416, PMID:12740060, PMID:11880608	*Bacteroides* species are well established to produce succinate. Also, growth of *B. fragilis* is stimulated by uptake of succinate in heme-resitricted culture (PMID:11880608). Annotation based on NCBI Gene.	
SUCR	sucrose hydrolyzing enzyme	BT_1765	Plant Polysaccharide Degradation	Evidence from literature	PMID:20603004	*B. thetaiotaomicron* can utilize sucrose as carbon source.	3.2.1.26
SUCRt2	sucrose transport in via proton symport		Transport, Extracellular	Evidence from literature	PMID:20603004	*B. thetaiotaomicron* can utilize sucrose as carbon source.	
T2DECAI	trans-2-decenoyl-ACP isomerase		Cell Envelope Biosynthesis	Manual gapfilling	PMID:6102980	This reaction is carried out by FabA. *B. thetaiotaomicron* does not have this enzyme. However, production of monounsaturated fatty acids in *B. thetaiotaomicron* is confirmed.	
TAURtex2	taurine transport via diffusion		Transport, Extracellular	Evidence from literature	PMID: 14665678	Diffusion through a porine assumed due to metabolites small size.	
TCHOLAH	Bile acid hydrolase (taurocholate)	(BT_1259 or BT_2086)	Bile Acid Metabolism	Evidence from literature	PMID:10993, Dworkin, M. and S. Falkow (2006). The prokaryotes : a handbook on the biology of bacteria. New York ; [London], Springer	This enzyme was demonstrated in *B. thetaiotaomicron* (PMID:10993). Growth is stimulated by 20 % bile (textbook The Prokaryotes).	3.5.1.24

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
TCHOLAt2	taurocholate transport via sodium cotransport		Transport, Extracellular	Evidence from literature	PMID:10993	B. thetaiotaomicron metabolizes glycocholate and taurocholate. A bile acid/ sodium symporter is annotated for *Bacteroides salanitronis* (NCBI Gene, last updated 18.05.11).	
TGBPA	Tagatose-bisphosphate aldolase		Alternate Carbon Metabolism	Evidence from literature	PMID:2845859, PMID:10931310	*B. thetaiotaomicron* grows on N-acetyl-galactosamine (PMID:2845859), but the utilization pathway is poorly studied. In *E. coli*, this enzyme is involved in GalNAc utilization (PMID:10931310).	4.1.2.40
THMDP	thiamin diphosphatase	BT_3017	Thiamine Metabolism	Manually added gene annotation from databases		The enzyme is an acid phosphatase with wide specifity. Added based on annotation from The SEED Viewer (last checked 01.07.11)	3.1.3.2
THRt2r	L-threonine reversible transport via proton symport		Transport, Extracellular	Evidence from literature	Dworkin, M. and S. Falkow (2006). The prokaryotes : a handbook on the biology of bacteria. New York ; [London], Springer	B. thetaiotaomicron is weakly proteolytic, so a transport reaction for all amino acids is assumed to be present.	
TREHe	alpha,alpha-trehalase		Alternate Carbon Metabolism	Evidence from literature	PMID:10993, Dworkin, M. and S. Falkow (2006). The prokaryotes : a handbook on the biology of bacteria. New York ; [London], Springer	*B. thetaiotaomicron* grows on trehalose. The reaction may be carried out be another enzyme, no annotation available.	3.2.1.28
U23GAAT_BT	UDP-3-O-(anteiso-C17)glycosamine acyltransferase	BT_4207	Lipopolysaccharide Biosynthesis	Evidence from literature	PMID:18931137, PMID:19460428, PMID:20974832	Based on *H. pylori* LPS biosynthesis (BIGG database), as in the *P. gingivalis* reconstruction (PMID:18931137). *P. gingivalis* LPS is similar in structure to the *Bacteroides* LPS. Based on structural information taken from (PMID:19460428, PMID:20974832).	

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
U2GAAT_BT	u2gaat		Lipopolysaccharide Biosynthesis	Evidence from literature	PMID:18931137, PMID:19460428, PMID:20974832	Based on *H. pylori* LPS biosynthesis (BIGG database), as in the *P. gingivalis* reconstruction (PMID:18931137). *P. gingivalis* LPS is similar in structure to the *Bacteroides* LPS. Based on structural information taken from (PMID:19460428, PMID:20974832).	
U2GAAT2_BT	u2gaat2		Lipopolysaccharide Biosynthesis	Evidence from literature	PMID:18931137, PMID:19460428, PMID:20974832	Based on *H. pylori* LPS biosynthesis (BIGG database), as in the *P. gingivalis* reconstruction (PMID:18931137). *P. gingivalis* LPS is similar in structure to the *Bacteroides* LPS. Based on structural information taken from (PMID:19460428, PMID:20974832).	
UACMAMO	UDP-N-acetyl-D-mannosamine oxidoreductase	BT_0602	Capsular Polysaccharide Biosynthesis	Evidence from literature	PMID:17579514	Annotation taken from PMID:17579514, Table S5	
UAGAAT_HP	UDP-N-acetylglucosamine acyltransferase	(BT_3336 or BT_4205)	Lipopolysaccharide Biosynthesis	Based on existing metabolic reconstruction	PMID:18931137, PMID:19460428, PMID:20974832	Based on *H. pylori* LPS biosynthesis (BIGG database), as in the *P. gingivalis* reconstruction (PMID:18931137). *P. gingivalis* LPS is similar in structure to the *Bacteroides* LPS. Based on structural information taken from (PMID:19460428, PMID:20974832).	
UAGDP	UDP-N-acetylglucosamine diphosphorylase		Aminosugar Metabolism	Manual gapfilling	PMID:7240086	Manually filled in based on KEGG Pathway to to make N-acetylglucosamine, a substrate known to support growth, usable.	2.7.7.23
UAGDP2	UDP-glucosamine diphosphorylase		Aminosugar Metabolism	Based on existing metabolic reconstruction	PMID:18931137, PMID:19460428, PMID:20974832	Based on *H. pylori* LPS biosynthesis (BIGG database), as in the *P. gingivalis* reconstruction (PMID:18931137). *P. gingivalis* LPS is similar in structure to the *Bacteroides* LPS. Based on structural information taken from (PMID:19460428, PMID:20974832).	2.7.7.23

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
UDPGLCURE	UDP-glucuronate 5-epimerase	(BT_0600 or BT_1342 or BT_0380)	Pentose and Glucuronate Interconversions	Manually added gene annotation from databases		Annotation taken from The SEED. This reaction is probably involved in chondroitin sulfate degradation, but the exact pathway is unknown.	5.1.3.12
UDPGLDC	UDP-D-glucuronate decarboxylase	BT_1059	Capsular Polysaccharide Biosynthesis	Evidence from literature	PMID:21804000	The product is likely a precursor for capsule polysaccharide biosynthesis, but the exact function is unknown.	4.1.1.35
UGLT	UDPglucose--hexose-1-phosphate uridylyltransferase		Alternate Carbon Metabolism	Manual gapfilling	PMID:16887504	The reaction is needed for galactose utilization.	2.7.7.12
UHGADA_HP	UDP-3-O-acetylglucosamine deacetylase		Lipopolysaccharide Biosynthesis	Based on existing metabolic reconstruction	PMID:18931137, PMID:19460428, PMID:20974832	Based on *H. pylori* LPS biosynthesis (BIGG database), as in the *P. gingivalis* reconstruction (PMID:18931137). *P. gingivalis* LPS is similar in structure to the *Bacteroides* LPS. Based on structural information taken from (PMID:19460428, PMID:20974832).	
USHD_BT	UDP-sugar hydrolase	BT_3697	Lipopolysaccharide Biosynthesis	Evidence from literature	PMID:18931137, PMID:19460428, PMID:20974832	Based on *H. pylori* LPS biosynthesis (BIGG database), as in the *P. gingivalis* reconstruction (PMID:18931137). *P. gingivalis* LPS is similar in structure to the *Bacteroides* LPS. Based on structural information taken from (PMID:19460428, PMID:20974832).	
VALO	Valine oxidation by gut bacteria		Valine, Leucine, and Isoleucine Metabolism	Evidence from literature	PMID:3572204, PMID:16887608, Krieg NR (2010) Bergey's manual of systematic bacteriology, 2nd ed., volume 4 (Springer, New York).	Valine and leucine are oxidized by gut bacteria to BCFA (branched-chain fatty acids) with one less carbon atom (isobutyrate and isovalerate, respectively), CO2 and ammonia.This reaction formula is hypothetical, no information on exact pathway and involved enzymes is avaiable. KEGG does not provide any pathway information either.Isobutyrate and isovalerate are known secretion products of *B. thetaiotaomicron*.	

BIGG Rxn ID	Function	GPR	Subsystem	Reason for addition	Reference	Notes	EC Number
VALt2r	L-valine reversible transport via proton symport		Transport, Extracellular	Evidence from literature	PMID:7462155	*B. thetaiotaomicron* incorporates leucine, valine and isoleucine into its phospholipids,which suggests the presence of a transporter for these amino acids. However, it is not known which gene encodes this transporter.	

Table S10f: Reactions which underwent a change in directionality during manual curation based on directionalities found in other reconstructions (BIGG Database).

SEED Rxn ID	BIGG Rxn ID	Function	Directionality in iAH991	Directionality in *BΘ_Seed_v1*
rxn00020	BGLA	1,4-beta-D-Glucan glucohydrolase	Irreversible	Reversible
rxn00022	MALT	alpha-glucosidase	Irreversible	Reversible
rxn00056	FERO	ferroxidase	Irreversible	Reversible
rxn00077	NADK	NAD kinase	Irreversible	Reversible
rxn00085	GLUSy	glutamate synthase (NADPH)	Irreversible	Reversible
rxn00119	URIDK1	uridylate kinase (UMP)	Irreversible	Reversible
rxn00124	PYDXK	pyridoxal kinase	Irreversible	Reversible
rxn00131	AMPN	AMP nucleosidase	Irreversible	Reversible
rxn00148	PYK	pyruvate kinase	Irreversible	Reversible
rxn00151	PPDK	Pyruvate phosphate dikinase	Irreversible	Reversible
rxn00157	PFL	pyruvate formate lyase	Irreversible	Reversible
rxn00179	GLU5K	glutamate 5-kinase	Irreversible	Reversible
rxn00182	GLUDxi	glutamate dehydrogenase (NAD)	Irreversible	Reversible
rxn00183	PUTA3	puta3	Irreversible	Reversible
rxn00216	HEX1	hexokinase (D-glucose:ATP)	Irreversible	Reversible
rxn00247	PPCKr	phosphoenolpyruvate carboxykinase	Reversible	Irreversible
rxn00250	PC	pyruvate carboxylase	Irreversible	Reversible
rxn00303	GTPDPK	GTP diphosphokinase	Irreversible	Reversible
rxn00347	ASPT	L-aspartase	Irreversible	Reversible
rxn00361	ADSK	adenylyl-sulfate kinase	Irreversible	Reversible
rxn00365	CYTDK1	ATPcytidine 5-phosphotransferase	Irreversible	Reversible
rxn00368	CYTDK4	UTPcytidine 5-phosphotransferase	Irreversible	Reversible
rxn00369	CYTDK2	cytidine kinase (GTP)	Irreversible	Reversible

SEED Rxn ID	BIGG Rxn ID	Function	Directionality in iAH991	Directionality in *BΘ_Seed_v1*
rxn00379	SADT	sulfate adenylyltransferase	Irreversible	Reversible
rxn00392	RBFK	riboflavin kinase	Irreversible	Reversible
rxn00394	ARGN	arginase	Irreversible	Reversible
rxn00410	CTPS1	CTP synthase (NH3)	Irreversible	Reversible
rxn00440	TMDPK	Thiamin pyrophosphokinase (EC 2.7.6.2)	Irreversible	Reversible
rxn00469	ACODA	acetylornithine deacetylase	Irreversible	Reversible
rxn00473	TRPAS2	Tryptophanase (L-tryptophan)	Reversible	Irreversible
rxn00474	TRPS2	tryptophan synthase (indole)	Irreversible	Reversible
rxn00503	P5CD	1-pyrroline-5-carboxylate dehydrogenase	Irreversible	Reversible
rxn00533	ACCOAC	acetyl-CoA carboxylase	Irreversible	Reversible
rxn00545	PFK	phosphofructokinase	Irreversible	Reversible
rxn00547	HEX7	hexokinase (D-fructose:ATP)	Irreversible	Reversible
rxn00551	PFK(ppi)	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase, beta subunit (EC 2.7.1.90)	Irreversible	Reversible
rxn00609	MI1PS	myo-Inositol-1-phosphate synthase	Irreversible	Reversible
rxn00650	AMPTASECG	alanyl aminopeptidase (cys-gly)	Irreversible	Reversible
rxn00670	PTA2	Phosphate acetyltransferase	Irreversible	Reversible
rxn00690	FTHFLi	formate-tetrahydrofolate ligase	Irreversible	Reversible
rxn00707	CYTDK3	ITPcytidine 5-phosphotransferase	Irreversible	Reversible
rxn00709	URIK1	uridine kinase (ATP:Uridine)	Irreversible	Reversible
rxn00713	URIK2	uridine kinase (GTP:Uridine)	Irreversible	Reversible
rxn00715	URIK3	uridine kinase (ITP:Uridine)	Irreversible	Reversible
rxn00758	GPDDA1	Glycerophosphodiester phosphodiesterase (Glycerophosphocholine)	Irreversible	Reversible
rxn00772	RBK	ribokinase	Irreversible	Reversible
rxn00808	GALK	galactokinase	Irreversible	Reversible
rxn00817	GALS3	a-galactosidase (melibiose)	Irreversible	Reversible

SEED Rxn ID	BIGG Rxn ID	Function	Directionality in iAH991	Directionality in *BΘ_Seed_v1*
rxn00818	RAFGH	Raffinose galactohydrolase	Irreversible	Reversible
rxn00834	IMPD	IMP dehydrogenase	Irreversible	Reversible
rxn00892	ACGAMK	N-acetylglucosamine kinase	Irreversible	Reversible
rxn00910	MTHFR3	5,10-methylenetetrahydrofolatereductase (NADPH)	Irreversible	Reversible
rxn00912	MOHMT	3-methyl-2-oxobutanoate hydroxymethyltransferase	Irreversible	Reversible
rxn00927	ADNUC	adenosine hydrolase	Irreversible	Reversible
rxn00929	PRO1x	L-ProlineNAD+ 5-oxidoreductase	Irreversible	Reversible
rxn00947	FACOAL160	fatty-acid--CoA ligase (hexadecanoate)	Reversible	Irreversible
rxn01021	MTAN	methylthioadenosine nucleosidase	Irreversible	Reversible
rxn01068	THRD	L-threonine dehydrogenase	Irreversible	Reversible
rxn01073	GPDDA2	Glycerophosphodiester phosphodiesterase (Glycerophosphoethanolamine)	Irreversible	Reversible
rxn01102	GLYCK	glycerate kinase	Irreversible	Reversible
rxn01114	RBK_D	D-ribulokinase	Irreversible	Reversible
rxn01143	TMDK1	thymidine kinase (ATP:thymidine)	Irreversible	Reversible
rxn01169	HEXb	ATPD-glucose 6-phosphotransferase	Irreversible	Reversible
rxn01217	DCMPDA	dCMP deaminase	Reversible	Irreversible
rxn01226	GNNUC	gnnuc	Irreversible	Reversible
rxn01236	BUTK	Butyrate kinase	Irreversible	Reversible
rxn01257	PABB	Chorismate L-glutamine aminotransferase	Irreversible	Reversible
rxn01265	NAMNPP	nicotinic acid mononucleotide pyrophosphorylase	Irreversible	Reversible
rxn01299	INSH	Inosine hydrolase	Irreversible	Reversible
rxn01300	HSK	homoserine kinase	Irreversible	Reversible
rxn01301	HSDxi2	homoserine dehydrogenase (NADH), irreversible	Irreversible	Reversible
rxn01302	HSDyi2	homoserine dehydrogenase (NADPH), irreversible	Irreversible	Reversible
rxn01343	PFK_3	ATPSedoheptulose 7-phosphate 1-phosphotransferase	Irreversible	Reversible

SEED Rxn ID	BIGG Rxn ID	Function	Directionality in iAH991	Directionality in *BΘ_Seed_v1*
rxn01362	ORPT	orotate phosphoribosyltransferase	Reversible	Irreversible
rxn01396	PYDXNK	pyridoxine kinase	Irreversible	Reversible
rxn01476	PGL	6-phosphogluconolactonase	Irreversible	Reversible
rxn01484	AGDC	N-acetylglucosamine-6-phosphate deacetylase	Irreversible	Reversible
rxn01518	DURIK1	deoxyuridine kinase (ATP:Deoxyuridine)	Irreversible	Reversible
rxn01545	XTSNH	Xanthosine hydrolase	Irreversible	Reversible
rxn01675	G1PTT	glucose-1-phosphate thymidylyltransferase	Irreversible	Reversible
rxn01737	RAFH	raffinose hydrolyzing enzyme	Irreversible	Reversible
rxn01739	SHKK	shikimate kinase	Irreversible	Reversible
rxn01763	RBK_L1	L-ribulokinase (L-ribulose)	Irreversible	Reversible
rxn01790	DPR	2-dehydropantoate 2-reductase	Irreversible	Reversible
rxn01807	PYDAMK	pyridoxamine kinase	Irreversible	Reversible
rxn01834	LGTHL	lactoylglutathione lyase	Irreversible	Reversible
rxn01917	ACGK	acetylglutamate kinase	Irreversible	Reversible
rxn01964	TRPS1	tryptophan synthase (indoleglycerol phosphate)	Irreversible	Reversible
rxn02000	TDPDRE	dTDP-4-dehydrorhamnose 3,5-epimerase	Irreversible	Reversible
rxn02003	TDPDRR	dTDP-4-dehydrorhamnose reductase	Irreversible	Reversible
rxn02085	URCN	urocanase	Irreversible	Reversible
rxn02160	HISTP	histidinol-phosphatase	Irreversible	Reversible
rxn02161	RMK	rhamnulokinase	Irreversible	Reversible
rxn02200	DHPS	dihydropteroate synthase	Irreversible	Reversible
rxn02269	OIVD3	2-oxoisovalerate dehydrogenase (acylating; 3-methyl-2-oxopentanoate)	Irreversible	Reversible
rxn02297	AOXSr	8-amino-7-oxononanoate synthase	Reversible	Irreversible
rxn02305	TMPPP	thiamine-phosphate diphosphorylase	Irreversible	Reversible
rxn02314	PFK_2	Phosphofructokinase	Irreversible	Reversible

SEED Rxn ID	BIGG Rxn ID	Function	Directionality in iAH991	Directionality in *BΘ_Seed_v1*
rxn02319	FCLK	L-fuculokinase	Irreversible	Reversible
rxn02339	EHGLAT	L-erythro-4-Hydroxyglutamate:2-oxoglutarate aminotransferase	Irreversible	Reversible
rxn02374	G5SADs	L-glutamate 5-semialdehyde dehydratase (spontaneous)	Reversible	Irreversible
rxn02465	AGPR	N-acetyl-g-glutamyl-phosphate reductase	Reversible	Irreversible
rxn02474	APRAUR	5-amino-6-(5-phosphoribosylamino)uracil reductase	Irreversible	Reversible
rxn02503	HPPK	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase	Irreversible	Reversible
rxn02504	DHNPA	dihydroneopterin aldolase	Irreversible	Reversible
rxn02835	PRAMPC	phosphoribosyl-AMP cyclohydrolase	Irreversible	Reversible
rxn02875	AMAA	N-acetylmuramoyl-L-alanine amidase	Irreversible	Reversible
rxn02929	DHDPRy	dihydrodipicolinate reductase (NADPH)	Irreversible	Reversible
rxn02937	PRAIS	phosphoribosylaminoimidazole synthase	Irreversible	Reversible
rxn02938	AIRCr	phosphoribosylaminoimidazole carboxylase	Reversible	Irreversible
rxn03004	GARFTi	phosphoribosylglycinamide formyltransferase, irreversible	Irreversible	Reversible
rxn03108	PMPK	phosphomethylpyrimidine kinase	Irreversible	Reversible
rxn03395	OHPHM	2-octaprenyl-6-hydroxyphenol methylase	Irreversible	Reversible
rxn03408	UAGPT3	UDP-N-acetylglucosamine-N-acetylmuramyl-(pentapeptide)pyrophosphoryl-undecaprenol N-acetylglucosamine transferase	Irreversible	Reversible
rxn03903	PAPPT2	phospho-N-acetylmuramoyl-pentapeptide-transferase (gamma-glutamate)	Irreversible	Reversible
rxn03904	PAPPT3	phospho-N-acetylmuramoyl-pentapeptide-transferase (meso-2,6-diaminopimelate)	Irreversible	Reversible
rxn03907	MEPCT	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	Irreversible	Reversible
rxn03908	CDPMEK	4-(cytidine 5-diphospho)-2-C-methyl-D-erythritol kinase	Irreversible	Reversible
rxn03910	MECDPS	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	Irreversible	Reversible
rxn03933	UAGPT2	UDP-N-acetylglucosamine-N-acetylmuramyl-(pentapeptide)pyrophosphoryl-undecaprenol N-acetylglucosamine transferase	Irreversible	Reversible
rxn03958	DXPRIi	1-deoxy-D-xylulose reductoisomerase	Irreversible	Reversible

SEED Rxn ID	BIGG Rxn ID	Function	Directionality in iAH991	Directionality in *BΘ_Seed_v1*
rxn03962	GFUCS	GDP-L-fucose synthase	Irreversible	Reversible
rxn04794	OBTFL	2-Oxobutanoate formate lyase	Irreversible	Reversible
rxn04954	MTHFR2	5,10-methylenetetrahydrofolate reductase (NADH)	Irreversible	Reversible
rxn05144	PLPS	Pyridoxine biosynthesis glutamine amidotransferase	Irreversible	Reversible
rxn05145	PIabc	phosphate transport via ABC system	Irreversible	Reversible
rxn05200	THMDt2	thymidine transport in via proton symport	Irreversible	Reversible
rxn05247	FACOALI14	fatty-acid--CoA ligase (ISO14)	Reversible	Irreversible
rxn05248	FACOALAI15	fatty-acid--CoA ligase (ANTEISO15)	Reversible	Irreversible
rxn05249	FACOALI15	fatty-acid--CoA ligase (ISO15)	Reversible	Irreversible
rxn05250	FACOALI16	fatty-acid--CoA ligase (ISO16)	Reversible	Irreversible
rxn05251	FACOALAI17	fatty-acid--CoA ligase (ANTEISO17)	Reversible	Irreversible
rxn05252	FACOALI17	fatty-acid--CoA ligase (ISO17)	Reversible	Irreversible
rxn05313	PIt8i	phosphate transport in via Na+ symporter, irreversible	Irreversible	Reversible
rxn05318	ADNt2	adenosine transport in via proton symport	Irreversible	Reversible
rxn05319	H2Ot	H2O transport via diffusion	Reversible	Irreversible
rxn05329	3HAD40	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C4:0)	Irreversible	Reversible
rxn05330	3HAD60	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C6:0)	Irreversible	Reversible
rxn05331	3HAD120	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C12:0)	Irreversible	Reversible
rxn05332	3HAD160	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C16:0)	Irreversible	Reversible
rxn05333	3HAD100	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C10:0)	Irreversible	Reversible
rxn05334	3HAD80	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C8:0)	Irreversible	Reversible
rxn05335	3HAD140	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C14:0)	Irreversible	Reversible
rxn05361	3HAD4M6	4-methyl-3-hydroxy-hexanoyl-ACP hydro-lyase	Irreversible	Reversible
rxn05365	3HAD6M8	6-methyl-3-hydroxy-octanoyl-ACP hydro-lyase	Irreversible	Reversible
rxn05369	3HAD8M10	8-methyl-3-hydroxy-decanoyl-ACP hydro-lyase	Irreversible	Reversible

SEED Rxn ID	BIGG Rxn ID	Function	Directionality in iAH991	Directionality in *BΘ_Seed_v1*
rxn05373	3HAD10M12	10-methyl-3-hydroxy-dodecanoyl-ACP hydro-lyase	Irreversible	Reversible
rxn05377	3HAD12M14	12-methyl-3-hydroxy-tetra-decanoyl-ACP hydro-lyase	Irreversible	Reversible
rxn05381	3HAD14M16	14-methyl-3-hydroxy-hexa-decanoyl-ACP hydro-lyase	Irreversible	Reversible
rxn05386	3HAD5M6	5-methyl-3-hydroxy-hexanoyl-ACP hydro-lyase	Irreversible	Reversible
rxn05390	3HAD7M8	7-methyl-3-hydroxy-octanoyl-ACP hydro-lyase	Irreversible	Reversible
rxn05394	3HAD9M10	9-methyl-3-hydroxy-decanoyl-ACP hydro-lyase	Irreversible	Reversible
rxn05398	3HAD11M12	11-methyl-3-hydroxy-dodecanoyl-ACP hydro-lyase	Irreversible	Reversible
rxn05402	3HAD13M14	13-methyl-3-hydroxy-tetra-decanoyl-ACP hydro-lyase	Irreversible	Reversible
rxn05406	3HAD15M16	15-methyl-3-hydroxy-hexa-decanoyl-ACP hydro-lyase	Irreversible	Reversible
rxn05411	3HAD4M5	4-methyl-3-hydroxy-pentanoyl-ACP hydro-lyase	Irreversible	Reversible
rxn05415	3HAD6M7	6-methyl-3-hydroxy-heptanoyl-ACP hydro-lyase	Irreversible	Reversible
rxn05419	3HAD8M9	8-methyl-3-hydroxy-nonanoyl-ACP hydro-lyase	Irreversible	Reversible
rxn05423	3HAD10M11	10-methyl-3-hydroxy-undecanoyl-ACP hydro-lyase	Irreversible	Reversible
rxn05427	3HAD12M13	12-methyl-3-hydroxy-tridecanoyl-ACP hydro-lyase	Irreversible	Reversible
rxn05431	3HAD14M15	14-methyl-3-hydroxy-pentadecanoyl-ACP hydro-lyase	Irreversible	Reversible
rxn05462	3HAD180	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C18:0)	Irreversible	Reversible
rxn05616	MGt5	magnesium transport in/out via permease (no H+)	Reversible	Irreversible
rxn05646	RMNt	L-rhamnose transport via proton symport	Irreversible	Reversible
rxn05671	XYLt2	D-xylose transport in via proton symport	Irreversible	Reversible
rxn05736	FACOAL140	fatty-acid--CoA ligase (tetradecanoate)	Reversible	Irreversible
rxn05740	GLCP	glycogen phosphorylase	Irreversible	Reversible
rxn06023	ACPS1	acyl-carrier protein synthase	Irreversible	Reversible
rxn06077	METSOXR1	L-methionine-S-oxide reductase	Irreversible	Reversible
rxn06493	GCCc	glycine-cleavage complex	Irreversible	Reversible
rxn06673	BTNPL	holocarboxylase synthestase (biotin protein ligase)	Irreversible	Reversible

SEED Rxn ID	BIGG Rxn ID	Function	Directionality in iAH991	Directionality in *BΘ_Seed_v1*
rxn07441	26DAPLLATi	L,L-diaminopimelate aminotransferase (irreversible)	Irreversible	Reversible
rxn08040	ACGAMT	UDP-N-acetylglucosamine:undecaprenylphosphate N-acetylglucosamine -1-phosphate transferase	Irreversible	Reversible
rxn08126	AMALT1	Amylomaltase (maltotriose)	Irreversible	Reversible
rxn08127	AMALT2	Amylomaltase (maltotetraose)	Irreversible	Reversible
rxn08128	AMALT3	Amylomaltase (maltopentaose)	Irreversible	Reversible
rxn08129	AMALT4	Amylomaltase (maltohexaose)	Irreversible	Reversible
rxn08306	DASYN120	CDP-diacylglycerol synthetase (n-C12:0)	Irreversible	Reversible
rxn08307	DASYN140	CDP-diacylglycerol synthetase (n-C14:0)	Irreversible	Reversible
rxn08309	DASYN160	CDP-diacylglycerol synthetase (n-C16:0)	Irreversible	Reversible
rxn08311	DASYN180	CDP-diacylglycerol synthetase (n-C18:0)	Irreversible	Reversible
rxn08312	DASYN181	CDP-diacylglycerol synthetase (n-C18:1)	Irreversible	Reversible
rxn08527	FRD2	fumarate reductase	Irreversible	Reversible
rxn08528	FRD3	fumarate reductase	Irreversible	Reversible
rxn08669	GPDDA4	Glycerophosphodiester phosphodiesterase (Glycerophosphoglycerol)	Irreversible	Reversible
rxn09108	PGSA120	Phosphatidylglycerol synthase (n-C12:0)	Irreversible	Reversible
rxn09109	PGSA140	Phosphatidylglycerol synthase (n-C14:0)	Irreversible	Reversible
rxn09111	PGSA160	Phosphatidylglycerol synthase (n-C16:0)	Irreversible	Reversible
rxn09113	PGSA180	Phosphatidylglycerol synthase (n-C18:0)	Irreversible	Reversible
rxn09114	PGSA181	Phosphatidylglycerol synthase (n-C18:1)	Irreversible	Reversible
rxn09188	PROD2	Proline dehydrogenase	Irreversible	Reversible
rxn09197	PSD120	Phosphatidylserine decarboxylase (n-C12:0)	Irreversible	Reversible
rxn09198	PSD140	Phosphatidylserine decarboxylase (n-C14:0)	Irreversible	Reversible
rxn09200	PSD160	Phosphatidylserine decarboxylase (n-C16:0)	Irreversible	Reversible
rxn09202	PSD180	Phosphatidylserine decarboxylase (n-C18:0)	Irreversible	Reversible
rxn09203	PSD181	Phosphatidylserine decarboxylase (n-C18:1)	Irreversible	Reversible

SEED Rxn ID	BIGG Rxn ID	Function	Directionality in iAH991	Directionality in *BΘ_Seed_v1*
rxn09240	SADT2	Sulfate adenyltransferase	Irreversible	Reversible
rxn09272	SUCDi	succinate dehydrogenase (irreversible)	Irreversible	Reversible
rxn09448	FACOAL181	fatty-acid--CoA ligase (octadecenoate)	Reversible	Irreversible
rxn09449	FACOAL180	fatty-acid--CoA ligase (octadecanoate)	Reversible	Irreversible
rxn09450	FACOAL161	fatty-acid--CoA ligase (hexadecenoate)	Reversible	Irreversible
rxn09657	THMt2	Thiamine transport in via proton antiport	Reversible	Irreversible
rxn09685	DURIt2	deoxyuridine transport in via proton symport	Irreversible	Reversible
rxn09687	DINSt2	deoxyinosine transport in via proton symport	Irreversible	Reversible
rxn09688	DGSNt2	deoxyguanosine transport in via proton symport	Irreversible	Reversible
rxn09997	AHMMPS	4-amino-5-hydroxymethyl-2-methylpyrimidine synthetase	Irreversible	Reversible
rxn10042	ATPS4	ATP synthase (four protons for one ATP)	Irreversible	Reversible
rxn10060	NADK2	NAD kinase (dTTP)	Irreversible	Reversible
rxn10199	PPTGS	Peptidoglycan subunit synthesis	Irreversible	Reversible
rxn10220	DASYNI17	isoheptadecanoyl-phosphatidate cytidylyltransferase	Irreversible	Reversible
rxn10221	DASYNAI17	anteisoheptadecanoyl-phosphatidate cytidylyltransferase	Irreversible	Reversible
rxn10222	DASYNI14	isotetradecanoyl-phosphatidate cytidylyltransferase	Irreversible	Reversible
rxn10223	DASYNI15	isopentadecanoyl-phosphatidate cytidylyltransferase	Irreversible	Reversible
rxn10224	DASYNAI15	anteisopentadecanoyl-phosphatidate cytidylyltransferase	Irreversible	Reversible
rxn10225	DASYNI16	isohexadecanoyl-phosphatidate cytidylyltransferase	Irreversible	Reversible
rxn10232	PSDI17	isoheptadecanoyl-phosphatidylserine decarboxylase	Irreversible	Reversible
rxn10233	PSDAI17	anteisoheptadecanoyl-phosphatidylserine decarboxylase	Irreversible	Reversible
rxn10234	PSDI14	isotetradecanoyl-phosphatidylserine decarboxylase	Irreversible	Reversible
rxn10235	PSDI15	isopentadecanoyl-phosphatidylserine decarboxylase	Irreversible	Reversible
rxn10236	PSDAI15	anteisopentadecanoyl-phosphatidylserine decarboxylase	Irreversible	Reversible
rxn10237	PSDI16	isohexadecanoyl-phosphatidylserine decarboxylase	Irreversible	Reversible

SEED Rxn ID	BIGG Rxn ID	Function	Directionality in iAH991	Directionality in *BΘ_Seed_v1*
rxn10259	PGSAI17	isoheptadecanoyl-CDPdiacylglycerolsn-glycerol-3-phosphate 3-phosphatidyltransferase	Irreversible	Reversible
rxn10260	PGSAAI17	anteisoheptadecanoyl-CDPdiacylglycerolsn-glycerol-3-phosphate 3-phosphatidyltransferase	Irreversible	Reversible
rxn10261	PGSAI14	isotetradecanoyl-CDPdiacylglycerolsn-glycerol-3-phosphate 3-phosphatidyltransferase	Irreversible	Reversible
rxn10262	PGSAI15	isopentadecanoyl-CDPdiacylglycerolsn-glycerol-3-phosphate 3-phosphatidyltransferase	Irreversible	Reversible
rxn10263	PGSAAI15	anteisopentadecanoyl-CDPdiacylglycerolsn-glycerol-3-phosphate 3-phosphatidyltransferase	Irreversible	Reversible
rxn10264	PGSAI16	isohexadecanoyl-CDPdiacylglycerolsn-glycerol-3-phosphate 3-phosphatidyltransferase	Irreversible	Reversible
rxn10474	COBALTt5	cobalt transport in/out via permease (no H+)	Reversible	Irreversible
rxn11946	DMQMT	3-Dimethylubiquinonol 3-methyltransferase	Irreversible	Reversible
rxn12510	PNTK	pantothenate kinase	Irreversible	Reversible

Table S10g: Changes in gene-protein-reaction (GPR) association based on manual inspection of the automated reconstruction.

Falsely annotated genes

Gene	SEED annotation	SEED Rxn ID SEED annotation	BIGG Rxn ID SEED annotation	Curated annotation	BIGG Rxn ID curated annotation	Source
BT_4151, BT_3292	beta-galactosidase	rxn00816	LACZ	beta-glucuronidase	GLCAASEe, GLCAASE8e, GLCAASE9e, GLCAASE_HSe	NCBI Gene
BT_1780, BT_1872, BT_4714, BT_2854, BT_3567	cytosolic beta-glucosidase	rxn00020	BGLA	periplasmatic beta-glucosidase (extracellular for modeling purposes)	BGLAe	NCBI Gene
BT_4315	Inorganic pyrophosphatase	rxn00001	PPA	Phosphoglycolate phosphatase	PGLYCP	KEGG database

Manually updated GPR associations

Reaction	SEED Rxn ID	BIGG Rxn ID	SEED GPR association	Curated GPR association	Source
1,4-dihydroxy-2-naphthoate octaprenyltransferase (EC 2.5.1.74)	rxn08333	DHNAOT4	BT_2015	BT_2014 or BT_2015	NCBI Gene
Phosphoglucomutase (5.4.2.2)	rxn00704	PGMT	BT_1548	BT_1548 or BT_3950	NCBI Gene
Phosphoglycolate phosphatase (EC 3.1.3.18)	rxn00980	PGLYCP	BT_4184	(BT_4184 or BT_4315)	KEGG database
Glutamine synthetase (6.3.1.2)	rxn00187	GLNS	(BT_0785 or BT_0453 or BT_4339)	(BT_0785 or BT_0453 or BT_4339 or BT_0543)	NCBI Gene
N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28)	rxn02875	AMAA	(BT_0402 or BT_1641 or BT_1706 or BT_4031)	(BT_1991 or BT_2027 or BT_2141 or BT_3200 or BT_4736 or BT_0706 or BT_1168 or BT_1519 or BT_1641 or BT_1706 or BT_4031)	NCBI Gene
Alpha-glucosidase (EC 3.2.1.20)	rxn00022	MALT	(BT_0132 or BT_0683 or BT_2620 or BT_3163 or BT_3169 or BT_3294 or BT_3299 or BT_3664)	(BT_0132 or BT_0683 or BT_2620 or BT_3163 or BT_3169 or BT_3294 or BT_3299 or BT_3664 or BT_4581)	NCBI Gene
Peptidoglycan synthetase (EC 2.4.1.129)	rxn10199	PPTGS	(BT_0162 or BT_2501)	(BT_3453 or BT_0943 or BT_0162 or BT_2501)	NCBI Gene, The SEED Viewer

Table S11a: All reactions included in mouse reconstruction iSS1393.

Rev = Reversibility (1 = reversible, 0 = irreversible), CS = Confidence score, LB = Lower bound, UB = Upper Bound

BIGG Rxn ID	Rxn Name	Rxn Formula	Rev	GPR	LB	UB	CS	Subsystem	References	Notes	EC Number
10FTHF5GLUtl	5-glutamyl-10FTHF transport, lysosomal	10fthf5glu[c] -> 10fthf5glu[l]	0		0	1000		Transport, Lysosomal			
10FTHF5GLUtm	5-glutamyl-10FTHF transport, mitochondrial	10fthf5glu[m] -> 10fthf5glu[c]	0		0	1000		Transport, Mitochondrial			
10FTHF6GLUtl	6-glutamyl-10FTHF transport, lysosomal	10fthf6glu[c] -> 10fthf6glu[l]	0		0	1000		Transport, Lysosomal			
10FTHF6GLUtm	6-glutamyl-10FTHF transport, mitochondrial	10fthf6glu[m] -> 10fthf6glu[c]	0		0	1000		Transport, Mitochondrial			
10FTHF7GLUtl	7-glutamyl-10FTHF transport, lysosomal	10fthf7glu[c] -> 10fthf7glu[l]	0		0	1000		Transport, Lysosomal			
10FTHF7GLUtm	7-glutamyl-10FTHF transport, mitochondrial	10fthf7glu[m] -> 10fthf7glu[c]	0		0	1000		Transport, Mitochondrial			
10FTHFtl	10-Formyltetrahydrofolate lysosomal transport via diffusion	10fthf[c] <=> 10fthf[l]	1		-1000	1000		Transport, Lysosomal			
10FTHFtm	10-Formyltetrahydrofolate mitochondrial transport via diffusion	10fthf[c] <=> 10fthf[m]	1		-1000	1000		Transport, Mitochondrial			
11DOCRTSLtm	11-deoxycortisol intracellular transport	11docrtsl[c] <=> 11docrtsl[m]	1		-1000	1000		Transport, Mitochondrial			
11DOCRTSLtr	11-deoxycortisol intracellular transport	11docrtsl[c] <=> 11docrtsl[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
11DOCRTSTRNtm	11-deoxycorticosterone intracellular transport	11docrtstrn[c] <=> 11docrtstrn[m]	1		-1000	1000		Transport, Mitochondrial			
11DOCRTSTRNtr	11-deoxycorticosterone intracellular transport	11docrtstrn[c] <=> 11docrtstrn[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
13DAMPPOX	1,3-Diaminopropane:oxygen oxidoreductase (deaminating)	13dampp[c] + h2o[c] + o2[c] -> bamppald[c] + h2o2[c] + nh4[c]	0	237940.1 or 237940.2 or 11754.1 or 76507.1	0	1000		beta-Alanine metabolism			
1MNCAMti	N1-Methylnicotinamide transport	h2o[c] + 1mncam[c] + atp[c] -> adp[c] + h[c] + pi[c] + 1mncam[e]	0		0	1000		Transport, Extracellular			
1PPDCRp	delta1-piperideine-2-carboxylate reductase, perixosomal	1pipdn2c[x] + h[x] + nadh[x] -> Lpipecol[x] + nad[x]	0		0	1000		Lysine Metabolism			
1a_24_25VITD2Hm	1-alpha-Vitamin D-24,25-hydroxylase (D2)	2425dhvitd2[m] + h[m] + nadph[m] + o2[m] -> 1a2425thvitd2[m] + h2o[m] + nadp[m]	0		0	1000		Vitamin D			
1a_24_25VITD3Hm	1-alpha-Vitamin D-24,25-hydroxylase (D3)	h[m] + nadph[m] + o2[m] + 2425dhvitd3[m] -> h2o[m] + nadp[m] + 1a2425thvitd3[m]	0		0	1000		Vitamin D			
1a_25VITD2Hm	1-alpha,24R,25-Vitamin D-hydroxylase (D2)	h[m] + nadph[m] + o2[m] + 1a25dhvitd2[m] -> 1a2425thvitd2[m] + h2o[m] + nadp[m]	0		0	1000		Vitamin D			
1a_25VITD3Hm	1-alpha,24R,25-Vitamin D-hydroxylase (D3)	h[m] + nadph[m] + o2[m] + 1a25dhvitd3[m] -> h2o[m] + nadp[m] + 1a2425thvitd3[m]	0		0	1000		Vitamin D			
24NPHte	xenobiotic transport	24nph[e] <=> 24nph[c]	1		-1000	1000		Transport, Extracellular			
24_25DHVITD2t	24,25-Dihydroxyvitamin D2 transport from cytoplasm	2425dhvitd2[c] -> 2425dhvitd2[e]	0		0	1000		Transport, Extracellular			
24_25DHVITD2tm	24,25-Dihydroxyvitamin D2 transport from mitochondria	2425dhvitd2[m] -> 2425dhvitd2[c]	0		0	1000		Transport, Mitochondrial			
24_25DHVITD3t	24,25-Dihydroxyvitamin D3 transport from cytoplasm	2425dhvitd3[c] -> 2425dhvitd3[e]	0		0	1000		Transport, Extracellular			
24_25DHVITD3tm	24,25-Dihydroxyvitamin D3 transport from mitochondria	2425dhvitd3[m] -> 2425dhvitd3[c]	0		0	1000		Transport, Mitochondrial			
24_25VITD2Hm	24R-Vitamin D-25-hydroxylase (D2)	h[m] + nadph[m] + o2[m] + 25hvitd2[m] -> 2425dhvitd2[m] + h2o[m] + nadp[m]	0	13081.1	0	1000		Vitamin D			
24_25VITD3Hm	24R-Vitamin D-25-hydroxylase (D3)	h[m] + nadph[m] + o2[m] + 25hvitd3[m] -> h2o[m] + nadp[m] + 2425dhvitd3[m]	0	13081.1	0	1000		Vitamin D			
25HVITD2t	25-hydroxyvitamin D2 transport from cytoplasm	25hvitd2[c] -> 25hvitd2[e]	0		0	1000		Transport, Extracellular			
25HVITD2tin	25-hydroxyvitamin D2 transport in cytoplasm	25hvitd2[e] -> 25hvitd2[c]	0		0	1000		Transport, Extracellular			
25HVITD2tin_m	25-hydroxyvitamin D2 transport in mitochondria	25hvitd2[c] -> 25hvitd2[m]	0		0	1000		Transport, Mitochondrial			
25HVITD2tm	25-hydroxyvitamin D2 transport from mitochondria	25hvitd2[m] -> 25hvitd2[c]	0		0	1000		Transport, Mitochondrial			
25HVITD3t	25-hydroxyvitamin D3 transport from cytoplasm	25hvitd3[c] -> 25hvitd3[e]	0		0	1000		Transport, Extracellular			
25HVITD3tc	transport of 25-Hydroxyvitamin D3 into the intestine for absorption and into the renal cells for hydroxylation into active form of vitamin D	25hvitd3[u] -> 25hvitd3[c]	0	(14473.1 and 14725.1 and 65969.1)	0	1000	3	Transport, Extracellular	PMID: 19646505, PMID: 15951480, PMID: 12401836	DBP has higher affinity for 25(OH)D than for D3 (G.F.M. Ball (2006) Vitamins their role in the human body, Blackwell publishing, chapter 8, page 195-196). 25(OH) D binds DBP and is then recruited by magalin and cubilin for further hydroxylation in kidney and cellular uptake in intestine (PMID: 15951480).	
25HVITD3tin	25-hydroxyvitamin D3 transport in cytoplasm	25hvitd3[e] -> 25hvitd3[c]	0		0	1000		Transport, Extracellular			
25HVITD3tin_m	25-hydroxyvitamin D3 transport in mitochondria	25hvitd3[c] -> 25hvitd3[m]	0		0	1000		Transport, Mitochondrial			
25HVITD3tm	25-hydroxyvitamin D3 transport from mitochondria	25hvitd3[m] -> 25hvitd3[c]	0		0	1000		Transport, Mitochondrial			
25VITD2Hm	1-alpha-Vitamin D-25-hydroxylase (D2)	h[m] + nadph[m] + o2[m] + 25hvitd2[m] -> h2o[m] + nadp[m] + 1a25dhvitd2[m]	0	13115.1	0	1000		Vitamin D			
25VITD3Hm	1-alpha-Vitamin D-25-hydroxylase (D3)	h[m] + nadph[m] + o2[m] + 25hvitd3[m] -> h2o[m] + nadp[m] + 1a25dhvitd3[m]	0	13115.1	0	1000		Vitamin D			
2AMACHYD	2-Aminoacrylate hydrolysis	h2o[c] + 2amac[c] -> nh4[c] + pyr[c]	0		0	1000		Glycine, Serine, and Threonine Metabolism			
2AMACSULT	2-Aminoacrylate sulfotransferase	2amac[c] + nadph[c] + paps[c] -> Lcyst[c] + nadp[c] + pap[c]	0		0	1000		Cysteine Metabolism			
2AMADPTm	L-2-aminoadipate shuttle (cytosol/mitochondria)	L2aadp[c] + akg[m] <=> akg[c] + L2aadp[m]	1	217593.1	-1000	1000		Lysine Metabolism			
2DR1PP	2-deoxy-D-ribose 1-phosphate phosphorylase	h2o[c] + 2dr1p[c] -> pi[c] + drib[c]	0		0	1000		Pyrimidine Catabolism			
2HBt2	2-hydroxybutyrate cotransport with proton	2hb[e] + h[e] <=> h[c] + 2hb[c]	1	20503.1 or 80879.1 or 20501.1	-1000	1000		Transport, Extracellular			
2HCO3_NAt	bicarbonate transport (Na/HCO3 1:2 cotransport)	2 hco3[e] + na1[e] <=> 2 hco3[c] + na1[c]	1	232156.1 or 232156.2 or 232156.3 or 54403.1 or 232156.4	-1000	1000		Transport, Extracellular			
2MCITt	2-methylcitrate transport via diffusion	2mcit[c] <=> 2mcit[e]	1		-1000	1000		Transport, Extracellular			
2OXOADOXm	2-Oxoadipate:lipoamde 2-oxidoreductase(decarboxylating and acceptor-succinylating) (mitochondria)	2oxoadp[m] + coa[m] + nad[m] -> co2[m] + glutcoa[m] + nadh[m]	0	78920.1 or 18293.1 or (27402.1 and 13382.1) or 18293.2	0	1000		Lysine Metabolism			
2OXOADPTm	2-oxoadipate shuttle (cytosol/mitochondria)	akg[m] + 2oxoadp[c] <=> akg[c] + 2oxoadp[m]	1	217593.1	-1000	1000		Tryptophan metabolism			
34DHOXPEGt	3,4-Dihydroxyphenylethyleneglycol transport (diffusion)	34dhoxpeg[c] <=> 34dhoxpeg[e]	1		-1000	1000		Transport, Extracellular			
34DHPHAMT	3,4-Dihydroxyphenylacetate:amet O-methyltransferase	34dhpha[c] + amet[c] -> h[c] + ahcys[c] + homoval[c]	0	12846.1 or 12846.2	0	1000		Tyrosine metabolism			
34DHPHELAT1tc	transport of 3,4-Dihydroxy-L-phenylalanine by LAT1 in association with 4F2hc, across the apical surface of the memebranes.	34dhphe[u] + leu-L[c] -> 34dhphe[c] + leu-L[u]	0	(20539.1 and 17254.1)	0	1000	3	Tyrosine metabolism	Hans Gerhard Vogel, Franz J. Hock, Jochen Maas, Dieter Mayer (2006), Drug discovery and evaluation: Safety and pharmacokinetic assays, Springer publication, Chapter II D, page 456, table 3, PMID: 19035290, PMID: 12634921, European Journal of Pharmacology 441 (2002) 127-132. Am J Physiol Cell Physiol 281:C1077-C1093, 2001. Amino Acids (2005) 29: 229–233 DOI 10.1007/s00726-005-0221-x. PMID: 11901210	leucine is the only amino acid tested for efflux. Expressed in ovary, placenta, brain, spleen, testis, activated lymphocytes and some tumor cells. Functions as a antiport transport system (DOI 10.1016/j.cell.2009.01.02), requires heterodimerization with glycoprotein CD98 (Pflugers Arch-Eur J Physiol (2000) 440:503-512, DOI 10.1007/s004240000274, PMID: 10958334).	
34DHPLACOX	3,4-Dihydroxyphenylacetaldehyde:NAD+ oxidoreductase	h2o[c] + nad[c] + 34dhpac[c] -> 2 h[c] + 34dhpha[c] + nadh[c]	0	11670.1 or 67689.1 or 56847.1	0	1000	0	Tyrosine metabolism			
34DHPLACOX_NADP_	3,4-Dihydroxyphenylacetaldehyde:NADP+ oxidoreductase	h2o[c] + nadp[c] + 34dhpac[c] <=> 2 h[c] + nadph[c] + 34dhpha[c]	1	11670.1 or 67689.1 or 56847.1	-1000	1000	0	Tyrosine metabolism			
34DHXMANDACOX	3,4-Dihydroxymandelaldehyde:NAD+ oxidoreductase	h2o[c] + nad[c] + 34dhmald[c] -> 2 h[c] + nadh[c] + 34dhoxmand[c]	0	11670.1 or 67689.1 or 56847.1	0	1000	2	Tyrosine metabolism			
34DHXMANDACOX_NADP_	3,4-Dihydroxymandelaldehyde:NADP+ oxidoreductase	h2o[c] + nadp[c] + 34dhmald[c] <=> 2 h[c] + nadph[c] + 34dhoxmand[c]	1	11670.1 or 67689.1 or 56847.1	-1000	1000	0	Tyrosine metabolism			
34HPLFM	3-(4-hydroxyphenyl-)lactate formation	h[m] + nadh[m] + 34hpp[m] -> nad[m] + 34hpl[m]	0		0	1000		Ubiquinone Biosynthesis			
34HPPOR	4-Hydroxyphenylpyruvate:oxygen oxidoreductase	o2[c] + 34hpp[c] -> co2[c] + hgentis[c]	0	15445.1	0	1000		Tyrosine metabolism			
35CGMPtn	35cGMP nuclear transport	35cgmp[c] <=> 35cgmp[n]	1		-1000	1000		Transport, Nuclear			
3AIBTm	L-3-aminoisobutyrate transaminase, mitochondrial	2mop[m] + glu-L[m] <=> akg[m] + 3aib[m]	1	268860.2 or 268860.1	-1000	1000		Valine, Leucine, and Isoleucine Metabolism			
3AIBt	L-3-aminoisobutyrate transaminase	3aib[c] -> 3aib[e]	0		0	1000		Transport, Extracellular			
3AIBtm	L-3-aminoisobutyrate transaminase, mitochondrial	3aib[m] -> 3aib[c]	0		0	1000		Transport, Mitochondrial			
3DPHBH1	Hydroxylation of 3-Decaprenyl-4-hydroxybenzoate (NADH)	h[m] + o2[m] + nadh[m] + 3dphb[m] -> h2o[m] + nad[m] + 3dpdhb[m]	0		0	1000		Ubiquinone Biosynthesis			
3DPHBH2	Hydroxylation of 3-Decaprenyl-4-hydroxybenzoate (NADPH)	h[m] + nadph[m] + o2[m] + 3dphb[m] -> h2o[m] + nadp[m] + 3dpdhb[m]	0		0	1000		Ubiquinone Biosynthesis			
3DSPHR	3-Dehydrosphinganine reductase	h[c] + nadph[c] + 3dsphgn[c] -> nadp[c] + sphgn[c]	0	70750.1	0	1000		Sphingolipid Metabolism			
3HAO	3-hydroxyanthranilate 3,4-dioxygenase	o2[c] + 3hanthrn[c] -> h[c] + cmusa[c]	0	107766.1	0	1000		Tryptophan metabolism			
3HBCDm	3-hydroxybutyryl-CoA dehydratase, mitochondrial	h2o[m] + b2coa[m] <=> 3hbcoa-R[m]	1	52430.1	-1000	1000		Butanoate Metabolism			
3HBCOAHLm	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	h2o[m] + 3hibutcoa[m] -> h[m] + coa[m] + 3hmp[m]	0		0	1000		Valine, Leucine, and Isoleucine Metabolism			
3HCO3_NAt	bicarbonate transport (Na/HCO3 1:3 cotransport)	3 hco3[e] + na1[e] <=> 3 hco3[c] + na1[c]	1	232156.1 or 232156.2 or 232156.3 or 54403.1 or 232156.4	-1000	1000		Transport, Extracellular			
3HKYNAKGAT	3-Hydroxy-L-kynurenine:2-oxoglutarate aminotransferase	akg[c] + hLkynr[c] -> 42A3HP24DB[c] + glu-L[c]	0	23923.1 or 70266.1 or 23923.2	0	1000		Tryptophan metabolism			
3HLYTCL	3-Hydroxy-L-tyrosine carboxy-lyase	h[c] + 34dhphe[c] -> co2[c] + dopa[c]	0	13195.1	0	1000		Tyrosine metabolism			
3HPCOAHYD	3-hydroxyisobutyryl-Coenzyme A hydrolase	h2o[c] + 3hpcoa[c] -> h[c] + 3hpp[c] + coa[c]	0	227095.1 or 227095.2	0	1000		beta-Alanine metabolism			
3HPPD	3-hydroxypropionate dehydrogenase	nad[c] + 3hpp[c] <=> h[c] + nadh[c] + msa[c]	1		-1000	1000		Propanoate Metabolism			
3HXKYNDCL	3-Hydroxykynurenamine decarboxy-lyase	h[c] + hLkynr[c] -> co2[c] + 3hxkynam[c]	0	13195.1	0	1000		Tryptophan metabolism			
3HXKYNOXDA	3-Hydroxykynurenamine:oxygen oxidoreductase(deaminating)(flavin-containing)	o2[c] + 3hxkynam[c] -> h2o2[c] + nh4[c] + 48dhoxquin[c]	0	109731.1 or 17161.1	0	1000		Tryptophan metabolism			
3M4HDXPAC	3-Methoxy-4-hydroxyphenylacetaldehyde:NAD+ oxidoreductase	h2o[c] + nad[c] + 3mox4hpac[c] <=> 2 h[c] + homoval[c] + nadh[c]	1	11670.1 or 67689.1 or 56847.1	-1000	1000		Tyrosine metabolism			
3MLDAt	3MLDA extracellular transport via diffusion	3mlda[c] <=> 3mlda[e]	1		-1000	1000		Transport, Extracellular			
3MOBt2im	3-methyl-2-oxobutanoate mitochondrial transport via proton symport	h[c] + 3mob[c] -> h[m] + 3mob[m]	0		0	1000		Transport, Mitochondrial			
3MOPt2im	3-Methyl-2-oxopentanoate mitochondrial transport via proton symport	h[c] + 3mop[c] -> h[m] + 3mop[m]	0		0	1000		Transport, Mitochondrial			
3MOX4HOXPGALDOX	3-Methoxy-4-hydroxyphenylglycolaldehyde:NAD+ oxidoreductase	h2o[c] + nad[c] + 3m4hpga[c] -> 2 h[c] + nadh[c] + 3mox4hoxm[c]	0	11670.1 or 67689.1 or 56847.1	0	1000	2	Tyrosine metabolism			
3MOX4HOXPGALDOX_NADP_	3-Methoxy-4-hydroxyphenylglycolaldehyde:NADP+ oxidoreductase	h2o[c] + nadp[c] + 3m4hpga[c] <=> 2 h[c] + nadph[c] + 3mox4hoxm[c]	1	212647.1 or 212647.2	-1000	1000	0	Tyrosine metabolism			
3MOXTYROX	3-Methoxytyramine:oxygen oxidoreductase (deaminating)	h2o[c] + o2[c] + 3moxtyr[c] -> h2o2[c] + nh4[c] + 3mox4hpac[c]	0	109731.1 or 17161.1	0	1000		Tyrosine metabolism			
3NTD7l	3'-nucleotidase (AMP), lysosome	3amp[l] + h2o[l] -> adn[l] + pi[l]	0	11432.1	0	1000		Nucleic acid degradation			
3SALAASPm	cysteinesulfinate-aspartate mitochondrial shuttle	asp-L[c] + 3sala[m] <=> 3sala[c] + asp-L[m]	1	78830.1 or 50799.1	-1000	1000		Transport, Mitochondrial			

3SALACBOXL	3-Sulfino-L-alanine carboxy-lyase	h[c] + 3sala[c] -> co2[c] + hyptaur[c]	0	246277.1 or 14415.1 or 14417.1 or 14415.2	0	1000		Taurine and hypotaurine metabolism			
3SALAOX	cysteinesulfinic acid oxidase	o2[c] + 2 h[c] + 2 3sala[c] -> 2 Lcyst[c]	0		0	1000		Taurine and hypotaurine metabolism			
3SALATAi	3-sulfino-alanine transaminase (irreversible)	h[c] + akg[c] + 3sala[c] -> glu-L[c] + 3snpyr[c]	0	14718.1	0	1000		Cysteine Metabolism			
3SALATAim	3-sulfino-alanine transaminase (irreversible), mitochondrial	h[m] + akg[m] + 3sala[m] -> glu-L[m] + 3snpyr[m]	0	14719.1	0	1000		Cysteine Metabolism			
3SPYRSP	3-sulfinopyruvate hydrolase (spotaneous reaction)	h2o[c] + 3snpyr[c] -> h[c] + pyr[c] + so3[c]	0		0	1000		Cysteine Metabolism			
3SPYRSPm	3-sulfinopyruvate hydrolase (spotaneous reaction), mitochondrial	h2o[m] + 3snpyr[m] -> h[m] + pyr[m] + so3[m]	0		0	1000		Cysteine Metabolism			
41R1H2MAE12BOOX	4-[(1R)-1-Hydroxy-2-(methylamino)ethyl]-1,2-benzenediol:oxygen oxidoreductase(deaminating)(flavin-containing)	h2o[c] + o2[c] + adrnl[c] -> h2o2[c] + 34dhmald[c] + mma[c]	0	109731.1 or 17161.1	0	1000		Tyrosine metabolism			
41R2A1H12BOOX	4-[(1R)-2-Amino-1-hydroxyethyl]-1,2-benzenediol:oxygen oxidoreductase(deaminating)(flavin-containing)	h2o[c] + o2[c] + nrpphr[c] -> h2o2[c] + nh4[c] + 34dhmald[c]	0	109731.1 or 17161.1	0	1000		Tyrosine metabolism			
42A12BOOX	4-(2-Aminoethyl)-1,2-benzenediol:oxygen oxidoreductase(deaminating)(flavin-containing)	h2o[c] + o2[c] + dopa[c] -> h2o2[c] + nh4[c] + 34dhpac[c]	0	237940.1 or 109731.1 or 17161.1 or 237940.2 or 11754.1 or 76507.1	0	1000		Tyrosine metabolism			
4ABUTtm	4-aminobutanoate mitochondrial transport via diffusion	4abut[c] <=> 4abut[m]	1		-1000	1000		Transport, Mitochondrial			
4HBZCOAFm	4-hydroxybenzoyl-CoA formation	h2o[m] + coa[m] + nad[m] + coucoa[m] -> h[m] + nadh[m] + 4hbzcoa[m] + accoa[m]	0		0	1000		Ubiquinone Biosynthesis			
4HBZFm	4-hydroxybenzoate formation	h2o[m] + 4hbzcoa[m] -> h[m] + coa[m] + 4hbz[m]	0		0	1000		Ubiquinone Biosynthesis			
4HDEBRISOQUINEte	xenobiotic transport	4hdebrisoquine[e] <=> 4hdebrisoquine[c]	1		-1000	1000		Transport, Extracellular			
4HGLSDm	L-4-hydroxyglutamate semialdehyde dehydrogenase, mitochondrial	h2o[m] + nad[m] + 4hglusa[m] <=> 2 h[m] + nadh[m] + e4hglu[m]	1	212647.1 or 212647.2	-1000	1000	0	Arginine and Proline Metabolism			
4HOXPACDOX_NADP_	4-Hydroxyphenylacetaldehyde:NADP+ oxidoreductase	h2o[c] + nadp[c] + 4hoxpacd[c] <=> 2 h[c] + nadph[c] + 4hphac[c]	1	212647.1 or 212647.2	-1000	1000	0	Tyrosine metabolism			
4HPRO_LTt	trans-4-hydroxy-L-proline transport	h[e] + 4hpro-LT[e] <=> h[c] + 4hpro-LT[c]	1		-1000	1000	1	Transport, Extracellular		Needed to provide this metabolite for reaction 4OHPROIMINOtc in joint model.	
4MOPt2im	4-methyl-2-oxopentanoate mitochondrial transport via proton symport	h[c] + 4mop[c] -> h[m] + 4mop[m]	0		0	1000		Transport, Mitochondrial			
4MPTNLte	4 methylpentanal transmembrane transport	4mptnl[c] <=> 4mptnl[e]	1		-1000	1000		Transport, Extracellular			
4MPTNLtm	4 methylpentanal intracellular transport	4mptnl[c] <=> 4mptnl[m]	1		-1000	1000		Transport, Mitochondrial			
4MPTNLtr	4 methylpentanal intracellular transport	4mptnl[c] <=> 4mptnl[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
4MTOLBUTAMIDEte	xenobiotic transport	4mtolbutamide[e] <=> 4mtolbutamide[c]	1		-1000	1000		Transport, Extracellular			
4NPHSFte	xenobiotic transport	4nphsf[e] <=> 4nphsf[c]	1		-1000	1000		Transport, Extracellular			
4NPHte	xenobiotic transport	4nph[e] <=> 4nph[c]	1		-1000	1000		Transport, Extracellular			
4OHPROIMINOtc	transport of L-OH-Proline by the apical IMINO amino acid transporters in kidney and intestine	4hpro-LT[u] + 2 na1[u] + cl[u] -> 2 na1[c] + 4hpro-LT[c] + cl[c]	0	(102680.1 and 57394.1)	0	1000	3	Transport, Lumen	PMID: 19657969, PMID: 15632147, PMID: 18195088, PMID: 18400692, PMID:19184091	IMINO transporter is suggested to be a candidate for iminoglycinuria (PMID: 16052352). Associted with collectrin in kidney.	
4PYRDX	4-Pyridoxal secretion	h2o[c] + atp[c] + 4pyrdx[c] -> adp[c] + h[c] + pi[c] + 4pyrdx[e]	0		0	1000		Transport, Extracellular			
5ADTSTSTERONEGLCte	glucuronidated compound transport	h2o[c] + atp[c] + 5adtststeroneglc[c] -> adp[c] + h[c] + pi[c] + 5adtststeroneglc[e]	0	17250.1	0	1000		Transport, Extracellular			
5ADTSTSTERONEGLCtr	glucuronidated compound transport	5adtststeroneglc[c] <=> 5adtststeroneglc[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
5ADTSTSTERONESULT	5alpha-Dihydrotestosterone sulfotransferase	paps[c] + 5adtststerone[c] -> h[c] + pap[c] + 5adtststerones[c]	0	20859.1	0	1000		Steroid Metabolism			
5ADTSTSTERONESte	sulfonated testosterone transport	5adtststerones[c] <=> 5adtststerones[e]	1		-1000	1000		Transport, Extracellular			
5ADTSTSTERONEte	5 alpha dihydrotesterone transport	5adtststerone[e] <=> 5adtststerone[c]	1		-1000	1000		Transport, Extracellular			
5ADTSTSTERONEtr	5 alpha dihydrotesterone intracellular transport	5adtststerone[r] <=> 5adtststerone[c]	1		-1000	1000		Transport, Endoplasmic Reticular			
5AOPtm	5-Aminolevulinate mitochondrial transport	5aop[c] <=> 5aop[m]	1		-1000	1000		Heme Biosynthesis			
5DHFtl	5-glutamyl-DHF transport, lysosomal	5dhf[c] -> 5dhf[l]	0		0	1000		Transport, Lysosomal			
5FTHFt2	5-formyltetrahydrofolate transport via anion exchange	oh1[c] + 5fthf[e] <=> 5fthf[c] + oh1[e]	1	20509.1 or 20509.2	-1000	1000		Transport, Extracellular			
5HLTDL	5-Hydroxy-L-tryptophan decarboxy-lyase	h[c] + 5htrp[c] -> co2[c] + srtn[c]	0	13195.1	0	1000		Tryptophan metabolism			
5HOMEPRAZOLEte	xenobiotic transport	5homeprazole[e] <=> 5homeprazole[c]	1		-1000	1000		Transport, Extracellular			
5HOXINDACTO2OX	5-Hydroxyindoleacetaldehyde:oxygen oxidoreductase	h2o[c] + o2[c] + 5hoxindact[c] -> h2o2[c] + h[c] + 5hoxindoa[c]	0	11761.1	0	1000		Tryptophan metabolism			
5HOXINDACTOX	5-Hydroxyindoleacetaldehyde:NAD+ oxidoreductase	h2o[c] + nad[c] + 5hoxindact[c] -> 2 h[c] + nadh[c] + 5hoxindoa[c]	0	19378.1 or 56752.1 or 110695.1 or 11668.1 or 11671.1 or 19378.2 or 19378.3	0	1000		Tryptophan metabolism			
5HOXINDACTOXm	5-Hydroxyindoleacetaldehyde:NAD+ oxidoreductase (mito)	h2o[m] + nad[m] + 5hoxindact[m] -> 2 h[m] + nadh[m] + 5hoxindoa[m]	0	212647.1 or 11669.1 or 212647.2 or 72535.1	0	1000		Tryptophan metabolism			
5HOXINOXDA	5-Hydroxytryptamine:oxygen oxidoreductase(deaminating)(flavin-containing)	h2o[c] + o2[c] + srtn[c] -> h2o2[c] + nh4[c] + 5hoxindact[c]	0	109731.1 or 17161.1	0	1000		Tryptophan metabolism			
5HTRPDOX	5-Hydroxy-L-tryptophan:oxygen 2,3-dioxygenase (indole-decyclizing)	o2[c] + 5htrp[c] -> 5hoxnfkyn[c]	0	15930.1	0	1000		Tryptophan metabolism			
5HTRPVESSEC	5-hydroxy-L-tryptophan secretion via secretory vesicle (ATP driven)	2 h2o[c] + 2 atp[c] + 3 5htrp[c] -> 2 adp[c] + 2 h[c] + 2 pi[c] + 3 5htrp[e]	0	214084.1 or 110877.1	0	1000		Transport, Extracellular			
5HXKYNDCL	5-Hydroxykynurenamine decarboxy-lyase	h[c] + 5hxkyn[c] -> co2[c] + 5hxkynam[c]	0	13195.1	0	1000		Tryptophan metabolism			
5HXKYNOXDA	5-Hydroxykynurenamine:oxygen oxidoreductase(deaminating)(flavin-containing)	o2[c] + 5hxkynam[c] -> h2o2[c] + nh4[c] + 46dhoxquin[c]	0	109731.1 or 17161.1	0	1000		Tryptophan metabolism			
5MTHFt2	5-methyltetrahydrofolate transport via anion exchange	oh1[c] + 5mthf[e] <=> oh1[e] + 5mthf[c]	1	20509.1 or 20509.2	-1000	1000		Transport, Extracellular			
5MTHFtc	transport of 5-Methyltetrahydrofolate by folate receptor protein	5mthf[u] -> 5mthf[c]	0	(14275.1 or 14276.1)	0	1000	3	Transport, Lumen	Janos Zempleni, Robert B. Rucker, Donald B. McCormick, John W. Suttie (2007) Handbook of vitamins, CRC press, chapter 12, page 390-391, Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Advanced nutrition and human metabolism, Wadsworth cengage learning, 5th edition, page 349-351, G.F.M. Ball (2006) Vitamins their role in the human body, Blackwell publishing, chapter 17, page 351-356	the folate receptor is encoded by atleast 3 genes, most tissues expressing the alpha form. The folate receptor like protein mediates unidirectional flux following internalization of the folate-receptor complex. (Janos Zempleni, Robert B. Rucker, Donald B. McCormick, John W. Suttie (2007) Handbook of vitamins, CRC press, chapter 12, page 390-391)	
5THFtl	5-glutamyl-THF transport, lysosomal	5thf[c] -> 5thf[l]	0		0	1000		Transport, Lysosomal			
5THFtm	5-glutamyl-THF transport,m mitochondrial	5thf[m] -> 5thf[c]	0		0	1000		Transport, Mitochondrial			
6DHFtl	6-glutamyl-DHF transport, lysosomal	6dhf[c] -> 6dhf[l]	0		0	1000		Transport, Lysosomal			
6DHFtm	6-glutamyl-DHF transport,m mitochondrial	6dhf[m] -> 6dhf[c]	0		0	1000		Transport, Mitochondrial			
6HTSTSTERONEte	hydroxylated testosterone transport	6htststerone[c] <=> 6htststerone[e]	1		-1000	1000		Transport, Extracellular			
6HTSTSTERONEtr	hydroxylated testosterone transport	6htststerone[c] <=> 6htststerone[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
6THFtl	6-glutamyl-THF transport, lysosomal	6thf[c] -> 6thf[l]	0		0	1000		Transport, Lysosomal			
6THFtm	6-glutamyl-THF transport,m mitochondrial	6thf[m] -> 6thf[c]	0		0	1000		Transport, Mitochondrial			
7DHCHSTEROLtr	cholesterol precursor intracellular transport	7dhchsterol[r] <=> 7dhchsterol[c]	1		-1000	1000		Transport, Endoplasmic Reticular			
7DHFtl	7-glutamyl-DHF transport, lysosomal	7dhf[c] -> 7dhf[l]	0		0	1000		Transport, Lysosomal			
7DHFtm	7-glutamyl-DHF transport,m mitochondrial	7dhf[m] -> 7dhf[c]	0		0	1000		Transport, Mitochondrial			
7THFtl	7-glutamyl-THF transport, lysosomal	7thf[c] -> 7thf[l]	0		0	1000		Transport, Lysosomal			
7THFtm	7-glutamyl-THF transport,m mitochondrial	7thf[m] -> 7thf[c]	0		0	1000		Transport, Mitochondrial			
A4GALTc	Lactosylceramide 4-alpha-galactosyltransferase	galgluside_hs[c] + udpgal[c] -> h[c] + thcrm_hs[c] + udp[c]	0	239559.1	0	1000		Sphingolipid Metabolism			
A4GALTg	Lactosylceramide 4-alpha-galactosyltransferase	galgluside_hs[g] + udpgal[g] -> h[g] + thcrm_hs[g] + udp[g]	0	239559.1	0	1000		Sphingolipid Metabolism			
A4GNT1g	alpha 1,4-N-acetylglucosaminyltransferase, Golgi apparatus	T_antigen[g] + uacgam[g] -> h[g] + udp[g] + gncore1[g]	0	333424.1	0	1000		O-Glycan Biosynthesis			
A4GNT2g	alpha 1,4-N-acetylglucosaminyltransferase, Golgi apparatus	uacgam[g] + core2[g] -> h[g] + udp[g] + gncore2[g]	0	333424.1	0	1000		O-Glycan Biosynthesis			
AACOAT	Acetoacetyl-CoA:acetate CoA-transferase	atp[c] + coa[c] + acac[c] <=> aacoa[c] + amp[c] + ppi[c]	1	78894.1	-1000	1000		Propanoate Metabolism			
AACTOOR	Aminoacetone:oxygen oxidoreductase(deaminating)(flavin-containing)	h2o[c] + o2[c] + aact[c] -> h2o2[c] + nh4[c] + mthgxl[c]	0	11754.1	0	1000		Glycine, Serine, and Threonine Metabolism			
AACTtm	Aminoacetone transport (mitochondrial)	aact[m] -> aact[c]	0		0	1000		Transport, Mitochondrial			
AAPSAS	AAPSAS	h2o[c] + h[c] + thp2c[c] -> L2aadp6sa[c]	0		0	1000		Lysine Metabolism			
AASAD3	L-aminoadipate-semialdehyde dehydrogenase (NADH)	h2o[c] + nad[c] + L2aadp6sa[c] -> 2 h[c] + L2aadp[c] + nadh[c]	0		0	1000		Lysine Metabolism			
AASAD3m	L-aminoadipate-semialdehyde dehydrogenase (NADH), mitochondrial	h2o[m] + nad[m] + L2aadp6sa[m] -> 2 h[m] + L2aadp[m] + nadh[m]	0		0	1000		Lysine Metabolism			
AATAi	2-aminoadipate transaminase, irreversible	L2aadp[c] + akg[c] -> 2oxoadp[c] + glu-L[c]	0	23923.1 or 23923.2	0	1000		Lysine Metabolism			
ABTArm	4-aminobutyrate transaminase, reversible (mitochondrial)	akg[m] + 4abut[m] <=> glu-L[m] + sucsal[m]	1	268860.2 or 268860.1	-1000	1000		Glutamate metabolism			
ABTD	L-arabinitol 4-dehydrogenase	nad[c] + abt[c] <=> h[c] + nadh[c] + xylu-L[c]	1		-1000	1000		Pentose and Glucuronate Interconversions			
ABTti	L-arabinitol transport via passive diffusion	abt[c] -> abt[e]	0		0	1000		Transport, Extracellular			
ABUTD	Aminobutyraldehyde dehydrogenase	h2o[c] + nad[c] + 4abutn[c] -> 2 h[c] + nadh[c] + 4abut[c]	0	56752.1	0	1000		beta-Alanine metabolism			
ABUTt2r	4-aminobutyrate reversible transport in via proton symport	h[e] + 4abut[e] <=> h[c] + 4abut[c]	1	215335.1	-1000	1000		Transport, Extracellular			
ABUTt2rL	4-aminobutyrate reversible transport in via proton symport (lysosome)	4abut[l] + h[l] <=> h[c] + 4abut[c]	1	215335.1	-1000	1000	0	Transport, Lysosomal			
ABUTt4_2_r	4-aminobutyrate reversible transport in via sodium symport (1:2)	2 na1[e] + 4abut[e] <=> 2 na1[c] + 4abut[c]	1	14412.1 or 14411.1 or 243616.1 or 232333.1	-1000	1000	0	Transport, Extracellular			
ACACT1	acetyl-CoA C-acetyltransferase	2 accoa[c] -> coa[c] + aacoa[c]	0	224530.1	0	1000		Cholesterol Metabolism			
ACACT10m	acetyl-CoA C-acetyltransferase, mitochondrial	coa[m] + 2maacoa[m] <=> accoa[m] + ppcoa[m]	1	110446.1	-1000	1000		Valine, Leucine, and Isoleucine Metabolism			
ACACT1r	acetyl-CoA C-acetyltransferase	2 accoa[c] <=> coa[c] + aacoa[c]	1	224530.1	-1000	1000		Tryptophan metabolism			
ACACT1rm	acetyl-CoA C-acetyltransferase, mitochondrial	2 accoa[m] <=> coa[m] + aacoa[m]	1	110446.1 or 231086.1 or 97212.1	-1000	1000		Tryptophan metabolism			
ACACT1x	acetyl-CoA C-acetyltransferase, mitochondrial	2 accoa[x] -> aacoa[x] + coa[x]	0	224530.1	0	1000		Cholesterol Metabolism			
ACACT4p	acetyl-CoA C-acetyltransferase (octanoyl-CoA), peroxisomal	coa[x] + 3odcoa[x] -> accoa[x] + occoa[x]	0	113868.1	0	1000		Fatty Acid Metabolism			
ACACT5p	acetyl-CoA C-acyltransferase (decanoyl-CoA), peroxisomal	coa[x] + 3oddcoa[x] -> accoa[x] + dcacoa[x]	0	113868.1	0	1000		Fatty Acid Metabolism			
ACACT6p	acetyl-CoA C-acetyltransferase (dodecanoyl), peroxisomal	coa[x] + 3otdcoa[x] -> accoa[x] + ddcacoa[x]	0	113868.1	0	1000		Fatty Acid Metabolism			
ACACT7p	acetyl-CoA acyltransferase (tetradecanoyl-CoA), peroxisomal	coa[x] + 3ohdcoa[x] -> accoa[x] + tdcoa[x]	0	113868.1	0	1000		Fatty Acid Metabolism			

ACACT8p	acetyl-CoA acyltransferase (hexadecanoyl-CoA), peroxisomal	coa[x] + 3ohodcoa[x] -> accoa[x] + pmtcoa[x]	0	113868.1	0	1000		Fatty Acid Metabolism			
ACACT9p	acetyl-CoA acyltransferase (tetracosanoyl-CoA), peroxisomal	coa[x] + 3ohxccoa[x] -> accoa[x] + ttccoa[x]	0	113868.1	0	1000		Fatty Acid Metabolism			
ACACt2	acetoacetate transport via proton symport	h[e] + acac[e] <=> h[c] + acac[c]	1	20503.1 or 20501.1	-1000	1000		Transport, Extracellular			
ACACt2m	Acetoacetate mitochondrial transport via H+ symport	h[c] + acac[c] <=> h[m] + acac[m]	1	20501.1	-1000	1000		Transport, Mitochondrial			
ACACtx	acetoacetate intracellular transport unknown mechanism	acac[c] <=> acac[x]	1		-1000	1000		Transport, Peroxisomal			
ACALDt	acetaldehyde reversible transport	acald[e] <=> acald[c]	1		-1000	1000		Transport, Extracellular			
ACALDtm	acetaldehyde mitochondrial diffusion	acald[m] <=> acald[c]	1		-1000	1000		Transport, Mitochondrial			
ACALDtr	acetaldehyde transport intracellular	acald[r] <=> acald[c]	1		-1000	1000		Transport, Endoplasmic Reticular			
ACALDtx	acetaldehyde peroxisomal diffusion	acald[x] <=> acald[c]	1		-1000	1000		Transport, Peroxisomal			
ACCOAC	acetyl-CoA carboxylase	atp[c] + hco3[c] + accoa[c] -> adp[c] + h[c] + pi[c] + malcoa[c]	0	107476.2 or 107476.1 or 100705.1 and 107476.3 or 100705.1 and 107476.5 or 107476.4 or 100705.1 and 107476.4 or 107476.1 and 100705.1 or 107476.5 or 107476.3 or 100705.1 and 107476.4	0	1000		Fatty Acid Metabolism			
ACCOACm	Acetyl-Coa carboxylase, beta isoform	accoa[m] + atp[m] + hco3[m] -> h[m] + adp[m] + malcoa[m] + pi[m]	0	100705.1	0	1000		Fatty Acid Metabolism			
ACCOAL	acetate-CoA ligase (ADP-forming)	atp[c] + coa[c] + ppa[c] -> adp[c] + pi[c] + ppcoa[c]	0	60525.1 or 60525.2	0	1000		Propanoate Metabolism			
ACCOALm	acetate-CoA ligase (AMP-forming)	coa[m] + atp[m] + ppa[m] -> ppcoa[m] + amp[m] + ppi[m]	0	68738.1	0	1000		Propanoate Metabolism			
ACCOAgt	acetyl-coa transport	accoa[c] <=> accoa[g]	1	11416.1	-1000	1000		Transport, Extracellular			
ACCOAtn	acetyl-CoA transport, nuclear	accoa[c] <=> accoa[n]	1		-1000	1000		Transport, Nuclear			
ACCOAtr	acetyl-coa transport	accoa[c] <=> accoa[r]	1	11416.1	-1000	1000		Transport, Endoplasmic Reticular			
ACETONEt2	acetone transport via proton symport	h[e] + acetone[e] <=> h[c] + acetone[c]	1	20503.1 or 80879.1 or 20501.1	-1000	1000		Transport, Extracellular			
ACETONEt2m	acetone mitochondrial transport via proton symport	h[c] + acetone[c] <=> h[m] + acetone[m]	1	20501.1	-1000	1000		Transport, Mitochondrial			
ACGAGBSIDEtg	acgagbside_hs intracellular transport	acgagbside_hs[c] <=> acgagbside_hs[g]	1		-1000	1000		Transport, Golgi Apparatus			
ACGAGBSIDEtl	acgagbside_hs intracellular transport	acgagbside_hs[c] <=> acgagbside_hs[l]	1		-1000	1000		Transport, Lysosomal			
ACGALFUCGALACGALFUC12GAL14ACGLCGALGLUSIDEte	blood group intracellular transport	acgalfucgalacgalfuc12gal14acglcgalgluside_hs[e] <=> acgalfucgalacgalfuc12gal14acglcgalgluside_hs[c]	1		-1000	1000		Transport, Extracellular			
ACGALFUCGALACGALFUC12GAL14ACGLCGALGLUSIDEtg	blood group intracellular transport	acgalfucgalacgalfuc12gal14acglcgalgluside_hs[g] <=> acgalfucgalacgalfuc12gal14acglcgalgluside_hs[c]	1		-1000	1000		Transport, Golgi Apparatus			
ACGALFUCGALACGALFUCGALACGLCGAL14ACGLCGALGLUSIDEte	blood group intracellular transport	acgalfucgalacgalfucgalacglcgal14acglcgalgluside_hs[e] <=> acgalfucgalacgalfucgalacglcgal14acglcgalgluside_hs[c]	1		-1000	1000		Transport, Extracellular			
ACGALFUCGALACGALFUCGALACGLCGAL14ACGLCGALGLUSIDEtg	blood group intracellular transport	acgalfucgalacgalfucgalacglcgal14acglcgalgluside_hs[g] <=> acgalfucgalacgalfucgalacglcgal14acglcgalgluside_hs[c]	1		-1000	1000		Transport, Golgi Apparatus			
ACGALK	N-acetylgalactosamine kinase	atp[c] + acgal[c] -> adp[c] + h[c] + acgal1p[c]	0		0	1000		Aminosugar Metabolism			
ACGALK2	N-acetylgalactosamine kinase (ITP)	acgal[c] + itp[c] -> h[c] + acgal1p[c] + idp[c]	0		0	1000		Aminosugar Metabolism			
ACGALtlg	N-acetyl-galactosamine intracellular transport	acgal[g] <=> acgal[c]	1		-1000	1000		Transport, Golgi Apparatus			
ACGALtly	N-acetyl-galactosamine lysosomal efflux	acgal[l] -> acgal[c]	0		0	1000		Transport, Lysosomal			
ACGALtr	N-acetylgalactosamine export	acgal[c] -> acgal[e]	0		0	1000	2	Transport, Extracellular	PMID: 15123798, PMID: 18180286	This metabolite is found in mucus and can serve as carbon source for intestinal microbes. It is assumed it appears in mucus through secretion from goblet cells and from epithelial cell debris.	
ACGAM2E	N-acetylglucosamine 2-epimerase	acgam[c] <=> acmana[c]	1	19703.1	-1000	1000		Aminosugar Metabolism			
ACGAM6PSi	N-acetylglucosamine-6-phosphate synthase	accoa[c] + gam6p[c] -> h[c] + coa[c] + acgam6p[c]	0	54342.1	0	1000		Aminosugar Metabolism			
ACGAMK	N-acetylglucosamine kinase	atp[c] + acgam[c] -> adp[c] + h[c] + acgam6p[c]	0	56174.1	0	1000		Aminosugar Metabolism			
ACGAMPM	phosphoacetylglucosamine mutase	acgam6p[c] <=> acgam1p[c]	1	109785.1	-1000	1000		Aminosugar Metabolism			
ACGAMtly	N-acetyl-glucosamine lysosomal efflux	acgam[l] -> acgam[c]	0		0	1000		Transport, Lysosomal			
ACGBGBSIDEtg	acgbgbside_hs intracellular transport	acgbgbside_hs[c] <=> acgbgbside_hs[g]	1		-1000	1000		Transport, Golgi Apparatus			
ACGBGBSIDEtl	acgbgbside_hs intracellular transport	acgbgbside_hs[c] <=> acgbgbside_hs[l]	1		-1000	1000		Transport, Lysosomal			
ACGPID	N-acetylglucosaminylphosphatidylinositol deacetylase	h2o[c] + acgpail_hs[c] -> ac[c] + gpail_hs[c]	0	327942.1	0	1000		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
ACGSm	N-acetylglutamate synthase, mitochondrial	glu-L[m] + accoa[m] -> h[m] + coa[m] + acglu[m]	0	217214.1	0	1000		Urea cycle/amino group metabolism			
ACHEe	Acetylcholinesterase	ach[e] + h2o[e] -> h[e] + ac[e] + chol[e]	0	11423.1 or 11423.2	0	1000		Glycerophospholipid Metabolism			
ACHVESSEC	Acetylcholine secretion via secretory vesicle (ATP driven)	2 h2o[c] + 2 atp[c] + 3 ach[c] -> 2 adp[c] + 2 h[c] + 2 pi[c] + 3 ach[e]	0	20508.1	0	1000		Transport, Extracellular			
ACHtn	Acetylcholin transport, nuclear trhough pores	ach[n] <=> ach[c]	1		-1000	1000		Transport, Nuclear			
ACITL	ATP-Citrate lyase	atp[c] + coa[c] + cit[c] -> adp[c] + pi[c] + accoa[c] + oaa[c]	0	104112.1 or 104112.2	0	1000		Citric Acid Cycle			
ACN13ACNGALGBSIDEte	acn13acngalgbside_hs transport	acn13acngalgbside_hs[c] <=> acn13acngalgbside_hs[e]	1		-1000	1000		Transport, Extracellular			
ACN13ACNGALGBSIDEtg	acn13acngalgbside_hs intracellular transport	acn13acngalgbside_hs[c] <=> acn13acngalgbside_hs[g]	1		-1000	1000		Transport, Golgi Apparatus			
ACN23ACNGALGBSIDEte	acn23acngalgbside transport	acn23acngalgbside_hs[c] <=> acn23acngalgbside_hs[e]	1		-1000	1000		Transport, Extracellular			
ACN23ACNGALGBSIDEtg	acn23acngalgbside intracellular transport	acn23acngalgbside_hs[c] <=> acn23acngalgbside_hs[g]	1		-1000	1000		Transport, Golgi Apparatus			
ACNACNGAL14ACGLCGALGLUSIDEte	blood group intracellular transport	acnacngal14acglcgalgluside_hs[e] <=> acnacngal14acglcgalgluside_hs[c]	1		-1000	1000		Transport, Extracellular			
ACNACNGAL14ACGLCGALGLUSIDEtg	blood group intracellular transport	acnacngal14acglcgalgluside_hs[g] <=> acnacngal14acglcgalgluside_hs[c]	1		-1000	1000		Transport, Golgi Apparatus			
ACNACNGALGBSIDEte	acnacngalgbside_hs transport	acnacngalgbside_hs[c] <=> acnacngalgbside_hs[e]	1		-1000	1000		Transport, Extracellular			
ACNACNGALGBSIDEtg	acnacngalgbside_hs intracellular transport	acnacngalgbside_hs[c] <=> acnacngalgbside_hs[g]	1		-1000	1000		Transport, Golgi Apparatus			
ACNAM9PL	N-Acetylneuraminate 9-phosphate pyruvate-lyase (pyruvate-phosphorylating)	h2o[c] + acmanap[c] + pep[c] -> pi[c] + acnamp[c]	0	94181.1	0	1000		Aminosugar Metabolism			
ACNAM9PL2	N-Acetylneuraminate 9-phosphate pyruvate-lyase (pyruvate-phosphorylating)	h2o[c] + pep[c] + man6p[c] -> pi[c] + kdnp[c]	0	94181.1	0	1000		Aminosugar Metabolism			
ACNAMPH	N-Acetylneuraminate 9-phosphate phosphohydrolase	h2o[c] + acnamp[c] -> pi[c] + acnam[c]	0		0	1000		Aminosugar Metabolism			
ACNAMlt	N-acetylneuraminate transport into lysososme	h[c] + acnam[c] <=> h[l] + acnam[l]	1	235504.1	-1000	1000		Transport, Lysosomal			
ACNAMtn	N-acetylneuraminate nuclear import	acnam[c] -> acnam[n]	0		0	1000		Transport, Nuclear			
ACNAMtr	N-acetylneuraminate export	acnam[c] -> acnam[e]	0		0	1000	2	Transport, Extracellular	PMID: 15123798, PMID: 18180286	This metabolite is found in mucus and can serve as carbon source for intestinal microbes. It is assumed it appears in mucus through secretion from goblet cells and from epithelial cell debris.	
ACNGALACGLCGAL14ACGLCGALGLUSIDEte	blood group intracellular transport	acngalacglcgal14acglcgalgluside_hs[e] <=> acngalacglcgal14acglcgalgluside_hs[c]	1		-1000	1000		Transport, Extracellular			
ACNGALACGLCGAL14ACGLCGALGLUSIDEtg	blood group intracellular transport	acngalacglcgal14acglcgalgluside_hs[g] <=> acngalacglcgal14acglcgalgluside_hs[c]	1		-1000	1000		Transport, Golgi Apparatus			
ACNMLr	N-Acetylneuraminate lyase (reversible)	acnam[c] <=> pyr[c] + acmana[c]	1		-1000	1000		Aminosugar Metabolism			
ACOAD10m	acyl-CoA dehydrogenase (2-methylbutanoyl-CoA), mitochondrial	2mbcoa[m] + fad[m] -> 2mb2coa[m] + fadh2[m]	0	11364.1 or 66885.1	0	1000		Valine, Leucine, and Isoleucine Metabolism			
ACOAD1fm	acyl-CoA dehydrogenase (butanoyl-CoA), mitochondrial	fad[m] + btcoa[m] -> b2coa[m] + fadh2[m]	0	102632.1 or 66948.1 or 11364.1 or 66885.1 or 11409.1 or 71985.1 or 229211.1	0	1000		Butanoate Metabolism			
ACOAD8m	acyl-CoA dehydrogenase (isovaleryl-CoA), mitochondrial	fad[m] + ivcoa[m] -> fadh2[m] + 3mb2coa[m]	0	56357.1	0	1000		Valine, Leucine, and Isoleucine Metabolism			
ACOAD9m	acyl-CoA dehydrogenase (isobutyryl-CoA), mitochondrial	fad[m] + ibcoa[m] -> fadh2[m] + 2mp2coa[m]	0	66948.1 or 11364.1	0	1000		Valine, Leucine, and Isoleucine Metabolism			
ACOAHi	acetyl-CoA hydrolase	h2o[c] + accoa[c] -> h[c] + coa[c] + ac[c]	0	74156.1	0	1000		Pyruvate Metabolism			
ACOAO7p	acyl-CoA oxidase (hexadecanoyl-CoA), peroxisomal	pmtcoa[x] + o2[x] -> h2o2[x] + hdd2coa[x]	0	11430.1 or 11430.2	0	1000		Fatty Acid Metabolism			
ACOATA	Acetyl-CoA ACP transacylase	accoa[c] + ACP[c] <=> coa[c] + acACP[c]	1	14104.1	-1000	1000		Fatty Acid Metabolism			
ACODA	acetylornithine deacetylase	h2o[c] + acorn[c] -> ac[c] + orn[c]	0	109652.1	0	1000		Urea cycle/amino group metabolism			
ACONT	aconitase	cit[c] <=> icit[c]	1	11428.1 or 64602.1	-1000	1000		Citric Acid Cycle			
ACONTm	Aconitate hydratase	cit[m] <=> icit[m]	1	11429.1	-1000	1000		Citric Acid Cycle			
ACOX22x	acyl-Coenzyme A oxidase 2, branched chain	0.5 o2[x] + dhcholoylcoa[x] + fadh2[x] -> fad[x] + thcholoylcoa[x]	0	93732.1	0	1000		Bile Acid Biosynthesis			
ACOX2x	acyl-Coenzyme A oxidase 2, branched chain	o2[x] + fadh2[x] + cholcoas[x] -> fad[x] + cholcoads[x] + 2 h2o[x]	0	212647.1 or 212647.2	0	1000	0	Bile Acid Biosynthesis			
ACP1_FMN	acid phosphatase (FMN)	h2o[c] + fmn[c] -> pi[c] + ribflv[c]	0	11431.1 or 11431.2 or 11431.3	0	1000	2	Riboflavin Metabolism			
ACRNtm	O-acetylcarnintine transport into mitochondria via diffusion	acrn[c] -> acrn[m]	0	57279.1	0	1000		Transport, Mitochondrial			
ACS	acetyl-CoA synthetase	atp[c] + coa[c] + ac[c] -> amp[c] + ppi[c] + accoa[c]	0	60525.1 or 78894.1 or 60525.2	0	1000		Glycolysis/Gluconeogenesis			
ACS2	acetyl-CoA synthase (propionate)	atp[c] + coa[c] + ppa[c] -> amp[c] + ppi[c] + ppcoa[c]	0	60525.1 or 78894.1 or 60525.2	0	1000		Propanoate Metabolism			
ACSm	acetyl-CoA synthetase	coa[m] + atp[m] + ac[m] -> accoa[m] + amp[m] + ppi[m]	0	68738.1	0	1000		Glycolysis/Gluconeogenesis			
ACTLMO	acetol monooxygenase	o2[c] + h[c] + nadph[c] + acetol[c] -> 2 h2o[c] + nadp[c] + mthgxl[c]	0	13106.1	0	1000		Pyruvate Metabolism			
ACTNMO	acetone monooxygenase	o2[c] + h[c] + nadph[c] + acetone[c] -> h2o[c] + nadp[c] + acetol[c]	0	13106.1	0	1000		Pyruvate Metabolism			
ACYP	acylphosphatase	h2o[c] + 13dpg[c] -> h[c] + pi[c] + 3pg[c]	0	69519.1 or 66204.1 or 66204.2 or 75572.1	0	1000		Glycolysis/Gluconeogenesis			
ACt2m	acetate mitochondrial transport via proton symport	h[c] + ac[c] <=> h[m] + ac[m]	1		-1000	1000		Transport, Mitochondrial			
ACt2r	acetate reversible transport via proton symport	h[e] + ac[e] <=> h[c] + ac[c]	1		-1000	1000		Transport, Extracellular			
ACtg	acetate transport, Golgi apparatus	ac[c] <=> ac[g]	1		-1000	1000		Transport, Golgi Apparatus			
ADA	Adenosine deaminase	h2o[c] + h[c] + adn[c] -> nh4[c] + ins[c]	0	11486.1	0	1000		Purine Catabolism			
ADAe	Adenosine deaminase, extracellular	h[e] + h2o[e] + adn[e] -> ins[e] + nh4[e]	0	11486.1	0	1000		Nucleotides			
ADCim	Acetoacetate decarboxylation (irreversible), mitochondrial	h[m] + acac[m] -> co2[m] + acetone[m]	0		0	1000		Propanoate Metabolism			
ADEt	adenine reversible transport, cytosol	ade[e] <=> ade[c]	1	13340.1	-1000	1000		Transport, Extracellular			
ADEtl	adenine facilated transport from lysosome	ade[l] <=> ade[c]	1	71279.1	-1000	1000		Transport, Lysosomal			
ADHAPtx	intracellular transport (peroxisome)	adhap_hs[c] <=> adhap_hs[x]	1		-1000	1000		Transport, Peroxisomal			
ADK1	adenylate kinase	atp[c] + amp[c] <=> 2 adp[c]	1	11636.1 or 229949.1 or 229949.2 or 78801.1	-1000	1000		Nucleotides			
ADK3	adentylate kinase (GTP)	amp[c] + gtp[c] <=> adp[c] + gdp[c]	1	229949.1 or 229949.2	-1000	1000		Nucleotides			
ADK3m	adentylate kinase (GTP)	amp[m] + gtp[m] <=> adp[m] + gdp[m]	1	56248.1	-1000	1000		Nucleotides			
ADKd	adenylate kinase (d form)	damp[c] + datp[c] <=> 2 dadp[c]	1	229949.1 or 229949.2	-1000	1000		Nucleotides			
ADMDC	adenosylmethionine decarboxylase	h[c] + amet[c] -> co2[c] + ametam[c]	0	11702.1	0	1000		Arginine and Proline Metabolism			

ADNCYC	adenylate cyclase	atp[c] -> ppi[c] + camp[c]	0	224129.1 or 11515.1 or 432530.1 or 11512.1 or 104311.1 or 1043.10.1 or 271639.1 or 11512.2 or 11513.1 or 11514.1 or 271639.1 or 210044.1	0	1000		Nucleotides			
ADNK1	adenosine kinase	atp[c] + ado[c] -> adp[c] + h[c] + amp[c]	0	11534.1 or 11534.2	0	1000		Nucleotides			
ADNK1m	adenosine kinase, mitochondrial	atp[m] + ado[m] -> h[m] + adp[m] + amp[m]	0		0	1000		Nucleotides			
ADN6	adenosine facilated transport in cytosol	ado[e] <=> ado[c]	1	13340.1 or 63959.1	-1000	1000		Transport, Extracellular			
ADN4	adenosine transport (Na/Ado cotransport)	na1[e] + ado[e] -> na1[c] + ado[c]	0	114304.1 or 454203.1 or 454203.2 or 269346.1	0	1000		Transport, Extracellular			
ADN5	adenosine transport (1:2 Na/Ado cotransport)	2 na1[e] + ado[e] -> 2 na1[c] + ado[c]	0	114304.1	0	1000		Transport, Extracellular			
ADN6l	adenosine facilated transport from lysosome	ado[l] <=> ado[c]	1	71279.1	-1000	1000		Transport, Lysosomal			
ADN6m	adenosine facilated transport in mitochondria	ado[c] <=> ado[m]	1	63959.1	-1000	1000		Transport, Mitochondrial			
ADPGLC	ADPglucose diphosphatase	h2o[c] + adpglc[c] -> 2 h[c] + amp[c] + g1p[c]	0	53893.1	0	1000		Nucleotides			
ADPMAN	ADPmannose diphosphatase	h2o[c] + adpman[c] -> 2 h[c] + amp[c] + man1p[c]	0	53893.1	0	1000		Nucleotides			
ADPRDP	ADPribose diphosphatase	h2o[c] + adprib[c] -> 2 h[c] + amp[c] + r5p[c]	0	53893.1	0	1000		Nucleotides			
ADPRDPm	ADPribose diphosphatase (mitochondrial)	h2o[m] + adprib[m] -> 2 h[m] + amp[m] + r5p[m]	0	74167.1 or 74167.2 or 74167.3	0	1000		Nucleotides			
ADPRIBTe	ADPribose transport	adprib[e] -> adprib[c]	0	12494.1	0	1000		Transport, Extracellular			
ADPT	adenine phosphoribosyltransferase	ade[c] + prpp[c] -> amp[c] + ppi[c]	0	11821.1	0	1000		Salvage Pathway			
ADPtx	ADP transporter, peroxisomal	adp[c] <=> adp[x]	1		-1000	1000		Transport, Peroxisomal			
ADRNCOAtx	fatty acid intracellular transport	adrncoa[c] <=> adrncoa[x]	1		-1000	1000		Transport, Peroxisomal			
ADRNCPT1	carnitine O-palmitoyltransferase	adrncoa[c] + crn[c] -> coa[c] + adrncrn[c]	0	12895.4 or 12894.1 or 78670.1 or 12895.2 or 12895.3 or 12895.1	0	1000		Carnitine shuttle			
ADRNCPT2	carnitine transferase	coa[m] + adrncrn[m] -> adrncoa[m] + crn[m]	0	12896.1	0	1000		Carnitine shuttle			
ADRNCRNt	transport into the mitochondria (carnitine)	adrncrn[c] -> adrncrn[m]	0	57279.1	0	1000		Carnitine shuttle			
ADRNLPVESSEC	Adrenaline secretion via secretory vesicle (ATP driven)	2 h2o[c] + 2 atp[c] + 3 adrnl[c] -> 2 adp[c] + 2 h[c] + 2 pi[c] + 3 adrnlp[e]	0	214084.1 or 110877.1	0	1000		Transport, Extracellular			
ADRNt	fatty acid transport via diffusion	adrn[e] <=> adrn[c]	1		-1000	1000		Transport, Extracellular			
ADSELK	adenylyl-sulfate kinase	atp[c] + aps[c] -> adp[c] + h[c] + paps[c]	0	23972.1 or 23971.1	0	1000		Selenoamino acid metabolism			
ADSK	adenylyl-sulfate kinase	atp[c] + aps[c] -> adp[c] + h[c] + paps[c]	0	23972.1 or 23971.1	0	1000		Nucleotides			
ADSL1	adenylosuccinate lyase	4saspc[c] -> amp[c] + fum[c]	0	11564.1 or 11564.2	0	1000		Nucleotides			
ADSL2	adenylosuccinate lyase	25aics[c] -> fum[c] + aicar[c]	0	11564.1 or 11564.2	0	1000		IMP Biosynthesis			
ADSS	adenylosuccinate synthase	asp-L[c] + gtp[c] + imp[c] -> 2 h[c] + pi[c] + gdp[c] + dcsamp[c]	0	11565.1 or 11565.2 or 11566.1	0	1000		Nucleotides			
AFLATOXINte	xenobiotic transport	aflatoxin[e] <=> aflatoxin[c]	1		-1000	1000		Transport, Extracellular			
AG13T10g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	uacgam[g] + ksi_prot18[g] -> h[g] + udp[g] + ksi_prot19[g]	0	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	0	1000		Keratan sulfate biosynthesis			
AG13T11g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	uacgam[g] + ksi_prot21[g] -> h[g] + udp[g] + ksi_prot22[g]	0	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	0	1000		Keratan sulfate biosynthesis			
AG13T12g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	uacgam[g] + ksi_prot24[g] -> h[g] + udp[g] + ksi_prot25[g]	0	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	0	1000		Keratan sulfate biosynthesis			
AG13T13g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	uacgam[g] + ksi_prot27[g] -> h[g] + udp[g] + ksi_prot28[g]	0	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	0	1000		Keratan sulfate biosynthesis			
AG13T14g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	uacgam[g] + ksi_prot30[g] -> h[g] + udp[g] + ksi_prot31[g]	0	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	0	1000		Keratan sulfate biosynthesis			
AG13T15g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	uacgam[g] + ksi_prot33[g] -> h[g] + udp[g] + ksi_prot34[g]	0	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	0	1000		Keratan sulfate biosynthesis			
AG13T16g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	uacgam[g] + ksi_core4_prot2[g] -> h[g] + udp[g] + ksi_core4_prot3[g]	0	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	0	1000		Keratan sulfate biosynthesis			
AG13T17g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	uacgam[g] + ksi_core4_prot4[g] -> h[g] + udp[g] + ksi_core4_prot5[g]	0	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	0	1000		Keratan sulfate biosynthesis			
AG13T18g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	uacgam[g] + ksi_core4_prot7[g] -> h[g] + udp[g] + ksi_core4_prot8[g]	0	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	0	1000		Keratan sulfate biosynthesis			
AG13T1g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	uacgam[g] + ksi_core2_prot2[g] -> h[g] + udp[g] + ksi_core2_prot3[g]	0	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	0	1000		Keratan sulfate biosynthesis			
AG13T2g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	uacgam[g] + ksi_core2_prot4[g] -> h[g] + udp[g] + ksi_core2_prot5[g]	0	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	0	1000		Keratan sulfate biosynthesis			
AG13T3g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	uacgam[g] + ksi_core2_prot7[g] -> h[g] + udp[g] + ksi_core2_prot8[g]	0	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	0	1000		Keratan sulfate biosynthesis			
AG13T4g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	uacgam[g] + ksi_prot1[g] -> h[g] + udp[g] + ksi_prot2[g]	0	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	0	1000		Keratan sulfate biosynthesis			
AG13T5g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	uacgam[g] + ksi_prot3[g] -> h[g] + udp[g] + ksi_prot4[g]	0	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	0	1000		Keratan sulfate biosynthesis			
AG13T6g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	uacgam[g] + ksi_prot6[g] -> h[g] + udp[g] + ksi_prot7[g]	0	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	0	1000		Keratan sulfate biosynthesis			
AG13T7g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	uacgam[g] + ksi_prot9[g] -> h[g] + udp[g] + ksi_prot10[g]	0	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	0	1000		Keratan sulfate biosynthesis			
AG13T8g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	uacgam[g] + ksi_prot12[g] -> h[g] + udp[g] + ksi_prot13[g]	0	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	0	1000		Keratan sulfate biosynthesis			

AG13T9g	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase, Golgi apparatus	uacgam[g] + ksi_pre15[g] -> h[g] + udp[g] + ksi_pre16[g]	0	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	0	1000		Keratan sulfate biosynthesis			
AGDC	N-acetylglucosamine-6-phosphate deacetylase	h2o[c] + acgam6p[c] -> gam6p[c] + ac[c]	0	245847.1	0	1000		Aminosugar Metabolism			
AGLPC	alkyl acylglycerol phosphocholine transferase	ak2g_hs[c] + cdpchol[c] -> h2o[c] + h[c] + ak2gchol_hs[c] + cmp[c]	0		0	1000		Glycerophospholipid Metabolism			
AGLPED	alkyl acyl glycerophosphoethanolamine desaturase	o2[c] + h[c] + nadph[c] + ak2gpe_hs[c] -> 2 h2o[c] + nadp[c] + dak2gpe_hs[c]	0		0	1000		Glycerophospholipid Metabolism			
AGLPET	alkyl acylglycerol phosphoethanolamine transferase	h[c] + ak2g_hs[c] + cdpea[c] -> h2o[c] + cmp[c] + ak2gpe_hs[c]	0		0	1000		Glycerophospholipid Metabolism			
AGLPH	alkyl glycerol phosphate hydrolase	h2o[c] + ak2gp_hs[c] -> pi[c] + ak2g_hs[c]	0		0	1000		Glycerophospholipid Metabolism			
AGLPR	alkyl glycerol phosphate reductase	h[c] + nadph[c] + akdhap_hs[c] -> nadp[c] + akgp_hs[c]	0		0	1000		Glycerophospholipid Metabolism			
AGLPT	alkyl glycerol phosphate acyltransferase	h[c] + akgp_hs[c] + Rtotal2[c] -> h2o[c] + ak2gp_hs[c]	0		0	1000		Glycerophospholipid Metabolism			
AGMTm	agmatinase (m)	h2o[m] + agm[m] -> ptrc[m] + urea[m]	0	75986.1	0	1000		Arginine and Proline Metabolism			
AGPAT1	1-acylglycerol-3-phosphate O-acyltransferase 1	Rtotal2coa[c] + alpa_hs[c] -> coa[c] + pa_hs[c]	0	52123.1 or 28169.1 or 28169.2 or 55979.1 or 67512.1 or 68262.1 or 102247.1	0	1000		Triacylglycerol Synthesis			
AGPRim	N-acetyl-g-glutamyl-phosphate reductase, irreversible, mitochondrial	h[m] + nadph[m] + acg5p[m] -> nadp[m] + pi[m] + acg5sa[m]	0	56454.1	0	1000		Urea cycle/amino group metabolism			
AGPSx	alkylglycerone phosphate synthase	adhap_hs[x] + alkylR1oh[x] -> h[x] + Rtotal[x] + akdhap_hs[x]	0	228061.1	0	1000		Glycerophospholipid Metabolism			
AGPex	alkyl glycerol phosphate transport	akdhap_hs[c] <=> akdhap_hs[x]	1		-1000	1000		Transport, Peroxisomal			
AGTim	alanine-glyoxylate transaminase (irreversible), mitochondrial	ala-L[m] + glx[m] -> pyr[m] + gly[m]	0	268782.1 or 71760.1	0	1000		Alanine and Aspartate Metabolism			
AGTix	alanine-glyoxylate transaminase (irreversible), (peroxisomal)	ala-L[x] + glx[x] -> gly[x] + pyr[x]	0	11611.1	0	1000		Alanine and Aspartate Metabolism			
AHANDROSTANGLCte	glucuronidated compound transport	h2o[c] + atp[c] + ahandrostanglc[c] -> adp[c] + h[c] + pi[c] + ahandrostanglc[e]	0	17250.1	0	1000		Transport, Extracellular			
AHANDROSTANGLCtr	glucuronidated compound transport	ahandrostanglc[c] <=> ahandrostanglc[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
AHC	adenosylhomocysteinase	h2o[c] + ahcys[c] <=> adn[c] + hcys-L[c]	1	229709.1 or 229709.2 or 269378.1	-1000	1000		Methionine Metabolism			
AHCYStn	S-adenosyl-L-homocysteine nuclear transport	ahcys[c] <=> ahcys[n]	1		-1000	1000		Transport, Nuclear			
AHCYStr	S-Adenosyl-L-homocysteine intracellular diffusion	ahcys[c] <=> ahcys[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
AHEXASE2ly	beta-N-acetylhexosaminidase, lysosomal	3 h2o[l] + n2m2nmn[l] -> 3 acgam[l] + m2mn[l]	0	(15211.1 or 15212.1 or (15212.1 and 15211.1))	0	1000		N-Glycan Degradation			
AHEXASEly	beta-N-acetylhexosaminidase, lysosomal	2 h2o[l] + n2m2mn[l] -> 2 acgam[l] + m2mn[l]	0	(15211.1 or 15212.1 or (15212.1 and 15211.1))	0	1000		N-Glycan Degradation			
AICART	phosphoribosylaminoimidazolecarboxamide formyltransferase	10fthf[c] + aicar[c] <=> fprica[c] + thf[c]	1	108147.1	-1000	1000		IMP Biosynthesis			
AIRCr	phosphoribosylaminoimidazole carboxylase	co2[c] + air[c] <=> h[c] + 5aizc[c]	1	67054.1	-1000	1000		IMP Biosynthesis			
AK2LGCHOLt	1 alkyl 2 lysoglycerol 3-phosphocholine (homo sapiens) transport	ak2lgchol_hs[e] <=> ak2lgchol_hs[c]	1		-1000	1000		Transport, Extracellular			
AKGDm	2-oxoglutarate dehydrogenase	akg[m] + coa[m] + nad[m] -> co2[m] + nadh[m] + succoa[m]	0	(78920.1 or 18293.1 or (27402.1 and 13382.1) or 18293.2)	0	1000		Citric Acid Cycle			
AKGMALtm	alpha-ketoglutarate/malate transporter	akg[m] + mal-L[c] <=> akg[c] + mal-L[m]	1	67863.1	-1000	1000		Transport, Mitochondrial			
AKGt4_3	AKG transport via sodium symport	3 na1[e] + akg[e] <=> akg[c] + 3 na1[c]	1	114644.1 or 114644.2	-1000	1000		Transport, Extracellular			
AKGtp	AKG transporter, peroxisome	akg[c] <=> akg[x]	1		-1000	1000		Transport, Peroxisomal			
AKR1C1	aldo-keto reductase family 1, member C1 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihydrodiol dehydrogenase 4)	h[c] + nadph[c] + prgstrn[c] -> nadp[c] + aprgstrn[c]	0	77337.1	0	1000		Steroid Metabolism			
AKR1C41	aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihydrodiol dehydrogenase 4)	h[c] + nadh[c] + xol7ah[c] -> nad[c] + xol7ah2[c]	0	83702.1	0	1000		Bile Acid Biosynthesis			
AKR1C42	aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihydrodiol dehydrogenase 4)	h[c] + nadh[c] + xoldioloneh[c] -> nad[c] + xoltriol[c]	0	83702.1	0	1000		Bile Acid Biosynthesis			
AKR1D	aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase)	h[c] + nadph[c] + xol7aone[c] -> nadp[c] + xol7ah[c]	0	208665.1	0	1000		Bile Acid Biosynthesis			
AKR1D2	aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase)	h[c] + nadph[c] + xoldiolone[c] -> nadp[c] + xoldioloneh[c]	0	208665.1	0	1000		Bile Acid Biosynthesis			
ALAALACNc	ALAALACNc	h2o[c] + alaala[c] <=> 2 ala-L[c]	1	(338403.1 or 66054.1)	-1000	1000	4	Dipeptide Degradation	PMID: 6993048, PMCID: PMC1412501, PMID: 4919261, PMID: 20178671, PMID: 12473676	Dipeptides and tripeptides enter the brush border of the intestinal mucosal cells, where they are hydrolyzed to free amino acids, which are then transported into hepatic portal vein. Peptides entering by transcellular or paracellular mechanisms elicit allergic reactions to food (Robert K. Murray, David A. Bender, Kathleen M. Botham, Peter J. kennelly, Victor W. Rodwell, P. Anthony Weil (2009) 28th edition, Harper's illustrated biochemistry,Mc Graw Hill, page 462). formation and hydrolysis of diglycine is a reversible process (David L. Nelson, Michael M. Cox, Lehniniger principles of biochemistry (2000), 3rd edition, worth publishers,page 69, figure 3a). CN1 is expressed in brain where as CN2 is more ubiquitously expressed (PMID: 12473676).	3.4.13.20 or 3.4.13.18
ALAALAPEPT1tc	transport of Alanylalanine by the apical PEPT1 amino acid transporters across the brush border cells of the enterocytes of the intestine and renal cells	alaala[u] + h[u] -> h[c] + alaala[c]	0	215335.1	0	1000	3	Transport, Lumen	PMID: 7858848, PMID: 14965252, PMID: 14977407, PMID: 10330047	PEPT1 appears to transport all di- and tri- peptides across the brush border of the intestinal cells (Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Advanced nutrition and human metabolism, Wadsworth cengage learning, 5th edition, page 193). PEPT1 is expressed highly in intestinal cells where as PEPT2 is localized to renal cells (PMID: 10330047).	
ALAASNNaEx	L-alanine/L-asparagine Na-dependent exchange (Ala-L in)	na1[e] + asn-L[c] + ala-L[e] -> na1[c] + ala-L[c] + asn-L[e]	0	20514.1	0	1000		Transport, Extracellular			
ALAATB0tc	transport of L-Alanine into the intestinal cells by ATB0 transporter	2 na1[u] + cl[u] + ala-L[u] -> 2 na1[c] + cl[c] + ala-L[c]	0	56774.1	0	1000	3	Transport, Lumen	PMID:18195088	ATB0 is both sodium and chloride coupled, with reaction stoichiometry 2Na+:1cl:1amino acid. The transporter is localted in the intestine, has a broad substrate specificity (both neutral and cationic amino acids), but is not involved in the transport of aspartate, glutamate and proline (PMID:18195088).	
ALACYSNaEx	L-alanine/L-cysteine Na-dependent exchange (Ala-L in)	na1[e] + ala-L[e] + cys-L[c] -> na1[c] + ala-L[c] + cys-L[e]	0	20514.1 or 55963.1	0	1000		Transport, Extracellular			
ALADGLNexR	L-alanine/glutamine reversible exchange	gln-L[c] + ala-D[e] <=> ala-D[c] + gln-L[e]	1	53896.1 or 17254.1	-1000	1000		Transport, Extracellular			
ALADGLYexR	D-alanine/glycine reversible exchange	ala-D[e] + gly[c] <=> ala-D[c] + gly[e]	1	53896.1 or 17254.1	-1000	1000		Transport, Extracellular			
ALADPATtc	transport of D-Alanine by the apical PAT2 or PAT1 amino acid transporters in kidney and intestine	h[u] + ala-D[u] -> h[c] + ala-D[c]	0	215335.1	0	1000	3	Transport, Lumen	PMID:18195088, PMID:18400692, PMID: 15345686, PMID: 17123464, PMCID: PMC34647	PAT2 is strongly expressed in heart and lung and more weakly in kidney and muscle (PMID:18400692). PAT2 doest not strongly discriminate between L and D isomers (PMID: 18400692). PAT1 proton-amino acid co-transporter with 1:1 stoichiometry, does not discriminate between L and D isomers, located on the apical membrane of kidney and intestine (PMID: 18400692, PMID: 18195088).	
ALAGLNNaEx	L-alanine/L-glutamine Na-dependent exchange (Ala-L in)	na1[e] + ala-L[e] + gln-L[c] -> na1[c] + ala-L[c] + gln-L[e]	0	20514.1	0	1000		Transport, Extracellular			
ALAGLNexR	L-alanine/glutamine reversible exchange	ala-L[e] + gln-L[c] <=> ala-L[c] + gln-L[e]	1	53896.1 or 17254.1	-1000	1000		Transport, Extracellular			
ALAGLYexR	L-alanine/glycine reversible exchange	ala-L[e] + gly[c] <=> ala-L[c] + gly[e]	1	53896.1 or 17254.1	-1000	1000		Transport, Extracellular			
ALAILELAT2tc	transport of L-Alanine into the cell and efflux of L-Isoleucine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	ala-L[e] + ile-L[c] -> ala-L[c] + ile-L[e]	0	(20539.1 and 17254.1)	0	1000	3	Transport, Lumen	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s00420000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	higher affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for traficking of the complex to the mebrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s00420000274).	
ALALPATtc	transport of L-Alanine by the apical PAT2 or PAT1 amino acid transporters in kidney and intestine	h[u] + ala-L[u] -> h[c] + ala-L[c]	0	215335.1	0	1000	3	Transport, Lumen	PMID:18195088, PMID:18400692, PMID: 17123464, PMCID: PMC34647, PMID: 15345686	PAT2 is strongly expressed in heart and lung and more weakly in kidney and muscle (PMID:18400692). PAT2 doest not strongly discriminate between L and D isomers (PMID: 18400692). PAT1 proton-amino acid co-transporter with 1:1 stoichiometry, does not discriminate between L and D isomers, located on the apical membrane of kidney and intestine (PMID: 18400692, PMID: 18195088).	
ALAPHELAT2tc	transport of L-Alanine into the cell and efflux of L-Phenylalanine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	ala-L[e] + phe-L[c] -> ala-L[c] + phe-L[e]	0	(20539.1 and 17254.1)	0	1000	3	Transport, Extracellular	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s00420000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	higher affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for traficking of the complex to the mebrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s00420000274).	
ALAR	alanine racemase	ala-L[c] <=> ala-D[c]	1	114863.1	-1000	1000		Alanine and Aspartate Metabolism			
ALASERNaEx	L-alanine/L-serine Na-dependent exchange (Ala-L in)	na1[e] + ala-L[e] + ser-L[c] -> na1[c] + ala-L[c] + ser-L[e]	0	20514.1 or 55963.1	0	1000		Transport, Extracellular			
ALASm	5-aminolevulinate synthase	h[m] + gly[m] + succoa[m] -> coa[m] + co2[m] + 5aop[m]	0	26912.1 or 11655.1 or 11656.1 or 11655.2	0	1000		Glycine, Serine, and Threonine Metabolism			
ALATA_L	L-alanine transaminase	akg[c] + ala-L[c] <=> pyr[c] + glu-L[c]	1	108682.1 or 76282.1	-1000	1000		Glutamate metabolism			
ALATHRNaEx	L-alanine/L-threonine Na-dependent exchange (Ala-L in)	na1[e] + ala-L[e] + thr-L[c] -> na1[c] + ala-L[c] + thr-L[e]	0	20514.1 or 55963.1	0	1000		Transport, Extracellular			
ALAt2r	L-alanine reversible transport via proton symport	h[e] + ala-L[e] <=> h[c] + ala-L[c]	1	215335.1	-1000	1000		Transport, Extracellular			
ALAt2rL	L-alanine reversible transport via proton symport (lysosome)	h[l] + ala-L[l] <=> h[c] + ala-L[c]	1	215335.1	-1000	1000		Transport, Lysosomal			
ALAt4	Alanine-Sodium symporter	na1[e] + ala-L[e] -> na1[c] + ala-L[c]	0	105727.1 or 67760.1 or 69354.1 or 56774.1 or 11989.1 or 11988.1 or 11987.1	0	1000		Transport, Extracellular			
ALAt4lu	transport of L-Alanine by the apical neutral amino acid transporters in kidney and intestine	na1[u] + ala-L[u] -> na1[c] + ala-L[c]	0	(70008.1 or (74338.1 and 57394.1))	0	1000	3	Transport, Lumen	PMID: 19472175, PMID: 15804236, PMID: 18400692	transports all the neutral amino acids with preference for methionine, leucine and valine. Reaction stoichiometry is 1:1. Requires heterodimerization with collectrin protein for increased affinity. Found in kidney and intestine, however also reported to be expressed in skin. Requires association with ACE2 for expression in intestine but with collectrin for expression in kidney.	3.4.17.23
ALAtN1	Alanine transport (Na, H coupled)	h[c] + 2 na1[e] + ala-L[e] <=> h[e] + 2 na1[c] + ala-L[c]	1	209837.1 or 76257.1	-1000	1000		Transport, Extracellular			
ALAyLATtc	transport of L-Alanine by y+LAT1 or y+LAT2 transporters in small intestine and kidney	na1[e] + ala-L[e] + arg-L[c] -> na1[c] + ala-L[c] + arg-L[e]	0	(20540.1 or (330836.1 and 17254.1))	0	1000	3	Transport, Extracellular	PMID: 11546643, PMID:18195088	y+LAT1 and y+LAT2 transporters requires CD98 for sequesterization to the plasma membrane. Acts as an amino acid exchanger, with influx of neutral aminoa acids and efflux of cationic amino acid, requires Na+ for optimal activity. Can also operate with H+ in absence of Na+ (PMID: 11546643).	
ALAyLATthc	transport of Alanine by y+LAT1 or y+LAT2 with co-transporter of h in small intestine and kidney	h[e] + ala-L[e] + arg-L[c] -> h[c] + ala-L[c] + arg-L[e]	0	(20540.1 or (330836.1 and 17254.1))	0	1000	3	Transport, Extracellular	PMID: 11546643, PMID:18195088	y+LAT1 and y+LAT2 transporters requires CD98 for sequesterization to the plasma membrane. Acts as an amino acid exchanger, with influx of neutral aminoa acids and efflux of cationic amino acid, requires Na+ for optimal activity. Can also operate with H+ in absence of Na+ (PMID: 11546643).	

ALCD2ey	alcohol dehydrogenase (ethanol, NADP), forward reaction	nadp[c] + etoh[c] -> h[c] + nadph[c] + acald[c]	0	58810.1 or 58810.2	0	1000		Glycolysis/Gluconeogenesis			
ALDD19x	aldehyde dehydrogenase (phenylacetaldehyde, NAD)	h2o[c] + nad[c] + pacald[c] -> 2 h[c] + nadh[c] + pac[c]	0	11670.1 or 67689.1 or 56847.1	0	1000		Phenylalanine metabolism			
ALDD19x(P)	aldehyde dehydrogenase (phenylacetaldehyde, NADP)	h2o[c] + nadp[c] + pacald[c] -> 2 h[c] + nadph[c] + pac[c]	0	11670.1 or 67689.1 or 56847.1	0	1000		Phenylalanine metabolism			
ALDD20x	aldehyde dehydrogenase (indole-3-acetaldehyde, NAD)	h2o[c] + nad[c] + id3acald[c] -> 2 h[c] + nadh[c] + indlac[c]	0	19378.1 or 56752.1 or 110695.1 or 11668.1 or 11671.1 or 19378.2 or 19378.3	0	1000		Tryptophan metabolism			
ALDD20xm	aldehyde dehydrogenase (indole-3-acetaldehyde, NAD), mitochondrial	h2o[m] + nad[m] + id3acald[m] -> 2 h[m] + nadh[m] + indlac[m]	0	212647.1 or 11669.1 or 212647.2 or 72535.1	0	1000		Tryptophan metabolism			
ALDD21	aldehyde dehydrogenase (prixanal, NAD)	h2o[c] + nad[c] + prixanal[c] -> 2 h[c] + nadh[c] + peta[c]	0	11671.1	0	1000		Fatty Acid Metabolism			
ALDD2x	aldehyde dehydrogenase (acetaldehyde, NAD)	h2o[c] + nad[c] + acald[c] -> 2 h[c] + nadh[c] + ac[c]	0	19378.1 or 56752.1 or 11670.1 or 110695.1 or 67689.1 or 56847.1 or 11668.1 or 11671.1 or 19378.2 or 19378.3	0	1000		Glycolysis/Gluconeogenesis			
ALDD2xm	aldehyde dehydrogenase (acetylaldehyde, NAD), mitochondrial	h2o[m] + nad[m] + acald[m] -> 2 h[m] + nadh[m] + ac[m]	0	11669.1 or 72535.1	0	1000		Glycolysis/Gluconeogenesis			
ALDD2y	aldehyde dehydrogenase (acetaldehyde, NADP)	h2o[c] + nadp[c] + acald[c] -> 2 h[c] + nadph[c] + ac[c]	0	19378.1 or 56752.1 or 11670.1 or 67689.1 or 11671.1 or 19378.2 or 19378.3	0	1000		Glycolysis/Gluconeogenesis			
ALDSTRNte	aldosterone transport	aldstr[c] <=> aldstr[e]	1		-1000	1000		Transport, Extracellular			
ALDSTRNtm	aldosterone intracellular transport	aldstr[c] <=> aldstr[m]	1		-1000	1000		Transport, Mitochondrial			
ALINOFABPpmtc	uptake of alpha-Linolenic acid by the enterocytes	lnlnca[u] -> lnlnca[c]	0	(14719.1 or 12491.1)	0	1000	3	Transport, Lumen	PMID: 20086080, PMID: 10617989, PMID: 8717442, Progress in Lipid Research Volume 48, Issue 2, March 2009, Pages 101-115	GOT2 encodes FABPpm that may either act alone or in co-ordination with CD36, for the uptake of long chain fatty acids (exhibits a selective preference for long chain PUFA and essential fatty acids over non-essential fatty acids). The fatty acids alternatively can undergo passive diffusion. once inside the cell, they bind to the cytoplasmic fatty acid binding protein (FABPc) and thereby undergo activation or esterification. Additionally, a minority of fatty acids are thought to be transported by FATP1 and rapidly activated by plasma membrane acyl-CoA synthetase (ACS1) to form acyl-Co esters. (PMID: 20086080)	
ALKP	alkaline phosphatase	h2o[c] + dhap[c] -> pi[c] + dha[c]	0	11647.1 or 11650.1 or 76768.1	0	1000		Glycerophospholipid Metabolism			
ALOX12	Arachidonate 12-lipoxygenase	o2[c] + arachd[c] -> 12HPETc[c]	0	11684.1	0	1000		Eicosanoid Metabolism			
ALOX12R	Arachidonate 12-lipoxygenase R	o2[c] + arachd[c] -> 12HPETc[c]	0	11686.1	0	1000		Eicosanoid Metabolism			
ALOX15	Arachidonate 15-lipoxygenase	o2[c] + arachd[c] -> 15HPETc[c]	0	11687.1 or 11688.1	0	1000		Eicosanoid Metabolism			
ALOX5	Arachidonate 5-lipoxygenase	o2[c] + arachd[c] -> 5HPETc[c]	0	11689.1	0	1000		Eicosanoid Metabolism			
ALOX52	Arachidonate 5-lipoxygenase	5HPETc[c] -> h2o[c] + leuke5o[c]	0	11689.1	0	1000		Eicosanoid Metabolism			
ALR	Aldose reductase	h2o[c] + nadp[c] + mthgxl[c] -> 2 h[c] + pyr[c] + nadph[c]	0	11677.1	0	1000		Glycine, Serine, and Threonine Metabolism			
ALR2	Aldose reductase (NAD)	h[c] + nadph[c] + mthgxl[c] -> nadp[c] + acetol[c]	0	110198.1 or 58810.2 or 11677.1 or 58810.1	0	1000		Pyruvate Metabolism			
ALR3	aldose reductase (acetol)	h[c] + nadph[c] + acetol[c] -> nadp[c] + 12ppd-S[c]	0	110198.1 or 58810.2 or 11677.1 or 58810.1	0	1000		Pyruvate Metabolism			
AMHSAD	aminomuconate-semialdehyde dehydrogenase	h2o[c] + nad[c] + amfsal[c] -> 2 h[c] + nadh[c] + amuco[c]	0		0	1000		Tryptophan metabolism			
AMACR2p	alpha-methylacyl-CoA racemase (reductase)	0.5 o2[x] + dhcholestancoa[x] -> dhcholoxycoa[x] + h2o[x]	0	17117.1 or 17117.2	0	1000		Bile Acid Biosynthesis			
AMACR2r	alpha-methylacyl-CoA racemase (reductase)	dhcholestancoa[r] + 0.5 o2[r] -> dhcholoxycoa[r] + h2o[r]	0	17117.1 or 17117.2	0	1000		Bile Acid Biosynthesis			
AMACRp	alpha-methylacyl-CoA racemase	cholcoas[x] -> cholcoas[x]	0	17117.1 or 17117.2	0	1000		Bile Acid Biosynthesis			
AMACRr	alpha-methylacyl-CoA racemase	cholcoas[r] -> cholcoas[r]	0	17117.1 or 17117.2	0	1000		Bile Acid Biosynthesis			
AMANK	N-acetyl-D-mannosamine kinase	atp[c] + acmanas[c] -> adp[c] + h[c] + acmanap[c]	0	50798.1 or 56174.1	0	1000		Aminosugar Metabolism			
AMCOXO	2-aminomuconate reductase	h2o[c] + h[c] + nadph[c] + amuco[c] -> nh4[c] + nadp[c] + 2oxoadp[c]	0		0	1000		Tryptophan metabolism			
AMETr	S-Adenosyl-L-methionine intracellular diffusion	amet[c] <=> amet[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
AMETt2m	S-Adenosyl-L-methionine reversible transport, mitochondrial	amet[c] + ahcys[m] <=> ahcys[c] + amet[m]	1	67582.1 or 67582.2 or 67582.3	-1000	1000		Transport, Mitochondrial			
AMETtn	S-adenosyl-L-methionine nuclear transport	amet[c] <=> amet[n]	1		-1000	1000		Transport, Nuclear			
AMPDA	Adenosine monophosphate deaminase	h2o[c] + h[c] + amp[c] -> nh4[c] + imp[c]	0	109674.1 or 11717.1 or 109674.2 or 229665.1 or 109674.3	0	1000		Nucleotides			
AMPTASECG	alanyl aminopeptidase (cys-gly)	h2o[c] + cgly[c] -> cys-L[c] + gly[c]	0	16790.1	0	1000		Glutathione Metabolism			
AMPTASECGe	alanyl aminopeptidase (cys-gly) (e)	h2o[e] + cgly[e] -> cys-L[e] + gly[e]	0	16790.1	0	1000		Glutathione Metabolism			
AMPtp	AMP transporter, peroxisome	amp[c] <=> amp[x]	1		-1000	1000		Transport, Peroxisomal			
AMPtr	AMP transporter, endoplasmic reticulum	amp[c] <=> amp[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
AMY1e	alpha-amylase, extracellular (strch1 -> strch2)	8 h2o[e] + strch1[e] -> 8 glc-D[e] + strch2[e]	0	100043684.1 or 20532.1 and 30962.1 or 17254.1 or 11722.1 or 100043684.2	0	1000		Starch and Sucrose Metabolism			
AMY2e	alpha-amylase, extracellular (glygn2 -> glygn4)	8 h2o[e] + glygn2[e] -> 8 glc-D[e] + glygn4[e]	0	100043684.1 or 20532.1 and 30962.1 or 17254.1 or 11722.1 or 100043684.2	0	1000		Starch and Sucrose Metabolism			
ANDRSTRNGLCte	glucuronidated compound transport	h2o[c] + atp[c] + androstrngls[c] -> adp[c] + h[c] + pi[c] + androstrngls[e]	0	17250.1	0	1000		Transport, Extracellular			
ANDRSTRNGLCtr	glucuronidated compound transport	androstrngls[c] <=> androstrngls[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
ANDRSTRNte	androsterone transport	androstr[c] <=> androstr[e]	1		-1000	1000		Transport, Extracellular			
ANDRSTRNtr	androsterone intracellular transport	androstr[c] <=> androstr[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
ANTIPYRENEte	xenobiotic transport	antipyrene[e] <=> antipyrene[c]	1		-1000	1000		Transport, Extracellular			
AOBUTDsm	L-2-amino-3-oxobutanoate decarboxylation, mitochondrial (spontaneous)	h[m] + 2aobut[m] -> co2[m] + aact[m]	0		0	1000		Glycine, Serine, and Threonine Metabolism			
AP4AH1	Ap4A hydrolase, asymmetrically	h2o[c] + ap4a[c] -> atp[c] + 2 h[c] + amp[c]	0	66401.1 or 66401.2 or 66401.3	0	1000		Nucleotides			
APAT2rm	3-Aminopropanoate:2-oxoglutarate aminotransferase (m)	akg[m] + ala-B[m] <=> glu-L[m] + msa[m]	1	268860.2 or 268869.1	-1000	1000		beta-Alanine metabolism			
APNNO2te	xenobiotic transport	apnno2[e] <=> apnno2[c]	1		-1000	1000		Transport, Extracellular			
APOCF	Apocarboxylase formation	apoC-L[c] + lys-L[c] -> h2o[c] + h[c] + apoC-Lys[c]	0		0	1000		Biotin Metabolism			
APOCFm	Apocarboxylase formation, mitochondrial	apoC-L[m] + lys-L[m] -> h[m] + h2o[m] + apoC-Lys[m]	0		0	1000		Biotin Metabolism			
APOC_LYS_BTNP	proteolysis of apoC-Lys-btn	h2o[c] + apoC-Lys_btn[c] -> apoC-L[c] + biocy[c]	0		0	1000		Biotin Metabolism			
APOC_LYS_BTNPm	proteolysis of apoC-Lys-btn, mitochondrial	h2o[m] + apoC-Lys_btn[m] -> apoC-L[m] + biocy[m]	0		0	1000		Biotin Metabolism			
APPNNte	xenobiotic transport	appnn[e] <=> appnn[c]	1		-1000	1000		Transport, Extracellular			
APRGSTRNte	hydroxyprogesterone transport	aprgstrn[e] <=> aprgstrn[c]	1		-1000	1000		Transport, Extracellular			
APRTO2	N-acetylputrescine: oxygen oxireductase (deaminating)	h2o[c] + o2[c] + aprut[c] -> h2o2[c] + nh4[c] + 4nhutn[c]	0	109731.1 or 17161.1	0	1000		Arginine and Proline Metabolism			
AQCOBALt	Aquacobl(III)alamin uptake	aqcobal[c] -> aqcobal[c]	0		0	1000		Transport, Extracellular			
ARABR	arabinose reductase	h[c] + nadph[c] + arab-L[c] -> nadp[c] + abt[c]	0	110198.1 or 58810.2 or 11677.1 or 58810.1	0	1000		Pentose and Glucuronate Interconversions			
ARAB_Lt	L-arabinose extracellular transport	arab-L[e] <=> arab-L[c]	1		-1000	1000		Transport, Extracellular			
ARACHCOAtx	fatty acid intracellular transport	arachcoa[c] <=> arachcoa[x]	1		-1000	1000		Transport, Peroxisomal			
ARACHCPT1	carnitine transferase	crn[c] + arachcoa[c] -> coa[c] + arachcrn[c]	0	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	0	1000		Carnitine shuttle			
ARACHCPT2	carnitine transferase	coa[m] + arachcrn[m] -> crn[m] + arachcoa[m]	0	12896.1	0	1000		Carnitine shuttle			
ARACHCRNt	transport into the mitochondria (carnitine)	arachcrn[c] -> arachcrn[m]	0	57279.1	0	1000		Carnitine shuttle			
ARACHICOAtx	fatty acid intracellular transport	arachicoa[c] <=> arachicoa[x]	1		-1000	1000		Transport, Peroxisomal			
ARACHIDt2	fatty acid transport via diffusion	arachd[e] <=> arachd[c]	1		-1000	1000		Transport, Extracellular			
ARACHIDte	intracellular transport	arachd[c] <=> arachd[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
ARACHFABPpmtc	uptake of arachidonic acid by the enterocytes	arachd[u] -> arachd[c]	0	(14719.1 or 12491.1)	0	1000	3	Transport, Lumen	PMID: 20086080, PMID: 10617989, PMID: 8717442, Progress in Lipid Research Volume 48, Issue 2, March 2009, Pages 101-115	GOT2 encodes FABPpm that may either act alone or in co-ordination with CD36, for the uptake of long chain fatty acids (exhibits a selective preference for long chain PUFA and essential fatty acids over non-essential fatty acids). The fatty acids alternatively can undergo passive diffusion. once inside the cell, they bind to the cytoplasmic fatty acid binding protein (FABPc) and thereby undergo activation or esterification. Additionally, a minority of fatty acids are thought to be transported by FATP1 and rapidly activated by plasma membrane acyl-CoA synthetase (ACS1) to form acyl-Co esters. (PMID: 20086080)	
ARACHt	fatty acid transport via diffusion	arachd[e] <=> arachd[c]	1		-1000	1000		Transport, Extracellular			
ARGALArBATIc	transport of L-Arginine into the cell in exchange for L-Alanine by b0,+AT transporter at the apical surfaces of the membranes of small intestine and renal cells.	ala-L[c] + arg-L[u] -> ala-L[u] + arg-L[c]	0	(30962.1 and 20532.1)	0	1000	3	Transport, Lumen	PMID: 10958334, PMID: 19184091, PMID: 18195088, PMID: 11546643	sodium-independant antiport transport system, exchanges di-basic amino acids into the cells and neutral amino acids out of the cell. Located on the apical surfaces of transporting epithelia. Cellular localization being small intestine, kidney (proximal tubule), lung, placenta, brain and thymus. Requires the heterodimerization with rBAT glycoprotein. (PMID: 10958334).	
ARGATBItc	transport of L-Arginine into the intestinal cells by ATB0 transporter	2 na1[u] + cl[u] + arg-L[u] -> 2 na1[c] + cl[c] + arg-L[c]	0	56774.1	0	1000	3	Transport, Lumen	PMID:18195088	ATB0 is both sodium and chloride coupled, with reaction stoichiometry 2Na+:1cl-:1amino acid. The transporter is located in the intestine, has a broad substrate specificity (both neutral and cationic amino acids), but is not involved in the transport of aspartate, glutamate and proline (PMID:18195088).	
ARGDCm	arginine decarboxylase (m)	h[m] + arg-L[m] -> co2[m] + agm[m]	0	242669.1	0	1000		Arginine and Proline Metabolism			
ARGLEUtrBATIc	transport of L-Arginine into the cell in exchange for L-Leucine by b0,+AT transporter at the apical surfaces of the membranes of small intestine and renal cells.	leu-L[c] + arg-L[u] -> leu-L[u] + arg-L[c]	0	(30962.1 and 20532.1)	0	1000	3	Transport, Lumen	PMID: 10958334, PMID: 19184091, PMID: 18195088, PMID: 11546643	sodium-independant antiport transport system, exchanges di-basic amino acids into the cells and neutral amino acids out of the cell. Located on the apical surfaces of transporting epithelia. Cellular localization being small intestine, kidney (proximal tubule), lung, placenta, brain and thymus. Requires the heterodimerization with rBAT glycoprotein. (PMID: 10958334).	
ARGLYSex	Arginine/Lysine exchanger (Arg in)	arg-L[e] + lys-L[c] -> arg-L[c] + lys-L[e]	0	330836.1 and 17254.1	0	1000		Transport, Extracellular			
ARGN	arginase	h2o[c] + arg-L[c] -> orn[c] + urea[c]	0	11846.1	0	1000		Urea cycle/amino group metabolism			
ARGNm	arginase (m)	h2o[m] + arg-L[m] -> urea[m] + orn[m]	0	11847.1	0	1000		Urea cycle/amino group metabolism			
ARGSL	argininosuccinate lyase	argsuc[c] <=> fum[c] + arg-L[c]	1	109900.1	-1000	1000		Alanine and Aspartate Metabolism			
ARGSS	argininosuccinate synthase	atp[c] + asp-L[c] + citr-L[c] -> h[c] + amp[c] + ppi[c] + argsuc[c]	0	11898.1 or 11898.2	0	1000		Alanine and Aspartate Metabolism			
ARGt4	L-arginine transport in via sodium symport	na1[e] + arg-L[e] -> na1[c] + arg-L[c]	0	56774.1	0	1000		Transport, Extracellular			
ARGt5e	L-arginine transport via diffusion	arg-L[e] <=> arg-L[c]	1	11987.1	-1000	1000	2	Transport, Extracellular			
ARGtiDF	L-arginine transport via diffusion (extracellular to cytosol)	arg-L[e] -> arg-L[c]	0	69354.1 or 11989.1 or 11988.1 or 11987.1	0	1000		Transport, Extracellular			
ARGtm	arginine mitochondrial transport via ornithine carrier	h[m] + arg-L[c] <=> h[c] + arg-L[m]	1	18408.1 or 83885.1	-1000	1000		Transport, Mitochondrial			
ARSA	Arylsulfatase A	h2o[l] + sgalside_hs[l] -> h[l] + galside_hs[l] + so4[l]	0	11883.1	0	1000		Sphingolipid Metabolism			
ARTCOAL1	R group coenzyme a ligase	coa[c] + Rnstal[c] <=> Rnstalcoa[c]	1		-1000	1000		R Group Synthesis			

ARTCOAL2	R group coenzyme a ligase	coa[c] + Rtotal2[c] <=> Rtotal2coa[c]	1		-1000	1000		R Group Synthesis			
ARTCOAL3	R group coenzyme a ligase	coa[c] + Rtotal3[c] <=> Rtotal3coa[c]	1		-1000	1000		R Group Synthesis			
ARTFR11	R group artificial flux	pentcoa[c] -> R1coa_hs[c]	0		0	1000		R Group Synthesis			
ARTFR12	R group artificial flux (C16:1)	fadh2[m] + hdcoa[c] -> fad[m] + R1coa_hs[c]	0		0	1000		R Group Synthesis			
ARTFR13	R group artificial flux	tdcoa[c] -> 0.875 R1coa_hs[c]	0		0	1000		R Group Synthesis			
ARTFR202	R group artificial flux (C18:3, n-3)	h[m] + nadph[m] + 2 fadh2[m] + hdecacoa[c] -> nadp[m] + 2 fad[m] + 1.125 R2coa_hs[c]	0		0	1000		R Group Synthesis			
ARTFR203	R group artificial flux	h[m] + nadph[m] + 2 fadh2[m] + tdecapcoa[c] -> nadp[m] + 2 fad[m] + 1.125 R2coa_hs[c]	0		0	1000		R Group Synthesis			
ARTFR204	R group artificial flux	2 h[m] + 2 nadph[m] + 2 fadh2[m] + ttetdecoa[c] -> 2 nadp[m] + 2 fad[m] + 1.125 R2coa_hs[c]	0		0	1000		R Group Synthesis			
ARTFR205	R group artificial flux	h[m] + nadph[m] + 2 fadh2[m] + dhdcgcoa[c] -> nadp[m] + 2 fad[m] + 1.25 R2coa_hs[c]	0		0	1000		R Group Synthesis			
ARTFR206	R group artificial flux	2 h[m] + 2 nadph[m] + 2 fadh2[m] + arachdcoa[c] -> 2 nadp[m] + 2 fad[m] + 1.25 R2coa_hs[c]	0		0	1000		R Group Synthesis			
ARTFR207	R group artificial flux	arachcoa[c] -> 1.25 R2coa_hs[c]	0		0	1000		R Group Synthesis			
ARTFR208	R group artificial flux	2 h[m] + 2 nadph[m] + 3 fadh2[m] + tetrahexcoa[c] -> 2 nadp[m] + 3 fad[m] + 1.25 R2coa_hs[c]	0		0	1000		R Group Synthesis			
ARTFR209	R group artificial flux	2 h[m] + 2 nadph[m] + 2 fadh2[m] + adtricoa[c] -> 2 nadp[m] + 2 fad[m] + 1.375 R2coa_hs[c]	0		0	1000		R Group Synthesis			
ARTFR210	R group artificial flux	h[m] + nadph[m] + fadh2[m] + hdtcoa[c] -> nadp[m] + fad[m] + 1.125 R2coa_hs[c]	0		0	1000		R Group Synthesis			
ARTFR211	R group artificial flux	2 h[m] + 2 nadph[m] + 3 fadh2[m] + clpnhcoa[c] -> 2 nadp[m] + 3 fad[m] + 1.375 R2coa_hs[c]	0		0	1000		R Group Synthesis			
ARTFR212	R group artificial flux	2 h[m] + 2 nadph[m] + 3 fadh2[m] + dcoptn1coa[c] -> 2 nadp[m] + 3 fad[m] + 1.375 R2coa_hs[c]	0		0	1000		R Group Synthesis			
ARTFR213	R group artificial flux	3 h[m] + 3 nadph[m] + 3 fadh2[m] + c22fecoa[c] -> 3 nadp[m] + 3 fad[m] + 1.375 R2coa_hs[c]	0		0	1000		R Group Synthesis			
ARTFR31	R group artificial flux	stecoa[c] -> 1.125 R1coa_hs[c]	0		0	1000		R Group Synthesis			
ARTFR32	R group artificial flux	fadh2[m] + odecoa[c] -> fad[m] + 1.125 R1coa_hs[c]	0		0	1000		R Group Synthesis			
ARTFR33	R group artificial flux	fadh2[m] + vaccoa[c] -> fad[m] + 1.125 R3coa_hs[c]	0		0	1000		R Group Synthesis			
ARTFR34	R group artificial flux	2 fadh2[m] + hxdecoa[c] -> 2 fad[m] + 1.125 R1coa_hs[c]	0		0	1000		R Group Synthesis			
ARTFR41	R group artificial flux	fadh2[m] + hdcoa[c] -> fad[m] + R4coa_hs[c]	0		0	1000		R Group Synthesis			
ARTFR42	R group artificial flux	fadh2[m] + odecoa[c] -> fad[m] + 1.125 R4coa_hs[c]	0		0	1000		R Group Synthesis			
ARTFR43	R group artificial flux	fadh2[m] + vaccoa[c] -> fad[m] + 1.125 R4coa_hs[c]	0		0	1000		R Group Synthesis			
ARTFR44	R group artificial flux	2 fadh2[m] + hxdecoa[c] -> 2 fad[m] + 1.125 R4coa_hs[c]	0		0	1000		R Group Synthesis			
ARTFR45	R group artificial flux	fadh2[m] + nvvaccoa[c] -> fad[m] + 1.5 R4coa_hs[c]	0		0	1000		R Group Synthesis			
ARTFR46	R group artificial flux	fadh2[m] + od2coa[c] -> fad[m] + 1.125 R4coa_hs[c]	0		0	1000		R Group Synthesis			
ARTFR51	R group artificial flux	ligoccoa[c] -> 1.5 R5coa_hs[c]	0		0	1000		R Group Synthesis			
ARTFR52	R group artificial flux	hexccoa[c] -> 1.625 R5coa_hs[c]	0		0	1000		R Group Synthesis			
ARTFR53	R group artificial flux	2 h[m] + 2 nadph[m] + 2 fadh2[m] + eicosetricoa[c] -> 2 nadp[m] + 2 fad[m] + 1.25 R5coa_hs[c]	0		0	1000		R Group Synthesis			
ARTFR54	R group artificial flux	2 h[m] + 2 nadph[m] + 3 fadh2[m] + tetpentfacoa[c] -> 2 nadp[m] + 3 fad[m] + 1.5 R5coa_hs[c]	0		0	1000		R Group Synthesis			
ARTFR55	R group artificial flux	2 h[m] + 2 nadph[m] + 3 fadh2[m] + tetpent3coa[c] -> 2 nadp[m] + 3 fad[m] + 1.5 R5coa_hs[c]	0		0	1000		R Group Synthesis			
ARTFR56	R group artificial flux	2 h[m] + 2 nadph[m] + 2 fadh2[m] + tetrefficoa[c] -> 2 nadp[m] + 2 fad[m] + 1.5 R5coa_hs[c]	0		0	1000		R Group Synthesis			
ARTFR57	R group artificial flux	3 h[m] + 3 nadph[m] + 3 fadh2[m] + tethex3coa[c] -> 3 nadp[m] + 3 fad[m] + 1.5 R5coa_hs[c]	0		0	1000		R Group Synthesis			
ARTFR61	R group artificial flux	fadh2[m] + hdd2coa[c] -> fad[m] + R6coa_hs[c]	0		0	1000		R Group Synthesis			
ARTPLM1	R group to palmitate conversion	Rtotalcoa[c] <=> pmtcoa[c]	1		-1000	1000		R Group Synthesis			
ARTPLM1m	R group to palmitate conversion	Rtotalcoa[m] <=> pmtcoa[m]	1		-1000	1000		R Group Synthesis			
ARTPLM2	R group to palmitate conversion	Rtotal2coa[c] <=> pmtcoa[c]	1		-1000	1000		R Group Synthesis			
ARTPLM2m	R group to palmitate conversion	Rtotal2coa[m] <=> pmtcoa[m]	1		-1000	1000		R Group Synthesis			
ARTPLM3	R group to palmitate conversion	Rtotal3coa[c] <=> pmtcoa[c]	1		-1000	1000		R Group Synthesis			
ARTPLM3m	R group to palmitate conversion	Rtotal3coa[m] <=> pmtcoa[m]	1		-1000	1000		R Group Synthesis			
ASAH1	N-acylsphingosine amidohydrolase	h2o[l] + cer_hs[l] -> Rtotal[l] + sphings[l]	0	11886.1 or 11886.2	0	1000		Sphingolipid Metabolism			
ASCBOX	ascorbic acid oxidase	2 h[c] + asch-L[c] + 2 o2s[c] -> 2 h2o2[c] + dhdascb[c]	0		0	1000		Ascorbate and Aldarate Metabolism			
ASCBSVCTtc	transport of L-Ascorbate by SVCT1 or SVCT2 transporter	h2o[c] + atp[c] + 2 na1[e] + asch-L[a] -> adp[c] + h[c] + pi[c] + 2 na1[c] + asch-L[c]	0	20522.1 or 54338.1	0	1000	3	Transport, Lumen	PMID: 18094143, PMID: 11396616, G.F.M. Ball (2006) Vitamins their role in the human body, Blackwell publishing, chapter 19, page 395-398, PMID: 17222174	SVCT1 and SVCT2 differ in their tissue distribution, SVCT1 is more ubiquitously expressed, where as SVCT1 is confined to intestine, liver and kidney. The Na+ symport transport is energized by Na+/K+ ATPase, therefore its a secondary active transport (G.F.M. Ball (2006) Vitamins their role in the human body, Blackwell publishing, chapter 19, page 395-398). Vitamin C is absorbed only in ascorbate form, can be oxidized into dehydroascorbate, and can then enter the blood stream (Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Advanced nutrition and human metabolism, Wadsworth cengage learning, 5th edition, page 312-313).	
ASCBt	L-ascorbate transport via facilitated diffusion	asch-L[e] <=> asch-L[c]	1		-1000	1000		Transport, Extracellular			
ASCBt4	L-ascorbate transport via proton symport	na1[e] + asch-L[e] <=> na1[c] + asch-L[c]	1	54338.2 or 20522.1 or 20522.2 or 54338.1	-1000	1000		Transport, Extracellular			
ASNALANaEx	L-alanine/L-asparagine Na-dependent exchange (Asn-L:ini)	na1[e] + ala-L[c] + asn-L[e] -> na1[c] + asn-L[c] + ala-L[e]	0	20514.1	0	1000		Transport, Extracellular			
ASNATB0tc	transport of L-Asparagine into the intestinal cells by ATB0 transporter	2 na1[a] + cl[a] + asn-L[a] -> 2 na1[c] + cl[c] + asn-L[c]	0	5677.4.1	0	1000	3	Transport, Lumen	PMID:18195088	ATB0 is both sodium and chloride coupled, with reaction stoichiometry 2Na+:1cl: Lentiss acid. The transporter is localized in the intestine, has a broad substrate specificity (both neutral and cationic amino acids), but is not involved in the transport of aspartate, glutamate and proline (PMID:18195088).	
ASNB0ATtc	transport of L-Asparagine by the apical neutral amino acid transporters in kidney and intestine	na1[a] + asn-L[a] -> na1[c] + asn-L[c]	0	(70088.1 or (74338.1 and 57394.1))	0	1000	3	Transport, Lumen	PMID: 19472175, PMID: 15804236, PMID: 18400692	transports all the neutral amino acids with preference for methionine, leucine and valine. Reaction stoichiometry is 1:1. Requires heterodimerization with collectrin protein for increased affinity. Found in kidney and intestine, however also reported to be expressed in skin. Requires association with ACE2 for expression in intestine but with collectrin for expression in kidney.	3.4.17.23
ASNCYSNaEx	L-cysteine/L-asparagine Na-dependent exchange (Asn-L:ini)	na1[e] + asn-L[e] + cys-L[c] -> na1[c] + asn-L[c] + cys-L[e]	0	20514.1	0	1000		Transport, Extracellular			
ASNGLNNaEx	L-glutamine/L-asparagine Na-dependent exchange (Asn-L:ini)	na1[e] + asn-L[e] + gln-L[c] -> na1[c] + asn-L[c] + gln-L[e]	0	20514.1	0	1000		Transport, Extracellular			
ASNILELAT2tc	transport of L-Asparagine into the cell and efflux of L-Isoleucine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	asn-L[e] + ile-L[c] -> asn-L[c] + ile-L[e]	0	(20539.1 and 17254.1)	0	1000	3	Transport, Extracellular	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004280000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	Sigher affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004280000274).	
ASNNm	L-asparaginase (mitochondrial)	h2o[m] + asn-L[m] -> asp-L[m] + nh4[m]	0	66514.1	0	1000		Alanine and Aspartate Metabolism			
ASNPHELAT2tc	transport of L-Asparagine into the cell and efflux of L-Phenylalanine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	asn-L[e] + phe-L[c] -> asn-L[c] + phe-L[e]	0	(20539.1 and 17254.1)	0	1000	3	Transport, Extracellular	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004280000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	Sigher affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004280000274).	
ASNS1	asparagine synthase (glutamine-hydrolysing)	h2o[c] + atp[c] + asp-L[c] + gln-L[c] -> h[c] + glu-L[c] + amp[c] + ppi[c] + asn-L[c]	0	27053.1 or 27053.2 or 27053.3	0	1000		Alanine and Aspartate Metabolism			
ASNSERNaEx	L-serine/L-asparagine Na-dependent exchange (Asn-L:ini	na1[e] + asn-L[e] + ser-L[c] -> na1[c] + asn-L[c] + ser-L[e]	0	20514.1	0	1000		Transport, Extracellular			
ASNTHRNaEx	L-threonine/L-asparagine Na-dependent exchange (Asn-L:ini)	na1[e] + asn-L[e] + thr-L[c] -> na1[c] + asn-L[c] + thr-L[e]	0	20514.1	0	1000		Transport, Extracellular			
ASN_X_SER_THRtr	ASN_X_SER_THRtr	Asn_X_Ser_Thr[e] <=> Asn_X_Ser_Thr[l]	1		-1000	1000	0	Transport, Lysosomal			
ASNt4	L-asparagine transport in via sodium symport	na1[e] + asn-L[e] -> na1[c] + asn-L[c]	0	105727.1 or 67760.1 or 69354.1 or 56774.1	0	1000		Transport, Extracellular			
ASNtN1	Asparagine transport (Na, H coupled)	h[c] + 2 na1[e] + asn-L[e] <=> h[e] + 2 na1[c] + asn-L[c]	1	209837.1 or 76257.1	-1000	1000		Transport, Extracellular			
ASNtm	L-asparagine transport, mitochondrial	asn-L[c] -> asn-L[m]	0		0	1000		Transport, Mitochondrial			
ASP1DC	aspartate 1-decarboxylase	h[c] + asp-L[c] -> co2[c] + ala-B[c]	0	14415.1 or 14415.2	0	1000		beta-Alanine metabolism			
ASPCTr	aspartate carbamyltransferase (reversible)	asp-L[c] + cbp[c] <=> h[c] + pi[c] + cbasp[c]	1	69719.1	-1000	1000		Pyrimidine Biosynthesis			
ASPD6	D-aspartate transport via Na, H symport and K antiport	h[e] + 3 na1[e] + k[c] + asp-D[e] -> h[c] + 3 na1[c] + asp-D[c] + k[e]	0	242607.1 or 20511.1 or 20513.1 or 20510.1 or 20512.1	0	1000		Transport, Extracellular			
ASPDxt	D-aspartate transport, peroxisomal	asp-D[x] <=> asp-D[c]	1		-1000	1000		Transport, Peroxisomal			
ASPGLUm	aspartate–glutamate mitochondrial shuttle	h[c] + glu-L[c] + asp-L[m] <=> h[m] + glu-L[m] + asp-L[c]	1	78830.1 or 50799.1	-1000	1000		Transport, Mitochondrial			
ASPNATm	aspartate N-acetyltransferase, mitochondrial	asp-L[m] + accoa[m] -> h[m] + coa[m] + Nacasp[m]	0		0	1000		Alanine and Aspartate Metabolism			
ASPTA	aspartate transaminase	akg[c] + asp-L[c] <=> glu-L[c] + oaa[c]	1	14718.1	-1000	1000		Alanine and Aspartate Metabolism			
ASPTAm	aspartate transaminase	akg[m] + asp-L[m] <=> glu-L[m] + oaa[m]	1	14719.1	-1000	1000		Alanine and Aspartate Metabolism			
ASPt6	L-aspartate transport via Na, H symport and K antiport	h[e] + 3 na1[e] + k[c] + asp-L[e] -> h[c] + 3 na1[c] + asp-L[c] + k[e]	0	242607.1 or 20511.1 or 20513.1 or 20510.1 or 20512.1	0	1000		Transport, Extracellular			
ATP1er	ADP/ATP transporter, endoplasmic reticulum	atp[c] + adp[r] <=> adp[c] + atp[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
ATP2er	AMP/ATP transporter, endoplasmic reticulum	atp[c] + amp[r] <=> amp[c] + atp[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
ATPH1r	ATP diphosphohydrolase	2 h2o[r] + atp[r] -> 2 h[r] + amp[r] + 2 pi[r]	0	12495.1 or 12496.2 or 12497.1 or 12499.1 or 215446.1 or 12496.1	0	1000		Nucleotides			
ATPH2r	ATP diphosphohydrolase	h2o[r] + adp[r] -> h[r] + amp[r] + pi[r]	0	12495.1 or 12496.2 or 12497.1 or 12499.1 or 215446.1 or 12496.1	0	1000		Nucleotides			
ATPM	ATP maintenance requirement	h2o[c] + atp[c] -> adp[c] + h[c] + pi[c]	0		84.300	1000		Unassigned			

ATPS4m	ATP synthase (four protons for one ATP)	4 h[c] + adp[m] + pi[m] -> 3 h[m] + h2o[m] + atp[m]	0	11947.1 and 11946.1 and 67126.1 and 11949.1 and 66043.1 or 11947.1 and 11949.2 and 66043.2 and 11946.3 and 67126.2 or 11947.1 and 11946.1 and 67126.1 and 66043.1 and 11949.2 or 11947.1 and 11949.2 and 66043.1 and 67126.2 and 11946.3 or 11947.1 and 11949.2 and 66043.2 and 11946.2 and 67126.2 or 11947.1 and 11946.1 and 67126.1 and 11949.2 and 66043.2 or 11947.1 and 66043.1 and 11949.2 and 11946.2 and 67126.2 or 11947.1 and 11949.1 and 66043.2 and 67126.2 and 11946.3 or 11947.1 and 11946.1 and 11949.1 and 66043.2 and 67126.2 or 11947.1 and 11949.1 and 11946.2 and 66043.2 and 67126.2 or 11947.1 and 67126.1 and 66043.1 and 11949.2 and 11946.3 or 11947.1 and 67126.1 and 11949.1 and 66043.1 and 11946.3 or 11947.1 and 67126.1 and 11949.1 and	0	1000		Oxidative Phosphorylation			
ATPasel	V-type ATPase, H+ transporting, lysosomal	h2o[c] + atp[c] + 3 h[c] -> adp[c] + pi[c] + 4 h[l]	0	11984.1 and 11974.1 and 140494.2 and 242341.1 and 114143.1 or 11984.1 and 11974.1 and 11972.1 and 140494.2 and 114143.1 or 11984.1 and 11974.1 and 11975.1 and 242341.1 and 114143.1 or 11984.1 and 11974.1 and 242341.1 and 114143.1 and 21871.1 or 11984.1 and 11974.1 and 140494.3 and 242341.1 and 114143.1 or 11984.1 and 27060.1 and 11974.1 and 242341.1 and 114143.1 or 11984.1 and 140494.1 and 11974.1 and 242341.1 and 114143.1 or 11984.1 and 11974.1 and 11972.1 and 140494.3 and 114143.1 or 11984.1 and 27060.1 and 11974.1 and 11972.1 and 114143.1 or 11984.1 and 11974.1 and 27060.2 and 11972.1 and 114143.1 or 11984.1 and 11974.1 and 27060.2 and 242341.1 and 114143.1 or 11984.1 and 140494.1 and 11974.1 and 11972.1 and 114143.1 or 11984.1	0	1000		Transport, Lysosomal			
ATPtm	ADP/ATP transporter, mitochondrial	adp[c] + atp[m] -> atp[c] + adp[m]	0	11739.1 or 433923.1 or 11740.1	0	1000		Transport, Mitochondrial			
ATPtn	ATP diffusion in nucleus	atp[c] <=> atp[n]	1		-1000	1000		Transport, Nuclear			
ATPtx	ATP transporter, peroxisomal	atp[c] <=> atp[x]	1		-1000	1000		Transport, Peroxisomal			
AVITE1t	alpha-Tocopherol (Vit. E) transport	avite1[e] -> avite1[c]	0		0	1000		Transport, Extracellular			
AVITE2t	alpha-tocotrienol (Vit. E) transport	avite2[e] -> avite2[c]	0		0	1000		Transport, Extracellular			
A_MANASE	alpha-mannosidase	2 h2o[c] + m2mn[c] -> 2 man[c] + mn[c]	0	73744.1	0	1000		N-Glycan Degradation			
A_MANASEly	alpha-mannosidase, lysosomal	2 h2o[l] + m2mn[l] -> 2 man[l] + mn[l]	0	17159.1	0	1000		N-Glycan Degradation			
B3GALT3g	Beta-1,3-galactosyltransferase 3	thcrm_hs[g] + udpacgal[g] -> h[g] + udp[g] + gbside_hs[g]	0	26879.1 or 26879.2 or 26879.3 or 26879.4	0	1000		Sphingolipid Metabolism			
B3GALT41g	Beta-1,3-galactosyltransferase 4	udpgal[g] + ga2_hs[g] -> h[g] + udp[g] + ga1_hs[g]	0	54218.1	0	1000		Sphingolipid Metabolism			
B3GALT42g	Beta-1,3-galactosyltransferase 4	udpgal[g] + gm2_hs[g] -> h[g] + udp[g] + gm1_hs[g]	0	54218.1	0	1000		Sphingolipid Metabolism			
B3GALT43g	Beta-1,3-galactosyltransferase 4	udpgal[g] + gd2_hs[g] -> h[g] + udp[g] + gd1b_hs[g]	0	54218.1	0	1000		Sphingolipid Metabolism			
B3GALT44g	Beta-1,3-galactosyltransferase 4	udpgal[g] + gt2_hs[g] -> h[g] + udp[g] + gt1c_hs[g]	0	54218.1	0	1000		Sphingolipid Metabolism			
B3GALT5g	Beta-1,3-galactosyltransferase 5	udpgal[g] + gbside_hs[g] -> h[g] + udp[g] + galgbside_hs[g]	0	93961.1 or 93961.2 or 93961.3 or 93961.4 or 93961.5	0	1000		Sphingolipid Metabolism			
B3GALTg	Beta galactosyltransferase	udpgal[g] + acglcgalgluside_hs[g] -> h[g] + udp[g] + galacglcgalgluside_hs[g]	0		0	1000		Blood Group Biosynthesis			
B3GNT11g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1	uacgam[g] + gal14acglcgalgluside_hs[g] -> h[g] + udp[g] + acglcgal14acglcgalgluside_hs[g]	0	53625.1	0	1000		Blood Group Biosynthesis			
B3GNT12g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1	uacgam[g] + galacglcgal14acglcgalgluside_hs[g] -> h[g] + udp[g] + acglc13galacglcgal14acglcgalgluside_hs[g]	0	53625.1 or 53625.1	0	1000		Blood Group Biosynthesis			
B3GNT310g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus	udpgal[g] + acglcgalgluside_hs[g] -> h[g] + udp[g] + gal14acglcgalgluside_hs[g]	0	72297.1	0	1000		Blood Group Biosynthesis			
B3GNT311g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus	udpgal[g] + acgalfuc12gal14acglcgalgluside_hs[g] -> h[g] + udp[g] + galacgalfuc12gal14acglcgalgluside_hs[g]	0	72297.1	0	1000		Blood Group Biosynthesis			
B3GNT312g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus	udpgal[g] + acglcgal14acglcgalgluside_hs[g] -> h[g] + udp[g] + galacglcgal14acglcgalgluside_hs[g]	0	72297.1	0	1000		Blood Group Biosynthesis			
B3GNT313g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus	udpgal[g] + acgalfucgalacglcgal14acglcgalgluside_hs[g] -> h[g] + udp[g] + galacgalfucgalacglcgal14acglcgalgluside_hs[g]	0	72297.1	0	1000		Blood Group Biosynthesis			
B3GNT314g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus	udpgal[g] + acglcgalacglcgal14acglcgalgluside_hs[g] -> h[g] + udp[g] + galacglcgalacglcgal14acglcgalgluside_hs[g]	0	72297.1	0	1000		Blood Group Biosynthesis			
B3GNT315g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus	udpgal[g] + acglc13galacglcgal14acglcgalgluside_hs[g] -> h[g] + udp[g] + galacglc13galacglcgal14acglcgalgluside_hs[g]	0	72297.1	0	1000		Blood Group Biosynthesis			
B3GNT31g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus	udpgal[g] + thcrm_hs[g] -> h[g] + udp[g] + galthcrm_hs[g]	0	72297.1	0	1000		Sphingolipid Metabolism			
B3GNT32g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus	udpgal[g] + galthcrm_hs[g] -> h[g] + udp[g] + galgalthcrm_hs[g]	0	72297.1	0	1000		Sphingolipid Metabolism			
B3GNT33g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus	udpgal[g] + galgalthcrm_hs[g] -> h[g] + udp[g] + galgalgalthcrm_hs[g]	0	72297.1	0	1000		Sphingolipid Metabolism			
B3GNT34g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus	uacgam[g] + galgbside_hs[g] -> h[g] + udp[g] + acglcgalgbside_hs[g]	0	72297.1	0	1000		Sphingolipid Metabolism			
B3GNT35g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus	udpgal[g] + acglcgalgbside_hs[g] -> h[g] + udp[g] + galacglcgalgbside_hs[g]	0	72297.1	0	1000		Sphingolipid Metabolism			
B3GNT36g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus	acgal[g] + gbside_hs[g] -> acgbgbside_hs[g] + h2o[g]	0	72297.1	0	1000		Sphingolipid Metabolism			
B3GNT37g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus	udpgal[g] + gm2a_hs[g] -> h[g] + udp[g] + gm1a_hs[g]	0	72297.1	0	1000		Sphingolipid Metabolism			
B3GNT39g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3, Golgi apparatus	udpgal[g] + gluside_hs[g] -> galgluside_hs[g] + h[g] + udp[g]	0	72297.1	0	1000		Sphingolipid Metabolism			
B3GNT51g	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5	galgluside_hs[g] + uacgam[g] -> h[g] + udp[g] + acglcgalgluside_hs[g]	0	108105.1	0	1000		Blood Group Biosynthesis			
BAAT1x	bile acid Coenzyme A: amino acid N-acyltransferase	gly[x] + cholcoa[x] -> coa[x] + gchola[x]	0	12012.1	0	1000		Bile Acid Biosynthesis			
BAAT2x	bile acid Coenzyme A: amino acid N-acyltransferase	cholcoa[x] + taur[x] -> coa[x] + tchola[x]	0	12012.1	0	1000		Bile Acid Biosynthesis			
BAAT3x	bile acid Coenzyme A: amino acid N-acyltransferase	gly[x] + dgcholcoa[x] -> coa[x] + dgchol[x]	0	12012.1	0	1000		Bile Acid Biosynthesis			
BAAT4x	bile acid Coenzyme A: amino acid N-acyltransferase	gly[x] + dcholcoa[x] -> coa[x] + gdchola[x]	0	12012.1	0	1000		Bile Acid Biosynthesis			
BAAT5x	bile acid Coenzyme A: amino acid N-acyltransferase	taur[x] + dcholcoa[x] -> coa[x] + tdchola[x]	0	12012.1	0	1000		Bile Acid Biosynthesis			
BACCL	biotin-[acetyl-CoA-carboxylase] ligase	atp[c] + h[c] + btn[c] -> ppi[c] + btamp[c]	0	110948.1	0	1000		Biotin Metabolism			
BACCLm	biotin-[acetyl-CoA-carboxylase] ligase, mitochondrial	h[m] + atp[m] + btn[m] -> ppi[m] + btamp[m]	0	110948.1	0	1000		Biotin Metabolism			
BALABETAtc	transport of beta alanine into the intestinal cells by beta transport system	2 na1[u] + cl[u] + ala-B[u] -> 2 na1[c] + cl[c] + ala-B[c]	0	56774.1	0	1000	3	Transport, Lumen	PMID: 19074966, PMID: 2206910, PMID: 1324004, PMID: 16956961, PMID: 15166008, PMID: 18195088	beta transporter system requires chloride ions for optimal uptake of amino acids into the cells. Expressed on both apical and basolateral membranes of renal cells. Transports taurine and beta alanine. (PMID: 18195088)	
BALAPAT1tc	transport of beta alanine by PAT1 in renal and intestinal cells	h[u] + ala-B[u] -> h[c] + ala-B[c]	0	215335.1	0	1000	3	Transport, Lumen	PMID: 17123464, PMID: 18400692, PMCID: PMC34647, PMID: 15345686, PMID: 18195088	PAT1 proton-amino acid co-transporter with 1:1 stoichiometry, does not discriminate between L and D isomers, located on the apical membrane of kidney and intestine (PMID: 18400692, PMID: 18195088).	
BALAVECSEC	B-alanine secretion via secretory vesicle (ATP driven)	h2o[c] + atp[c] + 3 ala-B[c] -> adp[c] + h[c] + pi[c] + 3 ala-B[e]	0	22348.1	0	1000		Transport, Extracellular			
BALAtmr	Beta-alanine reversible mitochondrial transport (diffusion)	ala-B[c] <=> ala-B[m]	1		-1000	1000		Transport, Mitochondrial			
BAMPPALDOX	beta-Aminopropion aldehyde:NAD+ oxidoreductase	h2o[c] + bamppald[c] + nad[c] -> 2 h[c] + nadh[c] + ala-B[c]	0	19378.1 or 56752.1 or 110695.1 or 11668.1 or 11671.1 or 19378.2 or 19378.3	0	1000		beta-Alanine metabolism			
BAMPPALDOXm	beta-Aminopropion aldehyde:NAD+ oxidoreductase (m)	h2o[m] + nad[m] + bamppald[m] -> 2 h[m] + nadh[m] + ala-B[m]	0	11669.1 or 212647.1 or 212647.2 or 72535.1	0	1000		beta-Alanine metabolism			
BBHOX	4-Trimethylammoniobutanoate,2-oxoglutarate:oxygen oxidoreductase (3-hydroxylating)	o2[c] + akg[c] + 4tmeabutn[c] -> co2[c] + crn[c] + succ[c]	0	170442.1	0	1000		Lysine Metabolism			
BCDO	beta-Carotene dioxygenase	o2[c] + caro[c] -> 2 retinal[c]	0	63857.1	0	1000		Vitamin A Metabolism			
BDHm	(R)-3-Hydroxybutanoate:NAD+ oxidoreductase	nad[m] + bhb[m] <=> h[m] + nadh[m] + acac[m]	1	71911.1 or 71911.2 or 71911.3	-1000	1000		Butanoate Metabolism			
BDMT_L	GDPmannose:chitobiosyldiphosphodolichol beta-D-mannosyltransferase (liver)	0.1 chito2pdol_L[c] + gdpmann[c] -> h[c] + gdp[c] + 0.1 mpdol_L[c]	0	208211.1	0	1000		N-Glycan Biosynthesis			

BDMT_U	GDPmannose:chitobiosyldiphosphodolichol beta-D-mannosyltransferase (uterus)	gdpmann[c] + 0.1 chito2pdol_U[c] -> h[c] + gdp[c] + 0.1 mpdol_U[c]	0	208211.1	0	1000		N-Glycan Biosynthesis			
BETALDHx	betaine-aldehyde dehydrogenase	h2o[c] + nad[c] + betald[c] -> 2 h[c] + nadh[c] + glyb[c]	0	56752.1	0	1000		Glycine, Serine, and Threonine Metabolism			
BETALDHxm	betaine-aldehyde dehydrogenase, mitochondrial	h2o[m] + nad[m] + betald[m] -> 2 h[m] + nadh[m] + glyb[m]	0		0	1000		Glycine, Serine, and Threonine Metabolism			
BGLCt	beta-glucan transport	h[e] + bglc[e] <=> h[c] + bglc[c]	1		-1000	1000	1	Transport, Extracellular		Needed to provide this metabolite for reaction BGLUGCHe, BGLUTCHLe and BGLUTDECHOe in joint model.	
BGLUGCHe	binding of betaglucans with glycocholate in the intestinal lumen, reducing serum cholsterol	bglc[u] + gchola[u] -> glgchlo[u]	0		0	1000	3	Food processing, Lumen	"Park SY, Bae IY, Lee S, Lee HG. (2009). Journal of Agricultural and	oxidized beta glucan forms binds the bile acids more effectively. beta glucan binds bile acids and leads to enhanced excretion, there by the 7-alpha hydroxylase pathway is	
BGLUGCHt	binding of betaglucans with glycocholate transport	h[e] + glgchlo[e] <=> h[c] + glgchlo[c]	1		-1000	1000	1	Transport, Extracellular		Needed to provide this metabolite for reaction BGLUGCHe in joint model.	
BGLUTCHLe	binding of betaglucans with taurocholate in the intestinal lumen, reducing serum cholsterol levels.	bglc[u] + tchola[u] -> gltcho[u]	0		0	1000	3	Food processing, Lumen	Park SY, Bae IY, Lee S, Lee HG. (2009). Journal of Agricultural and Food Chemistry 57: 439-43, PMCID: PMC2663451, PMID: 17251929	oxidized beta glucan forms binds the bile acids more effectively. beta glucan binds bile acids and leads to enhanced excretion, there by the 7-alpha hydroxylase pathway is activated laeding to increased cholesterol catabolism for synthesis of more bile acids (regulates cholesterol metabolism). however the decreased serum cholesterol levels are brought about by many other cumulative effects (water unstirred action of dieatary fibres, glycemic role etc) (PMID: 18302966, Gunness P, Gidley MJ. (2010). Food & Function 1: 149-55).	
BGLUTCHLt	binding of betaglucans with taurocholate transport	h[e] + gltcho[e] <=> h[c] + gltcho[c]	1		-1000	1000	1	Transport, Extracellular		Needed to provide this metabolite for reaction BGLUTCHLe in joint model.	
BGLUTDECHOe	binding of betaglucans with taurodeoxycholate in the intestinal lumen, reducing serum cholsterol levels.	bglc[u] + tdechola[u] -> gltdechol[u]	0		0	1000	3	Food processing, Lumen	Park SY, Bae IY, Lee S, Lee HG. (2009). Journal of Agricultural and Food Chemistry 57: 439-43, PMCID: PMC2663451, PMID: 17251929	oxidized beta glucan forms binds the bile acids more effectively. beta glucan binds bile acids and leads to enhanced excretion, there by the 7-alpha hydroxylase pathway is activated laeding to increased cholesterol catabolism for synthesis of more bile acids (regulates cholesterol metabolism). however the decreased serum cholesterol levels are brought about by many other cumulative effects (water unstirred action of dieatary fibres, glycemic role etc) (PMID: 18302966, Gunness P, Gidley MJ. (2010). Food & Function 1: 149-55).	
BGLUTDECHOt	binding of betaglucans with taurodeoxycholate transport	h[e] + gltdechol[e] <=> h[c] + gltdechol[c]	1		-1000	1000	1	Transport, Extracellular		Needed to provide this metabolite for reaction BGLUTDECHOe in joint model.	
BHBt	(R)-3-Hydroxybutanoate transport via H+ symport	h[e] + bhb[e] <=> h[c] + bhb[c]	1		-1000	1000		Transport, Extracellular			
BHBtm	(R)-3-Hydroxybutanoate mitochondrial transport via H+ symport	h[c] + bhb[c] <=> h[m] + bhb[m]	1		-1000	1000		Transport, Mitochondrial			
BHMT	betaine-homocysteine S-methyltransferase	hcys-L[c] + glyb[c] -> dmgly[c] + met-L[c]	0	12116.1 or 64918.1	0	1000		Glycine, Serine, and Threonine Metabolism			
BILDGLCURte	bilirubin beta-diglucuronide transport MDR	h2o[c] + atp[c] + bildglcur[c] <=> adp[c] + h[c] + pi[c] + bildglcur[e]	1	17250.1	0	1000		Transport, Extracellular			
BILDGLCURtr	glucuronidated compound transport	bildglcur[c] <=> bildglcur[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
BILGLCURte	bilirubin monoglucuronide transport MDR	h2o[c] + atp[c] + bilglcur[c] <=> adp[c] + h[c] + pi[c] + bilglcur[e]	1	17250.1	0	1000		Transport, Extracellular			
BILGLCURtr	glucuronidated compound transport	bilglcur[c] <=> bilglcur[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
BILIRED	Nad(p)h biliverdin reductase	h[c] + nadph[c] + biliverd[c] -> nadp[c] + bilirub[c]	0	233016.1 or 109778.1	0	1000		Heme Degradation			
BILIRUBt2	bilirubin transport via bicarbonate countertransport	hco3[c] + bilirub[e] <=> hco3[e] + bilirub[c]	1	18669.1	-1000	1000	3	Transport, Extracellular	PMID: 20082599	Transporter is expressed in small and large intestine, transports various compounds. Mutations lead to conjugate hyperbilirubinemia.	
BILIRUBtr	lipid, flip-flop intracellular transport	bilirub[c] <=> bilirub[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
BIOCYTtn	biocytin transport, nuclear	biocyt[c] <=> biocyt[n]	1		-1000	1000		Transport, Nuclear			
BMTer_L	B mannosyltransferase, endoplasmic reticulum	0.1 dolmanp_L[r] + memgacpail_hs[r] -> 0.1 dolp_L[r] + h[r] + m2emgacpail_hs[r]	0	55981.1	0	1000		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
BMTer_U	B mannosyltransferase, endoplasmic reticulum	memgacpail_hs[r] + 0.1 dolmanp_U[r] -> h[r] + m2emgacpail_hs[r] + 0.1 dolp_U[r]	0	55981.1	0	1000		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
BPNT	3',5'-bisphosphate nucleotidase	h2o[c] + pap[c] -> pi[c] + amp[c]	0	23827.1	0	1000		Nucleotides			
BPNT2	3',5'-bisphosphate nucleotidase (paps)	h2o[c] + paps[c] -> pi[c] + aps[c]	0	23827.1	0	1000		Nucleotides			
BTND1	biotinidase (biotin)	h2o[c] + biocyt[c] -> lys-L[c] + btn[c]	0	26363.1	0	1000		Biotin Metabolism			
BTND1n	biotinidase (biotin), nuclear	biocyt[n] + h2o[n] -> btn[n] + lys-L[n]	0	26363.1	0	1000		Biotin Metabolism			
BTNDe	biotinidase (biotin), extracellular	h2o[e] + biocyt[e] -> lys-L[e] + btn[e]	0	26363.1	0	1000		Biotin Metabolism			
BTNDm	biotinidase (biotin), mitochondrial	h2o[m] + biocyt[m] -> lys-L[m] + btn[m]	0	26363.1	0	1000		Biotin Metabolism			
BTNPL	holocarboxylase synthestase (biotin protein ligase)	apoC-Lys[c] + btamp[c] -> h[c] + amp[c] + apoC-Lys_btn[c]	0	110948.1	0	1000		Biotin Metabolism			
BTNPLm	holocarboxylase synthestase (biotin protein ligase), mitochondrial	apoC-Lys[m] + btamp[m] -> h[m] + amp[m] + apoC-Lys_btn[m]	0	110948.1	0	1000		Biotin Metabolism			
BTNTe	release of biotin across the basolatral membrane	btn[c] -> btn[e]	0		0	1000	1	Transport, Extracellular	PMID: 1953660, PMID: 21749321, G.F.M. Ball (2006) Vitamins their role in the human body, Blackwell publishing, chapter 16, page 339-340.	biotin release from the enterocytes along the baso-lateral membrane is carrier protein mediated, Na+ independant and eletroneutral (exact protein involved needs to be further investigated). However pantothenic acid seems to compete with biotin for uptake. also in the presence of pantothenate, more amount of biotin exits enterocytes (PMID: 10064315).	
BTNt2	Biotin reversible transport via proton symport	h[e] + btn[e] <=> h[c] + btn[c]	1	20501.1	-1000	1000		Transport, Extracellular			
BTNt2m	Biotin reversible transport via proton symport, mitochondria	h[c] + btn[c] <=> h[m] + btn[m]	1	20501.1	-1000	1000		Transport, Mitochondrial			
BTNt3i	Biotin transport via sodium symport	h2o[c] + atp[c] + 2 na1[e] + btn[e] -> adp[c] + h[c] + pi[c] + 2 na1[c] + btn[c]	0	330064.1	0	1000		Transport, Extracellular			
BTNt4i	Biotin uptake (antiport)	h[c] + btn[e] -> h[e] + btn[c]	0	80721.1	0	1000		Transport, Extracellular			
BTNtn	Biotin transport, nuclear	btn[c] <=> btn[n]	1		-1000	1000		Transport, Nuclear			
BUP2	beta-ureidopropionase (D-3-amino-isobutanoate forming)	h2o[c] + 2 h[c] + 3uib[c] -> nh4[c] + co2[c] + 3aib-D[c]	0	103149.1	0	1000		Pyrimidine Catabolism			
BUTt2m	Butyrate mitochondrial transport via proton symport, reversible	h[c] + but[c] <=> h[m] + but[m]	1	20501.1	-1000	1000		Transport, Mitochondrial			
BUTt2r	Butyrate transport via proton symport, reversible	h[e] + but[e] <=> h[c] + but[c]	1	20501.1	-1000	1000		Transport, Extracellular			
BVITEt	beta-Tocopherol (Vit. E) transport	bvite[e] -> bvite[c]	0		0	1000		Transport, Extracellular			
BZt	benzoate transport (diffusion)	bz[e] <=> bz[c]	1		-1000	1000		Transport, Extracellular			
BZtr	Benzene transporter, endoplasmic reticulum	bz[c] <=> bz[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
B_MANNASEly	beta-mannosidase, lysosomal	h2o[l] + mn[l] -> acgam[l] + man[l]	0	110173.1	0	1000		N-Glycan Degradation			
C110CPT2m	C110 transport into the mitochondria	coa[m] + dmnoncrn[m] -> crn[m] + dmnoncoa[m]	0		0	1000		Fatty Acid Metabolism			
C14STRr	C-14 sterol reductase	h[r] + 44mctr[r] + nadph[r] -> 44mzym[r] + nadp[r]	0	73166.1	0	1000		Cholesterol Metabolism			
C160CPT1c	production of Palmitoylcarnitine	crn[c] + pmtcoa[c] <=> coa[c] + pmtcrn[c]	1	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	-1000	1000	4	Carnitine shuttle	PMID: 20392676, PMID: 20070908	mentioned in recon1 as C160CPT1	2.3.1.21
C160CPT2	C160 transport into the mitochondria	coa[m] + pmtcrn[m] -> crn[m] + pmtcoa[m]	0	12896.1	0	1000		Carnitine shuttle			
C160CRNt	C160 transport into the mitochondria	pmtcrn[c] -> pmtcrn[m]	0	57279.1	0	1000		Carnitine shuttle			
C161CPT12	carnitine O-palmitoyltransferase	crn[c] + hdd2coa[c] -> coa[c] + hdd2crn[c]	0	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	0	1000		Carnitine shuttle			
C161CPT1c	production of palmitoleoylcarnitine	crn[c] + hdcoa[c] <=> coa[c] + hdcecrn[c]	1	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	-1000	1000	4	Carnitine shuttle	Biochem. J. (1996) 319 (633–640)	in recon1 C161CPT1	2.3.1.21
C161CPT22	C161 transport into the mitochondria	coa[m] + hdd2crn[m] -> crn[m] + hdd2coa[m]	0	12896.1	0	1000		Carnitine shuttle			
C161CPT2m	transport of Hexadecenoyl-CoA into mitochondrial matrix	coa[m] + hdcecrn[m] <=> crn[m] + hdcoa[m]	1	12896.1	-1000	1000	4	Carnitine shuttle	Biochemica et Biophysica Acta 1486(2000) 1-17, Eur. J. Biochem. 244, 1-14 (1997) FEBS 1997, Biochemica et Biophysica Acta 1546(2001) 21-43.	in recon1 C161CPT2	2.3.1.21
C161CRN2t	C161 transport into the mitochondria	hdd2crn[c] -> hdd2crn[m]	0	57279.1	0	1000		Carnitine shuttle			
C161CRNt	C161 transport into the mitochondria	hdcecrn[c] -> hdcecrn[m]	0	57279.1	0	1000		Carnitine shuttle			
C180CPT1	carnitine O-stearoyl transferase	crn[c] + stcoa[c] -> coa[c] + stcrn[c]	0	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	0	1000		Carnitine shuttle			
C180CPT2	carnitine O-stearoyl transferase	coa[m] + stcrn[m] -> crn[m] + stcoa[m]	0	12896.1	0	1000		Carnitine shuttle			
C180CRNt	C180 transport into the mitochondria	stcrn[c] -> stcrn[m]	0	57279.1	0	1000		Carnitine shuttle			
C181CPT1c	transport of Octadecenoyl-CoA into mitochondrial matrix	crn[c] + odecoa[c] <=> coa[c] + odecrn[c]	1	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	-1000	1000	4	Carnitine shuttle	Biochemica et Biophysica Acta 1486(2000) 1-17, Eur. J. Biochem. 244, 1-14 (1997) FEBS 1997, Biochemica et Biophysica Acta 1546(2001) 21-43.	in recon1 C181CPT1	2.3.1.21
C181CPT2m	transport of Octadecenoyl-CoA into mitochondrial matrix	coa[m] + odecrn[m] <=> crn[m] + odecoa[m]	1	12896.1	-1000	1000	4	Carnitine shuttle	Biochemica et Biophysica Acta 1486(2000) 1-17, Eur. J. Biochem. 244, 1-14 (1997) FEBS 1997, Biochemica et Biophysica Acta 1546(2001) 21-43.	in recon1 C181CPT2	2.3.1.21
C181CRNt	C181 transport into the mitochondria	odecrn[c] -> odecrn[m]	0	57279.1	0	1000		Carnitine shuttle			
C204CPT1	carnitine C20:4 transferase	crn[c] + arachdcoa[c] -> coa[c] + arachdcrn[c]	0	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	0	1000		Carnitine shuttle			
C204CPT2	arachidonic acid transport into the mitochondria	coa[m] + arachdcrn[m] -> crn[m] + arachdcoa[m]	0	12896.1	0	1000		Carnitine shuttle			
C204CRNt	arachidonic acid transport into the mitochondria	arachdcrn[c] -> arachdcrn[m]	0		0	1000		Carnitine shuttle			
C20CPT1	C20CPT1	accoa[c] + crn[c] -> coa[c] + acrn[c]	0		0	1000	1	Carnitine shuttle	PMID: 21125791, PMID: 20590847, PMID: 20477950		2.3.1.21
C226COAtx	fatty acid intracellular transport	c226coa[c] <=> c226coa[x]	1		-1000	1000		Transport, Peroxisomal			
C226CPT1	carnitine C22:6 transferase	crn[c] + c226coa[c] -> coa[c] + c226crn[c]	0	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	0	1000		Carnitine shuttle			
C226CPT2	C226 transport into the mitochondria	coa[m] + c226crn[m] -> crn[m] + c226coa[m]	0	12896.1	0	1000		Carnitine shuttle			
C226CRNt	C226 transport into the mitochondria	c226crn[c] -> c226crn[m]	0		0	1000		Carnitine shuttle			
C2M26DCOAHLm	cis-2-Methyl-5-isopropylhexa-2,5-dienoyl-CoA hydro-lyase (m)	h2o[m] + c2m26dcoa[m] <=> 3h26dm5coa[m]	1	11992.1 or 231086.1 or 97212.1	-1000	1000		Limonene and pinene degradation			
C2M26DCOAHLx	cis-2-Methyl-5-isopropylhexa-2,5-dienoyl-CoA hydro-lyase (x)	h2o[x] + c2m26dcoa[x] <=> 3h26dm5coa[x]	1	74147.1 or 51798.1	-1000	1000		Limonene and pinene degradation			
C3STDH1Pr	C-3 sterol dehydrogenase (4-methylzymosterol)	nadp[r] + 4mzym_int1[r] -> h[r] + nadph[r] + 4mzym_int2[r] + co2[r]	0	18194.1	0	1000		Cholesterol Metabolism			
C3STDH1r	C-3 sterol dehydrogenase (4-methylzymosterol)	4mzym_int1[r] + nad[r] -> h[r] + 4mzym_int2[r] + co2[r] + nadh[r]	0	18194.1	0	1000		Cholesterol Metabolism			
C3STKR2r	C-3 sterol keto reductase (zymosterol)	h[r] + nadph[r] + zym_int2[r] -> nadp[r] + zymst[r]	0	15488.1	0	1000		Cholesterol Metabolism			
C4STMO1r	C-4 sterol methyl oxidase (4,4-dimethylzymosterol)	3 o2[r] + 3 h[r] + 3 nadph[r] + 44mzym[r] -> 4 h2o[r] + 3 nadp[r] + 4mzym_int1[r]	0	66234.1	0	1000		Cholesterol Metabolism			
C4STMO2Pr	C-4 methyl sterol oxidase	o2[r] + nadp[r] + 4mzym_int2[r] -> h[r] + nadph[r] + co2[r] + zym_int2[r]	0	18194.1	0	1000		Cholesterol Metabolism			
C4STMO2r	C-4 methyl sterol oxidase	o2[r] + 4mzym_int2[r] + nad[r] -> h[r] + co2[r] + nadh[r] + zym_int2[r]	0	66234.1 or 18194.1	0	1000		Cholesterol Metabolism			
CAATPS	Ca ATPase	h2o[c] + atp[c] + 2 ca2[c] -> adp[c] + pi[c] + h[e] + 2 ca2[e]	0	11941.1 or 67972.1 or 381290.1 or 320707.1	0	1000		Transport, Extracellular			
CAMPt	cAMP transport (ATP-dependent)	h2o[c] + atp[c] + camp[c] -> adp[c] + h[c] + pi[c] + camp[e]	0	27416.1 or 27416.2 or 239273.1	0	1000		Transport, Extracellular			
CARNCNc	hydrolysis of L-Carnosine for uptake	h2o[c] + carn[c] <=> ala-B[c] + his-L[c]	1	(338403.1 or 66054.1)	-1000	1000	3	Dipeptide Degradation	PMID: 6993048, PMCID: PMC1412501, PMID: 4919261, PMID: 20178671, PMID: 12473676	Dipeptides and tripeptides enter the brush border of the intestinal mucosal cells, where they are hydrolyzed to free amino acids, which are then transported into hepatic portal vein. Peptides entering by transcellular or paracellular mechanisms elicit allergic reactions to food (Robert K. Murray, David A. Bender, Kathleen M. Botham, Peter J. kennelly, Victor W. Rodwell, P. Anthony Weil (2009) 28th edition, Harper's illustrated biochemistry,Mc Graw Hill, page 462). formation and hydrolysis of diglycine is a reversible process (David L. Nelson, Michael M. Cox, Lehniniger principles of biochemistry (2000), 3rd edition, worth publishers,page 69, figure 3a). CN1 is expressed in brain where as CN2 is more ubiquitously expressed (PMID: 12473676). Recon 1 mentions this reaction as NBAHH_ir which needs to be replaced.	3.4.13.20 or 3.4.13.18

CAROe	beta-carotene transport via diffusion	caro[e] <=> caro[c]	1		-1000	1000		Transport, Extracellular			
CARPEPTtc	transport of L-Carnosine by the apical PEPT1 amino acid transporters across the brush border cells of the enterocytes of the intestine and renal cells	hl[u] + carn[u] -> hl[c] + carn[c]	0	215335.1	0	1000	3	Transport, Lumen	PMID: 7858848, PMID: 14965252, PMID: 14977407, PMID: 10330047	PEPT1 appears to transport all di- and tri- peptides across the brush border of the intestinal cells (Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Advanced nutrition and human metabolism. Wadsworth cengage learning, 5th edition, page 193). PEPT1 is expressed highly in intestinal cells where as PEPT2 is localized to renal cells (PMID: 10330047).	
CARVEOLse	xenobiotic transport	carveol[e] <=> carveol[c]	1		-1000	1000		Transport, Extracellular			
CARhPTtc	transport of L-Carnosine by hPT3 or hPT4 peptide transporter.	carn[l] -> hl[l] + carn[c]	0	(65221.1 or 100561.1)	0	1000	3	Transport, Lysosomal	PMID: 16289537, PMID: 12905028, PMID: 17681807	hPT3 (human peptide transporter 3) transports histidine and di-peptides from the lysosomes into the cytosol. Co-transports proton, expressed in lung, thymus, spleen and faintly in brain, placenta, liver, adrenal gland and heart (PMID: 12905028). hPT4 expressed in brain, placenta and retina. Transports carnosine and histidine in a proton symport mechanism. (PMID: 12905028).	
CAT2p	catalase A, peroxisomal (ethanol)	h2o2[x] + etoh[x] -> acald[x] + 2 h2o[x]	0	12359.1	0	1000		Glycolysis/Gluconeogenesis			
CATm	catalase	2 h2o2[m] -> o2[m] + 2 h2o[m]	0	12359.1	0	1000		ROS Detoxification			
CATp	catalase A, peroxisomal	2 h2o2[x] -> o2[x] + 2 h2o[x]	0	12359.1	0	1000		Miscellaneous			
CAtr	calcium / sodium antiporter (1:3), reversible	3 na1[e] + ca2[c] <=> 3 na1[c] + ca2[e]	1	110893.1 or 110893.2 or 110893.1 or 20541.1 or 110893.3 or 110893.4 or 110893.5 or 110893.6	-1000	1000		Transport, Extracellular			
CBL2OR	NADH:cob(II)alamine oxidoreductase	h[c] + nadh[c] + 2 aqcobal[c] -> 2 h2o[c] + nad[c] + 2 cbl2[c]	0		0	1000		Vitamin B12 Metabolism			
CBL2tm	Cob(II)alamine transport, mitochondrial	cbl2[c] -> cbl2[m]	0	109136.1	0	1000		Transport, Mitochondrial			
CBLATm	cob(I)alamin adenosyltransferase, mitochondrial	h[m] + atp[m] + cbl1[m] <=> adocbl[m] + ppp[m]	1	109136.1	-1000	1000		Vitamin B12 Metabolism			
CBLTDe_r	release of B12 by simple diffusion, reversible	adocbl[c] <=> adocbl[e]	1		-1000	1000	1	Transport, Extracellular	Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Advanced nutrition and human metabolism, Wadsworth cengage learning, 5th edition, page 359-360. AH: Made this reaction reversible for my model's functionality.	binds to transcobalamin II within the enterocyte before release into the portal blood.	
CBLtbi	transport of Adenosylcobalamin into the intestine	adocbl[u] -> adocbl[c]	0	(14603.1 or 65969.1 or 93835.1)	0	1000	3	Transport, Lumen	PMCID: PMC2669139, James Zempleni, Robert B. Rucker, Donald B. McCormick, John W. Suttie (2007) Handbook of vitamins, CRC press, chapter 13, page 418–422	Cobalamin binds intrinsic factor and then the complex binds cubilin and amnionless (that serve as anchors for the receptor). Even though megalin (MAG) and receptor-associated protein (RAP) can interact with CUB, the precise role if any, of these proteins in CUB-mediated absorption of IF-Cbl has not been determined (PMCID: PMC2809139). absorption of cobalamin can also occur by simple diffusion along the entire small intestine, this accounts for 1-3% of the dieatry vitamin, however significant role under pharmacological doses (G.F.M. Ball (2006) Vitamins their role in the human body, Blackwell publishing, chapter 18, page 386).	
CBPPer	Carbamoyl phosphate phosphotransferase, endoplasmic reticulum	hl[r] + chp[r] + glc-D[r] -> co2[r] + gfap[r] + sbd[r]	0	14378.1 or 14377.1 or 68401.1	0	1000		Glycolysis/Gluconeogenesis			
CBPS	carbamoyl-phosphate synthase (glutamine-hydrolysing)	h2o[c] + 2 atp[c] + hco3[c] + gln-L[c] -> 2 adp[c] + 2 h[c] + pi[c] + glu-L[c] + cbp[c]	0	69719.1	0	1000		Pyrimidine Biosynthesis			
CBPSam	carbamoyl-phosphate synthase (ammonia) (mitochondria)	2 atp[m] + hco3[m] + nh4[m] -> 2 h[m] + 2 adp[m] + pi[m] + cbp[m]	0	227231.1 or 227231.2	0	1000		Glutamate metabolism			
CBPter	carbamoyl phosphate transport, endoplasmic reticulum	pi[c] + ppi[c] + cbp[c] <=> cbp[r] + pi[r] + ppi[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
CBR1	Carbonyl reductase [NADPH] 1	h[c] + nadph[c] + prostg2[c] -> nadp[c] + prostgr1[c]	0	12408.1	0	1000		Eicosanoid Metabolism			
CBR2	Carbonyl reductase [NADPH] 1	h[c] + nadph[c] + prostge2[c] -> nadp[c] + prostgf2[c]	0	12408.1	0	1000		Eicosanoid Metabolism			
CCA_D3r	Calcitroic acid transport from cytosol	cca_d3[c] -> cca_d3[e]	0		0	1000		Transport, Extracellular			
CCA_D3tm	Calcitroic acid transport from mitochondria	cca_d3[m] -> cca_d3[c]	0		0	1000		Transport, Mitochondrial			
CDIPTr	phosphatidylinositol synthase (Homo sapiens)	cdpdag_hs[c] + inost[c] <=> h[c] + cmp[c] + pail_hs[c]	1	52858.1 or 52858.2	-1000	1000		Glycerophospholipid Metabolism			
CDPDAGtm	intracellular transport	cdpdag_hs[c] <=> cdpdag_hs[m]	1		-1000	1000		Transport, Mitochondrial			
CDS	phosphatidate cytidylyltransferase	h[c] + pa_hs[c] + ctp[c] -> ppi[c] + cdpdag_hs[c]	0	74596.1	0	1000		Glycerophospholipid Metabolism			
CDSm	phosphatidate cytidylyltransferase	h[m] + ctp[m] + pa_hs[m] -> ppi[m] + cdpdag_hs[m]	0	11091.1	0	1000		Glycerophospholipid Metabolism			
CEPTC	choline phosphotransferase	cdpchol[c] + dag_hs[c] -> h[c] + cmp[c] + pchol_hs[c]	0	212862.1 or 99712.1	0	1000		Glycerophospholipid Metabolism			
CEPTE	ethanolamine phosphotransferase	cdpea[c] + dag_hs[c] -> h[c] + cmp[c] + pe_hs[c]	0	99712.1	0	1000		Glycerophospholipid Metabolism			
CERK	Ceramide kinase	atp[c] + crm_hs[c] -> adp[c] + h[c] + crmp_hs[c]	0	223753.1 or 223753.2	0	1000		Sphingolipid Metabolism			
CERT1gt	ceramide transport protein	crm_hs[c] <=> crm_hs[g]	1	68018.1	-1000	1000		Transport, Golgi Apparatus			
CERT1rt	ceramide transport protein	crm_hs[c] <=> crm_hs[r]	1	68018.1	-1000	1000		Transport, Endoplasmic Reticular			
CERT2gt	ceramide transport protein	gluside_hs[c] <=> glusidе_hs[g]	1	68018.1	-1000	1000		Transport, Golgi Apparatus			
CERT2rt	ceramide transport protein	glusidе_hs[c] <=> glusidе_hs[r]	1	68018.1	-1000	1000		Transport, Endoplasmic Reticular			
CGLYG_2_	Cys-Gly transport in via proton symport	2 h[e] + cglyb[e] -> 2 h[c] + cglyb[c]	0	57738.1	0	1000	2	Transport, Extracellular			
CGMPt	cGMP transport (ATP-dependent)	h2o[c] + atp[c] + 35cgmp[c] -> adp[c] + h[c] + pi[c] + 35cgmp[e]	0	27416.1 or 27416.2 or 259273.1	0	1000		Transport, Extracellular			
CH25H	cholesterol 25-hydroxylase	ns2[r] + h[r] + nadph[r] + chsterol[r] -> h2o[r] + nadp[r] + ns225oh[r]	0	12642.1	0	1000		Bile Acid Biosynthesis			
CHAT	Choline O-acetyltransferase	accoa[c] + chol[c] <=> coa[c] + achl[c]	1	12647.1 or 12647.2 or 12647.3 or 12647.4	-1000	1000		Glycerophospholipid Metabolism			
CHATn	Choline O-acetyltransferase	accoa[n] + chol[n] <=> achl[n] + coa[n]	1	12647.1 or 12647.2 or 12647.3 or 12647.4	-1000	1000		Glycerophospholipid Metabolism			
CHLP	choline phosphate phosphatase	h2o[c] + cholp[c] -> pi[c] + chol[c]	0	237928.1	0	1000		Glycerophospholipid Metabolism			
CHLPCTD	choline phosphate cytidylyltransferase	h[c] + ctp[c] + cholp[c] -> ppi[c] + cdpchol[c]	0	13026.1 or 236899.1	0	1000		Glycerophospholipid Metabolism			
CHLtm	choline transport via diffusion (cytosol to mitochondria)	chol[c] <=> chol[m]	1		-1000	1000		Transport, Mitochondrial			
CHOLABCAet	efflux of Cholesterol into the lymph	h2o[c] + atp[c] + chsterol[c] -> adp[c] + h[c] + pi[c] + chsterol[e]	0	11303.1	0	1000	3	Transport, Extracellular	PMID: 21188557, PMID: 18692849, PMID: 20454462	ABCA1 is responible for the efflux of cholesterol from the enterocytes into the lymph, for incorporation into nascant HDL, accounts for 30% of reverse cholesterol transfer (PMID: 21188557)	
CHOLABSetc	efflux of Cholesterol from the enterocytes into lumen	h2o[c] + atp[c] + chsterol[c] -> adp[c] + h[c] + pi[c] + chsterol[u]	0	(27409.1 and 67470.1)	0	1000	3	Transport, Lumen	PMID: 18692849, PMID: 18850127, PMID: 15992510, PMID: 20454462	ABCG5 and ABCG8 are heterodimers, expressed in the enterocytes, involved in the efflux of the cholesterol from small intestine (i.e. Enterocytes) into the luminal cells of the small intestine, to reduce cholesterol uptake.	
CHOLATEt2	cholate transport via sodium cotransport	2 na1[u] + cholate[e] -> 2 na1[c] + cholate[c]	0	20494.1 or 20493.1	0	1000		Transport, Extracellular			
CHOLATEt3	ABC bile acid transporter	h2o[c] + atp[c] + cholate[c] -> adp[c] + h[c] + pi[c] + cholate[e]	0	27413.1 or 76408.2 or 76408.3 or 76408.1	0	1000		Transport, Extracellular			
CHOLD2tm	choline dehydrogenase (FAD acceptor), mitochondrial	fad[m] + chol[m] -> fadh2[m] + betald[m]	0	218865.1	0	1000		Glycine, Serine, and Threonine Metabolism			
CHOLESTTDe	Transport, extracellular	chsterol[c] -> chsterol[e]	0		0	1000	2	Transport, Extracellular	Sareen S. Gropper, jack L. Smith, James L. Groff (2009) Wadsworth cengage learning, Advanced nutrition and human metabolism, 5th edition, page 142-148.	transported in chylomicrons into lymph	
CHOLETDiu	diffussion of cholesterol accross the brush border membrane	chsterol[u] <=> chsterol[c]	1		-1000	1000	2	Transport, Lumen	Sareen S. Gropper, jack L. Smith, James L. Groff (2009) Wadsworth cengage learning, Advanced nutrition and human metabolism, 5th edition, page 142-144.		
CHOLK	Choline kinase	atp[c] + chol[c] -> adp[c] + h[c] + cholp[c]	0	12651.1 or 12660.1 or 12651.2 or 12660.2	0	1000		Glycerophospholipid Metabolism			
CHOLNPtc	uptake of Cholesterol from the lumen	chsterol[u] -> chsterol[c]	0	237636.1	0	1000	3	Transport, Lumen	PMID: 21188557, PMID: 21602275, PMID: 20454462, PMID: 18692849, PMID: 14976318, PMID: 18585981	Niemann-Pick C1-like protein 1 is indespensable for intestinal uptake of cholesterol from the mixed micelles. SR-BI has no apparent role in intestinal uptake of cholesterol and that NPC1L1 is mainly responsible (PMID: 18585981)	
CHOLPtg	choline phosphate intracellular transport	cholp[c] <=> cholp[g]	1		-1000	1000		Transport, Golgi Apparatus			
CHOLPtl	choline phosphate intracellular transport	cholp[c] <=> cholp[l]	1		-1000	1000		Transport, Lysosomal			
CHOLt4	choline, sodium cotransport	na1[e] + chol[e] <=> na1[c] + chol[c]	1	63993.1	-1000	1000		Transport, Extracellular			
CHOLtg	choline intracellular transport	chol[a] <=> chol[c]	1		-1000	1000		Transport, Golgi Apparatus			
CHOLtn	Choline transport, nuclear through pores	chol[c] <=> chol[n]	1		-1000	1000		Transport, Nuclear			
CHOLtr	choline intracellular transport	chol[r] <=> chol[c]	1		-1000	1000		Transport, Endoplasmic Reticular			
CHOLtu	Choline uniport	chol[e] <=> chol[c]	1	20518.1 or 20520.1 or 20518.2	-1000	1000		Transport, Extracellular			
CHSTEROLSULT	sterosil sulfotransferase	psyn[c] + chsterol[c] -> h[c] + psyp[c] + chsterolsd[c]	0	54260.1	0	1000		Steroid Metabolism			
CHSTEROLt	cholesterol efflux (ATP dependent)	h2o[c] + atp[c] + chsterol[c] -> adp[c] + h[c] + pi[c] + chsterol[e]	0	11303.1	0	1000		Transport, Extracellular			
CHSTEROLt1	cholesterol intracellular transport	chsterol[l] <=> chsterol[m]	1	59045.1	-1000	1000		Transport, Mitochondrial			
CHSTEROLt2	cholesterol intracellular transport	chsterol[r] <=> chsterol[m]	1		-1000	1000		Transport, Mitochondrial			
CHSTEROLt3	cholesterol intracellular transport	chsterol[r] <=> chsterol[m]	1		-1000	1000		Transport, Mitochondrial			
CHSTEROLtg	cholesterol efflux (ATP dependent), golgi	h2o[c] + atp[c] + chsterol[g] -> adp[c] + h[c] + pi[c] + chsterol[c]	0	11303.1	0	1000		Transport, Golgi Apparatus			
CHTNASE	chitinase	2 h2o[c] + chtn[c] -> 3 acgam[c]	0	81600.1 or 71884.1 or 67729.1	0	1000		Aminosugar Metabolism			
CHTNASEe	chitinase, extracellular	2 h2o[e] + chtn[e] -> 3 acgam[e]	0	81600.2	0	1000		Aminosugar Metabolism			
CITL	Citrate lyase	cit[c] -> ac[c] + oaa[c]	0	69634.1 or 69634.2	0	1000		Citric Acid Cycle			
CITMCOAHm	L-Citramalyl-CoA hydro-lyase, mitochondrial	h2o[m] + itaccoa[m] <=> cimcoa-L[m]	1		-1000	1000		C5-Branched dibasic acid metabolism			
CITMCOALm	L-Citramalyl-CoA pyruvate-lyase	cimcoa-L[m] -> pyr[m] + accoa[m]	0		0	1000		C5-Branched dibasic acid metabolism			
CITRtm	citrulline mitochondrial transport via proton antiport	citr-L[m] <=> citr-L[c]	1	18408.1 or 83885.1	-1000	1000		Transport, Mitochondrial			
CITt4_2	citrate transport via sodium symport	2 na1[e] + cit[e] <=> 2 na1[c] + cit[c]	1	20500.1	-1000	1000		Transport, Extracellular			
CITt4_4	citrate transport via sodium symport	4 na1[e] + cit[e] <=> 4 na1[c] + cit[c]	1	237831.1	-1000	1000		Transport, Extracellular			
CITtam	citrate transport, mitochondrial	cit[c] + mal-L[m] <=> cit[m] + mal-L[c]	1	13358.1	-1000	1000		Transport, Mitochondrial			
CITtim	citrate transport, mitochondrial	cit[c] + pep[m] <=> pep[c] + cit[m]	1	13358.1	-1000	1000		Transport, Mitochondrial			
CK	ATP Creatine kinase	atp[m] + crea[m] <=> adp[m] + pcrea[m]	1	76722.1	0	1000		Urea cycle/amino group metabolism			
CKc	ATP Creatine kinase (c)	atp[c] + crea[c] <=> adp[c] + pcrea[c]	1	12709.1 or 12715.1	-1000	1000		Urea cycle/amino group metabolism			
CLFORtex	chloride transport via formate countertransport	2 for[c] + cl[e] -> 2 cl[c] + for[e]	0	23985.1	0	1000		Transport, Extracellular			
CLFORtex2	chloride transport via formate countertransport (2:1)	for[c] + 2 cl[e] -> 2 cl[c] + for[e]	0	171429.1 or 171429.2 or 171429.3	0	1000		Transport, Extracellular			
CLHCO3tex2	chloride transport via bicarbonate countertransport (2:1)	hco3[c] + 2 cl[e] -> hco3[e] + 2 cl[c]	0	171429.1 or 171429.2 or 171429.3	0	1000		Transport, Extracellular			
CLHCOtex	chloride transport via bicarbonate countertransport	2 hco3[c] + cl[e] -> 2 hco3[e] + cl[c]	0	13487.1 or 224661.1 or 268880.1 or 224661.2 or 320718.1 or 13521.1 or 23985.1 or 268890.2 or 320718.2	0	1000		Transport, Extracellular			
CLI2tex	chloride transport via iodide countertransport	cl[e] + 2 i[c] -> cl[c] + 2 i[e]	0	23985.1	0	1000		Transport, Extracellular			

CLOHtex2	chloride transport via hydroxide countertransport (2:1)	oh1[c] + 2 cl[e] -> 2 cl[c] + oh1[e]	0	171429.1 or 171429.2 or 171429.3	0	1000		Transport, Extracellular			
CLOXAtex2	chloride transport via oxalate countertransport (2:1)	2 cl[e] + oxa[c] -> 2 cl[c] + oxa[e]	0	171429.1 or 171429.2 or 171429.3	0	1000		Transport, Extracellular			
CLPNDCOAtx	fatty acid intracellular transport	clpndcoa[c] <=> clpndcoa[x]	1		-1000	1000		Transport, Peroxisomal			
CLPNDCPT1	carnitine O-palmitoyltransferase	crn[c] + clpndcoa[c] -> coa[c] + clpndcrn[c]	0	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	0	1000		Carnitine shuttle			
CLPNDCPT2	carnitine transferase	coa[m] + clpndcrn[m] -> crn[m] + clpndcoa[m]	0	12896.1	0	1000		Carnitine shuttle			
CLPNDCRNt	transport into the mitochondria (carnitine)	clpndcrn[c] -> clpndcrn[m]	0	57279.1	0	1000		Carnitine shuttle			
CLPNDt	fatty acid transport via diffusion	clpnd[e] <=> clpnd[c]	1		-1000	1000		Transport, Extracellular			
CLS_hs	cardiolipin synthase (homo sapiens)	cdpdag_hs[c] + pglyc_hs[c] -> h[c] + cmp[c] + clpn_hs[c]	0	66586.1	0	1000		Glycerophospholipid Metabolism			
CMPACNAtg	CMP-Sia Golgi transport via CMP antiport	cmpacna[c] + cmp[g] <=> cmp[c] + cmpacna[g]	1	24060.1	-1000	1000		Transport, Golgi Apparatus			
CMPACNAtn	CMP-Sia nuclear export	cmpacna[n] -> cmpacna[c]	0		0	1000		Transport, Nuclear			
CMPSAS	CMP sialic acid synthase	acnam[c] + ctp[c] -> ppi[c] + cmpacna[c]	0	12764.1	0	1000		Aminosugar Metabolism			
CMPSASn	CMP sialic acid synthase, nuclear	acnam[n] + ctp[n] -> cmpacna[n] + ppi[n]	0	12764.1	0	1000		Aminosugar Metabolism			
CO2t	CO2 transporter via diffusion	co2[e] <=> co2[c]	1		-1000	1000		Transport, Extracellular			
CO2ter	CO2 endoplasmic reticular transport via diffusion	co2[c] <=> co2[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
CO2tg	CO2 Golgi transport	co2[c] <=> co2[g]	1		-1000	1000		Transport, Golgi Apparatus			
CO2tm	CO2 transport (diffusion), mitochondrial	co2[c] <=> co2[m]	1		-1000	1000		Transport, Mitochondrial			
CO2tn	CO2 nuclear transport via diffusion	co2[n] <=> co2[c]	1		-1000	1000		Transport, Nuclear			
CO2tp	CO2 peroxisomal transport	co2[c] <=> co2[x]	1		-1000	1000		Transport, Peroxisomal			
COAtg	CoA transport in golgi via diffusion	coa[c] <=> coa[g]	1		-1000	1000		Transport, Golgi Apparatus			
COAtl	CoA transport in lysosome via diffusion	coa[c] <=> coa[l]	1		-1000	1000		Transport, Lysosomal			
COAtm	CoA transporter	coa[c] <=> coa[m]	1	73132.1	-1000	1000		Transport, Mitochondrial			
COAtn	coenzyme A transport, nuclear	coa[c] <=> coa[n]	1		-1000	1000		Transport, Nuclear			
COAtp	coenzyme A transport, peroxisomal	coa[c] <=> coa[x]	1		-1000	1000		Transport, Peroxisomal			
COAtr	COA transporter, endoplasmic reticulum	coa[c] <=> coa[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
COKECBESr	Carboxylesterase (cocaine) (er)	h2o[r] + coke[r] -> h[r] + bz[r] + egme[r]	0	436059.1	0	1000		Alkaloid biosynthesis II			
COQ3m	methyltransferase COQ3	amet[m] + 2dpmhobq[m] -> h[m] + ahcys[m] + q10[m]	0	230027.1	0	1000		Ubiquinone Biosynthesis			
COQ5m	Ubiquinone biosynthesis methyltransferase COQ5	amet[m] + 2dp6mobq[m] -> h[m] + ahcys[m] + 2dp6mobq_me[m]	0		0	1000		Ubiquinone Biosynthesis			
COQ6m	Ubiquinone biosynthesis monooxgenase COQ6	o2[m] + 2dp6mep[m] -> h2o[m] + 2dp6mobq[m]	0	217707.1 or 217707.2	0	1000		Ubiquinone Biosynthesis			
COQ7m	Ubiquinone biosynthesis COQ7	h[m] + nadph[m] + o2[m] + 2dp6mobq_me[m] -> h2o[m] + nadp[m] + 2dpmhobq[m]	0	12850.1	0	1000		Ubiquinone Biosynthesis			
CORE3GTg	Core 3 beta-GlcNAc-transferase, Golgi apparatus	uacgam[g] + Tn_antigen[g] -> h[g] + udp[g] + core3[g]	0	272411.1	0	1000		O-Glycan Biosynthesis			
CORE4GTg	Core 4 beta6-GalNAc-transferase, Golgi apparatus	uacgam[g] + core3[g] -> h[g] + udp[g] + core4[g]	0	72077.1	0	1000		O-Glycan Biosynthesis			
CORE4t	Core4 (mucin O-glycan) export	core4[g] -> core4[e]	0		0	1000	2	Transport, Extracellular	PMID: 10430883, PMID: 848954	Reaction that provides mucin O-glycans to gut microbiota, e.g. B. thetaiotaomicron. BT is well known to degrade mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis.	
CORE5GTg	Core 5 alpha-GalNAc-transferase, Golgi apparatus	udpacgal[g] + Tn_antigen[g] -> h[g] + udp[g] + core5[g]	0		0	1000		O-Glycan Biosynthesis			
CORE5t	Core5 (mucin O-glycan) export	core5[g] -> core5[e]	0		0	1000	2	Transport, Extracellular	PMID: 10430883, PMID: 848954	Reaction that provides mucin O-glycans to gut microbiota, e.g. B. thetaiotaomicron. BT is well known to degrade mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis.	
CORE6GTg	Core 6 beta-GlcNAc-transferase A, Golgi apparatus	uacgam[g] + Tn_antigen[g] -> h[g] + udp[g] + core6[g]	0	14537.1	0	1000		O-Glycan Biosynthesis			
CORE7GTg	Core 7 alpha-GalNAc-transferase, Golgi apparatus	udpacgal[g] + Tn_antigen[g] -> h[g] + udp[g] + core7[g]	0		0	1000		O-Glycan Biosynthesis			
CORE7t	Core7 (mucin O-glycan) export	core7[g] -> core7[e]	0		0	1000	2	Transport, Extracellular	PMID: 10430883, PMID: 848954	Reaction that provides mucin O-glycans to gut microbiota, e.g. B. thetaiotaomicron. BT is well known to degrade mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis.	
CORE8GTg	N-acetylgalactosamine 3-alpha-galactosyltransferase, Golgi apparatus	udpgal[g] + Tn_antigen[g] -> h[g] + udp[g] + core8[g]	0		0	1000		O-Glycan Biosynthesis			
CORE8t	Core8 (mucin O-glycan) export	core8[g] -> core8[e]	0		0	1000	2	Transport, Extracellular	PMID: 10430883, PMID: 848954	Reaction that provides mucin O-glycans to gut microbiota, e.g. B. thetaiotaomicron. BT is well known to degrade mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis.	
COUCOAFm	p-coumaroyl-CoA formation	coa[m] + atp[m] + T4hcinnm[m] -> coucoa[m] + amp[m] + ppi[m]	0		0	1000		Ubiquinone Biosynthesis			
COUMARINte	xenobiotic transport	coumarin[e] <=> coumarin[c]	1		-1000	1000		Transport, Extracellular			
COt	CO transporter via diffusion	co[c] <=> co[e]	1		-1000	1000		Transport, Extracellular			
CPCTDTX	choline-phosphate cytidylyltransferase	h[c] + ctp[c] + ntm2amep[c] -> ppi[c] + cmpntm2amep[c]	0	13026.1 or 236899.1	0	1000		Glycerophospholipid Metabolism			
CPPPGO	coproporphyrinogen oxidase (O2 required)	o2[c] + 2 h[c] + cpppg3[c] -> 2 h2o[c] + 2 co2[c] + pppg9[c]	0	12892.1	0	1000		Heme Biosynthesis			
CREATt4_2_r	Creatine transport (sodium symport) (2:1)	2 na1[e] + creat[e] <=> 2 na1[c] + creat[c]	1	102857.1	-1000	1000	0	Transport, Extracellular			
CREATtmdiffir	Creatine transport to/from mitochondria via diffusion	creat[c] -> creat[m]	0		0	1000		Urea cycle/amino group metabolism			
CRMPte	crmp_hs transport	crmp_hs[c] <=> crmp_hs[e]	1		-1000	1000		Transport, Extracellular			
CRNCAR3tp	carnitine-propcarnitine carrier, peroxisomal	crn[c] + pcrn[x] -> pcrn[c] + crn[x]	0		0	1000		Transport, Peroxisomal			
CRNCARtp	carnitine-acetylcarnitine carrier, peroxisomal	crn[c] + acrn[x] -> acrn[c] + crn[x]	0		0	1000		Transport, Peroxisomal			
CRNt	L-carnitine reversible transport	crn[e] <=> crn[c]	1	20520.1	-1000	1000		Transport, Extracellular			
CRNtHa	L-carnitine outward transport (H+ antiport)	h[e] + crn[c] -> h[c] + crn[e]	0	30805.1	0	1000		Transport, Extracellular			
CRNtim	L-carnitine transport out of mitochondria via diffusion	crn[m] -> crn[c]	0	57279.1	0	1000		Transport, Mitochondrial			
CRNtuIR	L-carnitine inward uniport	crn[e] -> crn[c]	0	30805.1	0	1000		Transport, Extracellular			
CRNtuNa	L-carnitine inward transport by Na+ symport	na1[e] + crn[e] -> na1[c] + crn[c]	0	20520.1	0	1000		Transport, Extracellular			
CRNtx	carnitine transport peroxisome to mitochondria	dmnoncrn[x] <=> dmnoncrn[m]	1		-1000	1000		Transport, Peroxisomal			
CRTNsyn	Creatinine synthase	pcreat[c] -> h[c] + pi[c] + crtn[c]	0		0	1000		Urea cycle/amino group metabolism			
CRTSLt	cortisol transmembrane (homo sapiens) transport	crtsl[e] <=> crtsl[c]	1		-1000	1000		Transport, Extracellular			
CRTSLtm	cortisol intracellular transport	crtsl[c] <=> crtsl[m]	1		-1000	1000		Transport, Mitochondrial			
CRTSLtr	cortisol intracellular transport	crtsl[c] <=> crtsl[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
CRTSTRNt	corticosterone transmembrane (homo sapiens) transport	crtstrn[e] <=> crtstrn[c]	1		-1000	1000		Transport, Extracellular			
CRTSTRNtm	corticosterone intracellular transport	crtstrn[c] <=> crtstrn[m]	1		-1000	1000		Transport, Mitochondrial			
CRTSTRNtr	corticosterone intracellular transport	crtstrn[c] <=> crtstrn[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
CRVNCtr	fatty acid transport via diffusion	crvnc[e] <=> crvnc[c]	1		-1000	1000		Transport, Extracellular			
CSAPASEly	chondroitin sulfate A proteoglycan protease, lysosome (endosome)	h2o[l] + cspg_a[l] -> Ser_Gly_Ala_X_Gly[l] + cs_a[l]	0		0	1000		Chondroitin sulfate degradation			
CSBPASEly	chondroitin sulfate B proteoglycan protease, lysosome (endosome)	h2o[l] + cspg_b[l] -> Ser_Gly_Ala_X_Gly[l] + cs_b[l]	0		0	1000		Chondroitin sulfate degradation			
CSCPASEly	chondroitin sulfate C proteoglycan protease, lysosome (endosome)	h2o[l] + cspg_c[l] -> Ser_Gly_Ala_X_Gly[l] + cs_c[l]	0		0	1000		Chondroitin sulfate degradation			
CSDPASEly	chondroitin sulfate D proteoglycan protease, lysosome (endosome)	h2o[l] + cspg_d[l] -> Ser_Gly_Ala_X_Gly[l] + cs_d[l]	0		0	1000		Chondroitin sulfate degradation			
CSEPASEly	chondroitin sulfate E proteoglycan protease, lysosome (endosome)	h2o[l] + cspg_e[l] -> Ser_Gly_Ala_X_Gly[l] + cs_e[l]	0		0	1000		Chondroitin sulfate degradation			
CSNAT2m	carnitine O-aceyltransferase, mitochondrial	coa[m] + pcrn[m] <=> ppcoa[m] + crn[m]	1	12908.1	-1000	1000		Carnitine shuttle			
CSNAT2x	carnitine dimethyl nonanoyl transferase, revsible, peroxisomal	crn[x] + dmnoncoa[x] <=> coa[x] + dmnoncrn[x]	1	12908.2 or 74114.1	-1000	1000		Fatty Acid Metabolism			
CSNAT3x	carnitine O-aceyltransferase, peroxisomal	crn[x] + ppcoa[x] <=> coa[x] + pcrn[x]	1	12908.2	-1000	1000		Carnitine shuttle			
CSNATer	carnitine O-acetyltransferase, endolasmic reticulum	accoa[r] + crn[r] <=> coa[r] + acrn[r]	1	12908.3	-1000	1000		Fatty Acid Metabolism			
CSNATm	carnitine O-aceyltransferase, mitochondrial	coa[m] + acrn[m] <=> accoa[m] + crn[m]	1	12908.1	-1000	1000		Fatty Acid Metabolism			
CSNATp	carnitine O-acetyltransferase, reverse direction, peroxisomal	accoa[x] + crn[x] <=> coa[x] + acrn[x]	1	12908.2	-1000	1000		Fatty Acid Metabolism			
CSNATr	carnitine O-acetyltransferase	accoa[c] + crn[c] <=> coa[c] + acrn[c]	1		-1000	1000		Carnitine shuttle			
CSND	Cytosine deaminase	h2o[c] + h[c] + csn[c] -> nh4[c] + ura[c]	0		0	1000		Pyrimidine Catabolism			
CSNt	cytosine transport via facilated diffusion	csn[e] <=> csn[c]	1	13340.1	-1000	1000		Transport, Extracellular			
CSPG_At	chondroitin sulfate A transport, golgi to extracellular	cspg_a[g] -> cspg_a[e]	0		0	1000		Transport, Extracellular			
CSPG_Atly	chondroitin sulfate A transport, extracellular to lysosome	cspg_a[e] -> cspg_a[l]	0		0	1000		Transport, Lysosomal			
CSPG_Bt	chondroitin sulfate B transport, golgi to extracellular	cspg_b[g] -> cspg_b[e]	0		0	1000		Transport, Extracellular			
CSPG_Btly	chondroitin sulfate B transport, extracellular to lysosome	cspg_b[e] -> cspg_b[l]	0		0	1000		Transport, Lysosomal			
CSPG_Ct	chondroitin sulfate C transport, golgi to extracellular	cspg_c[g] -> cspg_c[e]	0		0	1000		Transport, Extracellular			
CSPG_Ctly	chondroitin sulfate C transport, extracellular to lysosome	cspg_c[e] -> cspg_c[l]	0		0	1000		Transport, Lysosomal			
CSPG_Dt	chondroitin sulfate D transport, golgi to extracellular	cspg_d[g] -> cspg_d[e]	0		0	1000		Transport, Extracellular			
CSPG_Dtly	chondroitin sulfate D transport, extracellular to lysosome	cspg_d[e] -> cspg_d[l]	0		0	1000		Transport, Lysosomal			
CSPG_Et	chondroitin sulfate E transport, golgi to extracellular	cspg_e[g] -> cspg_e[e]	0		0	1000		Transport, Extracellular			
CSPG_Etly	chondroitin sulfate E transport, extracellular to lysosome	cspg_e[e] -> cspg_e[l]	0		0	1000		Transport, Lysosomal			
CSm	citrate synthase	h2o[m] + accoa[m] + oaa[m] -> h[m] + coa[m] + cit[m]	0	12974.1 or 12974.2	0	1000		Citric Acid Cycle			
CTPS1	CTP synthase (NH3)	nh4[c] + atp[c] + utp[c] -> adp[c] + 2 h[c] + pi[c] + ctp[c]	0	51797.1	0	1000		Nucleotides			
CTPS2	CTP synthase (glutamine)	h2o[c] + atp[c] + gln-L[c] + utp[c] -> adp[c] + 2 h[c] + pi[c] + glu-L[c] + ctp[c]	0	55936.1 or 55936.2	0	1000		Pyrimidine Biosynthesis			
CTPtn	CTP diffusion in nucleus	ctp[c] <=> ctp[n]	1		-1000	1000		Transport, Nuclear			
CYANSTm	Cyanide sulfurtransferase, mitochondrial	cyan[m] + tsul[m] -> h[m] + so3[m] + tcynt[m]	0	22117.1	0	1000		Cysteine Metabolism			
CYANt	Cyanide transport via diffusion (extracellular to cytosol)	cyan[e] <=> cyan[c]	1		-1000	1000		Transport, Extracellular			
CYANtm	Cyanide transport via diffusion (mitochondrial)	cyan[c] <=> cyan[m]	1		-1000	1000		Transport, Mitochondrial			
CYOOm2	CYOOm2	8 h[m] + o2[m] + 4 focytC[m] -> 4 h[c] + 2 h2o[m] + 4 ficytC[m]	0		0	1000		Oxidative Phosphorylation			
CYOOm3	cytochrome c oxidase, mitochondrial Complex IV	7.92 h[m] + o2[m] + 4 focytC[m] -> 4 h[c] + 1.96 h2o[m] + 4 ficytC[m] + 0.02 o2s[m]	0	78174.1 or 12864.1 or 11532.1 or 75483.1 or 629383.1 or 333182.1 or 84682.1 or 12647.1 or 110323.1 or 12857.1 or 12865.1 or 12859.1 or 17708.1 or 12868.1 or 12866.1 or 66142.1 or 12858.1 or 12861.1 or 12862.1	0	0		Oxidative Phosphorylation			

CYOR_u10m	ubiquinol-6 cytochrome c reductase, Complex III	2 h[m] + 2 ficytC[m] + q10h2[m] -> 4 h[c] + q10[m] + 2 focytC[m]	0	22273.1 and 100042918.1 and 66152.1 and 66594.1 and 17711.1 and 67683.1 and 66694.1 and 66445.1 and 22272.1 and 67538.1 or 22273.1 and 100042918.1 and 17711.1 and 66594.1 and 66152.2 and 67683.1 and 66445.1 and 66694.1 and 22272.1 and 67538.1	0	1000		Oxidative Phosphorylation				
CYSALANaEx	L-alanine/L-cysteine Na-dependent exchange (Cys-L tst)	na1[e] + ala-L[c] + cys-L[e] -> na1[c] + ala-L[e] + cys-L[c]	0	20514.1 or 55963.1	0	1000		Transport, Extracellular				
CYSAMO	Cysteamine oxygenase	o2[c] + cysam[c] -> 2 h[c] + hyptaur[c]	0		0	1000		Taurine and hypotaurine metabolism				
CYSASNNaEx	L-cysteine/L-asparagine Na-dependent exchange (Cys-L tst)	na1[e] + asn-L[c] + cys-L[e] -> na1[c] + asn-L[e] + cys-L[c]	0	20514.1	0	1000		Transport, Extracellular				
CYSATBlte	transport of L-Cysteine into the intestinal cells by ATB0 transporter	2 na1[su] + cl[su] + cys-L[su] -> 2 na1[c] + cl[c] + cys-L[c]	0	56774.1	0	1000	3	Transport, Lumen	PMID:18195088	ATB0 is both sodium and chloride coupled, with reaction stoichiometry 2Na+:1cl:1amino acid. The transporter is located in the intestine, has a broad substrate specificity (both neutral and cationic amino acids), but is not involved in the transport of aspartate, glutamate and proline (PMID:18195088).		
CYSB0AT1Ate	transport of L-Cysteine by the apical neutral amino acid transporters in kidney and intestine	na1[su] + cys-L[su] -> na1[c] + cys-L[c]	0	(70008.1 or (74338.1 and 57394.1))	0	1000	3	Transport, Lumen	PMID: 19472175, PMID: 15804236, PMID: 18400692	transports all the neutral amino acids with preference for methionine, leucine and valine. Reaction stoichiometry is 1:1. Requires heterodimerization with collectrin protein for increased affinity. Found in kidney and intestine, however also reported to be expressed in skin. Requires association with ACE2 for expression in intestine but with collectrin for expression in kidney.	3.4.17.23	
CYSGLNNaEx	L-cysteine/L-glutamine Na-dependent exchange (Cys-L tst)	na1[e] + cys-L[e] + gln-L[c] -> na1[c] + cys-L[c] + gln-L[e]	0	20514.1	0	1000		Transport, Extracellular				
CYSGLTH	Glutathione:cystine oxidoreductase	2cystin[c] + 2 gthrd[c] <=> 2 cys-L[c] + gthox[c]	1		-1000	1000		Cysteine Metabolism				
CYSGLUexR	L-cystine/L-glutamine reversible exchanger	cys-L[e] + gln-L[c] <=> cys-L[c] + gln-L[e]	1	53896.1 or 17254.1	-1000	1000		Transport, Extracellular				
CYSGLYex	L-cysteine/glycine exchanger	cys-L[c] + gly[e] -> cys-L[e] + gly[c]	0	56934.1 or 17254.1 or 50934.2	0	1000		Transport, Extracellular				
CYSGLYexR	L-cysteine/glycine reversible exchanger	cys-L[c] + gly[e] <=> cys-L[e] + gly[c]	1	53896.1 or 17254.1	-1000	1000		Transport, Extracellular				
CYSILELAT2tc	transport of L-Cysteine into the cell and efflux of L-Isoleucine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	cys-L[e] + ile-L[c] -> cys-L[c] + ile-L[e]	0	(20539.1 and 17254.1)	0	1000	3	Transport, Extracellular	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID 18195088, Am J Physiol (2001) 281:C1077-C1093.	higher affinity for small neutral amino acids than LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274).		
CYSLYSL	L-Cystine Lysinine-lyase (deaminating)	h2o[c] + Lcystin[c] -> nh4[c] + pyr[c] + thcys[c]	0		0	1000		Cysteine Metabolism				
CYSO	cysteine oxidase	o2[c] + cys-L[c] -> 2 h[c] + 3sala[c]	0	12583.1	0	1000		Taurine and hypotaurine metabolism				
CYSPHELAT2tc	transport of L-Cysteine into the cell and efflux of L-Phenylalanine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	cys-L[e] + phe-L[c] -> cys-L[c] + phe-L[e]	0	(20539.1 and 17254.1)	0	1000	3	Transport, Extracellular	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID 18195088, Am J Physiol (2001) 281:C1077-C1093.	higher affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274).		
CYSSERNaEx	L-serine/L-cysteine Na-dependent exchange (Cys-L tst)	na1[e] + cys-L[e] + ser-L[c] -> na1[c] + cys-L[c] + ser-L[e]	0	20514.1 or 55963.1	0	1000		Transport, Extracellular				
CYSSNAT3tc	transport of L-Cysteine into the cell coupled with co-transport with Sodium and counter transport with proton by SNAT5 transporter.	h[c] + na1[e] + cys-L[e] <=> na1[c] + h[e] + cys-L[c]	1	209837.1	-1000	1000	3	Transport, Lumen	PMID: 12845534, PMCID: PMC1665133, PMID:18195088	SNAT5 performs both symport with sodium and antiport with proton, for the net transport of neutral amino acid into the cell. Cellular localization has been reported in stomach, brain, liver, lung, small intestine, spleen, colon and kidney. (PMID: 12845534)		
CYSTA	cysteine transaminase	akg[c] + cys-L[c] <=> glu-L[c] + mercppyr[c]	1	14718.1	-1000	1000		Cysteine Metabolism				
CYSTALArBATe	transport of L-Cysteine into the cell in exchange for L-Alanine by b0,+AT transporter at the apical surfaces of the membranes of small intestine and renal cells.	ala-L[c] + Lcystin[a] -> ala-L[a] + Lcystin[c]	0	(30962.1 and 20532.1)	0	1000	3	Transport, Lumen	PMID: 10958334, PMID: 19184091, PMID: 18195088, PMID: 11546643	sodium-independant antiport transport system, exchanges di-basic amino acids into the cells and neutral amino acids out of the cell. Located on the apical surfaces of transporting epithelia. Cellular localization being small intestine, kidney (proximal tubule), lung, placenta, brain and thymus. Requires the heterodimerization with rBAT glycoprotein. (PMID: 10958334).		
CYSTAm	cysteine transaminase (mitochondrial)	akg[m] + cys-L[m] <=> glu-L[m] + mercppyr[m]	1	14719.1	-1000	1000		Cysteine Metabolism				
CYSTGL	cystathionine g-lyase	h2o[c] + cyst-L[c] -> nh4[c] + cys-L[c] + 2obut[c]	0	107869.1 or 107869.2	0	1000		Cysteine Metabolism				
CYSTGLUex	L-cystine/L-glutamate exchanger	glu-L[c] + Lcystin[e] -> Lcystin[c] + glu-L[e]	0	17254.1 and 26570.1	0	1000		Transport, Extracellular				
CYSTHRNaEx	L-cysteine/L-threonine Na-dependent exchange (Cys-L tst)	na1[e] + cys-L[e] + thr-L[c] -> na1[c] + cys-L[c] + thr-L[e]	0	20514.1 or 55963.1	0	1000		Transport, Extracellular				
CYSTLEUHBATe	transport of L-Cysteine into the cell in exchange for L-Leucine by b0,+AT transporter at the apical surfaces of the membranes of small intestine and renal cells.	leu-L[c] + Lcystin[a] -> leu-L[a] + Lcystin[c]	0	(30962.1 and 20532.1)	0	1000	3	Transport, Lumen	PMID: 10958334, PMID: 19184091, PMID: 18195088, PMID: 11546643	sodium-independant antiport transport system, exchanges di-basic amino acids into the cells and neutral amino acids out of the cell. Located on the apical surfaces of transporting epithelia. Cellular localization being small intestine, kidney (proximal tubule), lung, placenta, brain and thymus. Requires the heterodimerization with rBAT glycoprotein. (PMID: 10958334).		
CYSTS	cystathionine beta-synthase	hcys-L[c] + ser-L[c] -> h2o[c] + cyst-L[c]	0	12411.1	0	1000		Methionine Metabolism				
CYSTSERex	L-cystine/glycine exchanger (cystine in)	ser-L[c] + Lcystin[e] -> ser-L[e] + Lcystin[c]	0	20532.1 and 30962.1	0	1000		Transport, Extracellular				
CYSt4	L-cysteine reversible transport via sodium symport	na1[e] + cys-L[e] -> na1[c] + cys-L[c]	0	56774.1	0	1000		Transport, Extracellular				
CYStec	L-cysteine transport via diffusion (extracellular to cytosol)	cys-L[e] <=> cys-L[c]	1	215113.1	-1000	1000		Transport, Extracellular				
CYTD	cytidine deaminase	h2o[c] + h[c] + cytd[c] -> nh4[c] + urd[c]	0	72269.1 or 11628.1	0	1000		Pyrimidine Catabolism				
CYTDK1	cytidine kinase (ATP)	atp[c] + cytd[c] -> adp[c] + h[c] + cmp[c]	0	22245.1 or 80914.1	0	1000		Nucleotides				
CYTDK2m	cytidine kinase (ATP), mitochondrial	atp[m] + cytd[m] -> h[m] + adp[m] + cmp[m]	0		0	1000		Nucleotides				
CYTDn	cytidine deaminase, nuclear	h2o[n] + cytd[n] + h[n] -> nh4[n] + urd[n]	0	11628.1	0	1000		Nucleotides				
CYTDt	cytidine facilated transport in cytosol	cytd[e] <=> cytd[c]	1	13340.1 or 63959.1	-1000	1000		Transport, Extracellular				
CYTDt4	cytidine transport in via sodium symport	na1[e] + cytd[e] -> na1[c] + cytd[c]	0	114304.1 or 434203.1 or 434203.2	0	1000		Transport, Extracellular				
CYTDt5	cytidine transport (1:2 Na/cytd cotransport)	2 na1[e] + cytd[e] -> 2 na1[c] + cytd[c]	0	114304.1	0	1000		Transport, Extracellular				
CYTDtl	Cytidine facilated transport from lysosome	cytd[l] <=> cytd[c]	1	71279.1	-1000	1000		Transport, Lysosomal				
CYTDtm	cytidine facilated transport in mitochondria	cytd[c] <=> cytd[m]	1	63959.1	-1000	1000		Transport, Mitochondrial				
CYTDtn	cytidine transport in nucleus	cytd[c] <=> cytd[n]	1		-1000	1000		Transport, Nuclear				
CYTK1	cytidylate kinase (CMP)	atp[c] + cmp[c] <=> adp[c] + cdp[c]	1	66588.1	-1000	1000		Nucleotides				
CYTK10	cytidylate kinase (CMP,dGTP)	cmp[c] + dgtp[c] <=> cdp[c] + dgdp[c]	1	66588.1	-1000	1000		Nucleotides				
CYTK10n	cytidylate kinase (CMP,dGTP),nuclear	cmp[n] + dgtp[n] <=> cdp[n] + dgdp[n]	1	66588.1	-1000	1000		Nucleotides				
CYTK11	cytidylate kinase (dCMP,dGTP)	dgtp[c] + dcmp[c] <=> dgdp[c] + dcdp[c]	1	66588.1	-1000	1000		Nucleotides				
CYTK11n	cytidylate kinase (dCMP,dGTP),nuclear	dgtp[n] + dcmp[n] <=> dgdp[n] + dcdp[n]	1	66588.1	-1000	1000		Nucleotides				
CYTK12	cytidylate kinase (dCMP,dCTP)	dcmp[c] + dctp[c] <=> 2 dcdp[c]	1	66588.1	-1000	1000		Nucleotides				
CYTK12n	cytidylate kinase (dCMP,dCTP),nuclear	dcmp[n] + dctp[n] <=> 2 dcdp[n]	1	66588.1	-1000	1000		Nucleotides				
CYTK13	cytidylate kinase (dCMP,dATP)	datp[c] + dcmp[c] <=> dadp[c] + dcdp[c]	1	66588.1	-1000	1000		Nucleotides				
CYTK13n	cytidylate kinase (dCMP,dATP),nuclear	dcmp[n] + datp[n] <=> dcdp[n] + dadp[n]	1	66588.1	-1000	1000		Nucleotides				
CYTK14	cytidylate kinase (dCMP,UTP)	utp[c] + dcmp[c] <=> udp[c] + dcdp[c]	1	66588.1	-1000	1000		Nucleotides				
CYTK14n	cytidylate kinase (dCMP,CTP),nuclear	dcmp[n] + utp[n] <=> dcdp[n] + udp[n]	1	66588.1	-1000	1000		Nucleotides				
CYTK1m	cytidylate kinase (CMP),mitochondrial	atp[m] + cmp[m] <=> adp[m] + cdp[m]	1		-1000	1000		Nucleotides				
CYTK1n	cytidylate kinase (CMP),nuclear	atp[n] + cmp[n] <=> cdp[n] + adp[n]	1	66588.1	-1000	1000		Nucleotides				
CYTK2	cytidylate kinase (dCMP)	atp[c] + dcmp[c] <=> adp[c] + dcdp[c]	1	66588.1	-1000	1000		Nucleotides				
CYTK2n	cytidylate kinase (dCMP),nuclear	atp[n] + dcmp[n] <=> dcdp[n] + adp[n]	1	66588.1	-1000	1000		Nucleotides				
CYTK3	cytidylate kinase (CMP)(GTP)	gtp[c] + cmp[c] <=> gdp[c] + cdp[c]	1	229949.1 or 229949.2	-1000	1000		Nucleotides				
CYTK3n	cytidylate kinase (dCMP,CTP),nuclear	ctp[n] + dcmp[n] <=> cdp[n] + dcdp[n]	1	66588.1	-1000	1000		Nucleotides				
CYTK4	cytidylate kinase (dCMP)(GTP)	gtp[c] + dcmp[c] <=> gdp[c] + dcdp[c]	1	229949.1 or 229949.2	-1000	1000		Nucleotides				
CYTK4n	cytidylate kinase (dCMP,GTP),nuclear	dcmp[n] + gtp[n] <=> dcdp[n] + gdp[n]	1	66588.1	-1000	1000		Nucleotides				
CYTK5	cytidylate kinase (dCMP)	ctp[c] + dcmp[c] <=> cdp[c] + dcdp[c]	1	66588.1	-1000	1000		Nucleotides				
CYTK5n	cytidylate kinase (CMP),nuclear	cmp[n] + gtp[n] <=> cdp[n] + gdp[n]	1	66588.1	-1000	1000		Nucleotides				
CYTK6	cytidylate kinase (CMP,CTP)	cmp[c] + cmp[c] <=> 2 cdp[c]	1	66588.1	-1000	1000		Nucleotides				
CYTK6n	cytidylate kinase (CMP,CTP),nuclear	cmp[n] + cmp[n] <=> 2 cdp[n]	1	66588.1	-1000	1000		Nucleotides				
CYTK7	cytidylate kinase (CMP,UTP)	cmp[c] + utp[c] <=> udp[c] + cdp[c]	1	66588.1	-1000	1000		Nucleotides				
CYTK7n	cytidylate kinase (CMP,UTP),nuclear	cmp[n] + utp[n] <=> cdp[n] + udp[n]	1	66588.1	-1000	1000		Nucleotides				
CYTK8	cytidylate kinase (CMP,dATP)	datp[c] + cmp[c] <=> dadp[c] + cdp[c]	1	66588.1	-1000	1000		Nucleotides				
CYTK8n	cytidylate kinase (CMP,dATP),nuclear	cmp[n] + datp[n] <=> cdp[n] + dadp[n]	1	66588.1	-1000	1000		Nucleotides				
CYTK9	cytidylate kinase (CMP,dCTP)	cmp[c] + dctp[c] <=> cdp[c] + dcdp[c]	1	66588.1	-1000	1000		Nucleotides				
CYTK9n	cytidylate kinase (CMP,dCTP),nuclear	cmp[n] + dctp[n] <=> cdp[n] + dcdp[n]	1	66588.1	-1000	1000		Nucleotides				
CytOxe-	CytOxe-	focytC[m] -> ficytC[m] + e-[m]	0		0	1000	0	Oxidative Phosphorylation				
DHAIBTm	D-3-Amino-isobutanoate:pyruvate aminotransferase, mitochondrial	pyr[m] + 3aib-D[m] <=> 2mmp[m] + ala-L[m]	1		-1000	1000		Pyrimidine Catabolism				
DADA	Deoxyadenosine deaminase	h2o[c] + h[c] + dad-2[c] -> nh4[c] + din[c]	0	11486.1	0	1000		Nucleotides				
DADAe	Deoxyadenosine deaminase, extracellular	h[e] + h2o[e] + dad-2[e] -> nh4[e] + din[e]	0	11486.1	0	1000		Nucleotides				
DADNK	deoxyadenosine kinase	atp[c] + dad-2[c] -> adp[c] + h[c] + damp[c]	0		0	1000		Nucleotides				
DADN4	deoxyadenosine transport via diffusion	dad-2[e] <=> dad-2[c]	1		-1000	1000		Transport, Extracellular				
DAGHSTDIu	diffussion of di-acryl glycerol accross the brush border membrane	dag_hs[u] <=> dag_hs[c]	1		-1000	1000	2	Transport, Lumen	Sareen S. Gropper, jack L. Smith, James L. Groff (2009) Wadsworth cengage learning, Advanced nutrition and human metabolism, 5th edition, page 142-144.			
DAGKin_hs	Diacylglycerol phosphate kinase (homo sapiens)	atp[n] + dag_hs[n] <=> h[n] + adp[n] + pa_hs[n]	1	104418.1 or 3201.27.1	-1000	1000		Glycerophospholipid Metabolism				
DAG_HStor	diacylglycerol ER export	dag_hs[r] -> dag_hs[c]	0		0	1000		Transport, Endoplasmic Reticular				
DAGt	diacylglycerol 2 (homo sapiens) transport	dag_hs[e] <=> dag_hs[c]	1		-1000	1000		Transport, Extracellular				
DALAOXs	D-Alanine Oxidase (s)	o2[s] + h2o[s] + ala-D[s] -> h2o2[s] + pyr[s] + nh4[s]	0	13142.1	0	1000		D-alanine metabolism				
DALAt2r	D-alanine transport via proton symport	h[e] + ala-D[e] <=> h[c] + ala-D[c]	1	215335.1	-1000	1000		Transport, Extracellular				
DALAt2vL	D-alanine transport via proton symport (lysosome)	h[l] + ala-D[l] <=> h[c] + ala-D[c]	1	215335.1	-1000	1000		Transport, Lysosomal				
DALAxt	D-Alanine transport to peroxisome	ala-D[c] -> ala-D[x]	0		0	1000		D-alanine metabolism				
DARGOp	D-arginine oxidase, peroxisomal	o2[x] + h2o[x] + arg-D[x] -> h2o2[x] + nh4[x] + 5a2oxoadi[x]	0	13142.1	0	1000		D-arg and D-orn metabolism				
DASCBH	L-Dehydroascorbate lactonohydrolase	h2o[c] + dhlasc[c] -> h[c] + 23dogulo[c]	0		0	1000		Ascorbate and Aldarate Metabolism				

DASCBR	dehydroascorbate reductase	h[c] + nadph[c] + dhdascb[c] -> nadp[c] + ascb-L[c]	0	93692.1 or 69367.1 or 69367.2	0	1000		Ascorbate and Aldarate Metabolism			
DASPO1p	D-aspartate oxidase, peroxisomal	o2[x] + h2o[x] + asp-D[x] -> h2o2[x] + nh4[x] + oaa[x]	0	70503.1 or 70503.2	0	1000		Alanine and Aspartate Metabolism			
DATPtn	dATP diffusion in nucleus	datp[c] <=> datp[n]	1		-1000	1000		Transport, Nuclear			
DCIm	dodecenoyl-Coenzyme A delta isomerase	dd2coa[m] <=> dd3coa[m]	1	13177.1	-1000	1000		Fatty Acid Metabolism			
DCK1m	Deoxycytidine kinase, mitochondrial (ATP)	atp[m] + dcyt[m] <=> h[m] + adp[m] + dcmp[m]	1		-1000	1000		Nucleotides			
DCK1n	Deoxycytidine kinase, nuclear (ATP)	atp[n] + dcyt[n] <=> h[n] + dcmp[n] + adp[n]	1	13178.1	-1000	1000		Nucleotides			
DCK2n	Deoxycytidine kinase, nuclear (UTP)	utp[n] + dcyt[n] <=> h[n] + dcmp[n] + udp[n]	1	13178.1	-1000	1000		Nucleotides			
DCMPDA	dCMP deaminase	h2o[c] + h[c] + dcmp[c] <=> nh4[c] + dump[c]	1	320685.1	-1000	1000		Pyrimidine Catabolism			
DCSPTN1COAtx	fatty acid intracellular transport	dcsptn1coa[c] <=> dcsptn1coa[x]	1		-1000	1000		Transport, Peroxisomal			
DCSPTN1CPT1	carnitine O-palmitoyltransferase	crn[c] + dcsptn1coa[c] -> coa[c] + dcsptn1crn[c]	0	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	0	1000		Carnitine shuttle			
DCSPTN1CPT2	carnitine transferase	coa[m] + dcsptn1crn[m] -> crn[m] + dcsptn1coa[m]	0	12896.1	0	1000		Carnitine shuttle			
DCSPTN1CRNt	transport into the mitochondria (carnitine)	dcsptn1crn[c] -> dcsptn1crn[m]	0	57279.1	0	1000		Carnitine shuttle			
DCSPTN1t	fatty acid transport via diffusion	dcsptn1[e] <=> dcsptn1[c]	1		-1000	1000		Transport, Extracellular			
DCT	Dopachrome tautomerase	L-dpchrm[c] <=> 56dihindlcrbxlt[c]	1	13190.1	-1000	1000		Tyrosine metabolism			
DCTPtn	dCTP diffusion in nucleus	dctp[c] <=> dctp[n]	1		-1000	1000		Transport, Nuclear			
DCYTD	deoxycytidine deaminase	h2o[c] + h[c] + dcyt[c] -> nh4[c] + duri[c]	0	72269.1 or 11628.1	0	1000		Pyrimidine Catabolism			
DCYTDn	deoxycytidine deaminase, nuclear	h2o[n] + h[n] + dcyt[n] -> nh4[n] + duri[n]	0	11628.1	0	1000		Nucleotides			
DCYTt	deoxycytidine transport via diffusion	dcyt[e] <=> dcyt[c]	1		-1000	1000		Transport, Extracellular			
DDPGAm	2-dehydro-3-deoxy-phosphogluconate aldolase, mitochondrial	4h2oglt[m] <=> pyr[m] + glx[m]	1		-1000	1000		Arginine and Proline Metabolism			
DEBRISOQUINEt	debrisoquine uniport	debrisoquine[e] <=> debrisoquine[c]	1	20518.1 or 20518.2	-1000	1000		Transport, Extracellular			
DECDPtm	lipid, flip-flop intracellular transport	decdp[c] <=> decdp[m]	1		-1000	1000		Transport, Mitochondrial			
DEDOLP1_L	dehydrodolichol diphosphate phosphatase (liver)	h2o[c] + 0.1 dedoldp_L[c] -> h[c] + pi[c] + 0.1 dedolp_L[c]	0		0	1000		N-Glycan Biosynthesis			
DEDOLP1_U	dehydrodolichol diphosphate phosphatase (uterus)	h2o[c] + 0.1 dedoldp_U[c] -> h[c] + pi[c] + 0.1 dedolp_U[c]	0		0	1000		N-Glycan Biosynthesis			
DEDOLP2_L	dehydrodolichol phosphate phosphatase (liver)	h2o[c] + 0.1 dedolp_L[c] -> pi[c] + 0.1 dedol_L[c]	0		0	1000		N-Glycan Biosynthesis			
DEDOLP2_U	dehydrodolichol phosphate phosphatase (uterus)	h2o[c] + 0.1 dedolp_U[c] -> pi[c] + 0.1 dedol_U[c]	0		0	1000		N-Glycan Biosynthesis			
DEDOLR_L	dehydrodolichol reductase (liver)	h[c] + nadph[c] + 0.1 dedol_L[c] -> nadp[c] + 0.1 dolichol_L[c]	0		0	1000		N-Glycan Biosynthesis			
DEDOLR_U	dehydrodolichol reductase (uterus)	h[c] + nadph[c] + 0.1 dedol_U[c] -> nadp[c] + 0.1 dolichol_U[c]	0		0	1000		N-Glycan Biosynthesis			
DESAT16_2	palmitoyl-CoA desaturase (n-C16:0CoA -> n-C16:1CoA)	o2[c] + h[c] + nadh[c] + pmtcoa[c] -> 2 h2o[c] + nad[c] + hdcoa[c]	0	20249.1	0	1000		Fatty acid elongation			
DESAT18_10	fatty acyl-CoA desaturase (n-C18:2CoA -> n-C18:3CoA)	o2[c] + h[c] + nadh[c] + lnlncacoa[c] -> 2 h2o[c] + nad[c] + strdnccoa[c]	0	56473.1	0	1000		Fatty acid elongation			
DESAT18_3	stearoyl-CoA desaturase (n-C18:0CoA -> n-C18:1CoA)	o2[c] + h[c] + nadh[c] + stcoa[c] -> 2 h2o[c] + nad[c] + odecoa[c]	0	20249.1	0	1000		Fatty acid elongation			
DESAT18_4	stearoyl-CoA desaturase (n-C18:0CoA -> n-C18:1CoA)	o2[c] + h[c] + nadh[c] + stcoa[c] -> 2 h2o[c] + nad[c] + vacccoa[c]	0	20249.1	0	1000		Fatty acid elongation			
DESAT18_5	stearoyl-CoA desaturase (n-C18:0CoA -> n-C18:1CoA)	o2[c] + h[c] + nadh[c] + stcoa[c] -> 2 h2o[c] + nad[c] + od2coa[c]	0	20249.1	0	1000		Fatty acid elongation			
DESAT18_6	fatty acyl-CoA desaturase (n-C18:1CoA -> n-C18:2CoA)	o2[c] + h[c] + nadh[c] + odecoa[c] -> 2 h2o[c] + nad[c] + lneldccoa[c]	0	56473.1	0	1000		Fatty acid elongation			
DESAT18_7	fatty acyl-CoA desaturase (n-C18:1CoA -> n-C18:2CoA)	o2[c] + h[c] + nadh[c] + vacccoa[c] -> 2 h2o[c] + nad[c] + lneldccoa[c]	0	56473.1	0	1000		Fatty acid elongation			
DESAT18_8	fatty acyl-CoA desaturase (n-C18:1CoA -> n-C18:2CoA)	o2[c] + h[c] + nadh[c] + od2coa[c] -> 2 h2o[c] + nad[c] + lneldccoa[c]	0	56473.1	0	1000		Fatty acid elongation			
DESAT18_9	fatty acyl-CoA desaturase (n-C18:2CoA -> n-C18:3CoA)	o2[c] + h[c] + nadh[c] + lnlccoa[c] -> 2 h2o[c] + nad[c] + lnlncgcoa[c]	0	56473.1	0	1000		Fatty acid elongation			
DESAT20_1	fatty acyl-CoA desaturase (n-C20:3CoA -> n-C20:4CoA)	o2[c] + h[c] + nadh[c] + dlnlcgcoa[c] -> 2 h2o[c] + nad[c] + arachdcoa[c]	0	76267.1	0	1000		Fatty acid elongation			
DESAT20_2	fatty acyl-CoA desaturase (n-C20:4CoA -> n-C20:5CoA)	o2[c] + h[c] + nadh[c] + eicostetcoa[c] -> 2 h2o[c] + nad[c] + tmndnccoa[c]	0	76267.1	0	1000		Fatty acid elongation			
DESAT22_1p	fatty acyl-CoA desaturase (n-C22:4CoA -> n-C22:5CoA)	h[x] + nadh[x] + o2[x] + adrncoa[x] -> nad[x] + 2 h2o[x] + dcsptn1coa[x]	0		0	1000		Fatty acid elongation			
DESAT22_2p	fatty acyl-CoA desaturase (n-C22:5CoA -> n-C22:6CoA)	h[x] + nadh[x] + o2[x] + clpndcoa[x] -> nad[x] + 2 h2o[x] + c226coa[x]	0		0	1000		Fatty acid elongation			
DESAT24_1	fatty acyl-CoA desaturase (n-C24:5CoA -> n-C24:6CoA)	o2[c] + h[c] + nadh[c] + tetpent3coa[c] -> 2 h2o[c] + nad[c] + tethex3coa[c]	0	56473.1	0	1000		Fatty acid elongation			
DGAT	diacylglycerol acyltransferase	Rtotal3coa[c] + dag_hs[c] -> coa[c] + tag_hs[c]	0	13350.1 or 67800.1	0	1000		Triacylglycerol Synthesis			
DGCHOLte	bile acid intracellular transport	dgchol[e] <=> dgchol[c]	1		-1000	1000		Transport, Extracellular			
DGCHOLtx	bile acid intracellular transport	dgchol[x] <=> dgchol[c]	1		-1000	1000		Transport, Peroxisomal			
DGK1	deoxyguanylate kinase (dGMP:ATP)	atp[c] + dgmp[c] <=> adp[c] + dgdp[c]	1	14923.1	-1000	1000		Nucleotides			
DGK2m	deoxyguanylate kinase (dGMP:dATP) (mitochondrial)	datp[m] + dgmp[m] <=> dadp[m] + dgdp[m]	1		-1000	1000		Nucleotides			
DGNSKm	deoxyguanosine kinase	atp[m] + dgsn[m] -> h[m] + adp[m] + dgmp[m]	0	27369.1 or 27369.2 or 27369.3 or 27369.4 or 27369.5	0	1000		Nucleotides			
DGSNt	deoyguanosine transport via diffusion	dgsn[e] <=> dgsn[c]	1		-1000	1000		Transport, Extracellular			
DGSNtm	deoyguanosine transport in mitochondria	dgsn[c] <=> dgsn[m]	1		-1000	1000		Transport, Mitochondrial			
DGTPtn	dGTP diffusion in nucleus	dgtp[c] <=> dgtp[n]	1		-1000	1000		Transport, Nuclear			
DGULND	dehydro-L-gulonate decarboxylase	h[c] + 3dhguln[c] <=> co2[c] + xylu-L[c]	1		-1000	1000		Pentose and Glucuronate Interconversions			
DHAAt1r	dehydroascorbate transport (uniport)	dhdascb[e] <=> dhdascb[c]	1	20528.1 or 20527.1 or 20525.1	-1000	1000		Transport, Extracellular			
DHAPA	dihydroxyacetone phosphate acyltransferase	dhap[c] + Rtotalcoa[c] -> coa[c] + adhap_hs[c]	0	14712.1	0	1000		Triacylglycerol Synthesis			
DHAPAx	dihydroxyacetone phosphate acyltransferase	Rtotalcoa[x] + dhap[x] -> coa[x] + adhap_hs[x]	0	14712.1	0	1000		Triacylglycerol Synthesis			
DHCHOLESTANATEtm	lipid, flip-flop intracellular transport	dhcholestanate[m] <=> dhcholestanate[x]	1		-1000	1000		Transport, Peroxisomal			
DHCR241r	24-dehydrocholesterol reductase [Precursor]	zymst[r] + fadh2[r] -> fad[r] + zymstnl[r]	0	74754.1	0	1000		Cholesterol Metabolism			
DHCR242r	24-dehydrocholesterol reductase [Precursor]	fadh2[r] + chlstol[r] -> fad[r] + lthstrl[r]	0	74754.1	0	1000		Cholesterol Metabolism			
DHCR243r	24-dehydrocholesterol reductase [Precursor]	fadh2[r] + dsmsterol[r] -> chsterol[r] + fad[r]	0	74754.1	0	1000		Cholesterol Metabolism			
DHCR71r	7-dehydrocholesterol reductase	h[r] + nadph[r] + ddsmsterol[r] -> nadp[r] + dsmsterol[r]	0	13360.1	0	1000		Cholesterol Metabolism			
DHCR72r	7-dehydrocholesterol reductase	7dhchsterol[r] + h[r] + nadph[r] -> nadp[r] + chsterol[r]	0	13360.1	0	1000		Cholesterol Metabolism			
DHCRD1	dihydroceramide desaturase	nadp[c] + dhcrm_hs[c] -> h[c] + nadph[c] + crm_hs[c]	0	13244.2 or 13244.1	0	1000		Sphingolipid Metabolism			
DHCRD2	dihydroceramide desaturase	dhcrm_hs[c] + fad[c] -> crm_hs[c] + fadh2[c]	0	13244.2 or 13244.1	0	1000		Sphingolipid Metabolism			
DHDPBMTm	dihydroxydecaprenylbenzoate methyltransferase	3dpdhb[m] + amet[m] -> h[m] + ahcys[m] + 3dpdhb_me[m]	0	230027.1	0	1000		Ubiquinone Biosynthesis			
DHEASULT	Dehydroepiandrosterone sulfotransferase	paps[c] + dhea[c] -> h[c] + pap[c] + dheas[c]	0	20859.1 or 20860.1	0	1000		Steroid Metabolism			
DHEAStr	dheas intracellular transport	dheas[r] <=> dheas[c]	1		-1000	1000		Transport, Extracellular			
DHEAtr	dhea intracellular transport	dhea[r] <=> dhea[c]	1		-1000	1000		Transport, Endoplasmic Reticular			
DHFR	dihydrofolate reductase	h[c] + nadph[c] + dhf[c] <=> nadp[c] + thf[c]	1	13361.1	-1000	1000		Folate Metabolism			
DHFtl	dihydrofolate reversible lysosomal transport	dhf[c] <=> dhf[l]	1		-1000	1000		Transport, Lysosomal			
DHFtm	dihydrofolate reversible mitochondrial transport	dhf[c] <=> dhf[m]	1		-1000	1000		Transport, Mitochondrial			
DHORD9	dihydoorotic acid dehydrogenase (quinone10)	q10[m] + dhor-S[c] -> q10h2[m] + orot[c]	0	56749.1	0	1000		Pyrimidine Biosynthesis			
DHORTS	dihydroorotase	h2o[c] + dhor-S[c] <=> h[c] + cbasp[c]	1	69719.1	-1000	1000		Pyrimidine Biosynthesis			
DHPM1	dihydropyrimidinase (5,6-dihydrouracil)	h2o[c] + 56dura[c] -> h[c] + cala[c]	0	22240.1 or 64705.1 or 12934.1	0	1000		Pyrimidine Catabolism			
DHPM2	dihydropyrimidinase (dihydrothymine)	h2o[c] + 56dthm[c] -> h[c] + 3uib[c]	0		0	1000		Pyrimidine Catabolism			
DHPR	6,7-dihydropteridine reductase	h[c] + nadh[c] + dhbpt[c] -> nad[c] + thbpt[c]	0	110391.1	0	1000		Tetrahydrobiopterin			
DHPR2	6,7-dihydropteridine reduction	5mthf[c] + dhbpt[c] -> h[c] + thbpt[c] + mlthf[c]	0		0	1000		Tetrahydrobiopterin			
DIDPtn	dIDP nuclear transport	didp[c] <=> didp[n]	1		-1000	1000		Transport, Nuclear			
DIGALSGALSIDEte	digalsgalside_hs transport	digalsgalside_hs[c] <=> digalsgalside_hs[e]	1		-1000	1000		Transport, Extracellular			
DIGALSGALSIDEtg	digalsgalside_hs intracellular transport	digalsgalside_hs[c] <=> digalsgalside_hs[g]	1		-1000	1000		Transport, Golgi Apparatus			
DIGALSIDEtg	digalside_hs intracellular transport	digalside_hs[c] <=> digalside_hs[g]	1		-1000	1000		Transport, Golgi Apparatus			
DIGALSIDEtl	digalside_hs intracellular transport	digalside_hs[c] <=> digalside_hs[l]	1		-1000	1000		Transport, Lysosomal			
DINt	deoxyinosine transport via diffusion	din[e] <=> din[c]	1		-1000	1000		Transport, Extracellular			
DITPtn	dITP nuclear transport	ditp[c] <=> ditp[n]	1		-1000	1000		Transport, Nuclear			
DKMPPD	2,3-diketo-5-methylthio-1-phosphopentane degradation reaction	h2o[c] + o2[c] + dkmpp[c] -> 2 h[c] + pi[c] + for[c] + 2kmb[c]	0		0	1000		Arginine and Proline Metabolism			
DLNLCGCPT1	carnitine O-palmitoyltransferase	crn[c] + dlnlcgcoa[c] -> coa[c] + dlnlcgcrn[c]	0	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	0	1000		Carnitine shuttle			
DLNLCGCPT2	carnitine transferase	coa[m] + dlnlcgcrn[m] -> crn[m] + dlnlcgcoa[m]	0	12896.1	0	1000		Carnitine shuttle			
DLNLCGCRNt	transport into the mitochondria (carnitine)	dlnlcgcrn[c] -> dlnlcgcrn[m]	0	57279.1	0	1000		Carnitine shuttle			
DLNLCGt	fatty acid transport via diffusion	dlnlcg[e] <=> dlnlcg[c]	1		-1000	1000		Transport, Extracellular			
DMANTIPYRINEte	xenobiotic transport	dmantipyrine[e] <=> dmantipyrine[c]	1		-1000	1000		Transport, Extracellular			
DMATT	dimethylallyltranstransferase	dmpp[c] + ipdp[c] -> ppi[c] + grdp[c]	0	14593.1	0	1000		Cholesterol Metabolism			
DMATTx	dimethylallyltranstransferase	dmpp[x] + ipdp[x] -> grdp[x] + ppi[x]	0	110196.1	0	1000		Cholesterol Metabolism			
DMGDHm	dimethylglycine dehydrogenase, mitochondrial	h2o[m] + fad[m] + dmgly[m] -> fadh2[m] + fald[m] + sarcs[m]	0	74129.1	0	1000		Glycine, Serine, and Threonine Metabolism			
DMGtm	dimethylglycine transport via diffusion (cytosol to mitochondria)	dmgly[c] <=> dmgly[m]	1		-1000	1000		Transport, Mitochondrial			
DMHPTCRNCPT1	carnitine fatty-acyl transferase	crn[c] + dmhptcoa[c] <=> coa[c] + dmhptcrn[c]	1		-1000	1000		Carnitine shuttle			
DMHPTCRNCPT2	2,6 dimethylheptanoly CoA carnitine transferase	coa[m] + dmhptcrn[m] <=> crn[m] + dmhptcoa[m]	1		-1000	1000		Carnitine shuttle			
DMHPTCRNt	2,6 dimethylheptanoyl crn transport	dmhptcrn[c] <=> dmhptcrn[m]	1		-1000	1000		Carnitine shuttle			
DMHPTCRNte	2,6 dimethylheptanoyl carnitine transport	dmhptcrn[c] <=> dmhptcrn[e]	1		-1000	1000		Transport, Extracellular			
DMNONCOACRNCPT1	carnitine fatty-acyl transferase	crn[c] + dmnoncoa[c] <=> coa[c] + dmnoncrn[c]	1		-1000	1000		Carnitine shuttle			
DMNONCRNCPT2	DMNON carnitine transferase	coa[m] + dmnoncrn[m] <=> crn[m] + dmnoncoa[m]	1		-1000	1000		Carnitine shuttle			
DMNONCRNt	4,8 dimethylnonanoyl crn transport	dmnoncrn[c] <=> dmnoncrn[m]	1		-1000	1000		Carnitine shuttle			
DM_13_cis_oretn_n_	DM_13_cis_oretn_n_	13-cis-oretn[n] ->	0		0	0		Exchange/ demand			
DM_13_cis_retn_n_	DM_13_cis_retn_n_	13-cis-retn[n] ->	0		0	0		Exchange/ demand			
DM_Asn_X_Ser_Thr_ly_	DM_Asn_X_Ser_Thr_ly_	Asn_X_Ser_Thr[l] ->	0		0	1000		Exchange/ demand			
DM_Ser_Gly_Ala_X_Gly_ly_	DM_Ser_Gly_Ala_X_Gly_ly_	Ser_Gly_Ala_X_Gly[l] ->	0		0	1000		Exchange/ demand			
DM_Ser_Thr_ly_	DM_Ser_Thr_ly_	Ser_Thr[l] ->	0		0	1000		Exchange/ demand			
DM_T_antigen(g)	DM_T_antigen(g)	T_antigen[g] <=>	1		-1	1000		Exchange/ demand			
DM_avite1_c_	DM_avite1_c_	avite1[c] ->	0		0	1000		Exchange/ demand			
DM_avite2_c_	DM_avite2_c_	avite2[c] ->	0		0	1000		Exchange/ demand			
DM_bvite_c_	DM_bvite_c_	bvite[c] ->	0		0	1000		Exchange/ demand			
DM_core5_g_	DM_core5_g_	core5[g] ->	0		0	1000		Exchange/ demand			
DM_core7_g_	DM_core7_g_	core7[g] ->	0		0	1000		Exchange/ demand			
DM_core8_g_	DM_core8_g_	core8[g] ->	0		0	1000		Exchange/ demand			
DM_datp_m_	DM_datp_m_	datp[m] ->	0		0	1000		Exchange/ demand			
DM_datp_n_	DM_datp_n_	datp[n] ->	0		0	1000		Exchange/ demand			
DM_dctp(m)	DM_dctp(m)	dctp[m] ->	0		0	1000		Exchange/ demand			

DM_dctp(n)	DM_dctp(n)	dctp[n] ->	0		0	1000		Exchange/ demand			
DM_dem2emgacpail_prot_hs(r)	DM_dem2emgacpail_prot_hs(r)	dem2emgacpail_prot_hs[r] ->	0		0	1000		Exchange/ demand			
DM_dgpi_prot_hs(r)	DM_dgpi_prot_hs(r)	dgpi_prot_hs[r] ->	0		0	1000		Exchange/ demand			
DM_dgtp(m)	DM_dgtp(m)	dgtp[m] ->	0		0	1000		Exchange/ demand			
DM_dgtp(n)	DM_dgtp(n)	dgtp[n] ->	0		0	1000		Exchange/ demand			
DM_dsT_antigen(g)	DM_dsT_antigen(g)	dsT_antigen[g] ->	0		0	1000		Exchange/ demand			
DM_dttp(m)	DM_dttp(m)	dttp[m] ->	0		0	1000		Exchange/ demand			
DM_dttp(n)	DM_dttp(n)	dttp[n] ->	0		0	1000		Exchange/ demand			
DM_ethamp(r)	DM_ethamp(r)	ethamp[r] ->	0		0	1000		Exchange/ demand			
DM_gncore2(g)	DM_gncore2(g)	gncore2[g] ->	0		0	1000		Exchange/ demand			
DM_gpi_sig(er)	DM_gpi_sig(er)	gpi_sig[r] ->	0		0	1000		Exchange/ demand			
DM_hretn(n)	DM_hretn(n)	hretn[n] ->	0		0	1000		Exchange/ demand			
DM_kdn(c)	DM_kdn(c)	kdn[c] ->	0		0	1000		Exchange/ demand			
DM_m(em)3gacpail_prot_hs(r)	DM_m(em)3gacpail_prot_hs(r)	m[em]3gacpail_prot_hs[r] ->	0		0	1000		Exchange/ demand			
DM_melanin(c)	DM_melanin(c)	melanin[c] ->	0		0	1000		Exchange/ demand			
DM_mem2emgacpail_prot_hs(r)	DM_mem2emgacpail_prot_hs(r)	mem2emgacpail_prot_hs[r] ->	0		0	1000		Exchange/ demand			
DM_n5m2masn(g)	DM_n5m2masn(g)	n5m2masn[g] ->	0		0	1000		Exchange/ demand			
DM_oretn(n)	DM_oretn(n)	oretn[n] ->	0		0	1000		Exchange/ demand			
DM_sTn_antigen(g)	DM_sTn_antigen(g)	sTn_antigen[g] ->	0		0	1000		Exchange/ demand			
DM_sprm(c)	DM_sprm(c)	sprm[c] ->	0		0	1000		Exchange/ demand			
DM_yvite(c)	DM_yvite(c)	yvite[c] ->	0		0	1000		Exchange/ demand			
DNADDP	Deaminido NAD diphosphatase	h2o[c] + dnad[c] -> 2 h[c] + amp[c] + nicrnt[c]	0	18605.1 or 18606.1 or 209558.1	0	1000		NAD Metabolism			
DNADtn	dNAD transport, nuclear trhough pore	dnad[c] <=> dnad[n]	1		-1000	1000		Transport, Nuclear			
DNAMTSEn	DNA (cytosine-5-)-methyltransferase, nucleus	dna[n] + seasmet[n] -> h[n] + dna5mtc[n] + seahcys[n]	0	13434.1 or 13434.2 or 13434.3 or 13434.4 or 13433.1 or 13434.5 or 13436.1 or 13435.1 or 13435.2 or 13436.2 or 13436.4 or 13434.6 or 13435.3 or 13436.3 or 13435.4	0	1000		Selenoamino acid metabolism			
DNAMTn	DNA (cytosine-5-)-methyltransferase, nucleus	amet[n] + dna[n] -> ahcys[n] + h[n] + dna5mtc[n]	0	13434.1 or 13434.2 or 13434.3 or 13434.4 or 13433.1 or 13434.5 or 13436.1 or 13435.1 or 13435.2 or 13436.2 or 13436.4 or 13434.6 or 13435.3 or 13436.3 or 13435.4	0	1000		Methionine Metabolism			
DNDPt10m	dADP transport via dCDP antiport	dadp[c] + dcdp[m] -> dcdp[c] + dadp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt11m	dADP transport via dGDP antiport	dadp[c] + dgdp[m] -> dgdp[c] + dadp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt12m	dADP transport via ADP antiport	adp[m] + dadp[c] -> adp[c] + dadp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt13m	dADP transport via ATP antiport	atp[m] + dadp[c] -> atp[c] + dadp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt14m	dUDP transport via dTDP antiport	dudp[c] + dtdp[m] -> dtdp[c] + dudp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt15m	dUDP transport via dGDP antiport	dgdp[m] + dudp[c] -> dgdp[c] + dudp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt16m	dUDP transport via dADP antiport	dadp[m] + dudp[c] -> dadp[c] + dudp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt17m	dUDP transport via dCDP antiport	dcdp[m] + dudp[c] -> dcdp[c] + dudp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt18m	dUDP transport via ADP antiport	adp[m] + dudp[c] -> adp[c] + dudp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt19m	dUDP transport via ATP antiport	atp[m] + dudp[c] -> atp[c] + dudp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt1m	dATP transport via ADP antiport	adp[m] + datp[c] -> adp[c] + datp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt20m	dTDP transport via ATP antiport	atp[m] + dtdp[c] -> atp[c] + dtdp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt21m	dTDP transport via ADP antiport	adp[m] + dtdp[c] -> adp[c] + dtdp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt22m	dTDP transport via dUDP antiport	dtdp[c] + dudp[m] -> dudp[c] + dtdp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt23m	dTDP transport via dGTP antiport	dgdp[m] + dtdp[c] -> dgdp[c] + dtdp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt24m	dTDP transport via dADP antiport	dadp[m] + dtdp[c] -> dadp[c] + dtdp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt25m	dTDP transport via dCDP antiport	dcdp[m] + dtdp[c] -> dcdp[c] + dtdp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt26m	dCDP transport via dUDP antiport	dcdp[c] + dudp[m] -> dcdp[m] + dudp[c]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt27m	dCDP transport via dTDP antiport	dcdp[c] + dtdp[m] -> dcdp[m] + dtdp[c]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt28m	dCDP transport via dGDP antiport	dcdp[c] + dgdp[m] -> dgdp[c] + dcdp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt29m	dCDP transport via dADP antiport	dcdp[c] + dadp[m] -> dadp[c] + dcdp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt2m	dATP transport via ATP antiport	atp[m] + datp[c] -> atp[c] + datp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt30m	dCDP transport via ADP antiport	adp[m] + dcdp[c] -> adp[c] + dcdp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt31m	dCDP transport via ATP antiport	atp[m] + dcdp[c] -> atp[c] + dcdp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt32m	dGDP transport via ATP antiport	atp[m] + dgdp[c] -> atp[c] + dgdp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt33m	dGDP transport via dUDP antiport	dgdp[c] + dudp[m] -> dgdp[m] + dudp[c]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt34m	dGDP transport via dTDP antiport	dgdp[c] + dtdp[m] -> dgdp[m] + dtdp[c]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt35m	dGDP transport via dADP antiport	dgdp[c] + dadp[m] -> dadp[c] + dgdp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt36m	dGDP transport via dCDP antiport	dgdp[c] + dcdp[m] -> dcdp[c] + dgdp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt37m	dUTP transport via dTDP antiport	dtdp[m] + dutp[c] -> dtdp[c] + dutp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt38m	dUTP transport via dUDP antiport	dudp[m] + dutp[c] -> dudp[c] + dutp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt39m	dUTP transport via dGDP antiport	dgdp[m] + dutp[c] -> dgdp[c] + dutp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt3m	dATP transport via dCDP antiport	datp[c] + dcdp[m] -> dcdp[c] + datp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt40m	dUTP transport via dADP antiport	dadp[m] + dutp[c] -> dadp[c] + dutp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt41m	dUTP transport via dCDP antiport	dcdp[m] + dutp[c] -> dcdp[c] + dutp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt42m	dUTP transport via ADP antiport	adp[m] + dutp[c] -> adp[c] + dutp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt43m	dUTP transport via ATP antiport	atp[m] + dutp[c] -> atp[c] + dutp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt44m	dTTP transport via ATP antiport	atp[m] + dttp[c] -> atp[c] + dttp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt45m	dTTP transport via ADP antiport	adp[m] + dttp[c] -> adp[c] + dttp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt46m	dTTP transport via dUDP antiport	dudp[m] + dttp[c] -> dttp[m] + dudp[c]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt47m	dTTP transport via dTDP antiport	dtdp[m] + dttp[c] -> dttp[m] + dtdp[c]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt48m	dTTP transport via dGDP antiport	dgdp[m] + dttp[c] -> dgdp[c] + dttp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt49m	dTTP transport via dADP antiport	dadp[m] + dttp[c] -> dadp[c] + dttp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt4m	dATP transport via dUDP antiport	datp[c] + dudp[m] -> datp[m] + dudp[c]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt50m	dTTP transport via dCDP antiport	dcdp[m] + dttp[c] -> dcdp[c] + dttp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt51m	dCTP transport via dCDP antiport	dctp[c] + dcdp[m] -> dcdp[c] + dctp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt52m	dCTP transport via dUDP antiport	dctp[c] + dudp[m] -> dctp[m] + dudp[c]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt53m	dCTP transport via dGDP antiport	dctp[c] + dgdp[m] -> dgdp[c] + dctp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt54m	dCTP transport via dADP antiport	dctp[c] + dadp[m] -> dadp[c] + dctp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt55m	dCTP transport via ADP antiport	adp[m] + dctp[c] -> adp[c] + dctp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt56m	dCTP transport via ATP antiport	atp[m] + dctp[c] -> atp[c] + dctp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt57m	dGTP transport via ATP antiport	atp[m] + dgtp[c] -> atp[c] + dgtp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt58m	dGTP transport via ADP antiport	adp[m] + dgtp[c] -> adp[c] + dgtp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt59m	dGTP transport via dADP antiport	dgtp[c] + dadp[m] -> dadp[c] + dgtp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt5m	dATP transport via dTDP antiport	datp[c] + dtdp[m] -> datp[m] + dtdp[c]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt60m	dGTP transport via dUDP antiport	dgtp[c] + dudp[m] -> dgtp[m] + dudp[c]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt61m	dGTP transport via dTDP antiport	dgtp[c] + dtdp[m] -> dgtp[m] + dtdp[c]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt62m	dGTP transport via dGDP antiport	dgtp[c] + dgdp[m] -> dgdp[c] + dgtp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt63m	dGTP transport via dCDP antiport	dgtp[c] + dcdp[m] -> dcdp[c] + dgtp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt6m	dATP transport via dGDP antiport	datp[c] + dgdp[m] -> dgdp[c] + datp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt7m	dATP transport via dADP antiport	datp[c] + dadp[m] -> dadp[c] + datp[m]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt8m	dADP transport via dUDP antiport	dadp[c] + dudp[m] -> dadp[m] + dudp[c]	0	67283.1	0	1000		Transport, Mitochondrial			
DNDPt9m	dADP transport via dTDP antiport	dadp[c] + dtdp[m] -> dadp[m] + dtdp[c]	0	67283.1	0	1000		Transport, Mitochondrial			
DOGULND1	2,3-dioxo-L-gulonate decarboxylase (L-lyxonate-forming)	h2o[c] + 23doguln[c] -> co2[c] + lyxnt[c]	0		0	1000		Ascorbate and Aldarate Metabolism			
DOGULND2	2,3-dioxo-L-gulonate decarboxylase (L-xylonate-forming)	h2o[c] + 23doguln[c] -> co2[c] + xylnt[c]	0		0	1000		Ascorbate and Aldarate Metabolism			
DOGULNO1	2,3-dioxo-L-gulonate:hydrogen peroxide oxireductase	h2o2[c] + 23doguln[c] -> 2 h[c] + oxa[c] + thrnt[c]	0		0	1000		Ascorbate and Aldarate Metabolism			
DOGULNO2	2,3-dioxo-L-gulonate:hydrogen peroxide oxireductase	h2o[c] + 23doguln[c] -> h[c] + oxa[c] + eryth[c]	0		0	1000		Ascorbate and Aldarate Metabolism			
DOLASNT_Ler	Dolichyl-diphosphooligosaccharide:protein-L-asparagine oligopolysaccharidotransferase (liver)	Asn_X_Ser_Thr[r] + 0.1 g3m8mpdol_L[r] -> h[r] + 0.1 doldp_L[r] + g3m8masn[r]	0	20014.1 and 13200.1 and 103963.1 and 13135.1	0	1000		N-Glycan Biosynthesis			
DOLASNT_Uer	Dolichyl-diphosphooligosaccharide:protein-L-asparagine oligopolysaccharidotransferase (uterus)	Asn_X_Ser_Thr[r] + 0.1 g3m8mpdol_U[r] -> h[r] + g3m8masn[r] + 0.1 doldp_U[r]	0	20014.1 and 13200.1 and 103963.1 and 13135.1	0	1000		N-Glycan Biosynthesis			
DOLDPP_Ler	Dolichyl-diphosphate phosphohydrolase, human (liver)	h2o[r] + 0.1 doldp_L[r] -> 0.1 dolp_L[r] + h[r] + pi[r]	0	57170.1	0	1000		N-Glycan Biosynthesis			
DOLDPP_Uer	Dolichyl-diphosphate phosphohydrolase, human (uterus)	h2o[r] + 0.1 doldp_U[r] -> h[r] + 0.1 dolp_U[r] + pi[r]	0	57170.1	0	1000		N-Glycan Biosynthesis			
DOLGLCP_Lter	Dolichyl beta-D-glucosyl phosphate flippase (liver)	0.1 dolglcp_L[c] -> 0.1 dolglcp_L[r]	0		0	1000		N-Glycan Biosynthesis			
DOLGLCP_Uter	Dolichyl beta-D-glucosyl phosphate flippase (uterus)	0.1 dolglcp_U[c] -> 0.1 dolglcp_U[r]	0		0	1000		N-Glycan Biosynthesis			
DOLGPP_Ler	Dolichyl-beta-D-glucosyl-phosphate dolichylphosphohydrolase (liver)	h2o[r] + 0.1 dolglcp_L[r] -> 0.1 dolp_L[r] + h[r] + glc-D[r]	0		0	1000		N-Glycan Biosynthesis			
DOLGPP_Uer	Dolichyl-beta-D-glucosyl-phosphate dolichylphosphohydrolase (uterus)	h2o[r] + 0.1 dolglcp_U[r] -> h[r] + 0.1 dolp_U[r] + glc-D[r]	0		0	1000		N-Glycan Biosynthesis			
DOLICHOL_Lter	dolichol diffusion, human (liver)	0.1 dolichol_L[r] <=> 0.1 dolichol_L[c]	1		-1000	1000		N-Glycan Biosynthesis			
DOLICHOL_Uter	dolichol diffusion, human (uterus)	0.1 dolichol_U[r] <=> 0.1 dolichol_U[c]	1		-1000	1000		N-Glycan Biosynthesis			
DOLK_L	Dolichol kinase, human (liver)	ctp[c] + 0.1 dolichol_L[c] -> h[c] + cdp[c] + 0.1 dolp_L[c]	0		0	1000		N-Glycan Biosynthesis			
DOLK_U	Dolichol kinase, human (uterus)	ctp[c] + 0.1 dolichol_U[c] -> h[c] + cdp[c] + 0.1 dolp_U[c]	0		0	1000		N-Glycan Biosynthesis			
DOLMANP_Lter	dolichol-phosphate mannose flippase (liver)	0.1 dolmanp_L[c] -> 0.1 dolmanp_L[r]	0		0	1000		N-Glycan Biosynthesis			
DOLMANP_Uter	dolichol-phosphate mannose flippase (uterus)	0.1 dolmanp_U[c] -> 0.1 dolmanp_U[r]	0		0	1000		N-Glycan Biosynthesis			
DOLPGT1_Ler	dolichyl-phosphate-glucose-glycolipid alpha-glucosyltransferase (liver)	0.1 dolglcp_L[r] + 0.1 m8mpdol_L[r] -> 0.1 dolp_L[r] + h[r] + 0.1 g1m8mpdol_L[r]	0	320438.1	0	1000		N-Glycan Biosynthesis			
DOLPGT1_Uer	dolichyl-phosphate-glucose-glycolipid alpha-glucosyltransferase (uterus)	0.1 dolglcp_U[r] + 0.1 m8mpdol_U[r] -> h[r] + 0.1 dolp_U[r] + 0.1 g1m8mpdol_U[r]	0	320438.1	0	1000		N-Glycan Biosynthesis			
DOLPGT2_Ler	dolichyl-phosphate-glucose-glycolipid alpha-glucosyltransferase (liver)	0.1 dolglcp_L[r] + 0.1 g1m8mpdol_L[r] -> 0.1 dolp_L[r] + h[r] + 0.1 g2m8mpdol_L[r]	0	381903.1 or 381903.2 or 381903.3	0	1000		N-Glycan Biosynthesis			
DOLPGT2_Uer	dolichyl-phosphate-glucose-glycolipid alpha-glucosyltransferase (uterus)	0.1 dolglcp_U[r] + 0.1 g1m8mpdol_U[r] -> h[r] + 0.1 dolp_U[r] + 0.1 g2m8mpdol_U[r]	0	381903.1 or 381903.2 or 381903.3	0	1000		N-Glycan Biosynthesis			
DOLPGT3_Ler	dolichyl-phosphate-glucose-glycolipid alpha-glucosyltransferase (liver)	0.1 dolglcp_L[r] + 0.1 g2m8mpdol_L[r] -> 0.1 dolp_L[r] + h[r] + 0.1 g3m8mpdol_L[r]	0	380959.1	0	1000		N-Glycan Biosynthesis			
DOLPGT3_Uer	dolichyl-phosphate-glucose-glycolipid alpha-glucosyltransferase (uterus)	0.1 dolglcp_U[r] + 0.1 g2m8mpdol_U[r] -> h[r] + 0.1 dolp_U[r] + 0.1 g3m8mpdol_U[r]	0	380959.1	0	1000		N-Glycan Biosynthesis			
DOLPH_Ler	Dolichol-phosphate phosphohydrolase, human (liver)	h2o[r] + 0.1 dolp_L[r] -> pi[r] + 0.1 dolichol_L[r]	0		0	1000		N-Glycan Biosynthesis			
DOLPH_Uer	Dolichol-phosphate phosphohydrolase, human (uterus)	h2o[r] + 0.1 dolp_U[r] -> pi[r] + 0.1 dolichol_U[r]	0		0	1000		N-Glycan Biosynthesis			

DOLPMT1_Ler	dolichyl-phosphate-mannose-glycolipid alpha-mannosyltransferase (liver)	0.1 dolmanp_L[r] + 0.1 m4mpdol_L[r] -> 0.1 dolp_L[r] + h[r] + 0.1 m5mpdol_L[r]	0	208624.1 or 208624.2 or 208624.3 or 208624.4	0	1000		N-Glycan Biosynthesis			
DOLPMT1_Uer	dolichyl-phosphate-mannose-glycolipid alpha-mannosyltransferase (uterus)	0.1 dolmanp_U[r] + 0.1 m4mpdol_U[r] -> h[r] + 0.1 dolp_U[r] + 0.1 m5mpdol_U[r]	0	208624.1 or 208624.2 or 208624.3 or 208624.4	0	1000		N-Glycan Biosynthesis			
DOLPMT2_Ler	dolichyl-phosphate-mannose-glycolipid alpha-mannosyltransferase (liver)	0.1 dolmanp_L[r] + 0.1 m5mpdol_L[r] -> 0.1 dolp_L[r] + h[r] + 0.1 m6mpdol_L[r]	0		0	1000		N-Glycan Biosynthesis			
DOLPMT2_Uer	dolichyl-phosphate-mannose-glycolipid alpha-mannosyltransferase (uterus)	0.1 dolmanp_U[r] + 0.1 m5mpdol_U[r] -> h[r] + 0.1 dolp_U[r] + 0.1 m6mpdol_U[r]	0		0	1000		N-Glycan Biosynthesis			
DOLPMT3_Ler	dolichyl-phosphate-mannose-glycolipid alpha-mannosyltransferase (liver)	0.1 dolmanp_L[r] + 0.1 m6mpdol_L[r] -> 0.1 dolp_L[r] + h[r] + 0.1 m7mpdol_L[r]	0	223774.1	0	1000		N-Glycan Biosynthesis			
DOLPMT3_Uer	dolichyl-phosphate-mannose-glycolipid alpha-mannosyltransferase (uterus)	0.1 dolmanp_U[r] + 0.1 m6mpdol_U[r] -> h[r] + 0.1 dolp_U[r] + 0.1 m7mpdol_U[r]	0	223774.1	0	1000		N-Glycan Biosynthesis			
DOLPMT4_Ler	dolichyl-phosphate-mannose-glycolipid alpha-mannosyltransferase (liver)	0.1 dolmanp_L[r] + 0.1 m7mpdol_L[r] -> 0.1 dolp_L[r] + h[r] + 0.1 m8mpdol_L[r]	0		0	1000		N-Glycan Biosynthesis			
DOLPMT4_Uer	dolichyl-phosphate-mannose-glycolipid alpha-mannosyltransferase (uterus)	0.1 dolmanp_U[r] + 0.1 m7mpdol_U[r] -> h[r] + 0.1 dolp_U[r] + 0.1 m8mpdol_U[r]	0		0	1000		N-Glycan Biosynthesis			
DOLPMT_L	Dolichyl-phosphate D-mannosyltransferase (liver)	gdpmann[c] + 0.1 dolp_L[c] -> gdp[c] + 0.1 dolmanp_L[c]	0	68563.1 and 13481.1 and 13480.1 or 68563.2 and 13481.1 and 13480.1 or 13481.2 and 68563.1 and 13480.1 or 13481.2 and 68563.2 and 13480.1	0	1000		N-Glycan Biosynthesis			
DOLPMT_U	Dolichyl-phosphate D-mannosyltransferase (uterus)	gdpmann[c] + 0.1 dolp_U[c] -> gdp[c] + 0.1 dolmanp_U[c]	0	68563.1 and 13481.1 and 13480.1 or 68563.2 and 13481.1 and 13480.1 or 13481.2 and 68563.1 and 13480.1 or 13481.2 and 68563.2 and 13480.1	0	1000		N-Glycan Biosynthesis			
DOLP_Lter	dolichol phosphate flippase (liver)	0.1 dolp_L[r] -> 0.1 dolp_L[c]	0		0	1000		N-Glycan Biosynthesis			
DOLP_Uter	dolichol phosphate flippase (uterus)	0.1 dolp_U[r] -> 0.1 dolp_U[c]	0		0	1000		N-Glycan Biosynthesis			
DOPABMO	dopamine beta-monooxygenase	o2[c] + dopa[c] + ascb-L[c] -> h2o[c] + nrpphr[c] + dhdascb[c]	0	59012.1 or 13166.1	0	1000		Tyrosine metabolism			
DOPACHRMISO	L-dopachrome isomerase 1	o2[c] + 2 2c23dh56dhoxin[c] -> 2 h2o[c] + 2 L-dpchrm[c]	0	22173.1	0	1000		Tyrosine metabolism			
DOPAMT	Dopamine:amet O-methyltransferase	amet[c] + dopa[c] -> h[c] + ahcys[c] + 3moxtyr[c]	0	12846.1 or 12846.2	0	1000		Tyrosine metabolism			
DOPAQNISO1	Dopaquinone isomerase 1	dopaqn[c] <=> h[c] + 2c23dh56dhoxin[c]	1		-1000	1000		Tyrosine metabolism			
DOPASFt	Dopamine 3-0-sulfate transport (diffusion)	dopasf[c] -> dopasf[e]	0		0	1000		Transport, Extracellular			
DOPAVESSEC	Dopamine secretion via secretory vesicle (ATP driven)	2 h2o[c] + 2 atp[c] + 3 dopa[c] -> 2 adp[c] + 2 h[c] + 2 pi[c] + 3 dopa[e]	0	214084.1 or 110877.1	0	1000		Transport, Extracellular			
DOPAt4_2_r	Dopamine reversible transport in via sodium symport (1:2)	2 na1[e] + dopa[e] <=> 2 na1[c] + dopa[c]	1	20538.1 or 13162.1	-1000	1000	2	Transport, Extracellular			
DOPAtu	Dopamine uniport	dopa[e] <=> dopa[c]	1	20518.1 or 20519.1 or 20518.2	-1000	1000		Transport, Extracellular			
DORNOp	D-ornithine oxidase, perixosomal	o2[x] + h2o[x] + orn-D[x] -> h2o2[x] + nh4[x] + 5a2opntn[x]	0	13142.1	0	1000		D-arg and D-orn metabolism			
DPCOAK	dephospho-CoA kinase	atp[c] + dpcoa[c] -> adp[c] + h[c] + coa[c]	0	71743.1	0	1000		CoA Biosynthesis			
DPCOAPP	pyrophasphatase (dephospho-CoA)	h2o[c] + dpcoa[c] -> 2 h[c] + amp[c] + pan4p[c]	0		0	1000		CoA Catabolism			
DPCOAtl	dephospho-CoA transport from lysosome via diffusion	dpcoa[l] <=> dpcoa[c]	1		-1000	1000		Transport, Lysosomal			
DPGM	Diphosphoglyceromutase	13dpg[c] <=> h[c] + 23dpg[c]	1	12183.1 or 56012.1 or 18648.1 or 12183.2 or 56012.2	-1000	1000		Glycolysis/Gluconeogenesis			
DPGase	Diphosphoglycerate phosphatase	h2o[c] + 23dpg[c] -> pi[c] + 3pg[c]	0	12183.1 or 56012.1 or 18648.1 or 12183.2 or 56012.2	0	1000		Glycolysis/Gluconeogenesis			
DPHMBDCm	3-Decaprenyl-4-hydroxy-5-methoxybenzoate decarboxylation	h[m] + 3dpdhb_me[m] -> co2[m] + 2dp6mep[m]	0		0	1000		Ubiquinone Biosynthesis			
DPMVDx	diphosphomevalonate decarboxylase	atp[x] + 5dpmev[x] -> adp[x] + co2[x] + ipdp[x] + pi[x]	0	192156.1	0	1000		Cholesterol Metabolism			
DPPS	decaprenyl synthase	7 ipdp[c] + frdp[c] -> 7 ppi[c] + decdp[c]	0		0	1000		Miscellaneous			
DPROOp	D-proline oxidase, perixosomal	o2[x] + pro-D[x] -> h[x] + h2o2[x] + 1p2cbxl[x]	0	13142.1	0	1000		Arginine and Proline Metabolism			
DRBK	Deoxyribokinase	atp[c] + drib[c] -> adp[c] + h[c] + 2dr5p[c]	0	71336.1	0	1000		Pentose Phosphate Pathway			
DRIBt	deoxyribose transport via diffusion	drib[e] <=> drib[c]	1		-1000	1000		Transport, Extracellular			
DRPA	deoxyribose-phosphate aldolase	2dr5p[c] -> acald[c] + g3p[c]	0		0	1000		Pentose Phosphate Pathway			
DSAT	dihydrosphingosine N-acyltransferase	sphgn[c] + Rtotalcoa[c] -> h[c] + coa[c] + dhcrm_hs[c]	0		0	1000		Sphingolipid Metabolism			
DST_ANTIGENt	dsT_antigen (mucin O-glycan) export	dsT_antigen[g] -> dsT_antigen[e]	0		0	1000	2	Transport, Extracellular	PMID: 10430883, PMID: 848954	Reaction that provides mucin O-glycans to gut microbiota, e.g. B. thetaiotaomicron. BT is well known to degrade mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis.	
DTDPtn	dTDP nuclear transport	dtdp[c] <=> dtdp[n]	1		-1000	1000		Transport, Nuclear			
DTMPK	dTMP kinase	atp[c] + dtmp[c] <=> adp[c] + dtdp[c]	1	21915.1	-1000	1000		Nucleotides			
DTTPtn	dTTP diffusion in nucleus	dttp[c] <=> dttp[n]	1		-1000	1000		Transport, Nuclear			
DUDPtn	dUDP nuclear transport	dudp[c] <=> dudp[n]	1		-1000	1000		Transport, Nuclear			
DUMPtn	dUMP nuclear transport	dump[c] <=> dump[n]	1		-1000	1000		Transport, Nuclear			
DURAD	dihydrouracil dehydrogenase (NADP)	nadp[c] + 56dura[c] <=> h[c] + nadph[c] + ura[c]	1	99586.1	-1000	1000		Pyrimidine Catabolism			
DURAD2	dihydrothymin dehydrogenase (NADP)	nadp[c] + 56dthm[c] <=> h[c] + nadph[c] + thym[c]	1	99586.1	-1000	1000		Pyrimidine Catabolism			
DURIK1	deoxyuridine kinase (ATP:Deoxyuridine)	atp[c] + duri[c] -> adp[c] + h[c] + dump[c]	0	57813.1 or 619653.1	0	1000		Nucleotides			
DURIK1m	deoxyuridine kinase (ATP:Deoxyuridine), mitochondrial	atp[m] + duri[m] -> h[m] + adp[m] + dump[m]	0	57813.1	0	1000		Nucleotides			
DURIPP	deoxyuridine phosphorylase	pi[c] + duri[c] <=> 2dr1p[c] + ura[c]	1	667034.1 or 76654.1	-1000	1000		Nucleotides			
DURIt	deoxyuridine transport via diffusion	duri[e] <=> duri[c]	1		-1000	1000		Transport, Extracellular			
DURItn	deoxyuridine transport in nucleus	duri[c] <=> duri[n]	1		-1000	1000		Transport, Nuclear			
DUTPDPm	dUTP diphosphatase	h2o[m] + dutp[m] -> h[m] + ppi[m] + dump[m]	0	110074.1	0	1000		Nucleotides			
DUTPDPn	dUTP diphosphatase, nuclear	h2o[n] + dutp[n] -> ppi[n] + h[n] + dump[n]	0	110074.1	0	1000		Nucleotides			
D_3AIBt	D-3-amino-isobutyrate transport	3aib-D[c] -> 3aib-D[e]	0		0	1000		Transport, Extracellular			
D_LACt2	D-lactate transport via proton symport	h[e] + lac-D[e] <=> h[c] + lac-D[c]	1	20503.1 or 80879.1 or 20501.1 or 57274.1	-1000	1000		Transport, Extracellular			
D_LACtm	D-lactate transport, mitochondrial	h[c] + lac-D[c] <=> h[m] + lac-D[m]	1	20501.1	-1000	1000		Transport, Mitochondrial			
EAFLATOXINte	xenobiotic transport	eaflatoxin[e] <=> eaflatoxin[c]	1		-1000	1000		Transport, Extracellular			
EBASTINEOHte	xenobiotic transport	ebastineoh[e] <=> ebastineoh[c]	1		-1000	1000		Transport, Extracellular			
EBASTINEOHtr	xenobiotic transport	ebastineoh[r] <=> ebastineoh[c]	1		-1000	1000		Transport, Endoplasmic Reticular			
EBASTINEte	xenobiotic transport	ebastine[e] <=> ebastine[c]	1		-1000	1000		Transport, Extracellular			
EBASTINEtr	xenobiotic transport	ebastine[r] <=> ebastine[c]	1		-1000	1000		Transport, Endoplasmic Reticular			
EBP1r	3-beta-hydroxysteroid-delta(8),delta(7)-isomerase	zymst[r] -> chlstol[r]	0	13595.1	0	1000		Cholesterol Metabolism			
EBP2r	3-beta-hydroxysteroid-delta(8),delta(7)-isomerase	zymstnl[r] -> lthstrl[r]	0	13595.1	0	1000		Cholesterol Metabolism			
ECGISOr	Ecgonine isomerase (ER)	ecgon[r] <=> pecgon[r]	1		-1000	1000		Alkaloid biosynthesis II			
ECOAH12m	3-hydroxyacyl-CoA dehydratase (3-hydroxyisobutyryl-CoA) (mitochondria)	h2o[m] + 2mp2coa[m] <=> 3hibutcoa[m]	1	231086.1 or 97212.1 or 93747.1	-1000	1000		Valine, Leucine, and Isoleucine Metabolism			
ECOAH1m	3-hydroxyacyl-CoA dehydratase (3-hydroxybutanoyl-CoA) (mitochondria)	3hbcoa[m] <=> h2o[m] + b2coa[m]	1	11992.1 or 231086.1 or 97212.1 or 93747.1	-1000	1000		Tryptophan metabolism			
ECOAH1x	3-hydroxyacyl-CoA dehydratase (3-hydroxybutanoyl-CoA) (perioxisome)	3hbcoa[x] <=> h2o[x] + b2coa[x]	1	74147.1 or 51798.1	-1000	1000		Tryptophan metabolism			
ECOAH9m	2-Methylprop-2-enoyl-CoA (2-Methylbut-2-enoyl-CoA), mitochondrial	h2o[m] + 2mb2coa[m] <=> 3hmbcoa[m]	1	231086.1 or 97212.1 or 93747.1	-1000	1000		Valine, Leucine, and Isoleucine Metabolism			
EGMESTr	ecgonine methyl esterase (ER)	h2o[r] + egme[r] -> h[r] + ecgon[r] + meoh[r]	0	67758.1	0	1000		Alkaloid biosynthesis II			
EHGLAT	L-erythro-4-Hydroxyglutamate:2-oxoglutarate aminotransferase	akg[c] + e4hglu[c] -> glu-L[c] + 4h2oglt[c]	0	14718.1	0	1000		Arginine and Proline Metabolism			
EHGLAT2m	L-erythro-4-Hydroxyglutamate:2-oxoglutarate aminotransferase 2, mitochondrial	e4hglu[m] + oaa[m] -> asp-L[m] + 4h2oglt[m]	0	14719.1	0	1000		Arginine and Proline Metabolism			
EHGLATm	L-erythro-4-Hydroxyglutamate:2-oxoglutarate aminotransferase, mitochondrial	akg[m] + e4hglu[m] -> glu-L[m] + 4h2oglt[m]	0	14719.1	0	1000		Arginine and Proline Metabolism			
EICOSTETCPT1	carnitine O-palmitoyltransferase	crn[c] + eicostetcoa[c] -> coa[c] + eicostetcrn[c]	0	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	0	1000		Carnitine shuttle			
EICOSTETCPT2	carnitine transferase	coa[m] + eicostetcrn[m] -> crn[m] + eicostetcoa[m]	0	12896.1	0	1000		Carnitine shuttle			
EICOSTETCRNt	transport into the mitochondria (carnitine)	eicostetcrn[c] -> eicostetcrn[m]	0	57279.1	0	1000		Carnitine shuttle			
EICOSTETt	fatty acid transport via diffusion	eicostet[e] <=> eicostet[c]	1		-1000	1000		Transport, Extracellular			
ELAIDCPT1c	production of Elaidic carnitine	crn[c] + od2coa[c] <=> coa[c] + elaidcrn[c]	1	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	-1000	1000	4	Carnitine shuttle	PMID: 20508999, PMID: 10443971, PMID: 444549		2.3.1.21
ELAIDCPT2	carnitine transferase	coa[m] + elaidcrn[m] -> crn[m] + od2coa[m]	0	12896.1	0	1000		Carnitine shuttle			
ELAIDCRNt	transport into the mitochondria (carnitine)	elaidcrn[c] -> elaidcrn[m]	0	57279.1	0	1000		Carnitine shuttle			
ELAIDt	fatty acid transport via diffusion	elaid[e] <=> elaid[c]	1		-1000	1000		Transport, Extracellular			
ENGASE	endo-beta-N-acetylglucosaminidase	h2o[c] + s2l2n2m2m[c] -> acgam[c] + s2l2n2m2mn[c]	0	217364.1	0	1000		N-Glycan Degradation			
ENGASE2	endo-beta-N-acetylglucosaminidase	h2o[c] + n2m2nm[c] -> acgam[c] + n2m2nmn[c]	0	217364.1	0	1000		N-Glycan Degradation			
ENGASE2ly	endo-beta-N-acetylglucosaminidase, lysosomal	h2o[l] + n2m2nm[l] -> acgam[l] + n2m2nmn[l]	0		0	1000		N-Glycan Degradation			
ENGASE3ly	endo-beta-N-acetylglucosaminidase, lysosomal	h2o[l] + ksi_deg2[l] -> acgam[l] + ksi_deg3[l]	0		0	1000		Keratan sulfate degradation			
ENGASEly	endo-beta-N-acetylglucosaminidase, lysosomal	h2o[l] + s2l2n2m2m[l] -> acgam[l] + s2l2n2m2mn[l]	0		0	1000		N-Glycan Degradation			
ENMAN1g	Endomannosidase (glc1man-producing), Golgi apparatus	h2o[g] + g1m8masn[g] -> glc1man[g] + m7masnA[g]	0		0	1000		N-Glycan Biosynthesis			
ENMAN2g	Endomannosidase (glc2man-producing), Golgi apparatus	h2o[g] + g2m8masn[g] -> m7masnA[g] + glc2man[g]	0		0	1000		N-Glycan Biosynthesis			
ENMAN3g	Endomannosidase (glc3man-producing), Golgi apparatus	h2o[g] + g3m8masn[g] -> m7masnA[g] + glc3man[g]	0		0	1000		N-Glycan Biosynthesis			
ENMAN4g	Endomannosidase (m6masnC-producing), Golgi apparatus	h2o[g] + g1m7masnC[g] -> glc1man[g] + m6masnC[g]	0		0	1000		N-Glycan Biosynthesis			
ENMAN5g	Endomannosidase (m6masnB2-producing), Golgi apparatus	h2o[g] + g1m7masnB[g] -> glc1man[g] + m6masnB2[g]	0		0	1000		N-Glycan Biosynthesis			
ENMAN6g	Endomannosidase (m5masnB1-producing), Golgi apparatus	h2o[g] + g1m6masnB1[g] -> glc1man[g] + m5masnB1[g]	0		0	1000		N-Glycan Biosynthesis			
ENO	enolase	2pg[c] <=> h2o[c] + pep[c]	1	13807.1 or 13808.1 or 13808.2 or 13806.1	-1000	1000		Glycolysis/Gluconeogenesis			

EPAFABPpmtc	uptake of Eicosapentaenoic acid by the enterocytes	tmndnc[u] -> tmndnc[c]	0	(14719.1 or 12491.1)	0	1000	3	Transport, Lumen	PMID: 20086080, PMID: 10617989, PMID: 8717442, Progress in Lipid Research Volume 48, Issue 2, March 2009, Pages 101-115	GOT2 encodes FABPpm that may either act alone or in co-ordination with CD36, for the uptake of long chain fatty acids (exhibits a selective preference for long chain PUFA and essential fatty acids over non-essential fatty acids). The fatty acids alternatively can undergo passive diffusion. once inside the cell, they bind to the cytoplasmic fatty acid binding protein (FABPc) and thereby undergo actiavtion or esterification. Additionally, a minority of fatty acids are thought to be transported by FATP1 and rapidly activated by plasma membrane acyl-CoA synthetase (ACS1) to form acyl-Co esters. (PMID: 20086080)	
EPCTX	ethanolamine-phosphate cytidylyltransferase	h[c] + ctp[c] + 2ameph[c] -> ppi[c] + cmp2amep[c]	0	68671.1	0	1000		Glycerophospholipid Metabolism			
ESTRADIOLGLCt2	17-beta-D-glucuronide transport (ATP-dependent)	h2o[c] + atp[c] + estradiolglc[c] -> adp[c] + h[c] + pi[c] + estradiolglc[e]	0	239273.1	0	1000		Transport, Extracellular			
ESTRADIOLGLCtr	glucuronidated compound transport	estradiolglc[c] <=> estradiolglc[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
ESTRADIOLt	estradiol transmembrane (homo sapiens) transport	estradiol[e] <=> estradiol[c]	1		-1000	1000		Transport, Extracellular			
ESTRADIOLtr	estradiol intracellular transport	estradiol[r] <=> estradiol[c]	1		-1000	1000		Transport, Endoplasmic Reticular			
ESTRIOLGLCte	glucuronidated compound transport	h2o[c] + atp[c] + estriolglc[c] -> adp[c] + h[c] + pi[c] + estriolglc[e]	0	17250.1	0	1000		Transport, Extracellular			
ESTRIOLGLCtr	glucuronidated compound transport	estriolglc[c] <=> estriolglc[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
ESTRIOLtr	estriol intracellular transport	estriol[r] <=> estriol[c]	1		-1000	1000		Transport, Endoplasmic Reticular			
ESTRONEGLCt	ABC transporter	h2o[c] + atp[c] + estroneglc[c] -> adp[c] + h[c] + pi[c] + estroneglc[e]	0	76408.1 or 76408.2 or 76408.3	0	1000		Transport, Extracellular			
ESTRONEGLCtr	glucuronidated compound transport	estroneglc[c] <=> estroneglc[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
ESTRONESt2	estrone-3-sulfate transport via sodium cotransport	2 na1[e] + estrones[e] -> 2 na1[c] + estrones[c]	0	20493.1	0	1000		Transport, Extracellular			
ESTRONEtr	estrone intracellular transport	estrone[r] <=> estrone[c]	1		-1000	1000		Transport, Endoplasmic Reticular			
ESTSULT	Estrogen sulfotransferase	paps[c] + estrone[c] -> h[c] + pap[c] + estrones[c]	0	20887.1 or 20887.2 or 20887.3 or 20887.4 or 20860.1 or 20887.5	0	1000		Steroid Metabolism			
ETF	electron transfer flavoprotein	fadh2[m] + etfox[m] -> fad[m] + etfrd[m]	0	110826.1 or 110826.2 or 110842.1	0	1000		Fatty acid oxidation			
ETFQO	Electron transfer flavoprotein-ubiquinone oxidoreductase	q10[m] + etfrd[m] -> q10h2[m] + etfox[m]	0	66841.1	0	1000		Fatty acid oxidation			
ETHAK	Ethanolamine kinase	atp[c] + etha[c] -> adp[c] + h[c] + ethamp[c]	0	214253.1 or 12660.1 or 75320.1 or 12660.2	0	1000		Glycerophospholipid Metabolism			
ETHAtr	Ethanolamine export	etha[c] -> etha[e]	0		0	1000	2	Transport, Extracellular	PMID: 15123798, PMID: 18180286	This metabolite is found in mucus and can serve as carbon source for intestinal microbes. It is assumed it appears in mucus through secretion from goblet cells and from epithelial cell debris.	
ETHP	ethanolamine phosphate phosphatase	h2o[c] + ethamp[c] -> pi[c] + etha[c]	0	237928.1	0	1000		Glycerophospholipid Metabolism			
ETOHMO	ethanol monooxygenase	o2[c] + h[c] + nadph[c] + etoh[c] -> 2 h2o[c] + nadp[c] + acald[c]	0	13106.1	0	1000		Glycolysis/Gluconeogenesis			
ETOHt	ethanol reversible transport	etoh[e] <=> etoh[c]	1		-1000	1000		Transport, Extracellular			
ETOHtx	ethanol reversible peroxisomal transport	etoh[c] <=> etoh[x]	1		-1000	1000		Transport, Peroxisomal			
EX_10fthf(e)	EX_10fthf(e)	10fthf[e] <=>	1		-1000	1000		Exchange/ demand			
EX_10fthf5glu(e)	EX_10fthf5glu(e)	10fthf5glu[e] <=>	1		-1000	1000		Exchange/ demand			
EX_10fthf6glu(e)	EX_10fthf6glu(e)	10fthf6glu[e] <=>	1		-1000	1000		Exchange/ demand			
EX_10fthf7glu(e)	EX_10fthf7glu(e)	10fthf7glu[e] <=>	1		-1000	1000		Exchange/ demand			
EX_11_cis_retfa(e)	EX_11_cis_retfa(e)	11-cis-retfa[e] <=>	1		-1000	1000		Exchange/ demand			
EX_13_cis_retnglc(e)	EX_13_cis_retnglc(e)	13-cis-retnglc[e] <=>	1		-1000	1000		Exchange/ demand			
EX_1glyc_hs(e)	EX_1glyc_hs(e)	1glyc_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_1mncam(e)	EX_1mncam(e)	1mncam[e] <=>	1		-1000	1000		Exchange/ demand			
EX_2425dhvitd2(e)	EX_2425dhvitd2(e)	2425dhvitd2[e] <=>	1		-1000	1000		Exchange/ demand			
EX_2425dhvitd3(e)	EX_2425dhvitd3(e)	2425dhvitd3[e] <=>	1		-1000	1000		Exchange/ demand			
EX_24nph(e)	EX_24nph(e)	24nph[e] <=>	1		-1000	1000		Exchange/ demand			
EX_25HVITD3(u)	EX_25HVITD3(u)	25hvitd3[u] <=>	1		-1000	1000	1	Exchange/ demand		imported from Recon 1.	
EX_25hvitd2(e)	EX_25hvitd2(e)	25hvitd2[e] <=>	1		-1000	1000		Exchange/ demand			
EX_25hvitd3(e)	EX_25hvitd3(e)	25hvitd3[e] <=>	1		-1000	1000		Exchange/ demand			
EX_2hb(e)	EX_2hb(e)	2hb[e] <=>	1		-1000	1000		Exchange/ demand			
EX_2mcit(e)	EX_2mcit(e)	2mcit[e] <=>	1		-1000	1000		Exchange/ demand			
EX_34DHPHE(u)	exchange reaction for 3,4-Dihydroxy-L-phenylalanine	34dhphe[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_34dhoxpeg(e)	EX_34dhoxpeg(e)	34dhoxpeg[e] <=>	1		-1000	1000		Exchange/ demand			
EX_34dhphe(e)	EX_34dhphe(e)	34dhphe[e] <=>	1		-1000	1000		Exchange/ demand			
EX_35cgmp(e)	EX_35cgmp(e)	35cgmp[e] <=>	1		-1000	1000		Exchange/ demand			
EX_3aib(e)	EX_3aib(e)	3aib[e] <=>	1		-1000	1000		Exchange/ demand			
EX_3aib_D(e)	EX_3aib_D(e)	3aib-D[e] <=>	1		-1000	1000		Exchange/ demand			
EX_3mlda(e)	EX_3mlda(e)	3mlda[e] <=>	1		-1000	1000		Exchange/ demand			
EX_4ABUT(u)	exchange reaction for GABA	4abut[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_4HPRO(e)	exchange reaction for 4-hydroxy proline	4hpro_LT[e] <=>	1		-1000	1000	1	Exchange/ demand			
EX_4abut(e)	EX_4abut(e)	4abut[e] <=>	1		-1000	1000		Exchange/ demand			
EX_4hdebrisoquine(e)	EX_4hdebrisoquine(e)	4hdebrisoquine[e] <=>	1		-1000	1000		Exchange/ demand			
EX_4hphac(e)	EX_4hphac(e)	4hphac[e] <=>	1		-1000	1000		Exchange/ demand			
EX_4mptnl(e)	EX_4mptnl(e)	4mptnl[e] <=>	1		-1000	1000		Exchange/ demand			
EX_4mtolbutamide(e)	EX_4mtolbutamide(e)	4mtolbutamide[e] <=>	1		-1000	1000		Exchange/ demand			
EX_4nph(e)	EX_4nph(e)	4nph[e] <=>	1		-1000	1000		Exchange/ demand			
EX_4nphsf(e)	EX_4nphsf(e)	4nphsf[e] <=>	1		-1000	1000		Exchange/ demand			
EX_4pyrdx(e)	EX_4pyrdx(e)	4pyrdx[e] <=>	1		-1000	1000		Exchange/ demand			
EX_5adtststerone(e)	EX_5adtststerone(e)	5adtststerone[e] <=>	1		-1000	1000		Exchange/ demand			
EX_5adtststeroneglc(e)	EX_5adtststeroneglc(e)	5adtststeroneglc[e] <=>	1		-1000	1000		Exchange/ demand			
EX_5adtststerones(e)	EX_5adtststerones(e)	5adtststerones[e] <=>	1		-1000	1000		Exchange/ demand			
EX_5dhf(e)	EX_5dhf(e)	5dhf[e] <=>	1		-1000	1000		Exchange/ demand			
EX_5fthf(e)	EX_5fthf(e)	5fthf[e] <=>	1		-1000	1000		Exchange/ demand			
EX_5homeprazole(e)	EX_5homeprazole(e)	5homeprazole[e] <=>	1		-1000	1000		Exchange/ demand			
EX_5htrp(e)	EX_5htrp(e)	5htrp[e] <=>	1		-1000	1000		Exchange/ demand			
EX_5mthf(e)	EX_5mthf(e)	5mthf[e] <=>	1		-1000	1000		Exchange/ demand			
EX_5mthf(u)	exchange reaction for 5-Methyltetrahydrofolate	5mthf[u] <=>	1		-1000	1000	0	Exchange/ demand			
EX_5thf(e)	EX_5thf(e)	5thf[e] <=>	1		-1000	1000		Exchange/ demand			
EX_6dhf(e)	EX_6dhf(e)	6dhf[e] <=>	1		-1000	1000		Exchange/ demand			
EX_6htststerone(e)	EX_6htststerone(e)	6htststerone[e] <=>	1		-1000	1000		Exchange/ demand			
EX_6thf(e)	EX_6thf(e)	6thf[e] <=>	1		-1000	1000		Exchange/ demand			
EX_7dhf(e)	EX_7dhf(e)	7dhf[e] <=>	1		-1000	1000		Exchange/ demand			
EX_7thf(e)	EX_7thf(e)	7thf[e] <=>	1		-1000	1000		Exchange/ demand			
EX_9_cis_retfa(e)	EX_9_cis_retfa(e)	9-cis-retfa[e] <=>	1		-1000	1000		Exchange/ demand			
EX_ADPCBL(u)	exchange reaction for Adenosylcobalamin	adocbl[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_ALAALA(u)	exchange reaction for alanylalanine	alaala[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_ARACHD(u)	exchange reaction for arachidonic acid	arachd[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_ARG-L(u)	exchange reaction for L-arginine	arg-L[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_ASCB-L(u)	exchnage reaction for L-ascorbate	ascb-L[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_AVITE1(u)	exchange reaction for alpha-Tocopherol	avite1[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_BGLC(u)	exchange reaction for beta glucans	bglc[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_CARN(u)	exchange reaction for carnosine	carn[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_CLPND(e)	EX_CLPND(e)	clpnd[e] <=>	1		-1000	1000		Exchange/ demand			
EX_GCHOLA(u)	exchange reaction for glycocholate	gchola[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_GLGCHLO(u)	exchange reaction for beta glucan-glycocholate complex	glgchlo[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_GLTCHO(u)	exchange reaction for beta glucan-taurocholic acid complex	gltcho[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_GLTDECHOL(u)	exchange reaction for beta glucan-taurodeoxycholic acid complex	gltdechol[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_GLYGLY(u)	exchange reaction for glycylglycine	glygly[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_GLYLEU(u)	exchange reaction for glycylleucine	glyleu[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_GLYPHE(u)	exchange reaction for glycylphenylalaine	glyphe[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_GLYPRO(u)	exchange reaction for glycylproline	glypro[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_GLYSAR(u)	exchange reaction for glycylsarcosine	glysar[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_GUM(u)	exchange reaction for guar gums	gum[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_GUMDCHAC(u)	exchange reaction for guar gum-deoxyxholic acid complex	gumdchac[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_GUMGCHOL(u)	exchange reaction for guar gum-glycocholate complex	gumgchol[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_GUMTCHOL(u)	exchange reaction for guar gum-taurocholic acid complex	gumtchol[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_HDCA(u)	exchange reaction for Hexadecanoate (n-C16:0)	hdca[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_ILE-L(u)	exchange reaction for L-isoleucine	ile-L[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_LCYSTIN(u)	exchange reaction for cystine	Lcystin[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_LEUGLY(u)	exchange reaction for leucylglycine	leugly[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_LEULEU(u)	exchange reaction for leucylleucine	leuleu[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_LNLC(u)	exchange reaction for linoleic acid (all cis C18:2) n-6	lnlc[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_LNLNCA(u)	exchange reaction for alpha-Linolenic acid, C18:3, n-3	lnlnca[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_LNLNCG(u)	exchange reaction for gamma-linolenic acid	lnlncg[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_LYS(u)	exchange reaction for lysine	lys-L[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_Lcystin(e)	EX_Lcystin(e)	Lcystin[e] <=>	1		-1000	1000		Exchange/ demand			
EX_MET-L(u)	exchange reaction for methionine	met-L[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_NAC(u)	exchange reaction for nicotinate	nac[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_OCDCEA(u)	exchange reaction for octadecenoate (n-C18:1)	ocdcea[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_ORN(U)	exchange reaction for ornithine	orn[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_PECT(u)	exchange reaction for pectins	pect[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_PECTINDCHAC(u)	exchange reaction for pectin-deoxycholic acid complex	pectindchac[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_PECTINGCHOL(u)	exchange reaction for pectin-glycocholate complex	pectingchol[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_PECTINTCHOL(u)	exchange reaction for pectin-taurocholic acid complex	pectintchol[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_PRO-D(u)	exchange reaction for D-proline	pro-D[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_PRO-L(u)	exchange reaction for L-Proline	pro-L[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_PROGLY(u)	exchange reaction for prolyl-glycine	progly[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_PSYL(u)	exchange reaction for psyllium	psyl[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_PSYLCHOL(u)	exchange reaction for psyllium-glycocholic acid complex	psylchol[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_PSYLTCHOL(u)	exchange reaction for psyllium-taurocholic acid complex	psyltchol[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_PSYLTDECHOL(u)	exchange reaction for psyllium-taurodeoxycholic acid complex	psyltdechol[u] <=>	1		-1000	1000	1	Exchange/ demand			
EX_RETINOL(u)	exchange reaction for retinol	retinol[u] <=>	1		-1000	1000	1	Exchange/ demand			

EX_RTOTAL(u)	exchange reaction for Rtotal	Rtotal[u] <=>	1		-1000	1000	1	Exchange/ demand				
EX_RTOTAL2(u)	exchange reaction for Rtotal2	Rtotal2[u] <=>	1		-1000	1000	1	Exchange/ demand				
EX_RTOTAL3(u)	exchange reaction for Rtotal3	Rtotal3[u] <=>	1		-1000	1000	1	Exchange/ demand				
EX_Rtotal(e)	EX_Rtotal(e)	Rtotal[e] <=>	1		-1000	1000		Exchange/ demand				
EX_Rtotal2(e)	EX_Rtotal2(e)	Rtotal2[e] <=>	1		-1000	1000		Exchange/ demand				
EX_Rtotal3(e)	EX_Rtotal3(e)	Rtotal3[e] <=>	1		-1000	1000		Exchange/ demand				
EX_SRT-D(u)	exchange reaction for D-Sorbitol	sbt-D[u] <=>	1		-1000	1000	1	Exchange/ demand				
EX_TAUR(u)	exchange reaction for Taurine	taur[u] <=>	1		-1000	1000	1	Exchange/ demand				
EX_TCHOLA(u)	exchange reaction for taurocholic acid	tchola[u] <=>	1		-1000	1000	1	Exchange/ demand				
EX_TDECHOLA(u)	exchange reaction for Taurodeoxycholic acid	tdechola[u] <=>	1		-1000	1000	1	Exchange/ demand				
EX_TMNDNC(u)	exchange reaction for tinmodotic acid C20:5, n-3	tmndnc[u] <=>	1		-1000	1000	1	Exchange/ demand				
EX_TRP-L(u)	exchange reaction for L-tryptophan	trp-L[u] <=>	1		-1000	1000	1	Exchange/ demand				
EX_TYR-L(u)	exchange reaction for L-tyrosine	tyr-L[u] <=>	1		-1000	1000	1	Exchange/ demand				
EX_Tyr_ggn(e)	EX_Tyr_ggn(e)	Tyr-ggn[e] <=>	1		-1000	1000		Exchange/ demand				
EX_VAL-L(u)	exchange reaction for L-valine	val-L[u] <=>	1		-1000	1000	1	Exchange/ demand				
EX_ala(e)	EX_ala(e)	ala[e] <=>	1		-1000	1000		Exchange/ demand				
EX_ac(e)	EX_ac(e)	ac[e] <=>	1		-1000	1000		Exchange/ demand				
EX_acac(e)	EX_acac(e)	acac[e] <=>	1		-1000	1000		Exchange/ demand				
EX_acald(e)	EX_acald(e)	acald[e] <=>	1		-1000	1000		Exchange/ demand				
EX_acetone(e)	EX_acetone(e)	acetone[e] <=>	1		-1000	1000		Exchange/ demand				
EX_acgal(e)	N-Acetyl-D-galactosamine exchange	acgal[e] <=>	1		-1000	1000	0	Exchange/ demand				
EX_acgalfucgalacgalfuc12gal14ac glcgalglcside_3m(e)	EX_acgalfucgalacgalfuc12gal14acglcgalglcside_3m(e)	acgalfucgalacgalfuc12gal14acglcgalglcside_3m[e] <=>	1		-1000	1000		Exchange/ demand				
EX_acgalfucgalacgalfucgalacgalfucgalacglcgal14acglcgalgl cside_3m(e)	EX_acgalfucgalacgalfucgalacglcgal14acglcgalgl cside_3m(e)	acgalfucgalacgalfucgalacglcgal14acglcgalglcside_3m[e] <=>	1		-1000	1000		Exchange/ demand				
EX_acgam(e)	EX_acgam(e)	acgam[e] <=>	1		-1000	1000		Exchange/ demand				
EX_ach(e)	EX_ach(e)	ach[e] <=>	1		-1000	1000		Exchange/ demand				
EX_acnr13acngalglcside_3m(e)	EX_acnr13acngalglcside_3m(e)	acnr13acngalglcside_3m[e] <=>	1		-1000	1000		Exchange/ demand				
EX_acnr23acngalglcside_3m(e)	EX_acnr23acngalglcside_3m(e)	acnr23acngalglcside_3m[e] <=>	1		-1000	1000		Exchange/ demand				
EX_acnacngal14acglcgalglcside_3m(e)	EX_acnacngal14acglcgalglcside_3m(e)	acnacngal14acglcgalglcside_3m[e] <=>	1		-1000	1000		Exchange/ demand				
EX_acnacngalglcside_3m(e)	EX_acnacngalglcside_3m(e)	acnacngalglcside_3m[e] <=>	1		-1000	1000		Exchange/ demand				
EX_acnam(e)	N-Acetylneuraminate exchange	acnam[e] <=>	1		-1000	1000	0	Exchange/ demand				
EX_acngalacglcgal14acglcgalglcside_3m(e)	EX_acngalacglcgal14acglcgalglcside_3m(e)	acngalacglcgal14acglcgalglcside_3m[e] <=>	1		-1000	1000		Exchange/ demand				
EX_ade(e)	EX_ade(e)	ade[e] <=>	1		-1000	1000		Exchange/ demand				
EX_adn(e)	EX_adn(e)	adn[e] <=>	1		-1000	1000		Exchange/ demand				
EX_adocbl(e)	EX_adocbl(e)	adocbl[e] <=>	1		-1000	1000	0	Exchange/ demand				
EX_adp	EX_adp	adp[e] <=>	1		-1000	1000		Exchange/ demand				
EX_adprhp(e)	EX_adprhp(e)	adprhp[e] <=>	1		-1000	1000		Exchange/ demand				
EX_adprib(e)	EX_adprib(e)	adprib[e] <=>	1		-1000	1000		Exchange/ demand				
EX_adrn(e)	EX_adrn(e)	adrn[e] <=>	1		-1000	1000		Exchange/ demand				
EX_adrnr(e)	EX_adrnr(e)	adrnr[e] <=>	1		-1000	1000		Exchange/ demand				
EX_aflatoxin1(e)	EX_aflatoxin1(e)	aflatoxin1[e] <=>	1		-1000	1000		Exchange/ demand				
EX_ahandrostangl(e)	EX_ahandrostangl(e)	ahandrostangl[e] <=>	1		-1000	1000		Exchange/ demand				
EX_ak2lgchol_hs(e)	EX_ak2lgchol_hs(e)	ak2lgchol_hs[e] <=>	1		-1000	1000		Exchange/ demand				
EX_akg(e)	EX_akg(e)	akg[e] <=>	1		-1000	1000		Exchange/ demand				
EX_ala-B(u)	exchange reaction for beta alanine	ala-B[u] <=>	1		-1000	1000	1	Exchange/ demand				
EX_ala_B(e)	EX_ala_B(e)	ala-B[e] <=>	1		-1000	1000		Exchange/ demand				
EX_ala_D(e)	EX_ala_D(e)	ala-D[e] <=>	1		-1000	1000		Exchange/ demand				
EX_ala_L(e)	EX_ala_L(e)	ala-L[e] <=>	1		-1000	1000		Exchange/ demand				
EX_ala_L(u)	exchange reaction for L-alanine	ala-L[u] <=>	1		-1000	1000	0	Exchange/ demand				
EX_alaala(e)	EX_alaala(e)	alaala[e] <=>	1		-1000	1000	0	Exchange/ demand				
EX_aldstrn(e)	EX_aldstrn(e)	aldstrn[e] <=>	1		-1000	1000		Exchange/ demand				
EX_amp(e)	EX_amp(e)	amp[e] <=>	1		-1000	1000		Exchange/ demand				
EX_andrstrn(e)	EX_andrstrn(e)	andrstrn[e] <=>	1		-1000	1000		Exchange/ demand				
EX_andrstrngl(e)	EX_andrstrngl(e)	andrstrngl[e] <=>	1		-1000	1000		Exchange/ demand				
EX_antipyrene(e)	EX_antipyrene(e)	antipyrene[e] <=>	1		-1000	1000		Exchange/ demand				
EX_apmsn(e)	EX_apmsn(e)	apmsn[e] <=>	1		-1000	1000		Exchange/ demand				
EX_apprm(e)	EX_apprm(e)	apprm[e] <=>	1		-1000	1000		Exchange/ demand				
EX_aprgnstrn(e)	EX_aprgnstrn(e)	aprgnstrn[e] <=>	1		-1000	1000		Exchange/ demand				
EX_aqcobal(e)	EX_aqcobal(e)	aqcobal[e] <=>	1		-1000	1000		Exchange/ demand				
EX_arab_L(e)	EX_arab_L(e)	arab-L[e] <=>	1		-1000	1000		Exchange/ demand				
EX_arach(e)	EX_arach(e)	arach[e] <=>	1		-1000	1000		Exchange/ demand				
EX_arachd(e)	EX_arachd(e)	arachd[e] <=>	1		-1000	1000		Exchange/ demand				
EX_arg_L(e)	EX_arg_L(e)	arg-L[e] <=>	1		-1000	1000		Exchange/ demand				
EX_asclb_L(e)	EX_asclb_L(e)	asclb-L[e] <=>	1		-1000	1000		Exchange/ demand				
EX_asn_L(e)	EX_asn_L(e)	asn-L[e] <=>	1		-1000	1000		Exchange/ demand				
EX_asn_L(u)	exchange reaction for L-asparagine	asn-L[u] <=>	1		-1000	1000	0	Exchange/ demand				
EX_asp_D(e)	EX_asp_D(e)	asp-D[e] <=>	1		-1000	1000		Exchange/ demand				
EX_asp_L(e)	EX_asp_L(e)	asp-L[e] <=>	1		-1000	1000		Exchange/ demand				
EX_atp(e)	EX_atp(e)	atp[e] <=>	1		-1000	1000		Exchange/ demand				
EX_avite1(e)	EX_avite1(e)	avite1[e] <=>	1		-1000	1000		Exchange/ demand				
EX_avite2(e)	EX_avite2(e)	avite2[e] <=>	1		-1000	1000		Exchange/ demand				
EX_bglc(e)	exchange reaction for beta glucam	bglc[e] <=>	1		-1000	1000	0	Exchange/ demand				
EX_bhb(e)	EX_bhb(e)	bhb[e] <=>	1		-1000	1000		Exchange/ demand				
EX_bilglcur(e)	EX_bilglcur(e)	bilglcur[e] <=>	1		-1000	1000		Exchange/ demand				
EX_bilglcur(e)	EX_bilglcur(e)	bilglcur[e] <=>	1		-1000	1000		Exchange/ demand				
EX_bilirub(e)	EX_bilirub(e)	bilirub[e] <=>	1		-1000	1000		Exchange/ demand				
EX_biocyt(e)	EX_biocyt(e)	biocyt[e] <=>	1		-1000	1000		Exchange/ demand				
EX_btn(e)	EX_btn(e)	btn[e] <=>	1		-1000	1000		Exchange/ demand				
EX_but(e)	EX_but(e)	but[e] <=>	1		-1000	1000		Exchange/ demand				
EX_bvite(e)	EX_bvite(e)	bvite[e] <=>	1		-1000	1000		Exchange/ demand				
EX_ba(e)	EX_ba(e)	ba[e] <=>	1		-1000	1000		Exchange/ demand				
EX_ca2(e)	EX_ca2(e)	ca2[e] <=>	1		-1000	1000		Exchange/ demand				
EX_camp(e)	EX_camp(e)	camp[e] <=>	1		-1000	1000		Exchange/ demand				
EX_carn(e)	EX_carn(e)	carn[e] <=>	1		-1000	1000	0	Exchange/ demand				
EX_carot(e)	EX_carot(e)	carot[e] <=>	1		-1000	1000		Exchange/ demand				
EX_carvenol(e)	EX_carvenol(e)	carvenol[e] <=>	1		-1000	1000		Exchange/ demand				
EX_cca_cl3(e)	EX_cca_cl3(e)	cca_cl3[e] <=>	1		-1000	1000		Exchange/ demand				
EX_cgly(e)	EX_cgly(e)	cgly[e] <=>	1		-1000	1000		Exchange/ demand				
EX_chol(e)	EX_chol(e)	chol[e] <=>	1		-1000	1000		Exchange/ demand				
EX_cholate(e)	EX_cholate(e)	cholate[e] <=>	1		-1000	1000		Exchange/ demand				
EX_chsterol(e)	EX_chsterol(e)	chsterol[e] <=>	1		-1000	1000		Exchange/ demand				
EX_chsterol(u)	exchange reaction for cholesterol	chsterol[u] <=>	1		-1000	1000	0	Exchange/ demand				
EX_cit(e)	EX_cit(e)	cit[e] <=>	1		-1000	1000		Exchange/ demand				
EX_cl(e)	EX_cl(e)	cl[e] <=>	1		-1000	1000		Exchange/ demand				
EX_cl(u)	exchange reaction for Chloride	cl[u] <=>	1		-1000	1000	0	Exchange/ demand				
EX_cmp(e)	EX_cmp(e)	cmp[e] <=>	1		-1000	1000		Exchange/ demand				
EX_co(e)	EX_co(e)	co[e] <=>	1		-1000	1000		Exchange/ demand				
EX_co2(e)	EX_co2(e)	co2[e] <=>	1		-1000	1000		Exchange/ demand				
EX_core4(e)	Core4 (mucin O-glycan) exchange	core4[e] <=>	1		-1000	1000	0	Exchange/ demand				
EX_core5(e)	Core 5 exchange	core5[e] <=>	1		-1000	1000	0	Exchange/ demand				
EX_core7(e)	Core 7 exchange	core7[e] <=>	1		-1000	1000	0	Exchange/ demand				
EX_core8(e)	Core 8 exchange	core8[e] <=>	1		-1000	1000	0	Exchange/ demand				
EX_coumarin(e)	EX_coumarin(e)	coumarin[e] <=>	1		-1000	1000		Exchange/ demand				
EX_creat(e)	EX_creat(e)	creat[e] <=>	1		-1000	1000		Exchange/ demand				
EX_crmp_hs(e)	EX_crmp_hs(e)	crmp_hs[e] <=>	1		-1000	1000		Exchange/ demand				
EX_crn(e)	EX_crn(e)	crn[e] <=>	1		-1000	1000		Exchange/ demand				
EX_crn(e)	EX_crn(e)	crn[e] <=>	1		-1000	1000		Exchange/ demand				
EX_crnstn(e)	EX_crnstn(e)	crnstn[e] <=>	1		-1000	1000		Exchange/ demand				
EX_crvnc(e)	EX_crvnc(e)	crvnc[e] <=>	1		-1000	1000		Exchange/ demand				
EX_csn(e)	EX_csn(e)	csn[e] <=>	1		-1000	1000		Exchange/ demand				
EX_cspg_a(e)	EX_cspg_a(e)	cspg_a[e] <=>	1		-1000	1000		Exchange/ demand				
EX_cspg_b(e)	EX_cspg_b(e)	cspg_b[e] <=>	1		-1000	1000		Exchange/ demand				
EX_cspg_c(e)	EX_cspg_c(e)	cspg_c[e] <=>	1		-1000	1000		Exchange/ demand				
EX_cspg_d(e)	EX_cspg_d(e)	cspg_d[e] <=>	1		-1000	1000		Exchange/ demand				
EX_cspg_e(e)	EX_cspg_e(e)	cspg_e[e] <=>	1		-1000	1000		Exchange/ demand				
EX_cyan(e)	EX_cyan(e)	cyan[e] <=>	1		-1000	1000		Exchange/ demand				
EX_cys_L(e)	EX_cys_L(e)	cys-L[e] <=>	1		-1000	1000		Exchange/ demand				
EX_cys_L(u)	exchange reaction for L-cysteine	cys-L[u] <=>	1		-1000	1000	0	Exchange/ demand				
EX_cyst(e)	EX_cyst(e)	cyst[e] <=>	1		-1000	1000		Exchange/ demand				
EX_dad-5(e)	EX_dad-5(e)	dad-5[e] <=>	1		-1000	1000		Exchange/ demand				
EX_dad_2(e)	EX_dad_2(e)	dad-2[e] <=>	1		-1000	1000		Exchange/ demand				
EX_dag_hs(e)	EX_dag_hs(e)	dag_hs[e] <=>	1		-1000	1000		Exchange/ demand				
EX_dag_hs(u)	exchange reaction for diglyceride	dag_hs[u] <=>	1		-1000	1000	0	Exchange/ demand				
EX_dcspntn1(e)	EX_dcspntn1(e)	dcspntn1[e] <=>	1		-1000	1000		Exchange/ demand				
EX_dcyt(e)	EX_dcyt(e)	dcyt[e] <=>	1		-1000	1000		Exchange/ demand				
EX_debrisoquine(e)	EX_debrisoquine(e)	debrisoquine[e] <=>	1		-1000	1000		Exchange/ demand				
EX_dgchol(e)	EX_dgchol(e)	dgchol[e] <=>	1		-1000	1000		Exchange/ demand				
EX_dgsn(e)	EX_dgsn(e)	dgsn[e] <=>	1		-1000	1000		Exchange/ demand				
EX_dhdascb(e)	EX_dhdascb(e)	dhdascb[e] <=>	1		-1000	1000		Exchange/ demand				
EX_dhnsn(e)	EX_dhnsn(e)	dhnsn[e] <=>	1		-1000	1000		Exchange/ demand				
EX_dhtl(e)	EX_dhtl(e)	dhtl[e] <=>	1		-1000	1000		Exchange/ demand				
EX_digsluqside_hs(e)	EX_digsluqside_hs(e)	digsluqside_hs[e] <=>	1		-1000	1000		Exchange/ demand				
EX_din(e)	EX_din(e)	din[e] <=>	1		-1000	1000		Exchange/ demand				
EX_dlnlcg(e)	EX_dlnlcg(e)	dlnlcg[e] <=>	1		-1000	1000		Exchange/ demand				
EX_dmantityrene(e)	EX_dmantityrene(e)	dmantityrene[e] <=>	1		-1000	1000		Exchange/ demand				
EX_dmbptcrn(e)	EX_dmbptcrn(e)	dmbptcrn[e] <=>	1		-1000	1000		Exchange/ demand				
EX_dopa(e)	EX_dopa(e)	dopa[e] <=>	1		-1000	1000		Exchange/ demand				
EX_dopasf(e)	EX_dopasf(e)	dopasf[e] <=>	1		-1000	1000		Exchange/ demand				
EX_drib(e)	EX_drib(e)	drib[e] <=>	1		-1000	1000		Exchange/ demand				
EX_ds7_antigen(e)	disialyl-T antigen exchange	ds7_antigen[e] <=>	1		-1000	1000	0	Exchange/ demand				
EX_dtar(e)	EX_dtar(e)	dtar[e] <=>	1		-1000	1000		Exchange/ demand				

EX_eaflatoxin(e)	EX_eaflatoxin(e)	eaflatoxin[e] <=>	1		-1000	1000		Exchange/ demand			
EX_ebastine(e)	EX_ebastine(e)	ebastine[e] <=>	1		-1000	1000		Exchange/ demand			
EX_ebastineoh(e)	EX_ebastineoh(e)	ebastineoh[e] <=>	1		-1000	1000		Exchange/ demand			
EX_eicostet(e)	EX_eicostet(e)	eicostet[e] <=>	1		-1000	1000		Exchange/ demand			
EX_elaid(e)	EX_elaid(e)	elaid[e] <=>	1		-1000	1000		Exchange/ demand			
EX_estradiol(e)	EX_estradiol(e)	estradiol[e] <=>	1		-1000	1000		Exchange/ demand			
EX_estradiolglc(e)	EX_estradiolglc(e)	estradiolglc[e] <=>	1		-1000	1000		Exchange/ demand			
EX_estriolglc(e)	EX_estriolglc(e)	estriolglc[e] <=>	1		-1000	1000		Exchange/ demand			
EX_estroneglc(e)	EX_estroneglc(e)	estroneglc[e] <=>	1		-1000	1000		Exchange/ demand			
EX_estrones(e)	EX_estrones(e)	estrones[e] <=>	1		-1000	1000		Exchange/ demand			
EX_etha(e)	Ethanolamine exchange	etha[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_etoh(e)	EX_etoh(e)	etoh[e] <=>	1		-1000	1000		Exchange/ demand			
EX_f1a(e)	F1alpha (mucin O-glycan) exchange	f1a[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_fe2(e)	EX_fe2(e)	fe2[e] <=>	1		-1000	1000		Exchange/ demand			
EX_fe3(e)	EX_fe3(e)	fe3[e] <=>	1		-1000	1000		Exchange/ demand			
EX_fol(e)	EX_fol(e)	fol[e] <=>	1		-1000	1000		Exchange/ demand			
EX_fol(u)	exchange reaction for Folate	fol[u] <=>	1		-1000	1000	0	Exchange/ demand			
EX_for(e)	EX_for(e)	for[e] <=>	1		-1000	1000		Exchange/ demand			
EX_fru(e)	EX_fru(e)	fru[e] <=>	1		-1000	1000		Exchange/ demand			
EX_fuc13galacglcgal14acglcgalgluside_hs(e)	EX_fuc13galacglcgal14acglcgalgluside_hs(e)	fuc13galacglcgal14acglcgalgluside_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_fuc14galacglcgalgluside_hs(e)	EX_fuc14galacglcgalgluside_hs(e)	fuc14galacglcgalgluside_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_fuc_L(e)	EX_fuc_L(e)	fuc-L[e] <=>	1		-1000	1000		Exchange/ demand			
EX_fucacgalfucgalacglcgalgluside_hs(e)	EX_fucacgalfucgalacglcgalgluside_hs(e)	fucacgalfucgalacglcgalgluside_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_fucacngal14acglcgalgluside_hs(e)	EX_fucacngal14acglcgalgluside_hs(e)	fucacngal14acglcgalgluside_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_fucacngalacglcgalgluside_hs(e)	EX_fucacngalacglcgalgluside_hs(e)	fucacngalacglcgalgluside_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_fucfuc12gal14acglcgalgluside_hs(e)	EX_fucfuc12gal14acglcgalgluside_hs(e)	fucfuc12gal14acglcgalgluside_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_fucfuc132galacglcgal14acglcgalgluside_hs(e)	EX_fucfuc132galacglcgal14acglcgalgluside_hs(e)	fucfuc132galacglcgal14acglcgalgluside_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_fucfucfucgalacglc13galacglcgal14acglcgalgluside_hs(e)	EX_fucfucfucgalacglc13galacglcgal14acglcgalgluside_hs(e)	fucfucfucgalacglc13galacglcgal14acglcgalgluside_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_fucfucfucgalacglcgal14acglcgalgluside_hs(e)	EX_fucfucfucgalacglcgal14acglcgalgluside_hs(e)	fucfucfucgalacglcgal14acglcgalgluside_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_fucfucgalacglcgalgluside_hs(e)	EX_fucfucgalacglcgalgluside_hs(e)	fucfucgalacglcgalgluside_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_fucgal14acglcgalgluside_hs(e)	EX_fucgal14acglcgalgluside_hs(e)	fucgal14acglcgalgluside_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_fucgalfucgalacglcgalgluside_hs(e)	EX_fucgalfucgalacglcgalgluside_hs(e)	fucgalfucgalacglcgalgluside_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_fucgalgbside_hs(e)	EX_fucgalgbside_hs(e)	fucgalgbside_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_gal(e)	EX_gal(e)	gal[e] <=>	1		-1000	1000		Exchange/ demand			
EX_gal(u)	exchange reaction for D-Galactose	gal[u] <=>	1		-1000	1000	0	Exchange/ demand			
EX_galacglcgalgbside_hs(e)	EX_galacglcgalgbside_hs(e)	galacglcgalgbside_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_galam(e)	Galactosamine exchange	galam[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_galfuc12gal14acglcgalgluside_hs(e)	EX_galfuc12gal14acglcgalgluside_hs(e)	galfuc12gal14acglcgalgluside_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_galfucgalacglcgal14acglcgalgluside_hs(e)	EX_galfucgalacglcgal14acglcgalgluside_hs(e)	galfucgalacglcgal14acglcgalgluside_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_galgalfucfucgalacglcgalacglcgal14acglcgalgluside_hs(e)	EX_galgalfucfucgalacglcgalacglcgal14acglcgalgluside_hs(e)	galgalfucfucgalacglcgalacglcgal14acglcgalgluside_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_galgalgalthcrm_hs(e)	EX_galgalgalthcrm_hs(e)	galgalgalthcrm_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_gam(e)	EX_gam(e)	gam[e] <=>	1		-1000	1000		Exchange/ demand			
EX_gbside_hs(e)	EX_gbside_hs(e)	gbside_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_gchola(e)	EX_gchola(e)	gchola[e] <=>	1		-1000	1000		Exchange/ demand			
EX_gd1b2_hs(e)	EX_gd1b2_hs(e)	gd1b2_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_gd1c_hs(e)	EX_gd1c_hs(e)	gd1c_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_gdchola(e)	EX_gdchola(e)	gdchola[e] <=>	1		-1000	1000		Exchange/ demand			
EX_gdp(e)	EX_gdp(e)	gdp[e] <=>	1		-1000	1000		Exchange/ demand			
EX_glc(e)	EX_glc(e)	glc-D[e] <=>	1		-1000	1000		Exchange/ demand			
EX_glc_D(u)	exchange reaction for D-glucose	glc-D[u] <=>	1		-1000	1000	0	Exchange/ demand			
EX_glcur(e)	D-Glucuronate exchange	glcur[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_glgchlo(e)	exchange reaction for beta glucan-glycocholate complex	glgchlo[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_gln_L(e)	EX_gln_L(e)	gln-L[e] <=>	1		-1000	1000		Exchange/ demand			
EX_gln_L(u)	exchange reaction for L-glutamine	gln-L[u] <=>	1		-1000	1000	0	Exchange/ demand			
EX_gltcho(e)	exchange reaction for beta glucan-taurocholic acid complex	gltcho[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_gltdechol(e)	exchange reaction for beta glucan-taurodeoxycholic acid complex	gltdechol[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_glu_L(e)	EX_glu_L(e)	glu-L[e] <=>	1		-1000	1000		Exchange/ demand			
EX_gluala(e)	EX_gluala(e)	gluala[e] <=>	1		-1000	1000		Exchange/ demand			
EX_gly(e)	EX_gly(e)	gly[e] <=>	1		-1000	1000		Exchange/ demand			
EX_gly(u)	exchange reaction for Glycine	gly[u] <=>	1		-1000	1000	0	Exchange/ demand			
EX_glyb(e)	EX_glyb(e)	glyb[e] <=>	1		-1000	1000		Exchange/ demand			
EX_glyc(e)	EX_glyc(e)	glyc[e] <=>	1		-1000	1000		Exchange/ demand			
EX_glyc_S(e)	EX_glyc_S(e)	glyc-S[e] <=>	1		-1000	1000		Exchange/ demand			
EX_glygly(e)	exchange reaction for glycylglycine	glygly[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_glygn2(e)	EX_glygn2(e)	glygn2[e] <=>	1		-1000	1000		Exchange/ demand			
EX_glygn4(e)	EX_glygn4(e)	glygn4[e] <=>	1		-1000	1000		Exchange/ demand			
EX_glygn5(e)	EX_glygn5(e)	glygn5[e] <=>	1		-1000	1000		Exchange/ demand			
EX_glyleu(e)	EX_glyleu(e)	glyleu[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_glyphe(e)	exchange reaction for glycylphenylalaine	glyphe[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_glypro(e)	EX_glypro(e)	glypro[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_glysar(e)	exchange reaction for glycylsarcosine	glysar[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_gmp(e)	EX_gmp(e)	gmp[e] <=>	1		-1000	1000		Exchange/ demand			
EX_gncore1(e)	gncore1 (mucin O-glycan) exchange	gncore1[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_gncore2(e)	GlcNAc-alpha-1,4-Core 2 exchange	gncore2[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_gp1c_hs(e)	EX_gp1c_hs(e)	gp1c_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_gp1calpha_hs(e)	EX_gp1calpha_hs(e)	gp1calpha_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_gq1b_hs(e)	EX_gq1b_hs(e)	gq1b_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_gq1balpha_hs(e)	EX_gq1balpha_hs(e)	gq1balpha_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_gsn(e)	EX_gsn(e)	gsn[e] <=>	1		-1000	1000		Exchange/ demand			
EX_gt1a_hs(e)	EX_gt1a_hs(e)	gt1a_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_gthox(e)	EX_gthox(e)	gthox[e] <=>	1		-1000	1000		Exchange/ demand			
EX_gthrd(e)	EX_gthrd(e)	gthrd[e] <=>	1		-1000	1000		Exchange/ demand			
EX_gtp(e)	EX_gtp(e)	gtp[e] <=>	1		-1000	1000		Exchange/ demand			
EX_gua(e)	EX_gua(e)	gua[e] <=>	1		-1000	1000		Exchange/ demand			
EX_gum(e)	exchange reaction for guar gums	gum[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_gumdchac(e)	exchange reaction for guar gum-deoxyxholic acid complex	gumdchac[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_gumgchol(e)	exchange reaction for guar gum-glycocholate complex	gumgchol[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_gumtchol(e)	exchange reaction for guar gum-taurocholic acid complex	gumtchol[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_h(e)	EX_h(e)	h[e] <=>	1		-1000	1000		Exchange/ demand			
EX_h(u)	exchange reaction for proton	h[u] <=>	1		-1000	1000	0	Exchange/ demand			
EX_h2o(e)	EX_h2o(e)	h2o[e] <=>	1		-1000	1000		Exchange/ demand			
EX_h2o2(e)	EX_h2o2(e)	h2o2[e] <=>	1		-1000	1000		Exchange/ demand			
EX_ha(e)	EX_ha(e)	ha[e] <=>	1		-1000	1000		Exchange/ demand			
EX_ha_pre1(e)	EX_ha_pre1(e)	ha_pre1[e] <=>	1		-1000	1000		Exchange/ demand			
EX_hco3(e)	EX_hco3(e)	hco3[e] <=>	1		-1000	1000		Exchange/ demand			
EX_hcoumarin(e)	EX_hcoumarin(e)	hcoumarin[e] <=>	1		-1000	1000		Exchange/ demand			
EX_hdca(e)	EX_hdca(e)	hdca[e] <=>	1		-1000	1000		Exchange/ demand			
EX_hdcea(e)	EX_hdcea(e)	hdcea[e] <=>	1		-1000	1000		Exchange/ demand			
EX_hestratriol(e)	EX_hestratriol(e)	hestratriol[e] <=>	1		-1000	1000		Exchange/ demand			
EX_hexc(e)	EX_hexc(e)	hexc[e] <=>	1		-1000	1000		Exchange/ demand			
EX_his_L(e)	EX_his_L(e)	his-L[e] <=>	1		-1000	1000		Exchange/ demand			
EX_his_L(u)	exchange reaction for L-histidine	his-L[u] <=>	1		-1000	1000	0	Exchange/ demand			
EX_hista(e)	EX_hista(e)	hista[e] <=>	1		-1000	1000		Exchange/ demand			
EX_hom_L(e)	EX_hom_L(e)	hom-L[e] <=>	1		-1000	1000		Exchange/ demand			
EX_hpdca(e)	EX_hpdca(e)	hpdca[e] <=>	1		-1000	1000		Exchange/ demand			
EX_hspg(e)	EX_hspg(e)	hspg[e] <=>	1		-1000	1000		Exchange/ demand			
EX_htaxol(e)	EX_htaxol(e)	htaxol[e] <=>	1		-1000	1000		Exchange/ demand			
EX_hxan(e)	EX_hxan(e)	hxan[e] <=>	1		-1000	1000		Exchange/ demand			
EX_i(e)	EX_i(e)	i[e] <=>	1		-1000	1000		Exchange/ demand			
EX_idp(e)	EX_idp(e)	idp[e] <=>	1		-1000	1000		Exchange/ demand			
EX_ile_L(e)	EX_ile_L(e)	ile-L[e] <=>	1		-1000	1000		Exchange/ demand			
EX_imp(e)	EX_imp(e)	imp[e] <=>	1		-1000	1000		Exchange/ demand			
EX_inost(e)	EX_inost(e)	inost[e] <=>	1		-1000	1000		Exchange/ demand			
EX_ins(e)	EX_ins(e)	ins[e] <=>	1		-1000	1000		Exchange/ demand			
EX_k(e)	EX_k(e)	k[e] <=>	1		-1000	1000		Exchange/ demand			
EX_ksi(e)	EX_ksi(e)	ksi[e] <=>	1		-1000	1000		Exchange/ demand			
EX_ksi_deg1(e)	EX_ksi_deg1(e)	ksi_deg1[e] <=>	1		-1000	1000		Exchange/ demand			
EX_ksii_core2(e)	EX_ksii_core2(e)	ksii_core2[e] <=>	1		-1000	1000		Exchange/ demand			
EX_ksii_core4(e)	EX_ksii_core4(e)	ksii_core4[e] <=>	1		-1000	1000		Exchange/ demand			
EX_lac_D(e)	EX_lac_D(e)	lac-D[e] <=>	1		-1000	1000		Exchange/ demand			
EX_lac_L(e)	EX_lac_L(e)	lac-L[e] <=>	1		-1000	1000		Exchange/ demand			
EX_lcts(e)	EX_lcts(e)	lcts[e] <=>	1		-1000	1000		Exchange/ demand			
EX_leu_L(e)	EX_leu_L(e)	leu-L[e] <=>	1		-1000	1000		Exchange/ demand			
EX_leu_L(u)	exchange reaction for L-leucine	leu-L[u] <=>	1		-1000	1000	0	Exchange/ demand			
EX_leugly(e)	exchange reaction for leucylglycine	leugly[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_leuktrA4(e)	EX_leuktrA4(e)	leuktrA4[e] <=>	1		-1000	1000		Exchange/ demand			
EX_leuktrB4(e)	EX_leuktrB4(e)	leuktrB4[e] <=>	1		-1000	1000		Exchange/ demand			
EX_leuktrC4(e)	EX_leuktrC4(e)	leuktrC4[e] <=>	1		-1000	1000		Exchange/ demand			
EX_leuktrD4(e)	EX_leuktrD4(e)	leuktrD4[e] <=>	1		-1000	1000		Exchange/ demand			
EX_leuktrE4(e)	EX_leuktrE4(e)	leuktrE4[e] <=>	1		-1000	1000		Exchange/ demand			
EX_leuktrF4(e)	EX_leuktrF4(e)	leuktrF4[e] <=>	1		-1000	1000		Exchange/ demand			
EX_leuleu(e)	EX_leuleu(e)	leuleu[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_lgnc(e)	EX_lgnc(e)	lgnc[e] <=>	1		-1000	1000		Exchange/ demand			

EX_limnen(e)	EX_limnen(e)	limnen[e] <=>	1		-1000	1000		Exchange/ demand			
EX_lipoate(e)	EX_lipoate(e)	lipoate[e] <=>	1		-1000	1000		Exchange/ demand			
EX_lneldc(e)	EX_lneldc(e)	lneldc[e] <=>	1		-1000	1000		Exchange/ demand			
EX_lnlc(e)	EX_lnlc(e)	lnlc[e] <=>	1		-1000	1000		Exchange/ demand			
EX_lnlnca(e)	EX_lnlnca(e)	lnlnca[e] <=>	1		-1000	1000		Exchange/ demand			
EX_lnlncg(e)	EX_lnlncg(e)	lnlncg[e] <=>	1		-1000	1000		Exchange/ demand			
EX_lpchol_hs(e)	EX_lpchol_hs(e)	lpchol_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_lpchol_hs(u)	exchange reaction for lysophosphatidylcholine	lpchol_hs[u] <=>	1		-1000	1000	0	Exchange/ demand			
EX_lys_L(e)	EX_lys_L(e)	lys-L[e] <=>	1		-1000	1000		Exchange/ demand			
EX_mag_hs(e)	EX_mag_hs(e)	mag_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_mag_hs(u)	exchange reaction for monoacylglycerol 2	mag_hs[u] <=>	1		-1000	1000	0	Exchange/ demand			
EX_malt(e)	EX_malt(e)	malt[e] <=>	1		-1000	1000		Exchange/ demand			
EX_malttr(e)	EX_malttr(e)	malttr[e] <=>	1		-1000	1000		Exchange/ demand			
EX_man(e)	EX_man(e)	man[e] <=>	1		-1000	1000		Exchange/ demand			
EX_meoh(e)	EX_meoh(e)	meoh[e] <=>	1		-1000	1000		Exchange/ demand			
EX_mepi(e)	EX_mepi(e)	mepi[e] <=>	1		-1000	1000		Exchange/ demand			
EX_mercplaccys(e)	EX_mercplaccys(e)	mercplaccys[e] <=>	1		-1000	1000		Exchange/ demand			
EX_met_L(e)	EX_met_L(e)	met-L[e] <=>	1		-1000	1000		Exchange/ demand			
EX_mqn10(e)	Menaquinone 10 exchange	mqn10[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_mqn11(e)	Menaquinone 11 exchange	mqn11[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_mqn7(e)	Menaquinone 7 exchange	mqn7[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_mqn8(e)	Menaquinone 8 exchange	mqn8[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_mqn9(e)	Menaquinone 9 exchange	mqn9[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_mthgxl(e)	EX_mthgxl(e)	mthgxl[e] <=>	1		-1000	1000		Exchange/ demand			
EX_n2m2nmasn(e)	EX_n2m2nmasn(e)	n2m2nmasn[e] <=>	1		-1000	1000		Exchange/ demand			
EX_na1(e)	EX_na1(e)	na1[e] <=>	1		-1000	1000		Exchange/ demand			
EX_na1(u)	exchange reaction for Sodium	na1[u] <=>	1		-1000	1000	0	Exchange/ demand			
EX_nac(e)	EX_nac(e)	nac[e] <=>	1		-1000	1000		Exchange/ demand			
EX_nad(e)	EX_nad(e)	nad[e] <=>	1		-1000	1000		Exchange/ demand			
EX_nadp(e)	EX_nadp(e)	nadp[e] <=>	1		-1000	1000		Exchange/ demand			
EX_ncam(e)	EX_ncam(e)	ncam[e] <=>	1		-1000	1000		Exchange/ demand			
EX_nh4(e)	EX_nh4(e)	nh4[e] <=>	1		-1000	1000		Exchange/ demand			
EX_nifedipine(e)	EX_nifedipine(e)	nifedipine[e] <=>	1		-1000	1000		Exchange/ demand			
EX_no(e)	EX_no(e)	no[e] <=>	1		-1000	1000		Exchange/ demand			
EX_npthl(e)	EX_npthl(e)	npthl[e] <=>	1		-1000	1000		Exchange/ demand			
EX_nrpphr(e)	EX_nrpphr(e)	nrpphr[e] <=>	1		-1000	1000		Exchange/ demand			
EX_nrpphrsf(e)	EX_nrpphrsf(e)	nrpphrsf[e] <=>	1		-1000	1000		Exchange/ demand			
EX_nrvnc(e)	EX_nrvnc(e)	nrvnc[e] <=>	1		-1000	1000		Exchange/ demand			
EX_o2(e)	EX_o2(e)	o2[e] <=>	1		-1000	1000		Exchange/ demand			
EX_o2s(e)	EX_o2s(e)	o2s[e] <=>	1		-1000	1000		Exchange/ demand			
EX_oagd3_hs(e)	EX_oagd3_hs(e)	oagd3_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_oagt3_hs(e)	EX_oagt3_hs(e)	oagt3_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_ocdca(e)	EX_ocdca(e)	ocdca[e] <=>	1		-1000	1000		Exchange/ demand			
EX_ocdcea(e)	EX_ocdcea(e)	ocdcea[e] <=>	1		-1000	1000		Exchange/ demand			
EX_octa(e)	EX_octa(e)	octa[e] <=>	1		-1000	1000		Exchange/ demand			
EX_oh1	EX_oh1	oh1[e] <=>	1		-1000	1000		Exchange/ demand			
EX_omeprazole(e)	EX_omeprazole(e)	omeprazole[e] <=>	1		-1000	1000		Exchange/ demand			
EX_onpthl(e)	EX_onpthl(e)	onpthl[e] <=>	1		-1000	1000		Exchange/ demand			
EX_orn(e)	EX_orn(e)	orn[e] <=>	1		-1000	1000		Exchange/ demand			
EX_oxa(e)	EX_oxa(e)	oxa[e] <=>	1		-1000	1000		Exchange/ demand			
EX_paf_hs(e)	EX_paf_hs(e)	paf_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_pchol_hs(e)	EX_pchol_hs(e)	pchol_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_pe_hs(e)	EX_pe_hs(e)	pe_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_pect(e)	exchange reaction for pectins	pect[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_pectindchac(e)	exchange reaction for pectin-deoxycholic acid complex	pectindchac[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_pectingchol(e)	exchange reaction for pectin-glycocholate complex	pectingchol[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_pectintchol(e)	exchange reaction for pectin-taurocholic acid complex	pectintchol[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_peplys(e)	EX_peplys(e)	peplys[e] <=>	1		-1000	1000		Exchange/ demand			
EX_perillyl(e)	EX_perillyl(e)	perillyl[e] <=>	1		-1000	1000		Exchange/ demand			
EX_pglyc_hs(e)	EX_pglyc_hs(e)	pglyc_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_phe_L(e)	EX_phe_L(e)	phe-L[e] <=>	1		-1000	1000		Exchange/ demand			
EX_phe_L(u)	exchange reaction for L-phenylalanine	phe-L[u] <=>	1		-1000	1000	0	Exchange/ demand			
EX_pheacgln(e)	EX_pheacgln(e)	pheacgln[e] <=>	1		-1000	1000		Exchange/ demand			
EX_pheme(e)	EX_pheme(e)	pheme[e] <=>	1		-1000	1000		Exchange/ demand			
EX_phyQ(e)	EX_phyQ(e)	phyQ[e] <=>	1		-1000	1000		Exchange/ demand			
EX_phyt(e)	EX_phyt(e)	phyt[e] <=>	1		-1000	1000		Exchange/ demand			
EX_pi(e)	EX_pi(e)	pi[e] <=>	1		-1000	1000		Exchange/ demand			
EX_pnto_R(e)	EX_pnto_R(e)	pnto-R[e] <=>	1		-1000	1000		Exchange/ demand			
EX_ppa(e)	EX_ppa(e)	ppa[e] <=>	1		-1000	1000		Exchange/ demand			
EX_prgstrn(e)	EX_prgstrn(e)	prgstrn[e] <=>	1		-1000	1000		Exchange/ demand			
EX_pro_D(e)	EX_pro_D(e)	pro-D[e] <=>	1		-1000	1000		Exchange/ demand			
EX_pro_L(e)	EX_pro_L(e)	pro-L[e] <=>	1		-1000	1000		Exchange/ demand			
EX_progly(e)	EX_progly(e)	progly[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_prostgd2(e)	EX_prostgd2(e)	prostgd2[e] <=>	1		-1000	1000		Exchange/ demand			
EX_prostge1(e)	EX_prostge1(e)	prostge1[e] <=>	1		-1000	1000		Exchange/ demand			
EX_prostge2(e)	EX_prostge2(e)	prostge2[e] <=>	1		-1000	1000		Exchange/ demand			
EX_prostgf2(e)	EX_prostgf2(e)	prostgf2[e] <=>	1		-1000	1000		Exchange/ demand			
EX_ps_hs(e)	EX_ps_hs(e)	ps_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_psyl(e)	exchange reaction for psyllium	psyl[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_psylchol(e)	exchange reaction for psyllium-glycocholic acid complex	psylchol[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_psyltchol(e)	exchange reaction for psyllium-taurocholic acid complex	psyltchol[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_psyltdechol(e)	exchange reaction for psyllium-taurodeoxycholic acid complex	psyltdechol[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_ptdca(e)	EX_ptdca(e)	ptdca[e] <=>	1		-1000	1000		Exchange/ demand			
EX_pydam(e)	EX_pydam(e)	pydam[e] <=>	1		-1000	1000		Exchange/ demand			
EX_pydx(e)	EX_pydx(e)	pydx[e] <=>	1		-1000	1000		Exchange/ demand			
EX_pydxn(e)	EX_pydxn(e)	pydxn[e] <=>	1		-1000	1000		Exchange/ demand			
EX_pyr(e)	EX_pyr(e)	pyr[e] <=>	1		-1000	1000		Exchange/ demand			
EX_rbt(e)	EX_rbt(e)	rbt[e] <=>	1		-1000	1000		Exchange/ demand			
EX_retfa(e)	EX_retfa(e)	retfa[e] <=>	1		-1000	1000		Exchange/ demand			
EX_retinol(e)	EX_retinol(e)	retinol[e] <=>	1		-1000	1000		Exchange/ demand			
EX_retinol_9_cis(e)	EX_retinol_9_cis(e)	retinol-9-cis[e] <=>	1		-1000	1000		Exchange/ demand			
EX_retinol_cis_11(e)	EX_retinol_cis_11(e)	retinol-cis-11[e] <=>	1		-1000	1000		Exchange/ demand			
EX_retn(e)	EX_retn(e)	retn[e] <=>	1		-1000	1000		Exchange/ demand			
EX_retnglc(e)	EX_retnglc(e)	retnglc[e] <=>	1		-1000	1000		Exchange/ demand			
EX_rib_D(e)	EX_rib_D(e)	rib-D[e] <=>	1		-1000	1000		Exchange/ demand			
EX_ribflv(e)	EX_ribflv(e)	ribflv[e] <=>	1		-1000	1000		Exchange/ demand			
EX_ribflv(u)	exchange reaction for Riboflavin	ribflv[u] <=>	1		-1000	1000	0	Exchange/ demand			
EX_s2l2fn2m2masn(e)	EX_s2l2fn2m2masn(e)	s2l2fn2m2masn[e] <=>	1		-1000	1000		Exchange/ demand			
EX_s2l2n2m2m(e)	de-Fuc form of PA6 (w/o peptide linkage) exchange	s2l2n2m2m[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_s2l2n2m2masn(e)	EX_s2l2n2m2masn(e)	s2l2n2m2masn[e] <=>	1		-1000	1000		Exchange/ demand			
EX_sTn_antigen(e)	sialyl-Tn antigen exchange	sTn_antigen[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_sarcs(e)	EX_sarcs(e)	sarcs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_sbt_D(e)	EX_sbt_D(e)	sbt-D[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_sel(e)	EX_sel(e)	sel[e] <=>	1		-1000	1000		Exchange/ demand			
EX_ser_D(e)	EX_ser_D(e)	ser-D[e] <=>	1		-1000	1000		Exchange/ demand			
EX_ser_L(e)	EX_ser_L(e)	ser-L[e] <=>	1		-1000	1000		Exchange/ demand			
EX_ser_L(u)	exchange reaction for L-serine	ser-L[u] <=>	1		-1000	1000	0	Exchange/ demand			
EX_sl_L(e)	EX_sl_L(e)	sl-L[e] <=>	1		-1000	1000		Exchange/ demand			
EX_so4(e)	EX_so4(e)	so4[e] <=>	1		-1000	1000		Exchange/ demand			
EX_spc_hs(e)	EX_spc_hs(e)	spc_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_sph1p(e)	EX_sph1p(e)	sph1p[e] <=>	1		-1000	1000		Exchange/ demand			
EX_sphs1p(e)	EX_sphs1p(e)	sphs1p[e] <=>	1		-1000	1000		Exchange/ demand			
EX_srtn(e)	EX_srtn(e)	srtn[e] <=>	1		-1000	1000		Exchange/ demand			
EX_strch1(e)	EX_strch1(e)	strch1[e] <=>	1		-1000	1000		Exchange/ demand			
EX_strch2(e)	EX_strch2(e)	strch2[e] <=>	1		-1000	1000		Exchange/ demand			
EX_strdnc(e)	EX_strdnc(e)	strdnc[e] <=>	1		-1000	1000		Exchange/ demand			
EX_succ(e)	EX_succ(e)	succ[e] <=>	1		-1000	1000		Exchange/ demand			
EX_sucr(e)	EX_sucr(e)	sucr[e] <=>	1		-1000	1000		Exchange/ demand			
EX_tag_hs(e)	EX_tag_hs(e)	tag_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_tagat_D(e)	EX_tagat_D(e)	tagat-D[e] <=>	1		-1000	1000		Exchange/ demand			
EX_taur(e)	EX_taur(e)	taur[e] <=>	1		-1000	1000		Exchange/ demand			
EX_taxol(e)	EX_taxol(e)	taxol[e] <=>	1		-1000	1000		Exchange/ demand			
EX_tchola(e)	EX_tchola(e)	tchola[e] <=>	1		-1000	1000		Exchange/ demand			
EX_tcynt(e)	EX_tcynt(e)	tcynt[e] <=>	1		-1000	1000		Exchange/ demand			
EX_tdchola(e)	EX_tdchola(e)	tdchola[e] <=>	1		-1000	1000		Exchange/ demand			
EX_tdechola(e)	exchange reaction for Taurodeoxycholic acid	tdechola[e] <=>	1		-1000	1000	0	Exchange/ demand			
EX_tethex3(e)	EX_tethex3(e)	tethex3[e] <=>	1		-1000	1000		Exchange/ demand			
EX_tetpent3(e)	EX_tetpent3(e)	tetpent3[e] <=>	1		-1000	1000		Exchange/ demand			
EX_tetpent6(e)	EX_tetpent6(e)	tetpent6[e] <=>	1		-1000	1000		Exchange/ demand			
EX_tettet6(e)	EX_tettet6(e)	tettet6[e] <=>	1		-1000	1000		Exchange/ demand			
EX_thf(e)	EX_thf(e)	thf[e] <=>	1		-1000	1000		Exchange/ demand			
EX_thm(e)	EX_thm(e)	thm[e] <=>	1		-1000	1000		Exchange/ demand			
EX_thmmp(e)	EX_thmmp(e)	thmmp[e] <=>	1		-1000	1000		Exchange/ demand			
EX_thmtp(e)	EX_thmtp(e)	thmtp[e] <=>	1		-1000	1000		Exchange/ demand			
EX_thr_L(e)	EX_thr_L(e)	thr-L[e] <=>	1		-1000	1000		Exchange/ demand			
EX_thr_L(u)	exchange reaction for L-threonine	thr-L[u] <=>	1		-1000	1000	0	Exchange/ demand			
EX_thym(e)	EX_thym(e)	thym[e] <=>	1		-1000	1000		Exchange/ demand			
EX_thymd(e)	EX_thymd(e)	thymd[e] <=>	1		-1000	1000		Exchange/ demand			
EX_thyox_L(e)	EX_thyox_L(e)	thyox-L[e] <=>	1		-1000	1000		Exchange/ demand			
EX_tmndnc(e)	EX_tmndnc(e)	tmndnc[e] <=>	1		-1000	1000		Exchange/ demand			
EX_tolbutamide(e)	EX_tolbutamide(e)	tolbutamide[e] <=>	1		-1000	1000		Exchange/ demand			

EX_tre(e)	EX_tre(e)	tre[e] <=>	1		-1000	1000		Exchange/ demand			
EX_triodthy(e)	EX_triodthy(e)	triodthy[e] <=>	1		-1000	1000		Exchange/ demand			
EX_triodthysuf(e)	EX_triodthysuf(e)	triodthysuf[e] <=>	1		-1000	1000		Exchange/ demand			
EX_trp_L(e)	EX_trp_L(e)	trp-L[e] <=>	1		-1000	1000		Exchange/ demand			
EX_tststerone(e)	EX_tststerone(e)	tststerone[e] <=>	1		-1000	1000		Exchange/ demand			
EX_tststeroneglc(e)	EX_tststeroneglc(e)	tststeroneglc[e] <=>	1		-1000	1000		Exchange/ demand			
EX_tststerones(e)	EX_tststerones(e)	tststerones[e] <=>	1		-1000	1000		Exchange/ demand			
EX_tsul(e)	EX_tsul(e)	tsul[e] <=>	1		-1000	1000		Exchange/ demand			
EX_ttdca(e)	EX_ttdca(e)	ttdca[e] <=>	1		-1000	1000		Exchange/ demand			
EX_txa2(e)	EX_txa2(e)	txa2[e] <=>	1		-1000	1000		Exchange/ demand			
EX_tymsf(e)	EX_tymsf(e)	tymsf[e] <=>	1		-1000	1000		Exchange/ demand			
EX_tyr_L(e)	EX_tyr_L(e)	tyr-L[e] <=>	1		-1000	1000		Exchange/ demand			
EX_udp(e)	EX_udp(e)	udp[e] <=>	1		-1000	1000		Exchange/ demand			
EX_ump(e)	EX_ump(e)	ump[e] <=>	1		-1000	1000		Exchange/ demand			
EX_ura(e)	EX_ura(e)	ura[e] <=>	1		-1000	1000		Exchange/ demand			
EX_urate(e)	EX_urate(e)	urate[e] <=>	1		-1000	1000		Exchange/ demand			
EX_urea(e)	EX_urea(e)	urea[e] <=>	1		-1000	1000		Exchange/ demand			
EX_uri(e)	EX_uri(e)	uri[e] <=>	1		-1000	1000		Exchange/ demand			
EX_utp(e)	EX_utp(e)	utp[e] <=>	1		-1000	1000		Exchange/ demand			
EX_vacc(e)	EX_vacc(e)	vacc[e] <=>	1		-1000	1000		Exchange/ demand			
EX_val_L(e)	EX_val_L(e)	val-L[e] <=>	1		-1000	1000		Exchange/ demand			
EX_vitd2(e)	EX_vitd2(e)	vitd2[e] <=>	1		-1000	1000		Exchange/ demand			
EX_vitd3(e)	EX_vitd3(e)	vitd3[e] <=>	1		-1000	1000		Exchange/ demand			
EX_vitd3(u)	exchange reaction for calctriol	vitd3[u] <=>	1		-1000	1000	0	Exchange/ demand			
EX_whddca(e)	EX_whddca(e)	whddca[e] <=>	1		-1000	1000		Exchange/ demand			
EX_whhdca(e)	EX_whhdca(e)	whhdca[e] <=>	1		-1000	1000		Exchange/ demand			
EX_whtststerone(e)	EX_whtststerone(e)	whtststerone[e] <=>	1		-1000	1000		Exchange/ demand			
EX_whttdca(e)	EX_whttdca(e)	whttdca[e] <=>	1		-1000	1000		Exchange/ demand			
EX_xolest2_hs(e)	EX_xolest2_hs(e)	xolest2_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_xolest_hs(e)	EX_xolest_hs(e)	xolest_hs[e] <=>	1		-1000	1000		Exchange/ demand			
EX_xoltri24(e)	EX_xoltri24(e)	xoltri24[e] <=>	1		-1000	1000		Exchange/ demand			
EX_xoltri25(e)	EX_xoltri25(e)	xoltri25[e] <=>	1		-1000	1000		Exchange/ demand			
EX_xoltri27(e)	EX_xoltri27(e)	xoltri27[e] <=>	1		-1000	1000		Exchange/ demand			
EX_xyl_D(e)	EX_xyl_D(e)	xyl-D[e] <=>	1		-1000	1000		Exchange/ demand			
EX_xylt(e)	EX_xylt(e)	xylt[e] <=>	1		-1000	1000		Exchange/ demand			
EX_yvite(e)	EX_yvite(e)	yvite[e] <=>	1		-1000	1000	0	Exchange/ demand			
F1At	F1alpha (mucin O-glycan) export	f1a[g] -> f1a[e]	0		0	1000	2	Transport, Extracellular	PMID: 10430883, PMID: 848954	Reaction that provides mucin O-glycans to gut microbiota, e.g. B. thetaiotaomicron. BT is well known to degrade mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis.	
F1Atg	F1A intracellular transport	f1a[g] <=> f1a[l]	1		-1000	1000		Transport, Golgi Apparatus			
F1PGT	fucose-1-phosphate guanylyltransferase	h[c] + gtp[c] + fuc1p-L[c] <=> ppi[c] + gdpfuc[c]	1	75540.1	-1000	1000		Fructose and Mannose Metabolism			
F6Tg	glycoprotein 6-alpha-L-fucosyltransferase	gdpfuc[g] + n2m2masn[g] -> h[g] + fn2m2masn[g] + gdp[g]	0	53618.1 or 53618.2 or 53618.3 or 53618.4 or 53618.5	0	1000		N-Glycan Biosynthesis			
FA120ACPH	fatty-acyl-ACP hydrolase	h2o[c] + ddcaACP[c] <=> h[c] + ACP[c] + ddca[c]	1	99035.1	-1000	1000		Fatty Acid Metabolism			
FA140ACPH	fatty-acyl-ACP hydrolase	h2o[c] + myrsACP[c] <=> h[c] + ACP[c] + ttdca[c]	1	99035.1	-1000	1000		Fatty Acid Metabolism			
FA141ACPH	fatty-acyl-ACP hydrolase	h2o[c] + tdeACP[c] <=> h[c] + ACP[c] + ttdcea[c]	1	99035.1	-1000	1000		Fatty Acid Metabolism			
FA160ACPH	fatty-acyl-ACP hydrolase	h2o[c] + palmACP[c] <=> h[c] + ACP[c] + hdca[c]	1	99035.1	-1000	1000		Fatty Acid Metabolism			
FA161ACPH	fatty-acyl-ACP hydrolase	h2o[c] + hdeACP[c] <=> h[c] + ACP[c] + hdcea[c]	1	99035.1	-1000	1000		Fatty Acid Metabolism			
FA180ACPH	fatty-acyl-ACP hydrolase	h2o[c] + ocdcaACP[c] <=> h[c] + ACP[c] + ocdca[c]	1	99035.1	-1000	1000		Fatty Acid Metabolism			
FA181ACPH	fatty-acyl-ACP hydrolase	h2o[c] + octeACP[c] <=> h[c] + ACP[c] + ocdcea[c]	1	99035.1	-1000	1000		Fatty Acid Metabolism			
FA1821ACPH	fatty-acyl-ACP hydrolase	h2o[c] + lnlcACP[c] <=> h[c] + ACP[c] + lnlc[c]	1		-1000	1000		Fatty Acid Metabolism			
FA1822ACPH	fatty-acyl-ACP hydrolase	h2o[c] + lneldcACP[c] <=> h[c] + ACP[c] + lneldc[c]	1		-1000	1000		Fatty Acid Metabolism			
FA182ACPH	fatty-acyl-ACP hydrolase	h2o[c] + ocdcyaACP[c] <=> h[c] + ACP[c] + ocdcya[c]	1	99035.1	-1000	1000		Fatty Acid Metabolism			
FACOAL140i	fatty-acid--CoA ligase (tetradecanoate)	atp[c] + coa[c] + ttdca[c] -> amp[c] + ppi[c] + tdcoa[c]	0	74205.1	0	1000		Fatty acid activation			
FACOAL150	fatty-acid--CoA ligase	atp[c] + coa[c] + ptdca[c] <=> amp[c] + ppi[c] + ptdcacoa[c]	1	(74205.1 or 50790.1 or 14081.1 or 22305.2 or 22305.1 or 74205.2)	-1000	1000		Fatty acid activation			
FACOAL160i	C160 fatty acid activation	atp[c] + coa[c] + hdca[c] -> amp[c] + ppi[c] + pmtcoa[c]	0	(433256.1 or 74205.1 or 14081.1 or 22305.2 or 22305.1 or 74205.2)	0	1000		Fatty acid activation			
FACOAL161	fatty-acid--CoA ligase (hexadecenoate)	atp[c] + coa[c] + hdcea[c] <=> amp[c] + ppi[c] + hdcoa[c]	1	14081.1	-1000	1000		Fatty acid activation			
FACOAL170	fatty-acid--CoA ligase	atp[c] + coa[c] + hpdca[c] <=> amp[c] + ppi[c] + hpdcacoa[c]	1	(74205.1 or 50790.1 or 14081.1 or 22305.2 or 22305.1 or 74205.2)	-1000	1000		Fatty acid activation			
FACOAL180i	C180 fatty acid activation	atp[c] + coa[c] + ocdca[c] -> amp[c] + ppi[c] + stcoa[c]	0	(433256.1 or 74205.1 or 14081.1 or 22305.2 or 22305.1 or 74205.2)	0	1000		Fatty acid activation			
FACOAL1812	fatty-acid--CoA ligase	atp[c] + coa[c] + vacc[c] <=> amp[c] + ppi[c] + vacccoa[c]	1	14081.1	-1000	1000		Fatty acid activation			
FACOAL1813	fatty-acid--CoA ligase	atp[c] + coa[c] + elaid[c] <=> amp[c] + ppi[c] + od2coa[c]	1	14081.1	-1000	1000		Fatty acid activation			
FACOAL181i	C181 fatty acid activation	atp[c] + coa[c] + ocdcea[c] -> amp[c] + ppi[c] + odecoa[c]	0	74205.1 or 14081.1 or 74205.2	0	1000		Fatty acid activation			
FACOAL1821	fatty-acid--CoA ligase	atp[c] + coa[c] + lnlc[c] <=> amp[c] + ppi[c] + lnlccoa[c]	1	14081.1	-1000	1000		Fatty acid activation			
FACOAL1822	fatty-acid--CoA ligase	atp[c] + coa[c] + lneldc[c] <=> amp[c] + ppi[c] + lneldccoa[c]	1	14081.1	-1000	1000		Fatty acid activation			
FACOAL1831	fatty-acid--CoA ligase	atp[c] + coa[c] + lnlncg[c] <=> amp[c] + ppi[c] + lnlncgcoa[c]	1	14081.1	-1000	1000		Fatty acid activation			
FACOAL1832	fatty-acid--CoA ligase	atp[c] + coa[c] + lnlnca[c] <=> amp[c] + ppi[c] + lnlncacoa[c]	1	14081.1	-1000	1000		Fatty acid activation			
FACOAL184	fatty-acid--CoA ligase	atp[c] + coa[c] + strdnc[c] <=> amp[c] + ppi[c] + strdnccoa[c]	1	14081.1	-1000	1000		Fatty acid activation			
FACOAL191	fatty-acid--CoA ligase	atp[c] + coa[c] + prist[c] -> amp[c] + ppi[c] + pristcoa[c]	0	26458.1	0	1000		Fatty acid activation			
FACOAL200	fatty-acid--CoA ligase	atp[c] + coa[c] + arach[c] <=> amp[c] + ppi[c] + arachcoa[c]	1	14081.1	-1000	1000		Fatty acid activation			
FACOAL203	fatty-acid--CoA ligase	atp[c] + coa[c] + dlnlcg[c] <=> amp[c] + ppi[c] + dlnlcgcoa[c]	1	14081.1	-1000	1000		Fatty acid activation			
FACOAL204	fatty-acid--CoA ligase	atp[c] + coa[c] + arachd[c] <=> amp[c] + ppi[c] + arachdcoa[c]	1	14081.1	-1000	1000		Fatty acid activation			
FACOAL2042	fatty-acid--CoA ligase	atp[c] + coa[c] + eicostet[c] <=> amp[c] + ppi[c] + eicostetcoa[c]	1	14081.1	-1000	1000		Fatty acid activation			
FACOAL204i	arachidonic acid activation	atp[c] + coa[c] + arachd[c] -> amp[c] + ppi[c] + arachdcoa[c]	0	(50790.1 or 74205.1 or 50790.2 or 14081.1 or 22305.2 or 22305.1 or 74205.2)	0	1000		Fatty acid activation			
FACOAL205	fatty-acid--CoA ligase	atp[c] + coa[c] + tmndnc[c] <=> amp[c] + ppi[c] + tmndnccoa[c]	1	14081.1	-1000	1000		Fatty acid activation			
FACOAL206	fatty-acid--CoA ligase	atp[c] + coa[c] + phyt[c] <=> amp[c] + ppi[c] + phytcoa[c]	1	26458.1	-1000	1000		Fatty acid activation			
FACOAL224	fatty-acid--CoA ligase	atp[c] + coa[c] + adrn[c] <=> amp[c] + ppi[c] + adrncoa[c]	1	14081.1	-1000	1000		Fatty acid activation			
FACOAL2251	fatty-acid--CoA ligase	atp[c] + coa[c] + dcsptn1[c] <=> amp[c] + ppi[c] + dcsptn1coa[c]	1	14081.1	-1000	1000		Fatty acid activation			
FACOAL2252	fatty-acid--CoA ligase	atp[c] + coa[c] + clpnd[c] <=> amp[c] + ppi[c] + clpndcoa[c]	1	14081.1	-1000	1000		Fatty acid activation			
FACOAL226	fatty-acid--CoA ligase	atp[c] + coa[c] + crvnc[c] <=> amp[c] + ppi[c] + c226coa[c]	1	14081.1	-1000	1000		Fatty acid activation			
FACOAL226i	C226 fatty acid activation	atp[c] + coa[c] + crvnc[c] -> amp[c] + ppi[c] + c226coa[c]	0		0	1000		Fatty acid activation			
FACOAL240	fatty-acid--CoA ligase	atp[c] + coa[c] + lgnc[c] <=> amp[c] + ppi[c] + lgnccoa[c]	1	14081.1	-1000	1000		Fatty acid activation			
FACOAL241	fatty-acid--CoA ligase	atp[c] + coa[c] + nrvnc[c] <=> amp[c] + ppi[c] + nrvnccoa[c]	1	14081.1	-1000	1000		Fatty acid activation			
FACOAL244_1	fatty-acid--CoA ligase	atp[c] + coa[c] + tettet6[c] <=> amp[c] + ppi[c] + tettet6coa[c]	1	14081.1	-1000	1000		Fatty acid activation			
FACOAL245_1	fatty-acid--CoA ligase	atp[c] + coa[c] + tetpent6[c] <=> amp[c] + ppi[c] + tetpent6coa[c]	1	14081.1	-1000	1000		Fatty acid activation			
FACOAL245_2	fatty-acid--CoA ligase	atp[c] + coa[c] + tetpent3[c] <=> amp[c] + ppi[c] + tetpent3coa[c]	1	14081.1	-1000	1000		Fatty acid activation			
FACOAL246_1	fatty-acid--CoA ligase	atp[c] + coa[c] + tethex3[c] <=> amp[c] + ppi[c] + tethex3coa[c]	1	14081.1	-1000	1000		Fatty acid activation			
FACOAL260	fatty-acid--CoA ligase (n-C26:0)	atp[c] + coa[c] + hexc[c] <=> amp[c] + ppi[c] + hexccoa[c]	1	14081.1	-1000	1000		Fatty acid activation			
FACOAL40im	fatty-acid--CoA ligase (butanoate), mitochondrial	coa[m] + atp[m] + but[m] -> amp[m] + ppi[m] + btcoa[m]	0	117147.1	0	1000		Fatty acid activation			
FACOAL80i	fatty-acid--CoA ligase (octanoate)	atp[c] + coa[c] + octa[c] -> amp[c] + ppi[c] + occoa[c]	0	74205.1 or 74205.2	0	1000		Fatty acid activation			
FADDP	FAD diphosphatase	h2o[c] + fad[c] -> 2 h[c] + amp[c] + fmn[c]	0	18605.1	0	1000		Riboflavin Metabolism			
FADH2tru	FADH2 transporter, endoplasmic reticulum	fadh2[c] -> fadh2[r]	0		0	1000		Transport, Endoplasmic Reticular			
FADH2tx	FADH2 transporter, peroxisomal	fadh2[c] <=> fadh2[x]	1		-1000	1000		Transport, Peroxisomal			
FADtru	FAD transporter, endoplasmic reticulum	fad[r] -> fad[c]	0		0	1000		Transport, Endoplasmic Reticular			
FADtx	FAD transporter, peroxisomal	fad[c] <=> fad[x]	1		-1000	1000		Transport, Peroxisomal			
FAEL183	fatty-acyl-CoA elongation (n-C18:3CoA)	o2[c] + 5 h[c] + 4 nadph[c] + malcoa[c] + lnlncgcoa[c] -> 3 h2o[c] + 4 nadp[c] + co2[c] + coa[c] + dlnlcgcoa[c]	0	83603.1	0	1000		Fatty acid elongation			
FAEL184	fatty-acyl-CoA elongation (n-C20:4CoA)	o2[c] + 5 h[c] + 4 nadph[c] + malcoa[c] + strdnccoa[c] -> 3 h2o[c] + 4 nadp[c] + co2[c] + coa[c] + eicostetcoa[c]	0	83603.1	0	1000		Fatty acid elongation			
FAEL204	fatty-acyl-CoA elongation (n-C20:4CoA)	o2[c] + 5 h[c] + 4 nadph[c] + malcoa[c] + arachdcoa[c] -> 3 h2o[c] + 4 nadp[c] + co2[c] + coa[c] + adrncoa[c]	0	83603.1	0	1000		Fatty acid elongation			
FAEL205	fatty-acyl-CoA elongation (n-C20:5CoA)	o2[c] + 5 h[c] + 4 nadph[c] + malcoa[c] + tmndnccoa[c] -> 3 h2o[c] + 4 nadp[c] + co2[c] + coa[c] + clpndcoa[c]	0	83603.1	0	1000		Fatty acid elongation			
FAH1	Fatty acid omega-hydroxylase	o2[c] + h[c] + nadph[c] + ddca[c] -> h2o[c] + nadp[c] + whddca[c]	0	13117.1	0	1000		CYP Metabolism			
FAH2	Fatty acid omega-hydroxylase	o2[c] + h[c] + nadph[c] + ttdca[c] -> h2o[c] + nadp[c] + whttdca[c]	0	13117.1	0	1000		CYP Metabolism			
FAH3	Fatty acid omega-hydroxylase	o2[c] + h[c] + nadph[c] + hdca[c] -> h2o[c] + nadp[c] + whhdca[c]	0	13117.1	0	1000		CYP Metabolism			
FALDH	formaldehyde dehydrogenase	nad[c] + gthrd[c] + fald[c] <=> h[c] + nadh[c] + Sfglutth[c]	1	11532.1	-1000	1000		Tyrosine metabolism			
FALDtly	formaldehyde transport via diffusion (lysosomall)	fald[l] <=> fald[c]	1		-1000	1000		Transport, Lysosomal			
FALDtm	formaldehyde transport via diffusion (mitochondrial)	fald[m] <=> fald[c]	1		-1000	1000		Transport, Mitochondrial			

FAOXC11	Beta oxidation of long chain fatty acid	h2o[m] + coa[m] + nad[m] + dmnoncoa[m] -> h[m] + nadh[m] + accoa[m] + dmhexcoa[m]	0	11364.1	0	1000		Fatty acid oxidation			
FAOXC140	Beta oxidation of long chain fatty acid	6 h2o[m] + 6 coa[m] + 6 nad[m] + 6 fad[m] + hdcoa[m] -> 6 h[m] + 6 nadh[m] + 7 accoa[m] + 6 fadh2[m]	0	11364.1 or 11409.1	0	1000		Fatty acid oxidation			
FAOXC150m	Beta oxidation of long chain fatty acid (odd chain)	6 h2o[m] + 6 coa[m] + 6 nad[m] + 6 fad[m] + pmtcacoa[m] -> 6 h[m] + 6 nadh[m] + 6 accoa[m] + ppcoa[m] + 6 fadh2[m]	0	11364.1 or 11409.1	0	1000		Fatty acid oxidation			
FAOXC160	Beta oxidation of long chain fatty acid	7 h2o[m] + 7 coa[m] + 7 nad[m] + 7 fad[m] + pmtcoa[m] -> 7 h[m] + 7 nadh[m] + 8 accoa[m] + 7 fadh2[m]	0	11364.1 or 11409.1	0	1000		Fatty acid oxidation			
FAOXC160l0m	Beta oxidation of long chain fatty acid	4 h2o[m] + 4 coa[m] + 4 nad[m] + 4 fad[m] + pmtcoa[m] -> 4 h[m] + 4 nadh[m] + 4 accoa[m] + 4 fadh2[m] + occoa[m]	0	11364.1 or 11409.1	0	1000		Fatty acid oxidation			
FAOXC160l80x	Beta oxidation of long chain fatty acid	4 nad[x] + 4 coa[x] + pmtcoa[x] + 4 o2[x] + 4 h2o[x] -> 4 h[x] + 4 nadh[x] + 4 accoa[x] + occoa[x] + 4 h2o2[x]	0	74147.1 and 113868.1 and 11430.1 or 113868.1 and 11430.1 and 15488.1 or 74147.1 and 113868.1 and 11430.2 or 113868.1 and 15488.1 and 11430.2	0	1000		Fatty acid oxidation, peroxisome			
FAOXC161802m	Beta oxidation fatty acid	4 h2o[m] + 4 coa[m] + 4 nad[m] + 3 fad[m] + hdd2coa[m] -> 4 h[m] + 4 nadh[m] + 4 accoa[m] + 3 fadh2[m] + occoa[m]	0	11364.1 or 11409.1	0	1000		Fatty acid activation			
FAOXC161l80m	Beta oxidation fatty acid	4 h2o[m] + 4 coa[m] + 4 nad[m] + 3 fad[m] + hdcoa[m] -> 4 h[m] + 4 nadh[m] + 4 accoa[m] + 3 fadh2[m] + occoa[m]	0	11364.1 or 11409.1	0	1000		Fatty acid oxidation			
FAOXC170m	Beta oxidation of long chain fatty acid (odd chain)	7 h2o[m] + 7 coa[m] + 7 nad[m] + 7 fad[m] + hpdcoa[m] -> 7 h[m] + 7 nadh[m] + 7 accoa[m] + ppcoa[m] + 7 fadh2[m]	0	11364.1	0	1000		Fatty acid oxidation			
FAOXC180	Beta oxidation of long chain fatty acid	h2o[m] + coa[m] + nad[m] + fad[m] + stcoa[m] -> h[m] + nadh[m] + accoa[m] + fadh2[m] + pmtcoa[m]	0	11364.1 or 11409.1	0	1000		Fatty acid oxidation			
FAOXC180x	Beta oxidation of long chain fatty acid	nad[x] + coa[x] + o2[x] + h2o[x] + stcoa[x] -> h[x] + nadh[x] + accoa[x] + pmtcoa[x] + h2o2[x]	0	74147.1 and 113868.1 and 11430.1 or 113868.1 and 11430.1 and 15488.1 or 74147.1 and 113868.1 and 11430.2 or 113868.1 and 15488.1 and 11430.2	0	1000		Fatty acid oxidation, peroxisome			
FAOXC1811601m	Beta oxidation fatty acid	5 h2o[m] + 5 coa[m] + 5 nad[m] + 4 fad[m] + ot2coa[m] -> 5 h[m] + 5 nadh[m] + 5 accoa[m] + 4 fadh2[m] + occoa[m]	0	11364.1 or 11409.1	0	1000		Fatty acid oxidation			
FAOXC1811602m	Beta oxidation fatty acid	5 h2o[m] + 5 coa[m] + 5 nad[m] + 4 fad[m] + vaccoa[m] -> 5 h[m] + 5 nadh[m] + 5 accoa[m] + 4 fadh2[m] + occoa[m]	0	11364.1 or 11409.1	0	1000		Fatty acid oxidation			
FAOXC1811603m	Beta oxidation fatty acid	5 h2o[m] + 5 coa[m] + 5 nad[m] + 4 fad[m] + odecoa[m] -> 5 h[m] + 5 nadh[m] + 5 accoa[m] + 4 fadh2[m] + occoa[m]	0	11364.1 or 11409.1	0	1000		Fatty acid oxidation			
FAOXC1820806m	Beta oxidation of fatty acid	5 h2o[m] + 5 coa[m] + 5 nad[m] + 3 fad[m] + hdecoa[m] -> 5 h[m] + 5 nadh[m] + 5 accoa[m] + 3 fadh2[m] + occoa[m]	0	11364.1 or 11409.1	0	1000		Fatty acid oxidation			
FAOXC18280m	Beta oxidation of fatty acid	5 h2o[m] + 5 coa[m] + 5 nad[m] + 3 fad[m] + hxdcoa[m] -> 5 h[m] + 5 nadh[m] + 5 accoa[m] + 3 fadh2[m] + occoa[m]	0	11364.1 or 11409.1	0	1000		Fatty acid oxidation			
FAOXC1838003m	Beta oxidation of fatty acid	5 h2o[m] + 5 coa[m] + 5 nad[m] + 2 fad[m] + hdecacoa[m] -> 5 h[m] + 5 nadh[m] + 5 accoa[m] + 2 fadh2[m] + occoa[m]	0	11364.1 or 11409.1	0	1000		Fatty acid oxidation			
FAOXC1838006m	Beta oxidation of fatty acid	2 o2[m] + 5 h2o[m] + 5 coa[m] + 5 nad[m] + hdecgcoa[m] -> 5 h[m] + 5 nadh[m] + 5 accoa[m] + 2 h2o2[m] + occoa[m]	0	11364.1 or 11409.1	0	1000		Fatty acid oxidation			
FAOXC183806x	Beta oxidation of long chain fatty acid	5 nad[x] + 5 coa[x] + 2 o2[x] + 5 h2o[x] + hdecgcoa[x] -> 5 h[x] + 5 nadh[x] + 5 accoa[x] + occoa[x] + 2 h2o2[x]	0	74147.1 and 113868.1 and 11430.1 or 113868.1 and 11430.1 and 15488.1 or 74147.1 and 113868.1 and 11430.2 or 113868.1 and 15488.1 and 11430.2	0	1000		Fatty acid oxidation, peroxisome			
FAOXC18480m	Beta oxidation of fatty acid	5 h2o[m] + 5 coa[m] + 5 nad[m] + fad[m] + strdncoa[m] -> 5 h[m] + 5 nadh[m] + 5 accoa[m] + fadh2[m] + occoa[m]	0	11364.1 or 11409.1	0	1000		Fatty acid oxidation			
FAOXC18480x	Beta oxidation of long chain fatty acid	5 nad[x] + 5 coa[x] + o2[x] + 5 h2o[x] + strdncoa[x] -> 5 h[x] + 5 nadh[x] + 5 accoa[x] + occoa[x] + h2o2[x]	0	74147.1 and 113868.1 and 11430.1 or 113868.1 and 11430.1 and 15488.1 or 74147.1 and 113868.1 and 11430.2 or 113868.1 and 15488.1 and 11430.2	0	1000		Fatty acid oxidation, peroxisome			
FAOXC200180m	Beta oxidation of long chain fatty acid	h2o[m] + coa[m] + nad[m] + fad[m] + arachcoa[m] -> h[m] + nadh[m] + accoa[m] + fadh2[m] + stcoa[m]	0	11364.1 or 11409.1	0	1000		Fatty acid oxidation			
FAOXC200180x	Beta oxidation of long chain fatty acid	nad[x] + coa[x] + o2[x] + h2o[x] + arachcoa[x] -> h[x] + nadh[x] + accoa[x] + h2o2[x] + stcoa[x]	0	74147.1 and 113868.1 and 11430.1 or 113868.1 and 11430.1 and 15488.1 or 74147.1 and 113868.1 and 11430.2 or 113868.1 and 15488.1 and 11430.2	0	1000		Fatty acid oxidation, peroxisome			
FAOXC2031836m	Beta oxidation of fatty acid	h2o[m] + coa[m] + nad[m] + fad[m] + dhtdcgcoa[m] -> h[m] + nadh[m] + accoa[m] + fadh2[m] + hdecgcoa[m]	0	11364.1 or 11409.1	0	1000		Fatty acid oxidation			
FAOXC204	Beta oxidation of long chain fatty acid	9 h2o[m] + 9 coa[m] + 9 nad[m] + 5 fad[m] + arachdcoa[m] -> 9 h[m] + 9 nadh[m] + 10 accoa[m] + 5 fadh2[m]	0	11364.1 or 11409.1	0	1000		Fatty acid oxidation			
FAOXC20418dm	Beta oxidation fatty acid	h2o[m] + coa[m] + nad[m] + fad[m] + eicostetcoa[m] -> h[m] + nadh[m] + accoa[m] + fadh2[m] + strdncoa[m]	0	11364.1 or 11409.1	0	1000		Fatty acid oxidation			
FAOXC2051843m	Beta oxidation of fatty acid	h2o[m] + coa[m] + nad[m] + tmtdecoa[m] -> h[m] + nadh[m] + accoa[m] + strdncoa[m]	0	11364.1 or 11409.1	0	1000		Fatty acid oxidation			
FAOXC2051843x	Beta oxidation of long chain fatty acid	nad[x] + coa[x] + h2o[x] + tmtdecoa[x] -> h[x] + nadh[x] + accoa[x] + strdncoa[x]	0	74147.1 and 113868.1 and 11430.1 or 113868.1 and 11430.1 and 15488.1 or 74147.1 and 113868.1 and 11430.2 or 113868.1 and 15488.1 and 11430.2	0	1000		Fatty acid oxidation, peroxisome			
FAOXC2242046m	Beta oxidation of long chain fatty acid	h2o[m] + coa[m] + nad[m] + fad[m] + adrncoa[m] -> h[m] + nadh[m] + accoa[m] + fadh2[m] + arachdcoa[m]	0	11364.1 or 11409.1	0	1000		Fatty acid oxidation			
FAOXC2242046x	Beta oxidation of long chain fatty acid	nad[x] + coa[x] + o2[x] + h2o[x] + adrncoa[x] -> h[x] + nadh[x] + accoa[x] + h2o2[x] + arachdcoa[x]	0	74147.1 and 113868.1 and 11430.1 or 113868.1 and 11430.1 and 15488.1 or 74147.1 and 113868.1 and 11430.2 or 113868.1 and 15488.1 and 11430.2	0	1000		Fatty acid oxidation, peroxisome			
FAOXC2251836m	Beta oxidation of fatty acid	2 h2o[m] + 2 coa[m] + 2 nad[m] + dcspmtcoa[m] -> 2 h[m] + 2 nadh[m] + 2 accoa[m] + hdecgcoa[m]	0	11364.1 or 11409.1	0	1000		Fatty acid oxidation			
FAOXC2251836x	Beta oxidation of long chain fatty acid	2 nad[x] + 2 coa[x] + 2 h2o[x] + dcspmtcoa[x] -> 2 h[x] + 2 nadh[x] + 2 accoa[x] + hdecgcoa[x]	0	74147.1 and 113868.1 and 11430.1 or 113868.1 and 11430.1 and 15488.1 or 74147.1 and 113868.1 and 11430.2 or 113868.1 and 15488.1 and 11430.2	0	1000		Fatty acid oxidation, peroxisome			
FAOXC2252053m	Beta oxidation of long chain fatty acid	o2[m] + h2o[m] + coa[m] + nad[m] + dcspmtcoa[m] -> h[m] + nadh[m] + accoa[m] + h2o2[m] + tmtdecoa[m]	0	11364.1 or 11409.1	0	1000		Fatty acid oxidation			
FAOXC2252053x	Beta oxidation of long chain fatty acid	nad[x] + coa[x] + o2[x] + h2o[x] + dcspmtcoa[x] -> h[x] + nadh[x] + accoa[x] + h2o2[x] + tmtdecoa[x]	0	74147.1 and 113868.1 and 11430.1 or 113868.1 and 11430.1 and 15488.1 or 74147.1 and 113868.1 and 11430.2 or 113868.1 and 15488.1 and 11430.2	0	1000		Fatty acid oxidation, peroxisome			
FAOXC226	Beta oxidation of long chain fatty acid	10 h2o[m] + 10 coa[m] + 10 nad[m] + 4 fad[m] + c226coa[m] -> 10 h[m] + 10 nadh[m] + 11 accoa[m] + 4 fadh2[m]	0	11364.1 or 11409.1	0	1000		Fatty acid oxidation			
FAOXC226205m	Beta oxidation of long chain fatty acid	h2o[m] + coa[m] + nad[m] + c226coa[m] -> h[m] + nadh[m] + accoa[m] + tmtdecoa[m]	0	11364.1 or 11409.1	0	1000		Fatty acid oxidation			
FAOXC226205x	Beta oxidation of long chain fatty acid	nad[x] + coa[x] + h2o[x] + c226coa[x] -> h[x] + nadh[x] + accoa[x] + tmtdecoa[x]	0	74147.1 and 113868.1 and 11430.1 or 113868.1 and 11430.1 and 15488.1 or 74147.1 and 113868.1 and 11430.2 or 113868.1 and 15488.1 and 11430.2	0	1000		Fatty acid oxidation, peroxisome			

FAOXC240200x	Beta oxidation of long chain fatty acid	2 nad[x] + 2 coa[x] + 2 o2[x] + 2 h2o[x] + lgnccoa[x] -> 2 h[x] + 2 nadh[x] + 2 accoa[x] + 2 h2o2[x] + arachcoa[x]	0	74147.1 and 113868.1 and 11430.1 or 113868.1 and 11430.1 and 15488.1 or 74147.1 and 113868.1 and 11430.2 or 113868.1 and 15488.1 and 11430.2	0	1000		Fatty acid oxidation, peroxisome			
FAOXC241181x	Beta oxidation of long chain fatty acid	3 nad[x] + 3 coa[x] + 3 o2[x] + 3 h2o[x] + nvaccoa[x] -> 3 h[x] + 3 nadh[x] + 3 accoa[x] + 3 h2o2[x] + odecoa[x]	0	74147.1 and 113868.1 and 11430.1 or 113868.1 and 11430.1 and 15488.1 or 74147.1 and 113868.1 and 11430.2 or 113868.1 and 15488.1 and 11430.2	0	1000		Fatty acid oxidation, peroxisome			
FAOXC2442246x	Beta oxidation of long chain fatty acid	nad[x] + coa[x] + o2[x] + h2o[x] + tetrtetcoa[x] -> h[x] + nadh[x] + accoa[x] + h2o2[x] + adrncoa[x]	0	74147.1 and 113868.1 and 11430.1 or 113868.1 and 11430.1 and 15488.1 or 74147.1 and 113868.1 and 11430.2 or 113868.1 and 15488.1 and 11430.2	0	1000		Fatty acid oxidation, peroxisome			
FAOXC2452253x	Beta oxidation of long chain fatty acid	nad[x] + coa[x] + o2[x] + h2o[x] + tetpentcosa[x] -> h[x] + nadh[x] + accoa[x] + h2o2[x] + c1pndcoa[x]	0	74147.1 and 113868.1 and 11430.1 or 113868.1 and 11430.1 and 15488.1 or 74147.1 and 113868.1 and 11430.2 or 113868.1 and 15488.1 and 11430.2	0	1000		Fatty acid oxidation, peroxisome			
FAOXC2452256x	Beta oxidation of long chain fatty acid	nad[x] + coa[x] + o2[x] + h2o[x] + tetpentfcosa[x] -> h[x] + nadh[x] + accoa[x] + h2o2[x] + dctqntncoa[x]	0	74147.1 and 113868.1 and 11430.1 or 113868.1 and 11430.1 and 15488.1 or 74147.1 and 113868.1 and 11430.2 or 113868.1 and 15488.1 and 11430.2	0	1000		Fatty acid oxidation, peroxisome			
FAOXC246226x	Beta oxidation of long chain fatty acid	nad[x] + coa[x] + o2[x] + h2o[x] + tethexlcoa[x] -> h[x] + nadh[x] + accoa[x] + h2o2[x] + c226fcoa[x]	0	74147.1 and 113868.1 and 11430.1 or 113868.1 and 11430.1 and 15488.1 or 74147.1 and 113868.1 and 11430.2 or 113868.1 and 15488.1 and 11430.2	0	1000		Fatty acid oxidation, peroxisome			
FAOXC260240x	Beta oxidation of long chain fatty acid	nad[x] + coa[x] + o2[x] + h2o[x] + hexccoa[x] -> h[x] + nadh[x] + accoa[x] + h2o2[x] + lgnccoa[x]	0	74147.1 and 113868.1 and 11430.1 or 113868.1 and 11430.1 and 15488.1 or 74147.1 and 113868.1 and 11430.2 or 113868.1 and 15488.1 and 11430.2	0	1000		Fatty acid oxidation, peroxisome			
FAOXC80	Beta oxidation of med/long chain fatty acid	3 h2o[m] + 3 coa[m] + 3 nad[m] + 3 fad[m] + occoa[m] -> 3 h[m] + 3 nadh[m] + 4 accoa[m] + 3 fadh2[m]	0	11364.1 or 11409.1	0	1000		Fatty acid oxidation			
FAS100COA	fatty acyl-CoA synthase (n-C10:0CoA)	3 h[c] + 2 nadph[c] + malcoa[c] + occoa[c] -> h2o[c] + 2 nadp[c] + co2[c] + coa[c] + dcacoa[c]	0	14104.1	0	1000		Fatty acid elongation			
FAS120COA	fatty-acyl-CoA synthase (n-C12:0CoA)	3 h[c] + 2 nadph[c] + malcoa[c] + dcacoa[c] -> h2o[c] + 2 nadp[c] + co2[c] + coa[c] + ddcacoa[c]	0	14104.1	0	1000		Fatty acid elongation			
FAS140COA	fatty-acyl-CoA synthase (n-C14:0CoA)	3 h[c] + 2 nadph[c] + malcoa[c] + ddcacoa[c] -> h2o[c] + 2 nadp[c] + co2[c] + coa[c] + tdecoa[c]	0	14104.1	0	1000		Fatty acid elongation			
FAS160COA	fatty-acyl-CoA synthase (n-C16:0CoA)	3 h[c] + 2 nadph[c] + malcoa[c] + tdecoa[c] -> h2o[c] + 2 nadp[c] + co2[c] + coa[c] + pmtcoa[c]	0	14104.1	0	1000		Fatty acid elongation			
FAS180COA	fatty-acyl-CoA synthase (n-C18:0CoA)	3 h[c] + 2 nadph[c] + malcoa[c] + pmtcoa[c] -> h2o[c] + 2 nadp[c] + co2[c] + coa[c] + stcoa[c]	0	14104.1	0	1000		Fatty acid elongation			
FAS80COA_L	fatty acyl-CoA synthase (n-C8:0CoA), lumped reaction	9 h[c] + 6 nadph[c] + accoa[c] + 3 malcoa[c] -> 3 h2o[c] + 6 nadp[c] + 3 co2[c] + 3 coa[c] + occoa[c]	0	14104.1	0	1000		Fatty acid elongation			
FATP1t	fatty acid electroneutral transport	na1[c] + hdca[c] <=> na1[e] + hdca[e]	1	26457.1 or 26569.1 or 26568.1 or 26457.2	-1000	1000		Transport, Extracellular			
FATP2t	fatty acid electroneutral transport	na1[c] + ocdcea[c] <=> na1[e] + ocdcea[e]	1	26457.1 or 26457.2	-1000	1000		Transport, Extracellular			
FATP3t	fatty acid electroneutral transport	na1[c] + octica[c] <=> na1[e] + octica[e]	1	26457.1 or 26457.2	-1000	1000		Transport, Extracellular			
FATP4t	fatty acid electroneutral transport	na1[c] + arachf[c] <=> na1[e] + arachf[e]	1	26459.1	-1000	1000		Transport, Extracellular			
FATP5t	fatty acid electroneutral transport	na1[c] + arachd[c] <=> na1[e] + arachd[e]	1	26459.1	-1000	1000		Transport, Extracellular			
FATP6t	fatty acid electroneutral transport	na1[c] + adrn[c] <=> na1[e] + adrn[e]	1	26458.1 or 26459.1	-1000	1000		Transport, Extracellular			
FATP7t	fatty acid electroneutral transport	na1[c] + crvnc[c] <=> na1[e] + crvnc[e]	1	26458.1 or 26459.1	-1000	1000		Transport, Extracellular			
FATP8t	fatty acid electroneutral transport	na1[c] + lgnc[c] <=> na1[e] + lgnc[e]	1	26458.1 or 26459.1	-1000	1000		Transport, Extracellular			
FATP9t	fatty acid electroneutral transport	na1[c] + nrvnc[c] <=> na1[e] + nrvnc[e]	1	26458.1 or 26459.1	-1000	1000		Transport, Extracellular			
FBA	fructose-bisphosphate aldolase	fdp[c] <=> dhap[c] + g3p[c]	1	230163.1 or 11674.1 or 11674.3 or 11674.2 or 11676.1	-1000	1000		Glycolysis/Gluconeogenesis			
FBA2	D-Fructose 1-phosphate D-glyceraldehyde-3-phosphate-lyase	f1p[c] <=> dhap[c] + glyald[c]	1	230163.1 or 11674.1 or 11674.3 or 11674.2 or 11676.1	-1000	1000		Fructose and Mannose Metabolism			
FBA4	D-Fructose 1-phosphate D-glyceraldehyde-3-phosphate-lyase	xu1p-DE[c] <=> dhap[c] + gcald[c]	1	230163.1 or 11674.1 or 11674.3 or 11674.2 or 11676.1	-1000	1000		Glyoxylate and Dicarboxylate Metabolism			
FBA5	D-Tagatose 1-phosphate D-glyceraldehyde-3-phosphate-lyase	tag1p-DE[c] <=> dhap[c] + glyald[c]	1	230163.1	-1000	1000		Galactose metabolism			
FBP	fructose-bisphosphatase	h2o[c] + fdp[c] -> pi[c] + f6p[c]	0	14120.1 or 14121.1	0	1000		Glycolysis/Gluconeogenesis			
FBP26	Fructose-2,6-bisphosphate 2-phosphatase	h2o[c] + f26bp[c] -> pi[c] + f6p[c]	0	14120.1 or 18639.1 or 18640.1 or 14121.1 or 270198.1 or 170768.1	0	1000		Fructose and Mannose Metabolism			
FCLTm	Ferrochelatase, mitochondrial	fe2[m] + ppp9[m] -> 2 h[m] + pheme[m]	0	14151.1 or 14151.2	0	1000		Heme Biosynthesis			
FCOAH	formyl coa hydrolase	h2o[c] + formcoa[c] -> 5 h[c] + coa[c] + for[c]	0		0	1000		Fatty Acid Metabolism			
FDH	formate dehydrogenase	nad[c] + for[c] -> nadh[c] + co2[c]	0	107747.1	0	1000		Fatty Acid Metabolism			
FE2t	iron (II) transport	fe2[e] -> fe2[c]	0		0	1000		Transport, Extracellular			
FE2tm	iron (II) transport	h[c] + fe2[c] -> h[m] + fe2[m]	0		0	1000		Transport, Mitochondrial			
FE3R2e	Fe(III) reduction (ascorbate)	asch-L[e] + 2 fe3[e] -> 2 h[e] + dhdascb[e] + 2 fe2[e]	0	73649.1	0	1000		Heme Biosynthesis			
FK	Fucokinase	atp[c] + fuc-L[c] -> adp[c] + h[c] + fuc1p-L[c]	0	234730.1	0	1000		Fructose and Mannose Metabolism			
FKYNH	N-Formyl-L-kynurenine amidohydrolase	h2o[c] + L4mkynr[c] -> h[c] + for[c] + L4kynr[c]	0		0	1000		Tryptophan metabolism			
FMNAT	FMN adenylyltransferase	atp[c] + h[c] + fmn[c] -> ppi[c] + fad[c]	0	319945.1 or 319945.2	0	1000		Riboflavin Metabolism			
FOLR2	folate reductase	nadph[c] + fol[c] -> nadp[c] + dhf[c]	0	13361.1	0	1000		Folate Metabolism			
FOLTDIn	folate uptake into the enterocytes	fol[u] -> fol[c]	0		0	1000	2	Transport, Lumen	G.F.M. Ball (2006) Vitamins their role in the human body, Blackwell publishing, chapter 17, page 353.	uptake by diffusion.	
FOLTIu	folate uptake into the enterocytes	h[u] + fol[u] -> h[c] + fol[c]	0	52466.1	0	1000	3	Transport, Lumen	G.F.M. Ball (2006) Vitamins their role in the human body, Blackwell publishing, chapter 17, page 353, PMID: 19762432 .	carrier protein-mediated, H+ symport. Mutations in this gene is associated with hereditary folate mal-absorption syndrome (IEM) (PMID: 19762432) .	
FOLt2	folate transport via anion exchange	ohl[c] + fol[e] <=> ohl[e] + fol[c]	1	20509.1 or 20509.2	-1000	1000		Transport, Extracellular			
FORMCOAtx	formyl coa transport	formcoa[x] <=> formcoa[c]	1		-1000	1000		Transport, Peroxisomal			
FORt2m	formate mitochondrial transport	for[m] <=> for[c]	1		-1000	1000		Transport, Mitochondrial			
FORtr	FOR transporter, endoplasmic reticulum	for[c] <=> for[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
FORtrn	Formate transport, nuclear	for[c] <=> for[n]	1		-1000	1000		Transport, Nuclear			
FPGS	folylpolyglutamate synthetase	4 atp[c] + 4 glu-L[c] + thf[c] -> 4 adp[c] + 4 h[c] + 4 pi[c] + 5dhf[c]	0	14287.1	0	1000		Folate Metabolism			
FPGS2	folylpolyglutamate synthetase	atp[c] + glu-L[c] + 5dhf[c] -> adp[c] + h[c] + pi[c] + 6dhf[c]	0	14287.1	0	1000		Folate Metabolism			
FPGS2m	folylpolyglutamate synthetase, mitochondrial	glu-L[m] + 5dhf[m] + atp[m] -> h[m] + 6dhf[m] + adp[m] + pi[m]	0	14287.1	0	1000		Folate Metabolism			
FPGS3	folylpolyglutamate synthetase	atp[c] + glu-L[c] + 6dhf[c] -> adp[c] + h[c] + pi[c] + 7dhf[c]	0	14287.1	0	1000		Folate Metabolism			
FPGS3m	folylpolyglutamate synthetase, mitochondrial	glu-L[m] + 6dhf[m] + atp[m] -> h[m] + 7thf[m] + adp[m] + pi[m]	0	14287.1	0	1000		Folate Metabolism			
FPGS4	folylpolyglutamate synthetase (DHF)	4 atp[c] + 4 glu-L[c] + dhf[c] -> 4 adp[c] + 4 h[c] + 4 pi[c] + 5dhf[c]	0	14287.1	0	1000		Folate Metabolism			
FPGS4m	folylpolyglutamate synthetase (DHF), mitochondrial	4 glu-L[m] + 4 atp[m] + dhf[m] -> 4 h[m] + 4 adp[m] + 4 pi[m] + 5dhf[m]	0	14287.1	0	1000		Folate Metabolism			
FPGS5	folylpolyglutamate synthetase (DHF)	atp[c] + glu-L[c] + 5dhf[c] -> adp[c] + h[c] + pi[c] + 6dhf[c]	0	14287.1	0	1000		Folate Metabolism			
FPGS5m	folylpolyglutamate synthetase (DHF), mitochondrial	glu-L[m] + atp[m] + 5dhf[m] -> h[m] + 6dhf[m] + adp[m] + pi[m]	0	14287.1	0	1000		Folate Metabolism			
FPGS6	folylpolyglutamate synthetase (DHF)	atp[c] + glu-L[c] + 6dhf[c] -> adp[c] + h[c] + pi[c] + 7dhf[c]	0	14287.1	0	1000		Folate Metabolism			
FPGS6m	folylpolyglutamate synthetase (DHF), mitochondrial	glu-L[m] + 6dhf[m] + atp[m] -> h[m] + 7dhf[m] + adp[m] + pi[m]	0	14287.1	0	1000		Folate Metabolism			
FPGS7	folylpolyglutamate synthetase (10thf)	10thf[c] + 4 atp[c] + 4 glu-L[c] -> 10thf5glu[c] + 4 adp[c] + 4 h[c] + 4 pi[c]	0	14287.1	0	1000		Folate Metabolism			
FPGS7m	folylpolyglutamate synthetase (10thf), mitochondrial	10thf[m] + 4 glu-L[m] + 4 atp[m] -> 10thf5glu[m] + 4 h[m] + 4 adp[m] + 4 pi[m]	0	14287.1	0	1000		Folate Metabolism			
FPGS8	folylpolyglutamate synthetase (10thf)	10thf5glu[c] + atp[c] + glu-L[c] -> 10thf6glu[c] + adp[c] + h[c] + pi[c]	0	14287.1	0	1000		Folate Metabolism			
FPGS8m	folylpolyglutamate synthetase (10thf), mitochondrial	10thf5glu[m] + atp[m] + glu-L[m] + atp[m] -> 10thf6glu[m] + h[m] + adp[m] + pi[m]	0	14287.1	0	1000		Folate Metabolism			
FPGS9	folylpolyglutamate synthetase (10thf)	10thf6glu[c] + atp[c] + glu-L[c] -> 10thf7glu[c] + adp[c] + h[c] + pi[c]	0	14287.1	0	1000		Folate Metabolism			
FPGS9m	folylpolyglutamate synthetase (10thf), mitochondrial	10thf6glu[m] + glu-L[m] + atp[m] -> 10thf7glu[m] + h[m] + adp[m] + pi[m]	0	14287.1	0	1000		Folate Metabolism			

FPGSm	folylpolyglutamate synthetase, mitochondrial	4 glu-L[m] + 4 atp[m] + thf[m] -> 4 h[m] + 5thf[m] + 4 adp[m] + 4 pi[m]	0	14287.1	0	1000		Folate Metabolism			
FRDPtc	lipid, flip-flop intracellular transport	frdp[x] <=> frdp[c]	1		-1000	1000		Transport, Peroxisomal			
FRDPtr	lipid, flip-flop intracellular transport	frdp[x] <=> frdp[r]	1		-1000	1000		Transport, Peroxisomal			
FRTT	farnesyltranstransferase	ipdp[c] + frdp[c] -> ppi[c] + ggdp[c]	0	14593.1	0	1000		Cholesterol Metabolism			
FRUt4	D-fructose transport via sodium cotransport	na1[e] + fru[e] <=> na1[c] + fru[c]	1	230612.1	-1000	1000		Transport, Extracellular			
FT	farnesyltranstransferase (trans,trans,cis-geranylgeranyl diphosphate-generating)	ipdp[c] + frdp[c] -> ppi[c] + ttc-ggdp[c]	0		0	1000		N-Glycan Biosynthesis			
FTCD	formimidoyltransferase cyclodeaminase	2 h[c] + 5forthf[c] -> nh4[c] + methf[c]	0	14317.1 or 14317.2	0	1000		Folate Metabolism			
FTHFCL	5-formethyltetrahydrofolate cyclo-ligase	atp[c] + 5fthf[c] -> adp[c] + pi[c] + methf[c]	0	107885.1	0	1000		Folate Metabolism			
FTHFDH	formyltetrahydrofolate dehydrogenase	10fthf[c] + h2o[c] + nadp[c] -> h[c] + nadph[c] + co2[c] + thf[c]	0	107747.1	0	1000		Folate Metabolism			
FTHFL	formate-tetrahydrofolate ligase	atp[c] + thf[c] + for[c] <=> 10fthf[c] + adp[c] + pi[c]	1	108156.1	0	1000		Folate Metabolism			
FTHFLm	formate-tetrahydrofolate ligase, mitochondrial	atp[m] + for[m] + thf[m] <=> 10fthf[m] + adp[m] + pi[m]	1	270685.1	0	1000		Folate Metabolism			
FUC13GALACGLCGAL14ACGLCGALGLUSIDEte	blood group intracellular transport	fuc13galacglcgal14acglcgalgluside_hs[e] <=> fuc13galacglcgal14acglcgalgluside_hs[c]	1		-1000	1000		Transport, Extracellular			
FUC13GALACGLCGAL14ACGLCGALGLUSIDEtg	blood group intracellular transport	fuc13galacglcgal14acglcgalgluside_hs[g] <=> fuc13galacglcgal14acglcgalgluside_hs[c]	1		-1000	1000		Transport, Golgi Apparatus			
FUC14GALACGLCGALGLUSIDEte	blood group intracellular transport	fuc14galacglcgalgluside_hs[e] <=> fuc14galacglcgalgluside_hs[c]	1		-1000	1000		Transport, Extracellular			
FUC14GALACGLCGALGLUSIDEtg	blood group intracellular transport	fuc14galacglcgalgluside_hs[g] <=> fuc14galacglcgalgluside_hs[c]	1		-1000	1000		Transport, Golgi Apparatus			
FUCACGALFUCGALACGLCGALGLUSIDEte	blood group intracellular transport	fucacgalfucgalacglcgalgluside_hs[e] <=> fucacgalfucgalacglcgalgluside_hs[c]	1		-1000	1000		Transport, Extracellular			
FUCACGALFUCGALACGLCGALGLUSIDEtg	blood group intracellular transport	fucacgalfucgalacglcgalgluside_hs[g] <=> fucacgalfucgalacglcgalgluside_hs[c]	1		-1000	1000		Transport, Golgi Apparatus			
FUCACNGAL14ACGLCGALGLUSIDEte	blood group intracellular transport	fucacngal14acglcgalgluside_hs[e] <=> fucacngal14acglcgalgluside_hs[c]	1		-1000	1000		Transport, Extracellular			
FUCACNGAL14ACGLCGALGLUSIDEtg	blood group intracellular transport	fucacngal14acglcgalgluside_hs[g] <=> fucacngal14acglcgalgluside_hs[c]	1		-1000	1000		Transport, Golgi Apparatus			
FUCACNGALACGLCGALGLUSIDEte	blood group intracellular transport	fucacngalacglcgalgluside_hs[e] <=> fucacngalacglcgalgluside_hs[c]	1		-1000	1000		Transport, Extracellular			
FUCACNGALACGLCGALGLUSIDEtg	blood group intracellular transport	fucacngalacglcgalgluside_hs[g] <=> fucacngalacglcgalgluside_hs[c]	1		-1000	1000		Transport, Golgi Apparatus			
FUCASE2e	alpha-fucosidase, extracellular	h2o[e] + ksi[e] -> fuc-L[e] + ksi_deg1[e]	0	66848.1	0	1000		Keratan sulfate degradation			
FUCASE2ly	alpha-fucosidase, lysosomal	h2o[l] + ksi[l] -> fuc-L[l] + ksi_deg1[l]	0	71665.1	0	1000		Keratan sulfate degradation			
FUCASEe	alpha-fucosidase, extracellular	h2o[e] + s2l2fn2m2masn[e] -> fuc-L[e] + s2l2n2m2masn[e]	0	66848.1	0	1000		N-Glycan Degradation			
FUCASEly	alpha-fucosidase, lysosomal	h2o[l] + s2l2fn2m2masn[l] -> fuc-L[l] + s2l2n2m2masn[l]	0	71665.1	0	1000		N-Glycan Degradation			
FUCFUC12GAL14ACGLCGALGLUSIDEte	blood group intracellular transport	fucfuc12gal14acglcgalgluside_hs[e] <=> fucfuc12gal14acglcgalgluside_hs[c]	1		-1000	1000		Transport, Extracellular			
FUCFUC12GAL14ACGLCGALGLUSIDEtg	blood group intracellular transport	fucfuc12gal14acglcgalgluside_hs[g] <=> fucfuc12gal14acglcgalgluside_hs[c]	1		-1000	1000		Transport, Golgi Apparatus			
FUCFUC132GALACGLCGAL14ACGLCGALGLUSIDEte	blood group intracellular transport	fucfuc132galacglcgal14acglcgalgluside_hs[e] <=> fucfuc132galacglcgal14acglcgalgluside_hs[c]	1		-1000	1000		Transport, Extracellular			
FUCFUC132GALACGLCGAL14ACGLCGALGLUSIDEtg	blood group intracellular transport	fucfuc132galacglcgal14acglcgalgluside_hs[g] <=> fucfuc132galacglcgal14acglcgalgluside_hs[c]	1		-1000	1000		Transport, Golgi Apparatus			
FUCFUCFUCGALACGLC13GALACGLCGAL14ACGLCGALGLUSIDEte	blood group intracellular transport	fucfucfucgalacglc13galacglcgal14acglcgalgluside_hs[e] <=> fucfucfucgalacglc13galacglcgal14acglcgalgluside_hs[c]	1		-1000	1000		Transport, Extracellular			
FUCFUCFUCGALACGLC13GALACGLCGAL14ACGLCGALGLUSIDEtg	blood group intracellular transport	fucfucfucgalacglc13galacglcgal14acglcgalgluside_hs[g] <=> fucfucfucgalacglc13galacglcgal14acglcgalgluside_hs[c]	1		-1000	1000		Transport, Golgi Apparatus			
FUCFUCFUCGALACGLCGAL14ACGLCGALGLUSIDEte	blood group intracellular transport	fucfucfucgalacglcgal14acglcgalgluside_hs[e] <=> fucfucfucgalacglcgal14acglcgalgluside_hs[c]	1		-1000	1000		Transport, Extracellular			
FUCFUCFUCGALACGLCGAL14ACGLCGALGLUSIDEtg	blood group intracellular transport	fucfucfucgalacglcgal14acglcgalgluside_hs[g] <=> fucfucfucgalacglcgal14acglcgalgluside_hs[c]	1		-1000	1000		Transport, Golgi Apparatus			
FUCFUCGALACGLCGALGLUSIDEte	blood group intracellular transport	fucfucgalacglcgalgluside_hs[e] <=> fucfucgalacglcgalgluside_hs[c]	1		-1000	1000		Transport, Extracellular			
FUCFUCGALACGLCGALGLUSIDEtg	blood group intracellular transport	fucfucgalacglcgalgluside_hs[g] <=> fucfucgalacglcgalgluside_hs[c]	1		-1000	1000		Transport, Golgi Apparatus			
FUCGAL14ACGLCGALGLUSIDEte	blood group intracellular transport	fucgal14acglcgalgluside_hs[e] <=> fucgal14acglcgalgluside_hs[c]	1		-1000	1000		Transport, Extracellular			
FUCGAL14ACGLCGALGLUSIDEtg	blood group intracellular transport	fucgal14acglcgalgluside_hs[g] <=> fucgal14acglcgalgluside_hs[c]	1		-1000	1000		Transport, Golgi Apparatus			
FUCGALFUCGALACGLCGALGLUSIDEte	blood group intracellular transport	fucgalfucgalacglcgalgluside_hs[e] <=> fucgalfucgalacglcgalgluside_hs[c]	1		-1000	1000		Transport, Extracellular			
FUCGALFUCGALACGLCGALGLUSIDEtg	blood group intracellular transport	fucgalfucgalacglcgalgluside_hs[g] <=> fucgalfucgalacglcgalgluside_hs[c]	1		-1000	1000		Transport, Golgi Apparatus			
FUCGALGBSIDEte	fucgalgbside_hs transport	fucgalgbside_hs[c] <=> fucgalgbside_hs[e]	1		-1000	1000		Transport, Extracellular			
FUCGALGBSIDEtg	fucgalgbside_hs intracellular transport	fucgalgbside_hs[c] <=> fucgalgbside_hs[g]	1		-1000	1000		Transport, Golgi Apparatus			
FUCtly	L-fucose efflux from lysosome	fuc-L[l] -> fuc-L[c]	0		0	1000		Transport, Lysosomal			
FUM	fumarase	h2o[c] + fum[c] <=> mal-L[c]	1	14194.1	-1000	1000		Citric Acid Cycle			
FUMAC	fumarylacetoacetase	h2o[c] + 4fumacac[c] -> h[c] + acac[c] + fum[c]	0	14085.1	0	1000		Tyrosine metabolism			
FUMSO3tm	Fumarate:sulfite antiport, mitochondrial	so3[m] + fum[c] <=> so3[c] + fum[m]	1	27376.1	-1000	1000		Transport, Mitochondrial			
FUMSO4tm	Fumarate:sulfate antiport, mitochondrial	fum[c] + so4[m] <=> fum[m] + so4[c]	1	27376.1	-1000	1000		Transport, Mitochondrial			
FUMTSULtm	Fumarate:thiosulfate antiport, mitochondrial	fum[c] + tsul[m] <=> fum[m] + tsul[c]	1	27376.1	-1000	1000		Transport, Mitochondrial			
FUMm	fumarase, mitochondrial	h2o[m] + fum[m] <=> mal-L[m]	1	14194.1	-1000	1000		Citric Acid Cycle			
FUMtm	fumarate transport, mitochondrial	pi[m] + fum[c] <=> pi[c] + fum[m]	1	27376.1	-1000	1000		Transport, Mitochondrial			
FUT11g	Galactoside 2-alpha-L-fucosyltransferase 1	galgbside_hs[g] + gdpfuc[g] -> h[g] + gdp[g] + fucgalgbside_hs[g]	0	14343.1	0	1000		Sphingolipid Metabolism			
FUT12g	Galactoside 2-alpha-L-fucosyltransferase 1	galacglcgalgluside_hs[g] + gdpfuc[g] -> h[g] + gdp[g] + fucgalacglcgalgluside_hs[g]	0	14343.1	0	1000		Blood Group Biosynthesis			
FUT14g	Galactoside 2-alpha-L-fucosyltransferase 1	gal14acglcgalgluside_hs[g] + gdpfuc[g] -> h[g] + gdp[g] + fuc12gal14acglcgalgluside_hs[g]	0	14343.1	0	1000		Blood Group Biosynthesis			
FUT15g	Galactoside 2-alpha-L-fucosyltransferase 1	galacgalfuc12gal14acglcgalgluside_hs[g] + gdpfuc[g] -> h[g] + gdp[g] + fucgalacgalfuc12gal14acglcgalgluside_hs[g]	0	14343.1	0	1000		Blood Group Biosynthesis			
FUT16g	Galactoside 2-alpha-L-fucosyltransferase 1	galacglcgal14acglcgalgluside_hs[g] + gdpfuc[g] -> h[g] + gdp[g] + fucgalacglcgal14acglcgalgluside_hs[g]	0	14343.1	0	1000		Blood Group Biosynthesis			
FUT17g	Galactoside 2-alpha-L-fucosyltransferase 1	galacgalfucgalacglcgal14acglcgalgluside_hs[g] + gdpfuc[g] -> h[g] + gdp[g] + fucgalacgalfucgalacglcgal14acglcgalgluside_hs[g]	0	14343.1	0	1000		Blood Group Biosynthesis			
FUT18g	Galactoside 2-alpha-L-fucosyltransferase 1	galacglcgalacglcgal14acglcgalgluside_hs[g] + 2 gdpfuc[g] -> 2 h[g] + 2 gdp[g] + fucfucgalacglcgalacglcgal14acglcgalgluside_hs[g]	0	14343.1	0	1000		Blood Group Biosynthesis			
FUT910g	Alpha-(1,3)-fucosyltransferase	gdpfuc[g] + fucgalacglc13galacglcgal14acglcgalgluside_hs[g] -> h[g] + gdp[g] + fucfucgalacglc13galacglcgal14acglcgalgluside_hs[g]	0	14348.1	0	1000		Blood Group Biosynthesis			
FUT911g	Alpha-(1,3)-fucosyltransferase	gdpfuc[g] + fucfucgalacglc13galacglcgal14acglcgalgluside_hs[g] -> h[g] + gdp[g] + fucfucfucgalacglc13galacglcgal14acglcgalgluside_hs[g]	0	14348.1	0	1000		Blood Group Biosynthesis			
FUT91g	Alpha-(1,3)-fucosyltransferase	gal14acglcgalgluside_hs[g] + gdpfuc[g] -> h[g] + gdp[g] + fucgal14acglcgalgluside_hs[g]	0	14348.1	0	1000		Blood Group Biosynthesis			
FUT92g	Alpha-(1,3)-fucosyltransferase	gdpfuc[g] + acngal14acglcgalgluside_hs[g] -> h[g] + gdp[g] + fucacngal14acglcgalgluside_hs[g]	0	14348.1	0	1000		Blood Group Biosynthesis			
FUT93g	Alpha-(1,3)-fucosyltransferase	gdpfuc[g] + fuc12gal14acglcgalgluside_hs[g] -> h[g] + gdp[g] + fucfuc12gal14acglcgalgluside_hs[g]	0	14348.1	0	1000		Blood Group Biosynthesis			
FUT94g	Alpha-(1,3)-fucosyltransferase	gdpfuc[g] + fucgalacglcgal14acglcgalgluside_hs[g] -> h[g] + gdp[g] + fucfucgalacglcgal14acglcgalgluside_hs[g]	0	14348.1	0	1000		Blood Group Biosynthesis			
FUT95g	Alpha-(1,3)-fucosyltransferase	gdpfuc[g] + fucfucgalacglcgal14acglcgalgluside_hs[g] -> h[g] + gdp[g] + fucfucfucgalacglcgal14acglcgalgluside_hs[g]	0	14348.1	0	1000		Blood Group Biosynthesis			
FUT96g	Alpha-(1,3)-fucosyltransferase	galacglcgal14acglcgalgluside_hs[g] + gdpfuc[g] -> h[g] + gdp[g] + fuc132galacglcgal14acglcgalgluside_hs[g]	0	14348.1	0	1000		Blood Group Biosynthesis			
FUT97g	Alpha-(1,3)-fucosyltransferase	gdpfuc[g] + fuc132galacglcgal14acglcgalgluside_hs[g] -> h[g] + gdp[g] + fucfuc132galacglcgal14acglcgalgluside_hs[g]	0	14348.1	0	1000		Blood Group Biosynthesis			
FUT98g	Alpha-(1,3)-fucosyltransferase	galacglcgal14acglcgalgluside_hs[g] + gdpfuc[g] -> h[g] + gdp[g] + fuc13galacglcgal14acglcgalgluside_hs[g]	0	14348.1	0	1000		Blood Group Biosynthesis			
FUT99g	Alpha-(1,3)-fucosyltransferase	galacglc13galacglcgal14acglcgalgluside_hs[g] + gdpfuc[g] -> h[g] + gdp[g] + fucgalacglc13galacglcgal14acglcgalgluside_hs[g]	0	14348.1	0	1000		Blood Group Biosynthesis			
G12MT1_L	Glycolipid 1,2-alpha-D-mannosyltransferase (liver)	gdpmann[c] + 0.1 m2mpdol_L[c] -> h[c] + gdp[c] + 0.1 m3mpdol_L[c]	0		0	1000		N-Glycan Biosynthesis			
G12MT1_U	Glycolipid 1,2-alpha-D-mannosyltransferase (uterus)	gdpmann[c] + 0.1 m2mpdol_U[c] -> h[c] + gdp[c] + 0.1 m3mpdol_U[c]	0		0	1000		N-Glycan Biosynthesis			
G12MT2_L	Glycolipid 1,2-alpha-D-mannosyltransferase (liver)	gdpmann[c] + 0.1 m3mpdol_L[c] -> h[c] + gdp[c] + 0.1 m4mpdol_L[c]	0		0	1000		N-Glycan Biosynthesis			
G12MT2_U	Glycolipid 1,2-alpha-D-mannosyltransferase (uterus)	gdpmann[c] + 0.1 m3mpdol_U[c] -> h[c] + gdp[c] + 0.1 m4mpdol_U[c]	0		0	1000		N-Glycan Biosynthesis			
G13MT_L	Glycolipid 1,3-alpha-D-mannosyltransferase (liver)	gdpmann[c] + 0.1 mpdol_L[c] -> h[c] + gdp[c] + 0.1 m1mpdol_L[c]	0	56737.1 or 56737.2	0	1000		N-Glycan Biosynthesis			
G13MT_U	Glycolipid 1,3-alpha-D-mannosyltransferase (uterus)	gdpmann[c] + 0.1 mpdol_U[c] -> h[c] + gdp[c] + 0.1 m1mpdol_U[c]	0	56737.1 or 56737.2	0	1000		N-Glycan Biosynthesis			
G14T10g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	udpgal[g] + ksi_pre14[g] -> h[g] + udp[g] + ksi_pre15[g]	0	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	0	1000		Keratan sulfate biosynthesis			
G14T11g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	udpgal[g] + ksi_pre17[g] -> h[g] + udp[g] + ksi_pre18[g]	0	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	0	1000		Keratan sulfate biosynthesis			
G14T12g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	udpgal[g] + ksi_pre20[g] -> h[g] + udp[g] + ksi_pre21[g]	0	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	0	1000		Keratan sulfate biosynthesis			
G14T13g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	udpgal[g] + ksi_pre23[g] -> h[g] + udp[g] + ksi_pre24[g]	0	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	0	1000		Keratan sulfate biosynthesis			
G14T14g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	udpgal[g] + ksi_pre26[g] -> h[g] + udp[g] + ksi_pre27[g]	0	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	0	1000		Keratan sulfate biosynthesis			
G14T15g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	udpgal[g] + ksi_pre29[g] -> h[g] + udp[g] + ksi_pre30[g]	0	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	0	1000		Keratan sulfate biosynthesis			
G14T16g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	udpgal[g] + ksi_pre32[g] -> h[g] + udp[g] + ksi_pre33[g]	0	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	0	1000		Keratan sulfate biosynthesis			
G14T17g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	udpgal[g] + ksi_pre35[g] -> h[g] + udp[g] + ksi_pre36[g]	0	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	0	1000		Keratan sulfate biosynthesis			
G14T18g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	2 udpgal[g] + core4[g] -> 2 h[g] + 2 udp[g] + ksii_core4_pre1[g]	0	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	0	1000		Keratan sulfate biosynthesis			
G14T19g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	udpgal[g] + ksii_core4_pre3[g] -> h[g] + udp[g] + ksii_core4_pre4[g]	0	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	0	1000		Keratan sulfate biosynthesis			

G14T20g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	udpgal[g] + ksii_core4_pre6[g] -> h[g] + udp[g] + ksii_core4_pre7[g]	0	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	0	1000		Keratan sulfate biosynthesis			
G14T21g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	udpgal[g] + ksii_core4_pre9[g] -> h[g] + udp[g] + ksii_core4_pre10[g]	0	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	0	1000		Keratan sulfate biosynthesis			
G14T2g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	udpgal[g] + ksii_core2_pre1[g] -> h[g] + udp[g] + ksii_core2_pre2[g]	0	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	0	1000		Keratan sulfate biosynthesis			
G14T3g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	udpgal[g] + ksii_core2_pre3[g] -> h[g] + udp[g] + ksii_core2_pre4[g]	0	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	0	1000		Keratan sulfate biosynthesis			
G14T4g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	udpgal[g] + ksii_core2_pre6[g] -> h[g] + udp[g] + ksii_core2_pre7[g]	0	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	0	1000		Keratan sulfate biosynthesis			
G14T5g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	udpgal[g] + ksii_core2_pre9[g] -> h[g] + udp[g] + ksii_core2_pre10[g]	0	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	0	1000		Keratan sulfate biosynthesis			
G14T6g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	udpgal[g] + ksi_pre2[g] -> h[g] + udp[g] + ksi_pre3[g]	0	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	0	1000		Keratan sulfate biosynthesis			
G14T7g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	udpgal[g] + ksi_pre5[g] -> h[g] + udp[g] + ksi_pre6[g]	0	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	0	1000		Keratan sulfate biosynthesis			
G14T8g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	udpgal[g] + ksi_pre8[g] -> h[g] + udp[g] + ksi_pre9[g]	0	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	0	1000		Keratan sulfate biosynthesis			
G14T9g	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase, Golgi	udpgal[g] + ksi_pre11[g] -> h[g] + udp[g] + ksi_pre12[g]	0	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	0	1000		Keratan sulfate biosynthesis			
G14Tg	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase	2 udpgal[g] + fn2m2masn[g] -> 2 h[g] + 2 udp[g] + l2fn2m2masn[g]	0	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	0	1000		N-Glycan Biosynthesis			
G16MT_L	Glycolipid 1,6-alpha-D-mannosyltransferase (liver)	gdpmann[c] + 0.1 m1mpdol_L[c] -> h[c] + gdp[c] + 0.1 m2mpdol_L[c]	0		0	1000		N-Glycan Biosynthesis			
G16MT_U	Glycolipid 1,6-alpha-D-mannosyltransferase (uterus)	gdpmann[c] + 0.1 m1mpdol_U[c] -> h[c] + gdp[c] + 0.1 m2mpdol_U[c]	0		0	1000		N-Glycan Biosynthesis			
G1M6MASNB1terg	g1m6masnB1 endoplasmic reticulum to Golgi transport	g1m6masnB1[r] -> g1m6masnB1[g]	0		0	1000		N-Glycan Biosynthesis			
G1M7MASNBterg	g1m7masnC endoplasmic reticulum to Golgi transport	g1m7masnB[r] -> g1m7masnB[g]	0		0	1000		N-Glycan Biosynthesis			
G1M7MASNCterg	g1m7masnC endoplasmic reticulum to Golgi transport	g1m7masnC[r] -> g1m7masnC[g]	0		0	1000		N-Glycan Biosynthesis			
G1M8MASNterg	g1m8masn transport from endoplasmic reticulum to Golgi apparatus	g1m8masn[r] -> g1m8masn[g]	0		0	1000		N-Glycan Biosynthesis			
G1PTT	glucose-1-phosphate thymidylyltransferase	h[c] + g1p[c] + dttp[c] -> ppi[c] + dtdpglu[c]	0		0	1000		Nucleotide Sugar Metabolism			
G2M8MASNterg	g2m8masn transport from endoplasmic reticulum to Golgi apparatus	g2m8masn[r] -> g2m8masn[g]	0		0	1000		N-Glycan Biosynthesis			
G3M8MASNterg	g3m8masn transport from endoplasmic reticulum to Golgi apparatus	g3m8masn[r] -> g3m8masn[g]	0		0	1000		N-Glycan Biosynthesis			
G3PD1	glycerol-3-phosphate dehydrogenase (NAD)	nad[c] + glyc3p[c] <=> h[c] + nadh[c] + dhap[c]	1	14555.1	-1000	1000		Glycerophospholipid Metabolism			
G3PD2m	glycerol-3-phosphate dehydrogenase (FAD), mitochondrial	fad[m] + glyc3p[c] -> fadh2[m] + dhap[c]	0	14571.1	0	1000		Glycolysis/Gluconeogenesis			
G5SADrm	L-glutamate 5-semialdehyde dehydratase, reversible, mitochondrial	glu5sa[m] <=> h[m] + h2o[m] + 1pyr5c[m]	1		-1000	1000		Arginine and Proline Metabolism			
G5SADs	L-glutamate 5-semialdehyde dehydratase (spontaneous)	glu5sa[c] -> h2o[c] + h[c] + 1pyr5c[c]	0		0	1000		Urea cycle/amino group metabolism			
G5SDym	glutamate-5-semialdehyde dehydrogenase (m)	h[m] + nadph[m] + glu5p[m] -> nadp[m] + pi[m] + glu5sa[m]	0	56454.1	0	1000		Urea cycle/amino group metabolism			
G6PDA	glucosamine-6-phosphate deaminase	h2o[c] + gam6p[c] -> nh4[c] + f6p[c]	0	67980.1 or 26384.1	0	1000		Aminosugar Metabolism			
G6PDH1er	glucose-6-phosphate dehydrogenase, endoplasmic reticulum	nad[r] + g6p[r] -> h[r] + nadh[r] + 6pgl[r]	0	100198.1	0	1000		Pentose Phosphate Pathway			
G6PDH1rer	glucose-6-phosphate dehydrogenase, endoplasmic reticulum	nad[r] + g6p[r] <=> h[r] + nadh[r] + 6pgl[r]	1	100198.1	-1000	1000		Pentose Phosphate Pathway			
G6PDH2r	glucose 6-phosphate dehydrogenase	nadp[c] + g6p[c] <=> h[c] + nadph[c] + 6pgl[c]	1	14381.1	-1000	1000		Pentose Phosphate Pathway			
G6PDH2rer	glucose 6-phosphate dehydrogenase, endoplasmic reticulum	nadp[r] + g6p[r] <=> h[r] + nadph[r] + 6pgl[r]	1	100198.1	-1000	1000		Pentose Phosphate Pathway			
G6PPer	glucose-6-phosphate phosphatase, edoplasmic reticular	h2o[r] + g6p[r] -> glc-D[r] + pi[r]	0	14378.1 or 14377.1 or 68401.1	0	1000		Glycolysis/Gluconeogenesis			
G6Pter	glucose 6-phosphate endoplasmic reticular transport via diffusion	g6p[c] <=> g6p[r]	1	14385.1	-1000	1000		Transport, Endoplasmic Reticular			
GABAPAT1tc	transport of GABA by PAT1 in renal and intestinal cells	h[u] + 4abut[u] -> h[c] + 4abut[c]	0	215335.1	0	1000	3	Transport, Lumen	PMID: 17123464, PMID: 18400692, PMCID: PMC34647, PMID: 15345686, PMID: 18195088	PAT1 proton-amino acid co-transporter with 1:1 stoichiometry, does not discriminate between L and D isomers, located on the apical membrane of kidney and intestine (PMID: 18400692, PMID: 18195088).	
GABAVESSEC	GABA secretion via secretory vesicle (ATP driven)	h2o[c] + atp[c] + 3 4abut[c] -> adp[c] + h[c] + pi[c] + 3 4abut[e]	0	22348.1	0	1000		Transport, Extracellular			
GACMTRc	guanidinoacetate N-methyltransferase (c)	amet[c] + gudac[c] <=> h[c] + ahcys[c] + creat[c]	1	14431.1 or 14431.2	-1000	1000		Urea cycle/amino group metabolism			
GACPAILter	glucosaminyl-acylphosphatidylinositol ER flippase	gacpail_hs[c] -> gacpail_hs[r]	0		0	1000		Transport, Endoplasmic Reticular			
GAL3ST11	Galactosylceramide sulfotransferase	galside_hs[g] + paps[g] -> h[g] + pap[g] + sgalside_hs[g]	0	53897.1	0	1000		Sphingolipid Metabolism			
GAL3ST12	Galactosylceramide sulfotransferase	digalside_hs[g] + paps[g] -> h[g] + digalsgalside_hs[g] + pap[g]	0	53897.1	0	1000		Sphingolipid Metabolism			
GALACGLCGALGBSIDEte	galacglcgalgbside_hs transport	galacglcgalgbside_hs[c] <=> galacglcgalgbside_hs[e]	1		-1000	1000		Transport, Extracellular			
GALACGLCGALGBSIDEtg	galacglcgalgbside_hs intracellular transport	galacglcgalgbside_hs[c] <=> galacglcgalgbside_hs[g]	1		-1000	1000		Transport, Golgi Apparatus			
GALAMtr	Galactosamine import	galam[e] <=> galam[c]	1		-1000	1000	2	Transport, Extracellular	PMID: 15123798, PMID: 18180286	This metabolite is found in mucus and can serve as carbon source for intestinal microbes. Not sure if it is produced by human/ mouse or only imported through ingestion. Needed to provide this metabolite to the joint model.	
GALASE10ly	beta-galactosidase, lysosomal	h2o[l] + ksi_deg26[l] -> gal[l] + ksi_deg27[l]	0	50917.1 or 19025.1 or 12091.1 or 18010.1	0	1000		Keratan sulfate degradation			
GALASE11ly	beta-galactosidase, lysosomal	h2o[l] + ksi_deg29[l] -> gal[l] + ksi_deg30[l]	0	50917.1 or 19025.1 or 12091.1 or 18010.1	0	1000		Keratan sulfate degradation			
GALASE12ly	beta-galactosidase, lysosomal	h2o[l] + ksi_deg32[l] -> gal[l] + ksi_deg33[l]	0	50917.1 or 19025.1 or 12091.1 or 18010.1	0	1000		Keratan sulfate degradation			
GALASE13ly	beta-galactosidase, lysosomal	h2o[l] + ksi_deg35[l] -> gal[l] + ksi_deg36[l]	0	50917.1 or 19025.1 or 12091.1 or 18010.1	0	1000		Keratan sulfate degradation			
GALASE14ly	beta-galactosidase, lysosomal	h2o[l] + ksi_deg38[l] -> gal[l] + ksi_deg39[l]	0	50917.1 or 19025.1 or 12091.1 or 18010.1	0	1000		Keratan sulfate degradation			
GALASE15ly	beta-galactosidase, lysosomal	h2o[l] + ksi_deg40[l] -> gal[l] + ksi_deg41[l]	0	50917.1 or 19025.1 or 12091.1 or 18010.1	0	1000		Keratan sulfate degradation			
GALASE16ly	beta-galactosidase, lysosomal	2 h2o[l] + ksii_core2_deg2[l] -> 2 gal[l] + ksii_core2_deg3[l]	0	50917.1 or 19025.1 or 12091.1 or 18010.1	0	1000		Keratan sulfate degradation			
GALASE17ly	beta-galactosidase, lysosomal	h2o[l] + ksii_core2_deg5[l] -> gal[l] + ksii_core2_deg6[l]	0	50917.1 or 19025.1 or 12091.1 or 18010.1	0	1000		Keratan sulfate degradation			
GALASE18ly	beta-galactosidase, lysosomal	h2o[l] + ksii_core2_deg8[l] -> gal[l] + ksii_core2_deg9[l]	0	50917.1 or 19025.1 or 12091.1 or 18010.1	0	1000		Keratan sulfate degradation			
GALASE19ly	beta-galactosidase, lysosomal	h2o[l] + f1a[l] -> gal[l] + core6[l]	0	50917.1 or 19025.1 or 12091.1 or 18010.1	0	1000		Keratan sulfate degradation			
GALASE1ly	beta-galactosidase, lysosomal	2 h2o[l] + l2n2m2mn[l] -> n2m2mn[l] + 2 gal[l]	0	50917.1 or 19025.1 or 12091.1 or 18010.1	0	1000		N-Glycan Degradation			
GALASE20ly	beta-galactosidase, lysosomal	2 h2o[l] + ksii_core4_deg2[l] -> 2 gal[l] + ksii_core4_deg3[l]	0	50917.1 or 19025.1 or 12091.1 or 18010.1	0	1000		Keratan sulfate degradation			
GALASE3ly	beta-galactosidase, lysosomal	2 h2o[l] + ksi_deg5[l] -> 2 gal[l] + ksi_deg6[l]	0	50917.1 or 19025.1 or 12091.1 or 18010.1	0	1000		Keratan sulfate degradation			
GALASE4ly	beta-galactosidase, lysosomal	h2o[l] + ksi_deg8[l] -> gal[l] + ksi_deg9[l]	0	50917.1 or 19025.1 or 12091.1 or 18010.1	0	1000		Keratan sulfate degradation			
GALASE5ly	beta-galactosidase, lysosomal	h2o[l] + ksi_deg11[l] -> gal[l] + ksi_deg12[l]	0	50917.1 or 19025.1 or 12091.1 or 18010.1	0	1000		Keratan sulfate degradation			
GALASE6ly	beta-galactosidase, lysosomal	h2o[l] + ksi_deg14[l] -> gal[l] + ksi_deg15[l]	0	50917.1 or 19025.1 or 12091.1 or 18010.1	0	1000		Keratan sulfate degradation			
GALASE7ly	beta-galactosidase, lysosomal	h2o[l] + ksi_deg17[l] -> gal[l] + ksi_deg18[l]	0	50917.1 or 19025.1 or 12091.1 or 18010.1	0	1000		Keratan sulfate degradation			
GALASE8ly	beta-galactosidase, lysosomal	h2o[l] + ksi_deg20[l] -> gal[l] + ksi_deg21[l]	0	50917.1 or 19025.1 or 12091.1 or 18010.1	0	1000		Keratan sulfate degradation			
GALASE9ly	beta-galactosidase, lysosomal	h2o[l] + ksi_deg23[l] -> gal[l] + ksi_deg24[l]	0	50917.1 or 19025.1 or 12091.1 or 18010.1	0	1000		Keratan sulfate degradation			
GALC	Galactocerebrosidase	h2o[l] + galside_hs[l] -> crm_hs[l] + gal[l]	0	14420.1	0	1000		Sphingolipid Metabolism			
GALFUC12GAL14ACGLCGALGLUSIDEte	blood group intracellular transport	galfuc12gal14acglcgalgluside_hs[e] <=> galfuc12gal14acglcgalgluside_hs[c]	1		-1000	1000		Transport, Extracellular			
GALFUC12GAL14ACGLCGALGLUSIDEtg	blood group intracellular transport	galfuc12gal14acglcgalgluside_hs[g] <=> galfuc12gal14acglcgalgluside_hs[c]	1		-1000	1000		Transport, Golgi Apparatus			
GALFUCGALACGLCGAL14ACGLCGALGLUSIDEte	blood group intracellular transport	galfucgalacglcgal14acglcgalgluside_hs[e] <=> galfucgalacglcgal14acglcgalgluside_hs[c]	1		-1000	1000		Transport, Extracellular			
GALFUCGALACGLCGAL14ACGLCGALGLUSIDEtg	blood group intracellular transport	galfucgalacglcgal14acglcgalgluside_hs[g] <=> galfucgalacglcgal14acglcgalgluside_hs[c]	1		-1000	1000		Transport, Golgi Apparatus			
GALGALFUCFUCGALACGLCGALACGLCGAL14ACGLCGALGLUSIDEte	blood group intracellular transport	galgalfucfucgalacglcgalacglcgal14acglcgalgluside_hs[e] <=> galgalfucfucgalacglcgalacglcgal14acglcgalgluside_hs[c]	1		-1000	1000		Transport, Extracellular			
GALGALFUCFUCGALACGLCGALACGLCGAL14ACGLCGALGLUSIDEtg	blood group intracellular transport	galgalfucfucgalacglcgalacglcgal14acglcgalgluside_hs[g] <=> galgalfucfucgalacglcgalacglcgal14acglcgalgluside_hs[c]	1		-1000	1000		Transport, Golgi Apparatus			
GALGALGALTHCRMte	galgalgalthcrm_hs transport	galgalgalthcrm_hs[c] <=> galgalgalthcrm_hs[e]	1		-1000	1000		Transport, Extracellular			
GALGALGALTHCRMtg	galgalgalthcrm_hs intracellular transport	galgalgalthcrm_hs[c] <=> galgalgalthcrm_hs[g]	1		-1000	1000		Transport, Golgi Apparatus			
GALGLUSIDEtg	galgluside_hs intracellular transport	galgluside_hs[c] <=> galgluside_hs[g]	1		-1000	1000		Transport, Golgi Apparatus			
GALGLUSIDEtl	galgluside_hs intracellular transport	galgluside_hs[c] <=> galgluside_hs[l]	1		-1000	1000		Transport, Lysosomal			
GALGT1	Beta-1,4 N-acetylgalactosaminyltransferase	galgluside_hs[g] + udpacgal[g] -> h[g] + udp[g] + ga2_hs[g]	0	14421.1	0	1000		Sphingolipid Metabolism			
GALGT2	Beta-1,4 N-acetylgalactosaminyltransferase	udpacgal[g] + gm3_hs[g] -> h[g] + udp[g] + gm2_hs[g]	0	14421.1	0	1000		Sphingolipid Metabolism			
GALGT3	Beta-1,4 N-acetylgalactosaminyltransferase	udpacgal[g] + gd3_hs[g] -> h[g] + udp[g] + gd2_hs[g]	0	14421.1	0	1000		Sphingolipid Metabolism			
GALGT4	Beta-1,4 N-acetylgalactosaminyltransferase	udpacgal[g] + gt3_hs[g] -> h[g] + udp[g] + gt2_hs[g]	0	14421.1	0	1000		Sphingolipid Metabolism			
GALK	galactokinase	atp[c] + gal[c] -> adp[c] + h[c] + gal1p[c]	0	69976.1 or 69976.2 or 14635.1	0	1000		Galactose metabolism			
GALNACT1g	UDPGal-chondroitin acetylgalactosaminyltransferase I, Golgi	udpacgal[g] + cs_hs_linkage[g] -> h[g] + udp[g] + cs_pre[g]	0	78752.1 or 234356.1	0	1000		Chondroitin / heparan sulfate biosynthesis			
GALNACT2g	uridine diphosphoacetylgalactosamine-chondroitin acetylgalactosaminyltransferase II, Golgi	uacgam[g] + cs_a_b_pre2[g] -> h[g] + udp[g] + cs_a_b_pre3[g]	0	78752.1 or 78923.1 or 74241.1 or 269941.1 or 234356.1	0	1000		Chondroitin / heparan sulfate biosynthesis			
GALNACT3g	uridine diphosphoacetylgalactosamine-chondroitin acetylgalactosaminyltransferase II, Golgi	uacgam[g] + cs_c_pre2[g] -> h[g] + udp[g] + cs_c_pre3[g]	0	78752.1 or 78923.1 or 74241.1 or 269941.1 or 234356.1	0	1000		Chondroitin / heparan sulfate biosynthesis			

GALNACT4g	uridine diphosphoacetylgalactosamine-chondroitin acetylgalactosaminyltransferase II, Golgi	uacgam[g] + cs_d_pre3[g] -> h[g] + udp[g] + cs_d_pre4[g]	0	78752.1 or 78923.1 or 74241.1 or 269941.1 or 234356.1	0	1000		Chondroitin / heparan sulfate biosynthesis			
GALNACT5g	uridine diphosphoacetylgalactosamine-chondroitin acetylgalactosaminyltransferase II, Golgi	uacgam[g] + cs_e_pre3[g] -> h[g] + udp[g] + cs_e_pre4[g]	0	78752.1 or 78923.1 or 74241.1 or 269941.1 or 234356.1	0	1000		Chondroitin / heparan sulfate biosynthesis			
GALOR	D-Galactose:NADP+ 1-oxidoreductase	h[c] + nadph[c] + gal[c] <=> nadp[c] + galt[c]	1	58810.1 or 11677.1 or 58810.2	-1000	1000		Galactose metabolism			
GALSGLT1lu	transport of D-Galactose from extracellular space to cytosol of mucosal cells in small intestine	h2o[c] + atp[c] + 2 na1[u] + gal[u] -> adp[c] + h[c] + pi[c] + 2 na1[c] + gal[c]	0	20537.1	0	1000	3	Transport, Lumen	PMID: 20522896, PMID: 14642859, Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Advanced nutrition and human metabolism, Wadsworth cengage learning, 5th edition, page 71-72	SGLT-1 can also transport sugars coupled with H+ instead of Na+, under conditions of decreased extra-cellular ph. However, the affinity for glucose decreases with H+ coupled transport. (PMID: 17468205). The transport system is energized by Na/K ATPase activity (PMID: 7730974, Journal of animal science (2001) volume 79, (E suppl) E59:E72). Reversible transport for SGLT-1 has been suggested in a 6-state model in PMCID: PMC3000923.	
GALSIDEtg	galactocerebroside intracellular transport	galside_hs[c] <=> galside_hs[g]	1		-1000	1000		Transport, Golgi Apparatus			
GALSIDEtl	galactocerebroside intracellular transport	galside_hs[c] <=> galside_hs[l]	1		-1000	1000		Transport, Lysosomal			
GALT	galactose-1-phosphate uridylyltransferase	h[c] + utp[c] + gal1p[c] <=> udpgal[c] + ppi[c]	1	14430.1 or 14430.2 or 14430.3	-1000	1000		Galactose metabolism			
GALT2g	UDP-D-galactose:galactosylxylose galactosyltransferase, Golgi apparatus	udpgal[g] + lxser[g] -> h[g] + udp[g] + l2xser[g]	0	117592.1	0	1000		Chondroitin / heparan sulfate biosynthesis			
GALTg	UDP-D-galactose:D-xylose galactosyltransferase, Golgi apparatus	udpgal[g] + xser[g] -> h[g] + udp[g] + lxser[g]	0	218271.1	0	1000		Chondroitin / heparan sulfate biosynthesis			
GALU	UTP-glucose-1-phosphate uridylyltransferase	h[c] + g1p[c] + utp[c] <=> ppi[c] + udpg[c]	1	216558.1 or 216558.2	-1000	1000		Galactose metabolism			
GALt1r	galactose transport (uniport)	gal[e] <=> gal[c]	1	20527.1 or 20525.1 or 56017.1 or 170441.1 or 20526.1	-1000	1000		Transport, Extracellular			
GALt2_2	D-galactose transport via proton symport	2 h[e] + gal[e] <=> 2 h[c] + gal[c]	1	20537.1	-1000	1000		Transport, Extracellular			
GALt4	galactose transport via sodium symport	na1[e] + gal[e] <=> na1[c] + gal[c]	1	230612.1	-1000	1000		Transport, Extracellular			
GALt4_2	galactose transport via sodium symport	2 na1[e] + gal[e] <=> 2 na1[c] + gal[c]	1	20537.1	-1000	1000		Transport, Extracellular			
GALtly	galactose efflux from lysosome	gal[l] -> gal[c]	0		0	1000		Transport, Lysosomal			
GAMYe	glucoamylase, extracellular (glygn5 -> malt)	h2o[e] + glygn5[e] -> Tyr-ggn[e] + malt[e]	0	232714.1	0	1000		Starch and Sucrose Metabolism			
GAMt1r	glucosamine transport (uniport)	gam[e] <=> gam[c]	1	20528.1 or 20525.1 or 20526.1	-1000	1000		Transport, Extracellular			
GAO1	Ganglioside O-acetylation	accoa[c] + gd3_hs[c] -> coa[c] + oagd3_hs[c]	0	11416.1	0	1000		Sphingolipid Metabolism			
GAO1g	Ganglioside O-acetylation	accoa[g] + gd3_hs[g] -> coa[g] + oagd3_hs[g]	0	11416.1	0	1000		Sphingolipid Metabolism			
GAO2	Ganglioside O-acetylation	accoa[c] + gt3_hs[c] -> coa[c] + oagt3_hs[c]	0	11416.1	0	1000		Sphingolipid Metabolism			
GAO2g	Ganglioside O-acetylation	accoa[g] + gt3_hs[g] -> coa[g] + oagt3_hs[g]	0	11416.1	0	1000		Sphingolipid Metabolism			
GAPD	glyceraldehyde-3-phosphate dehydrogenase	pi[c] + nad[c] + g3p[c] <=> h[c] + nadh[c] + 13dpg[c]	1	100043349.1 or 14447.1	-1000	1000		Glycolysis/Gluconeogenesis			
GARFT	phosphoribosylglycinamide formyltransferase	10fthf[c] + gar[c] <=> h[c] + thf[c] + fgam[c]	1	14450.1 or 14450.2	-1000	1000		IMP Biosynthesis			
GASNASE2ly	glycosylasparaginase, lysosomal	h2o[l] + n2m2nmasn[l] -> Asn_X_Ser_Thr[l] + n2m2nm[l]	0	11593.1	0	1000		N-Glycan Degradation			
GASNASE3ly	glycosylasparaginase, lysosomal	h2o[l] + ksi_deg1[l] -> Asn_X_Ser_Thr[l] + ksi_deg2[l]	0	11593.1	0	1000		Keratan sulfate degradation			
GASNASEly	glycosylasparaginase, lysosomal	h2o[l] + s2l2n2m2masn[l] -> Asn_X_Ser_Thr[l] + s2l2n2m2m[l]	0	11593.1	0	1000		N-Glycan Degradation			
GBA	Glucosylceramidase	h2o[c] + gluside_hs[c] -> crm_hs[c] + glc-D[c]	0	14466.1 or 14466.2 or 14466.3 or 14466.4 or 14466.5	0	1000		Sphingolipid Metabolism			
GBAl	Glucosylceramidase	h2o[l] + gluside_hs[l] -> crm_hs[l] + glc-D[l]	0	14466.1 or 14466.2 or 14466.3 or 14466.4 or 14466.5	0	1000		Sphingolipid Metabolism			
GBGT1	globoside alpha-1,3-N-acetylgalactosaminyltransferase 1	udpacgal[g] + gbside_hs[g] -> h[g] + udp[g] + acgagbside_hs[g]	0	227671.1	0	1000		Sphingolipid Metabolism			
GBSIDEte	globoside transport	gbside_hs[c] <=> gbside_hs[e]	1		-1000	1000		Transport, Extracellular			
GBSIDEtl	globoside intracellular transport	gbside_hs[c] <=> gbside_hs[l]	1		-1000	1000		Transport, Lysosomal			
GCALDD	Glycolaldehyde dehydrogenase	h2o[c] + nad[c] + gcald[c] -> 2 h[c] + nadh[c] + glyclt[c]	0	19378.1 or 56752.1 or 11670.1 or 110695.1 or 67689.1 or 56847.1 or 11668.1 or 11671.1 or 19378.2 or 19378.3	0	1000		Glyoxylate and Dicarboxylate Metabolism			
GCALDDm	Glycolaldehyde dehydrogenase, mitochondrial	h2o[m] + nad[m] + gcald[m] -> 2 h[m] + nadh[m] + glyclt[m]	0	104776.1 or 212647.1 or 11669.1 or 214579.1 or 56454.1 or 214579.2 or 212647.2 or 72535.1	0	1000		Glyoxylate and Dicarboxylate Metabolism			
GCC2am	glycine-cleavage complex (lipoamide), mitochondrial	h[m] + gly[m] + lpam[m] <=> co2[m] + alpam[m]	1	68133.1 or 434437.1 or 13382.1 or 104174.1	-1000	1000		Glycine, Serine, and Threonine Metabolism			
GCC2bim	glycine-cleavage system (lipoamide) irreversible, mitochondrial	thf[m] + alpam[m] -> nh4[m] + dhlam[m] + mlthf[m]	0	68133.1 or 434437.1 or 13382.1 or 104174.1	0	1000		Glycine, Serine, and Threonine Metabolism			
GCC2cm	glycine-cleavage complex (lipoamide), mitochondrial	nad[m] + dhlam[m] <=> h[m] + nadh[m] + lpam[m]	1	68133.1 or 434437.1 or 13382.1 or 104174.1	-1000	1000		Glycine, Serine, and Threonine Metabolism			
GCCam	glycine-cleavage complex (lipoylprotein), mitochondrial	h[m] + gly[m] + lpro[m] <=> co2[m] + alpro[m]	1	68133.1 or 434437.1 or 13382.1 or 104174.1	-1000	1000		Glycine, Serine, and Threonine Metabolism			
GCCbim	glycine-cleavage complex (lipoylprotein) irreversible, mitochondrial	thf[m] + alpro[m] -> nh4[m] + mlthf[m] + dhlpro[m]	0	68133.1 or 434437.1 or 13382.1 or 104174.1	0	1000		Glycine, Serine, and Threonine Metabolism			
GCCcm	glycine-cleavage complex (lipoylprotein), mitochondrial	nad[m] + dhlpro[m] <=> h[m] + nadh[m] + lpro[m]	1	68133.1 or 434437.1 or 13382.1 or 104174.1	-1000	1000		Glycine, Serine, and Threonine Metabolism			
GCHOLAt2	glycocholate transport via sodium cotransport	2 na1[e] + gchola[e] -> 2 na1[c] + gchola[c]	0	20494.1 or 20493.1	0	1000		Transport, Extracellular			
GCHOLAt3	ABC bile acid transporter	h2o[c] + atp[c] + gchola[c] -> adp[c] + h[c] + pi[c] + gchola[e]	0	27413.1 or 76408.2 or 76408.3 or 76408.1	0	1000		Transport, Extracellular			
GCHOLAte	bile acid intracellular transport	gchola[e] <=> gchola[c]	1		-1000	1000		Transport, Extracellular			
GCHOLAtx	bile acid intracellular transport	gchola[x] <=> gchola[c]	1		-1000	1000		Transport, Peroxisomal			
GCNTg	N-acetyllactosaminide beta-1,6-N-acetylglucosaminyl-transferase	uacgam[g] + galacglcgal14acglcgalgluside_hs[g] -> h[g] + udp[g] + acglcgalacglcgal14acglcgalgluside_hs[g]	0	14538.1	0	1000		Blood Group Biosynthesis			
GD1B2te	gd1b2_hs transport	gd1b2_hs[c] <=> gd1b2_hs[e]	1		-1000	1000		Transport, Extracellular			
GD1B2tg	gd1b2_hs intracellular transport	gd1b2_hs[c] <=> gd1b2_hs[g]	1		-1000	1000		Transport, Golgi Apparatus			
GD1Cte	gd1c_hs transport	gd1c_hs[c] <=> gd1c_hs[e]	1		-1000	1000		Transport, Extracellular			
GD1Ctg	gd1c_hs intracellular transport	gd1c_hs[c] <=> gd1c_hs[g]	1		-1000	1000		Transport, Golgi Apparatus			
GDCHOLAte	bile acid intracellular transport	gdchola[e] <=> gdchola[c]	1		-1000	1000		Transport, Extracellular			
GDCHOLAtx	bile acid intracellular transport	gdchola[x] <=> gdchola[c]	1		-1000	1000		Transport, Peroxisomal			
GDPFUCtg	GDPFuc Golgi transport via CMP antiport	gdpfuc[c] + gmp[g] <=> gdpfuc[g] + gmp[c]	1	228368.1	-1000	1000		Transport, Golgi Apparatus			
GDPtg	GDP intracellular transport	gdp[c] <=> gdp[g]	1		-1000	1000		Transport, Golgi Apparatus			
GF6PTA	glutamine-fructose-6-phosphate transaminase	gln-L[c] + f6p[c] -> glu-L[c] + gam6p[c]	0	14584.1 or 14583.1	0	1000		Aminosugar Metabolism			
GFUCS	GDP-L-fucose synthase	h[c] + nadph[c] + gdpddman[c] -> nadp[c] + gdpfuc[c]	0	22122.1	0	1000		Fructose and Mannose Metabolism			
GGH_10FTHF5GLUe	Gamma-glutamyl hydrolase (10FTHF5GLU), extracellular	4 h2o[e] + 10fthf5glu[e] -> 4 glu-L[e] + 10fthf[e]	0	667301.1	0	1000		Folate Metabolism			
GGH_10FTHF5GLUl	Gamma-glutamyl hydrolase (10FTHF5GLU), lysosomal	10fthf5glu[l] + 4 h2o[l] -> 10fthf[l] + 4 glu-L[l]	0	667301.1	0	1000		Folate Metabolism			
GGH_10FTHF6GLUe	Gamma-glutamyl hydrolase (10FTHF6GLU), extracellular	h2o[e] + 10fthf6glu[e] -> glu-L[e] + 10fthf5glu[e]	0	667301.1	0	1000		Folate Metabolism			
GGH_10FTHF6GLUl	Gamma-glutamyl hydrolase (10FTHF6GLU), lysosomal	10fthf6glu[l] + h2o[l] -> 10fthf5glu[l] + glu-L[l]	0	667301.1	0	1000		Folate Metabolism			
GGH_10FTHF7GLUe	Gamma-glutamyl hydrolase (10FTHF7GLU), extracellular	h2o[e] + 10fthf7glu[e] -> glu-L[e] + 10fthf6glu[e]	0	667301.1	0	1000		Folate Metabolism			
GGH_10FTHF7GLUl	Gamma-glutamyl hydrolase (10FTHF7GLU), lysosomal	10fthf7glu[l] + h2o[l] -> 10fthf6glu[l] + glu-L[l]	0	667301.1	0	1000		Folate Metabolism			
GGH_5DHFe	Gamma-glutamyl hydrolase (5DHF), extracellular	4 h2o[e] + 5dhf[e] -> 4 glu-L[e] + dhf[e]	0	667301.1	0	1000		Folate Metabolism			
GGH_5DHFl	Gamma-glutamyl hydrolase (5DHF), lysosomal	4 h2o[l] + 5dhf[l] -> dhf[l] + 4 glu-L[l]	0	667301.1	0	1000		Folate Metabolism			
GGH_5THFe	Gamma-glutamyl hydrolase (5THF), extracellular	4 h2o[e] + 5thf[e] -> 4 glu-L[e] + thf[e]	0	667301.1	0	1000		Folate Metabolism			
GGH_5THFl	Gamma-glutamyl hydrolase (5THF), lysosomal	4 h2o[l] + 5thf[l] -> 4 glu-L[l] + thf[l]	0	667301.1	0	1000		Folate Metabolism			
GGH_6DHFe	Gamma-glutamyl hydrolase (6DHF), extracellular	h2o[e] + 6dhf[e] -> glu-L[e] + 5dhf[e]	0	667301.1	0	1000		Folate Metabolism			
GGH_6DHFl	Gamma-glutamyl hydrolase (6DHF), lysosomal	h2o[l] + 6dhf[l] -> 5dhf[l] + glu-L[l]	0	667301.1	0	1000		Folate Metabolism			
GGH_6THFe	Gamma-glutamyl hydrolase (6THF), extracellular	h2o[e] + 6thf[e] -> glu-L[e] + 5thf[e]	0	667301.1	0	1000		Folate Metabolism			
GGH_6THFl	Gamma-glutamyl hydrolase (6THF), lysosomal	h2o[l] + 6thf[l] -> 5thf[l] + glu-L[l]	0	667301.1	0	1000		Folate Metabolism			
GGH_7DHFe	Gamma-glutamyl hydrolase (7DHF), extracellular	h2o[e] + 7dhf[e] -> glu-L[e] + 6dhf[e]	0	667301.1	0	1000		Folate Metabolism			
GGH_7DHFl	Gamma-glutamyl hydrolase (7DHF), lysosomal	h2o[l] + 7dhf[l] -> 6dhf[l] + glu-L[l]	0	667301.1	0	1000		Folate Metabolism			
GGH_7THFe	Gamma-glutamyl hydrolase (7THF), extracellular	h2o[e] + 7thf[e] -> glu-L[e] + 6thf[e]	0	667301.1	0	1000		Folate Metabolism			
GGH_7THFl	Gamma-glutamyl hydrolase (7THF), lysosomal	h2o[l] + 7thf[l] -> 6thf[l] + glu-L[l]	0	667301.1	0	1000		Folate Metabolism			
GGLUCT	gamma-glutamylcyclotransferase	gluala[e] -> ala-L[c] + 5oxpro[c]	0		0	1000		Glutathione Metabolism			
GGNG	glycogenin self-glucosylation	8 udpg[c] + Tyr-ggn[c] -> 8 h[c] + 8 udp[c] + ggn[c]	0	14936.1 or 232493.1 or 27357.1	0	1000		Starch and Sucrose Metabolism			
GGT5r	Gamma-glutamyltransferase 5	h2o[r] + leuktrC4[r] <=> glu-L[r] + leuktrD4[r]	1	23887.1	-1000	1000		Eicosanoid Metabolism			
GGT6	Gamma-glutamyltransferase	glu-L[c] + leuktrE4[c] <=> h2o[c] + leuktrF4[c]	1		-1000	1000		Eicosanoid Metabolism			
GGT_L	geranylgeranyltransferase (liver)	17.6 ipdp[c] + ttc-ggdp[c] -> 17.6 ppi[c] + 0.1 dedoldp_L[c]	0		0	1000		N-Glycan Biosynthesis			
GGT_U	geranylgeranyltransferase (uterus)	16.5 ipdp[c] + ttc-ggdp[c] -> 16.5 ppi[c] + 0.1 dedoldp_U[c]	0		0	1000		N-Glycan Biosynthesis			
GHMT2r	glycine hydroxymethyltransferase, reversible	thf[c] + ser-L[c] <=> h2o[c] + gly[c] + mlthf[c]	1	20425.1 or 20425.2	-1000	1000		Glycine, Serine, and Threonine Metabolism			
GHMT2rm	glycine hydroxymethyltransferase, reversible, mitochondrial	thf[m] + ser-L[m] <=> h2o[m] + gly[m] + mlthf[m]	1	108037.1	-1000	1000		Glycine, Serine, and Threonine Metabolism			
GHMT3	glycine hydroxymethyltransferase	h[c] + 3htmelys[c] -> gly[c] + 4tmeabut[c]	0	20425.1 or 20425.2	0	1000		Lysine Metabolism			
GHMT3m	glycine hydroxymethyltransferase, mitochondrial	h[m] + 3htmelys[m] -> gly[m] + 4tmeabut[m]	0	108037.1	0	1000		Lysine Metabolism			
GK1	guanylate kinase (GMP:ATP)	atp[c] + gmp[c] <=> adp[c] + gdp[c]	1	14923.1	-1000	1000		Nucleotides			
GK1m	guanylate kinase (GMP:ATP), mitochondrial	atp[m] + gmp[m] <=> adp[m] + gdp[m]	1		-1000	1000		Nucleotides			

GLACO	D-Glucuronolactone:NAD+ oxidoreductase	2 h2o[c] + nad[c] + glac[c] -> 3 h[c] + nadh[c] + glcr[c]	0	19378.1 or 56752.1 or 11670.1 or 67689.1 or 56847.1 or 11668.1 or 11671.1 or 19378.2 or 19378.3	0	1000		Ascorbate and Aldarate Metabolism			
GLACOm	D-Glucuronolactone:NAD+ oxidoreductase, mitochondrial	2 h2o[m] + nad[m] + glac[m] -> 3 h[m] + nadh[m] + glcr[m]	0	212647.1 or 11669.1 or 212647.2 or 72535.1	0	1000		Ascorbate and Aldarate Metabolism			
GLACter	D-glucurono-6,3-lactone transport, endoplasmic reticulum	glac[c] <=> glac[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
GLAl	galactosidase, alpha	h2o[l] + digalside_hs[l] -> galside_hs[l] + gal[l]	0	11605.1	0	1000		Sphingolipid Metabolism			
GLB1	Beta-galactosidase	h2o[l] + galgluside_hs[l] -> gal[l] + gluside_hs[l]	0	50917.1 or 19025.1 or 12091.1 or 18010.1	0	1000		Sphingolipid Metabolism			
GLBRAN	1,4-alpha-glucan branching enzyme (glygn1 -> glygn2)	glygn1[c] -> glygn2[c]	0	74185.1	0	1000		Starch and Sucrose Metabolism			
GLCAASE1ly	beta-glucuronidase, lysosomal	h2o[l] + hs_deg9[l] -> glcur[l] + hs_deg10[l]	0	110006.1	0	1000		Heparan sulfate degradation			
GLCAASE4ly	beta-glucuronidase, lysosomal	h2o[l] + cs_a_deg2[l] -> glcur[l] + cs_a_deg3[l]	0	110006.1	0	1000		Chondroitin sulfate degradation			
GLCAASE5ly	beta-glucuronidase, lysosomal	h2o[l] + cs_c_deg2[l] -> glcur[l] + cs_c_deg3[l]	0	110006.1	0	1000		Chondroitin sulfate degradation			
GLCAASE6ly	beta-glucuronidase, lysosomal	h2o[l] + cs_d_deg3[l] -> glcur[l] + cs_d_deg4[l]	0	110006.1	0	1000		Chondroitin sulfate degradation			
GLCAASE7ly	beta-glucuronidase, lysosomal	h2o[l] + cs_e_deg3[l] -> glcur[l] + cs_e_deg4[l]	0	110006.1	0	1000		Chondroitin sulfate degradation			
GLCAASE8ly	beta-glucuronidase, lysosomal	h2o[l] + ha[l] -> glcur[l] + ha_deg1[l]	0	110006.1	0	1000		Hyaluronan Metabolism			
GLCAASE9ly	beta-glucuronidase, lysosomal	2 h2o[l] + ha_pre1[l] -> acgam[l] + glcur[l]	0	110006.1	0	1000		Hyaluronan Metabolism			
GLCAE1g	chondroitin-glucuronate 5-epimerase	cs_a_b_pre3[g] -> cs_b_pre4[g]	0		0	1000		Chondroitin / heparan sulfate biosynthesis			
GLCAE2g	heparosan-N-sulfate-glucuronate 5-epimerase	hs_pre10[g] -> hs_pre11[g]	0	93683.1	0	1000		Chondroitin / heparan sulfate biosynthesis			
GLCAT2g	chondroitin glucuronyltransferase II, Golgi apparatus	cs_a_b_e_pre1[g] + udpglcur[g] -> h[g] + udp[g] + cs_a_b_pre2[g]	0	78923.1 or 74241.1 and 269941.1 or 100910.1	0	1000		Chondroitin / heparan sulfate biosynthesis			
GLCAT3g	chondroitin glucuronyltransferase II, Golgi apparatus	udpglcur[g] + cs_c_d_e_pre1[g] -> h[g] + udp[g] + cs_c_pre2[g]	0	78923.1 or 74241.1 and 269941.1 or 100910.1	0	1000		Chondroitin / heparan sulfate biosynthesis			
GLCAT4g	chondroitin glucuronyltransferase II, Golgi apparatus	udpglcur[g] + cs_d_pre2[g] -> h[g] + udp[g] + cs_d_pre3[g]	0	78923.1 or 74241.1 and 269941.1 or 100910.1	0	1000		Chondroitin / heparan sulfate biosynthesis			
GLCAT5g	chondroitin glucuronyltransferase II, Golgi apparatus	udpglcur[g] + cs_e_pre2[g] -> h[g] + udp[g] + cs_e_pre3[g]	0	78923.1 or 74241.1 and 269941.1 or 100910.1	0	1000		Chondroitin / heparan sulfate biosynthesis			
GLCAT6g	heparan glucuronyltransferase II	udpglcur[g] + hs_pre1[g] -> h[g] + udp[g] + hs_pre2[g]	0	14043.1 and 14042.1 or 14042.1 and 14043.2	0	1000		Chondroitin / heparan sulfate biosynthesis			
GLCAT7g	heparan glucuronyltransferase II	udpglcur[g] + hs_pre3[g] -> h[g] + udp[g] + hs_pre4[g]	0	14043.1 and 14042.1 or 14042.1 and 14043.2	0	1000		Chondroitin / heparan sulfate biosynthesis			
GLCAT8g	heparan glucuronyltransferase II	udpglcur[g] + hs_pre5[g] -> h[g] + udp[g] + hs_pre6[g]	0	14043.1 and 14042.1 or 14042.1 and 14043.2	0	1000		Chondroitin / heparan sulfate biosynthesis			
GLCAT9g	heparan glucuronyltransferase II	udpglcur[g] + hs_pre7[g] -> h[g] + udp[g] + hs_pre8[g]	0	14043.1 and 14042.1 or 14042.1 and 14043.2	0	1000		Chondroitin / heparan sulfate biosynthesis			
GLCATg	UDP-D-glucuronate:galactosylgalactosylxylose glucuronosyltransferase, Golgi apparatus	l2xser[g] + udpglcur[g] -> h[g] + udp[g] + cs_hs_linkage[g]	0	76898.1 or 72727.1 or 280645.1 or 76898.2	0	1000		Chondroitin / heparan sulfate biosynthesis			
GLCMter	glucose transport via membrane vesicle	glc-D[r] -> glc-D[e]	0		0	1000		Transport, Extracellular			
GLCNACASE1ly	alpha-N-acetylglucosaminidase, lysosomal	h2o[l] + hs_deg3[l] -> acgam[l] + hs_deg4[l]	0	27419.1	0	1000		Heparan sulfate degradation			
GLCNACASE2ly	alpha-N-acetylglucosaminidase, lysosomal	h2o[l] + hs_deg8[l] -> acgam[l] + hs_deg9[l]	0	27419.1	0	1000		Heparan sulfate degradation			
GLCNACASE3ly	alpha-N-acetylglucosaminidase, lysosomal	h2o[l] + hs_deg14[l] -> acgam[l] + hs_deg15[l]	0	27419.1	0	1000		Heparan sulfate degradation			
GLCNACASE4ly	alpha-N-acetylglucosaminidase, lysosomal	h2o[l] + hs_deg20[l] -> acgam[l] + hs_deg21[l]	0	27419.1	0	1000		Heparan sulfate degradation			
GLCNACASE5ly	alpha-N-acetylglucosaminidase, lysosomal	h2o[l] + hs_deg24[l] -> acgam[l] + hs_deg25[l]	0	27419.1	0	1000		Heparan sulfate degradation			
GLCNACDASg	GlcNAc N-deacetylase / N-sulfotransferase	4 h2o[g] + 4 paps[g] + hs_pre9[g] -> 4 h[g] + 4 ac[g] + 4 pap[g] + hs_pre10[g]	0	17423.1 or 83398.1 or 64580.1 or 15531.1	0	1000		Chondroitin / heparan sulfate biosynthesis			
GLCNACPT_L	UDP-GlcNAc:dolichol-phosphate GlcNAc phosphotransferase (liver)	0.1 dolp_L[c] + uacgam[c] -> 0.1 naglc2p_L[c] + ump[c]	0	13478.1 or 13478.2	0	1000		N-Glycan Biosynthesis			
GLCNACPT_U	UDP-GlcNAc:dolichol-phosphate GlcNAc phosphotransferase (uterus)	0.1 dolp_U[c] + uacgam[c] -> ump[c] + 0.1 naglc2p_U[c]	0	13478.1 or 13478.2	0	1000		N-Glycan Biosynthesis			
GLCNACT1g	alpha-N-acetylglucosaminyltransferase I, Golgi apparatus	uacgam[g] + cs_hs_linkage[g] -> h[g] + udp[g] + hs_pre1[g]	0	54616.1 or 58193.1	0	1000		Chondroitin / heparan sulfate biosynthesis			
GLCNACT2g	alpha-N-acetylglucosaminyltransferase II	uacgam[g] + hs_pre2[g] -> h[g] + udp[g] + hs_pre3[g]	0	14043.1 and 14042.1 or 54616.1 or 56219.1 or 14042.1 and 14043.2	0	1000		Chondroitin / heparan sulfate biosynthesis			
GLCNACT3g	alpha-N-acetylglucosaminyltransferase II	uacgam[g] + hs_pre4[g] -> h[g] + udp[g] + hs_pre5[g]	0	14043.1 and 14042.1 or 54616.1 or 56219.1 or 14042.1 and 14043.2	0	1000		Chondroitin / heparan sulfate biosynthesis			
GLCNACT4g	alpha-N-acetylglucosaminyltransferase II	uacgam[g] + hs_pre6[g] -> h[g] + udp[g] + hs_pre7[g]	0	14043.1 and 14042.1 or 54616.1 or 56219.1 or 14042.1 and 14043.2	0	1000		Chondroitin / heparan sulfate biosynthesis			
GLCNACT5g	alpha-N-acetylglucosaminyltransferase II	uacgam[g] + hs_pre8[g] -> h[g] + udp[g] + hs_pre9[g]	0	14043.1 and 14042.1 or 54616.1 or 56219.1 or 14042.1 and 14043.2	0	1000		Chondroitin / heparan sulfate biosynthesis			
GLCNACT_L	UDP-GlcNAc:N-acetyl-D-glucosaminyl diphosphodolichol N-acetyl-D-glucosaminyltransferase (liver)	uacgam[c] + 0.1 naglc2p_L[c] -> h[c] + udp[c] + 0.1 chito2pdol_L[c]	0		0	1000		N-Glycan Biosynthesis			
GLCNACT_U	UDP-GlcNAc:N-acetyl-D-glucosaminyl diphosphodolichol N-acetyl-D-glucosaminyltransferase (uterus)	uacgam[c] + 0.1 naglc2p_U[c] -> h[c] + udp[c] + 0.1 chito2pdol_U[c]	0		0	1000		N-Glycan Biosynthesis			
GLCSGLT1lu	transport of D-glucose from lumen to cytosol of mucosal cells in small intestine	h2o[c] + atp[c] + 2 na1[u] + glc-D[u] -> adp[c] + h[c] + pi[c] + 2 na1[c] + glc-D[c]	0	20537.1	0	1000	3	Transport, Lumen	PMID: 20522896, PMID: 14642859, Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Advanced nutrition and human metabolism, Wadsworth cengage learning, 5th edition, page 71-72	SGLT-1 can also transport sugars coupled with H+ instead of Na+, under conditions of decreased extra-cellular ph. However, the affinity for glucose decreases with H+ coupled transport. (PMID: 17468205). The transport system is energized by Na/K ATPase activity (PMID: 7730974, Journal of animal science (2001) volume 79, (E suppl) E59:E72). Reversible transport for SGLT-1 has been suggested in a 6-state model in PMCID: PMC3000923.	
GLCURter	glucuronate endoplasmic reticular transport	glcur[c] -> glcur[r]	0		0	1000		Transport, Endoplasmic Reticular			
GLCURtly	glucuronate transport into lysososme	h[c] + glcur[c] <=> h[l] + glcur[l]	1	235504.1	-1000	1000		Transport, Lysosomal			
GLCURtr	D-Glucuronate export	glcur[c] -> glcur[e]	0		0	1000	2	Transport, Extracellular	PMID: 15123798, PMID: 18180286	This metabolite is found in mucus and can serve as carbon source for intestinal microbes. It is assumed it appears in mucus through secretion from goblet cells and from epithelial cell debris.	
GLCt2_2	D-glucose transport in via proton symport	2 h[e] + glc-D[e] <=> 2 h[c] + glc-D[c]	1	20537.1	-1000	1000		Transport, Extracellular			
GLCt2r	D-glucose transport in via proton symport	h[e] + glc-D[e] <=> h[c] + glc-D[c]	1	246787.1	-1000	1000		Transport, Extracellular			
GLCt4	glucose transport via sodium symport	na1[e] + glc-D[e] <=> na1[c] + glc-D[c]	1	53881.1 or 109342.1 or 241612.1 or 230612.1 or 246787.1	-1000	1000		Transport, Extracellular			
GLCt4_2	glucose transport via sodium symport	2 na1[e] + glc-D[e] <=> 2 na1[c] + glc-D[c]	1	20537.1	-1000	1000		Transport, Extracellular			
GLCter	glucose transport, endoplasmic reticulum	glc-D[c] <=> glc-D[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
GLCtg	glucose transport, Golgi apparatus	glc-D[c] <=> glc-D[g]	1	20525.1	-1000	1000		Transport, Golgi Apparatus			
GLCtly	glucose efflux from lysosome	glc-D[l] -> glc-D[c]	0		0	1000		Transport, Lysosomal			
GLDBRAN	glycogen debranching enzyme	h2o[c] + dxtrn[c] -> glc-D[c] + glygn3[c]	0	77559.1 or 77559.2 or 77559.3 or 77559.4 or 77559.5 or 77559.6	0	1000		Starch and Sucrose Metabolism			
GLGNS1	glycogen synthase (ggn -> glygn1)	3 udpg[c] + ggn[c] -> 3 h[c] + 3 udp[c] + glygn1[c]	0	14936.1 or 232493.1 or 27357.1	0	1000		Starch and Sucrose Metabolism			
GLINOFABPpmtc	uptake of gamma-linolenic acid by the enterocytes	lnlncg[u] -> lnlncg[c]	0	(14719.1 or 12491.1)	0	1000	3	Transport, Lumen	PMID: 20086080, PMID: 10617989, PMID: 8717442, Progress in Lipid Research Volume 48, Issue 2, March 2009, Pages 101-115	GOT2 encodes FABPpm that may either act alone or in co-ordination with CD36, for the uptake of long chain fatty acids (exhibits a selective preference for long chain PUFA and essential fatty acids over non-essential fatty acids). The fatty acids alternatively can undergo passive diffusion. once inside the cell, they bind to the cytoplasmic fatty acid binding protein (FABPc) and thereby undergo actiavtion or esterification. Additionally, a minority of fatty acids are thought to be transported by FATP1 and rapidly activated by plasma membrane acyl-CoA synthetase (ACS1) to form acyl-Co esters. (PMID: 20086080)	
GLNALANaEx	L-alanine/L-glutamine Na-dependent exchange (Gln-L in)	na1[e] + ala-L[c] + gln-L[e] -> na1[c] + ala-L[e] + gln-L[c]	0	20514.1	0	1000		Transport, Extracellular			
GLNASNNaEx	L-glutamine/L-asparagine Na-dependent exchange (Gln-L in)	na1[e] + asn-L[c] + gln-L[e] -> na1[c] + asn-L[e] + gln-L[c]	0	20514.1	0	1000		Transport, Extracellular			
GLNATB0tc	transport of L-Glutamine into the intestinal cells by ATB0 transporter	2 na1[u] + cl[u] + gln-L[u] -> 2 na1[c] + cl[c] + gln-L[c]	0	56774.1	0	1000	3	Transport, Lumen	PMID:18195088	ATB0 is both sodium and chloride coupled, with reaction stoichiometry 2Na+:1cl:1amino acid. The transporter is localted in the intestine, has a broad substrate specificity (both neutral and cationic amino acids), but is not involved in the transport of aspartate, glutamate and proline (PMID:18195088).	
GLNB0AT1tc	transport of L-Glutamine by the apical neutral amino acid transporters in kidney and intestine	na1[u] + gln-L[u] -> na1[c] + gln-L[c]	0	(70008.1 or (74338.1 and 57394.1))	0	1000	3	Transport, Lumen	PMID: 19472175, PMID: 15804236, PMID: 18400692	transports all the neutral amino acids with preference for methionine, leucine and valine. Reaction stoichiometry is 1:1. Requires heterodimerization with collectrin protein for increased affinity. Found in kidney and intestine, however also reported to be expressed in skin. Requires association with ACE2 for expression in intestine but with collectrin for expression in kidney.	3.4.17.23
GLNCYSNaEx	L-cysteine/L-glutamine Na-dependent exchange (Gln-L in)	na1[e] + cys-L[c] + gln-L[e] -> na1[c] + cys-L[e] + gln-L[c]	0	20514.1	0	1000		Transport, Extracellular			
GLNILELAT2tc	transport of L-Glutamine into the cell and efflux of L-Isoleucine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	gln-L[e] + ile-L[c] -> gln-L[c] + ile-L[e]	0	(20539.1 and 17254.1)	0	1000	3	Transport, Extracellular	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s00420000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	higer affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of memebranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for traficking of the complex to the mebrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s00420000274).	
GLNLASEer	gluconolactonase, endoplasmic reticulum	h[r] + guln[r] <=> h2o[r] + gullac[r]	1		-1000	1000		Ascorbate and Aldarate Metabolism			
GLNLAT1tc	transport of L-Glutamine by LAT1 in association with 4F2hc, across the apical surface of the memebranes.	leu-L[c] + gln-L[u] -> leu-L[u] + gln-L[c]	0	(20539.1 and 17254.1)	0	1000	3	Transport, Lumen	Hans Gerhard Vogel, Franz J. Hock, Jochen Maas, Dieter Mayer (2006), Drug discovery and evaluation: Safety and pharmacokinetic assays, Springer publication, Chapter II D, page 456, table 3, PMID: 19035290, PMID: 12634921, European Journal of Pharmacology 441 (2002) 127-132. Am J Physiol Cell Physiol 281:C1077-C1093, 2001. Amino Acids (2005) 29: 229–233 DOI 10.1007/s00726-005-0221-x. PMID: 11901210	leucine is the only amino acid tested for efflux. Expressed in ovary, placenta, brain, spleen, testis, activated lymphocytes and some tumor cells. Functions as a antiport transport system (DOI 10.1016/j.cell.2009.01.02), requires heterodimerization with glycoprotein CD98 (Pflugers Arch-Eur J Physiol (2000) 440:503-512, DOI 10.1007/s004240000274, PMID: 10958334).	

GLNPHELAT2tc	transport of L-Glutamine into the cell and efflux of L-Phenylalanine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	gln-L[e] + phe-L[c] -> gln-L[c] + phe-L[e]	0	(20539.1 and 17254.1)	0	1000	3	Transport, Extracellular	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s00420000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	higer affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of memebranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for traficking of the complex to the mebrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s00420000274).	
GLNS	glutamine synthetase	nh4[c] + atp[c] + glu-L[c] -> adp[c] + h[c] + pi[c] + gln-L[c]	0	266744.1 or 14645.1	0	1000		Glutamate metabolism			
GLNSERNaEx	L-serine/L-glutamine Na-dependent exchange (Gln-L in)	na1[e] + gln-L[e] + ser-L[c] -> na1[c] + gln-L[c] + ser-L[e]	0	20514.1	0	1000		Transport, Extracellular			
GLNTHRNaEx	L-threonine/L-glutamine Na-dependent exchange (Gln-L in)	na1[e] + gln-L[e] + thr-L[c] -> na1[c] + gln-L[c] + thr-L[e]	0	20514.1	0	1000		Transport, Extracellular			
GLNt4	L-glutamine reversible transport via sodium symport	na1[e] + gln-L[e] -> na1[c] + gln-L[c]	0	105727.1 or 67760.1 or 69354.1 or 56774.1	0	1000		Transport, Extracellular			
GLNtN1	Glutamine transport (Na, H coupled)	h[c] + 2 na1[e] + gln-L[e] <=> h[e] + 2 na1[c] + gln-L[c]	1	209837.1 or 76257.1	-1000	1000		Transport, Extracellular			
GLNtm	L-glutamine transport via electroneutral transporter	gln-L[c] -> gln-L[m]	0		0	1000		Transport, Mitochondrial			
GLNyLATtc	transport of L-Glutamine by y+LAT1 or y+LAT2 transporters in small intestine and kidney	na1[e] + gln-L[e] + arg-L[c] -> na1[c] + gln-L[c] + arg-L[e]	0	(20540.1 or (330836.1 and 17254.1))	0	1000	3	Transport, Extracellular	PMID: 11546643, PMID:18195088	y+LAT1 and y+LAT2 transporters requires CD98 for sequesterization to the plasma membrane. Acts as an amino acid exchanger, with influx of neutral aminoa acids and efflux of cationic amino acid, requires Na+ for optimal activity. Can also operate with H+ in absence of Na+ (PMID: 11546643).	
GLNyLATthc	transport of Glutamine by y+LAT1 or y+LAT2 with co-transporter of h in small intestine and kidney	h[e] + gln-L[e] + arg-L[c] -> h[c] + gln-L[c] + arg-L[e]	0	(20540.1 or (330836.1 and 17254.1))	0	1000	3	Transport, Extracellular	PMID: 11546643, PMID:18195088	y+LAT1 and y+LAT2 transporters requires CD98 for sequesterization to the plasma membrane. Acts as an amino acid exchanger, with influx of neutral aminoa acids and efflux of cationic amino acid, requires Na+ for optimal activity. Can also operate with H+ in absence of Na+ (PMID: 11546643).	
GLPASE1	glycogen phosphorylase (glygn2 -> dxtrn)	3 pi[c] + glygn2[c] -> 3 g1p[c] + dxtrn[c]	0	19309.1 or 110078.1 or 110095.1	0	1000		Starch and Sucrose Metabolism			
GLPASE2	glycogen phosphorylase (amyls -> glc-D)	7 h2o[c] + glygn3[c] -> 7 glc-D[c] + Tyr-ggn[c]	0	19309.1 or 110078.1 or 110095.1	0	1000		Starch and Sucrose Metabolism			
GLRASE	glucuronolactone reductase	nadp[c] + gullac[c] <=> h[c] + nadph[c] + glac[c]	1		-1000	1000		Ascorbate and Aldarate Metabolism			
GLU5Km	glutamate 5-kinase (m)	glu-L[m] + atp[m] -> adp[m] + glu5p[m]	0	56454.1	0	1000		Urea cycle/amino group metabolism			
GLUCYS	gamma-glutamylcysteine synthetase	atp[c] + glu-L[c] + cys-L[c] -> adp[c] + h[c] + pi[c] + glucys[c]	0	14630.1 or 14629.1	0	1000		Glutathione Metabolism			
GLUDC	Glutamate Decarboxylase	h[c] + glu-L[c] -> co2[c] + 4abut[c]	0	14415.1 or 14417.1 or 14415.2	0	1000		Glutamate metabolism			
GLUNm	glutaminase (mitochondrial)	h2o[m] + gln-L[m] -> glu-L[m] + nh4[m]	0	216456.1 or 14660.1 or 216456.2	0	1000		Glutamate metabolism			
GLUPRT	glutamine phosphoribosyldiphosphate amidotransferase	h2o[c] + prpp[c] + gln-L[c] -> glu-L[c] + ppi[c] + pram[c]	0	231327.1	0	1000		IMP Biosynthesis			
GLUTCOADHm	glutaryl-CoA dehydrogenase (mitochondria)	h[m] + glutcoa[m] + fad[m] -> co2[m] + b2coa[m] + fadh2[m]	0	270076.1 or 270076.2	0	1000		Tryptophan metabolism			
GLUt2m	L-glutamate reversible transport via proton symport, mitochondrial	h[c] + glu-L[c] <=> h[m] + glu-L[m]	1	71803.1 or 68267.1 or 78830.1 or 50799.1	-1000	1000		Transport, Mitochondrial			
GLUt6	Glutamate transport via Na, H symport and K antiport	h[e] + 3 na1[e] + k[c] + glu-L[e] -> h[c] + 3 na1[c] + glu-L[c] + k[e]	0	242607.1 or 20511.1 or 20513.1 or 20510.1 or 20512.1	0	1000		Transport, Extracellular			
GLUt7l	Glutamate transport, lysosomal	glu-L[l] -> glu-L[c]	0		0	1000		Transport, Lysosomal			
GLUtr	intracellular transport	glu-L[c] <=> glu-L[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
GLXO2p	glyoxylate oxidase, peroxisomal	o2[x] + h2o[x] + glx[x] -> h[x] + h2o2[x] + oxa[x]	0	15112.1 or 56185.1 or 56185.2	0	1000		Glyoxylate and Dicarboxylate Metabolism			
GLXtm	glyoxylate transport, mitochondrial	glx[c] <=> glx[m]	1		-1000	1000		Transport, Mitochondrial			
GLXtp	glyoxylate transport, peroxisomal	glx[c] <=> glx[x]	1		-1000	1000		Transport, Peroxisomal			
GLYAMDTRc	glycine amidinotransferase (c)	gly[c] + arg-L[c] <=> orn[c] + gudac[c]	1	67092.1	-1000	1000		Urea cycle/amino group metabolism			
GLYATB0tc	transport of Glycine into the intestinal cells by ATB0 transporter	2 na1[u] + cl[u] + gly[u] -> 2 na1[c] + cl[c] + gly[c]	0	56774.1	0	1000	3	Transport, Lumen	PMID:18195088	ATB0 is both sodium and chloride coupled, with reaction stoichiometry 2Na+:1cl:1amino acid. The transporter is localted in the intestine, has a broad substrate specificity (both neutral and cationic amino acids), but is not involved in the transport of aspartate, glutamate and proline (PMID:18195088).	
GLYATm	glycine C-acetyltransferase	accoa[m] + gly[m] <=> coa[m] + 2aobut[m]	1	26912.1	-1000	1000	2	Glycine, Serine, and Threonine Metabolism			
GLYB0AT1tc	transport of Glycine by the apical neutral amino acid transporters in kidney and intestine	na1[u] + gly[u] -> na1[c] + gly[c]	0	(70008.1 or (74338.1 and 57394.1))	0	1000	3	Transport, Lumen	PMID: 19472175, PMID: 15804236, PMID: 18400692	transports all the neutral amino acids with preference for methionine, leucine and valine. Reaction stoichiometry is 1:1. Requires heterodimerization with collectrin protein for increased affinity. Found in kidney and intestine, however also reported to be expressed in skin. Requires association with ACE2 for expression in intestine but with collectrin for expression in kidney.	3.4.17.23
GLYBt4_2_r	Betaine transport (sodium symport) (2:1)	2 na1[e] + glyb[e] <=> 2 na1[c] + glyb[c]	1	14411.1	-1000	1000		Transport, Extracellular			
GLYBtm	Glycine betaine transport via diffusion (mitochondria to cytosol)	glyb[m] <=> glyb[c]	1		-1000	1000		Transport, Mitochondrial			
GLYC3Ptm	glycerol-3-phosphate shuttle	glyc3p[c] -> glyc3p[m]	0		0	1000		Transport, Mitochondrial			
GLYCK2	glycerate kinase	atp[c] + glyc-R[c] -> adp[c] + h[c] + 2pg[c]	0		0	1000		Glyoxylate and Dicarboxylate Metabolism			
GLYCLTDy	Glycolate dehydrogenase (NADP)	h[c] + nadph[c] + glx[c] -> nadp[c] + glyclt[c]	0	76238.1	0	1000		Glyoxylate and Dicarboxylate Metabolism			
GLYCLTDym	Glycolate dehydrogenase (NADP), mitochondrial	h[m] + nadph[m] + glx[m] -> nadp[m] + glyclt[m]	0		0	1000		Glyoxylate and Dicarboxylate Metabolism			
GLYCLTtp	glycolate transport into peroxisome	glyclt[c] -> glyclt[x]	0		0	1000		Transport, Peroxisomal			
GLYCTO1p	Glycolate oxidase, peroxisome	o2[x] + glyclt[x] -> h2o2[x] + glx[x]	0	15112.1 or 56185.1 or 56185.2	0	1000		Glyoxylate and Dicarboxylate Metabolism			
GLYC_St	L-glycerate export	glyc-S[c] -> glyc-S[e]	0		0	1000		Transport, Extracellular			
GLYCt	glycerol transport via channel	glyc[c] <=> glyc[e]	1		-1000	1000		Transport, Extracellular			
GLYCtm	glycerol transport	glyc[c] <=> glyc[m]	1		-1000	1000		Transport, Mitochondrial			
GLYGLYCNc	hydrolysis of glycylycine for uptake	h2o[c] + glygly[c] <=> 2 gly[c]	1	(338403.1 or 66054.1)	-1000	1000	4	Dipeptide Degradation	PMID: 6993048, PMCID: PMC1412501, PMID: 4919261, PMID: 20178671, PMID: 12473676	Dipeptides and tripeptides enter the brush border of the intestinal mucosal cells, where they are hydrolyzed to free amino acids, which are then transported into hepatic portal vein. Peptides entering by transcellular or paracellular mechanisms elicit allergic reactions to food (Robert K. Murray, David A. Bender, Kathleen M. Botham, Peter J. kennelly, Victor W. Rodwell, P. Anthony Weil (2009) 28th edition, Harper's illustrated biochemistry,Mc Graw Hill, page 462). formation and hydrolysis of diglycine is a reversible process (David L. Nelson, Michael M. Cox, Lehniniger principles of biochemistry (2000), 3rd edition, worth publishers,page 69, figure 3a). CN1 is expressed in brain where as CN2 is more ubiquitously expressed (PMID: 12473676).	3.4.13.20 or 3.4.13.18
GLYGLYPEPT1tc	transport of Glycyl-glycine by the apical PEPT1 amino acid transporters across the brush border cells of the enterocytes of the intestine and renal cells	glygly[u] -> h[u] + glygly[c]	0	215335.1	0	1000	3	Transport, Lumen	PMID: 7858848, PMID: 14965252, PMID: 14977407, PMID: 10330047	PEPT1 appears to transport all di- and tri- peptides across the brush border of the intestinal cells (Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Advanced nutrition and human metabolism, Wadsworth cengage learning, 5th edition, page 193). PEPT1 is expressed highly in intestinal cells where as PEPT2 is localized to renal cells (PMID: 10330047).	
GLYGLYt	Glycylglycine transport	h[e] + glygly[e] <=> h[c] + glygly[c]	1		-1000	1000	1	Transport, Extracellular		Needed to provide this metabolite for reaction GLYGLYPEPT1tc in joint model.	
GLYK	glycerol kinase	atp[c] + glyc[c] -> adp[c] + h[c] + glyc3p[c]	0	14933.1 or 14933.2 or 14626.1	0	1000		Glycerophospholipid Metabolism			
GLYKm	glycerol kinase	atp[m] + glyc[m] -> h[m] + adp[m] + glyc3p[m]	0	14933.1 or 14933.2 or 14626.1	0	1000		Glycerophospholipid Metabolism			
GLYLEUHYDROc	hydrolysis of Glycylleucine in the small intestine for cellular uptake	h2o[c] + glyleu[c] <=> leu-L[c] + gly[c]	1	(13479.1 or 66054.1)	-1000	1000	3	Dipeptide Degradation	PMID: 4074331, PMID: 964683	BRENDA also lists beta-Ala-His dipeptidase (E.C. 3.4.13.20) as another enzyme catalyzing this reaction, but no literature evidence found.	3.4.13.19 or 3.4.13.18
GLYLEUPEPT1tc	transport of Glycylleucine by the apical PEPT1 amino acid transporters across the brush border cells of the enterocytes of the intestine and renal cells	h[u] + glyleu[u] -> h[c] + glyleu[c]	0	215335.1	0	1000	3	Transport, Lumen	PMID: 7858848, PMID: 14965252, PMID: 14977407, PMID: 10330047	PEPT1 appears to transport all di- and tri- peptides across the brush border of the intestinal cells (Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Advanced nutrition and human metabolism, Wadsworth cengage learning, 5th edition, page 193). PEPT1 is expressed highly in intestinal cells where as PEPT2 is localized to renal cells (PMID: 10330047).	
GLYOX	hydroxyacylglutathione hydrolase	h2o[c] + lgt-S[c] -> h[c] + gthrd[c] + lac-D[c]	0	14651.1 or 68977.2 or 68977.1	0	1000		Pyruvate Metabolism			
GLYOXm	hydroxyacylglutathione hydrolase, mitochondrial	h2o[m] + lgt-S[m] -> h[m] + lac-D[m] + gthrd[m]	0	14651.1	0	1000		Pyruvate Metabolism			
GLYOp	glycine oxidase, perixosomal	o2[x] + h2o[x] + gly[x] -> h2o2[x] + glx[x] + nh4[x]	0		0	1000		Glycine, Serine, and Threonine Metabolism			
GLYPATtc	transport of Glycine by the apical PAT2 or PAT1 amino acid transporters in kidney and intestine	h[u] + gly[u] -> h[c] + gly[c]	0	215335.1	0	1000	3	Transport, Lumen	PMID:18195088, PMID:18400692, PMID: 17123464, PMCID: PMC34647, PMID: 15345686	PAT2 is strongly expressed in heart and lung and more weakly in kidney and muscle (PMID:18400692). PAT2 can also transport glycine bidirectionally, depending on the membrane potential and substrate/proton gradient (PMID: 14600155). PAT1 proton-amino acid co-transporter with 1:1 stoichiometry, does not discriminate between L and D isomers, located on the apical membrane of kidney and intestine (PMID: 18400692, PMID: 18195088).	
GLYPHEPEPT1tc	transport of Glycylphenylalanine by the apical PEPT1 amino acid transporters across the brush border cells of the enterocytes of the intestine and renal cells	h[u] + glyphe[u] -> h[c] + glyphe[c]	0	215335.1	0	1000	3	Transport, Lumen	PMID: 7858848, PMID: 14965252, PMID: 14977407, PMID: 10330047	PEPT1 appears to transport all di- and tri- peptides across the brush border of the intestinal cells (Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Advanced nutrition and human metabolism, Wadsworth cengage learning, 5th edition, page 193). PEPT1 is expressed highly in intestinal cells where as PEPT2 is localized to renal cells (PMID: 10330047).	
GLYPHEt	Glycylphenylalanine transport	h[e] + glyphe[e] <=> h[c] + glyphe[c]	1		-1000	1000	1	Transport, Extracellular		Needed to provide this metabolite for reaction GLYPHEPEPT1tc in joint model.	
GLYPROPEPT1tc	transport of Glycylproline by the apical PEPT1 amino acid transporters across the brush border cells of the enterocytes of the intestine and renal cells	h[u] + glypro[u] -> h[c] + glypro[c]	0	215335.1	0	1000	3	Transport, Lumen	PMID: 7858848, PMID: 14965252, PMID: 14977407, PMID: 10330047	PEPT1 appears to transport all di- and tri- peptides across the brush border of the intestinal cells (Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Advanced nutrition and human metabolism, Wadsworth cengage learning, 5th edition, page 193). PEPT1 is expressed highly in intestinal cells where as PEPT2 is localized to renal cells (PMID: 10330047).	
GLYPROPRO1c	hydrolysis of Prolylglycine in the small intestine for cellular uptake	h2o[c] + glypro[c] <=> gly[c] + pro-L[c]	1	18624.1	-1000	1000	3	Dipeptide Degradation	PMID: 14580160, PMID: 2317925, PMID: 18340504, Rubino A, Pierro M, Torretta GL, Vetrella M, Martino DD, Auricch S. (1969). Pediatric Research 3: 313-9	prolidase 1 and 2 both have same E.C. Numbers, prolidase 1 has a substrate preference for glycylproline where as prolidase 2 catalyzes very slowly this reaction (PMID: 14580160).	3.4.13.9
GLYSARCNc	hydrolysis of glycylsarcosine for uptake	h2o[c] + glysar[c] <=> gly[c] + sarcs[c]	1	12751.1	-1000	1000	3	Dipeptide Degradation	PMID:6746633, PMID: 4778946, PMID: 7171621, PMID: 3293467	glycine-sarcosine is resistant to hydrolysis and the only enzyme to catalyze hydrolysis is prolidase in rabbit intestine (PMID:6746633). Further glycine-sarcosine and glycylalanine have been assumed to have a common transport system. It may also remain intact (PMID: 3293467).	3.4.14.9
GLYSARPEPT1tc	transport of Glycylsarcosine by the apical PEPT1 amino acid transporters across the brush border cells of the enterocytes of the intestine, renal cells and brain.	h[u] + glysar[u] -> h[c] + glysar[c]	0	215335.1	0	1000	3	Transport, Lumen	PMID: 7858848, PMID: 14965252, PMID: 14977407, PMID: 10330047	PEPT1 appears to transport all di- and tri- peptides across the brush border of the intestinal cells (Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Advanced nutrition and human metabolism, Wadsworth cengage learning, 5th edition, page 193). PEPT1 is expressed highly in intestinal cells where as PEPT2 is localized to renal cells (PMID: 10330047). glycine-sarcosine is also transported accros the brain specifically by PEPT2 (PMID: 20571525).	
GLYSARt	Glycylsarcosine transport	h[e] + glysar[e] <=> h[c] + glysar[c]	1		-1000	1000	1	Transport, Extracellular		Needed to provide this metabolite for reaction GLYSARPEPT1tc in joint model.	
GLYSNAT5tc	transport of Glycine into the cell coupled with co-transport with Sodium and counter transport with proton by SNAT5 transporter.	h[c] + na1[u] + gly[u] <=> na1[c] + h[u] + gly[c]	1	209837.1	-1000	1000	3	Transport, Lumen	PMID: 12845534, PMCID: PMC1665133, PMID:18195088	SNAT5 performs both symport with sodium and antiport with proton, for the net transport of neutral amino acid into the cell. Cellular localization has been reported in stomach, brain, liver, lung, small intestine, spleen, colon and kidney. (PMID: 12845534)	
GLYVESSEC	Glycine secretion via secretory vesicle (ATP driven)	h2o[c] + atp[c] + 3 gly[c] -> adp[c] + h[c] + pi[c] + 3 gly[e]	0	22348.1	0	1000		Transport, Extracellular			
GLYt2r	glycine reversible transport via proton symport	h[e] + gly[e] <=> h[c] + gly[c]	1	215335.1	-1000	1000		Transport, Extracellular			
GLYt2rL	glycine reversible transport via proton symport (lysosome)	h[l] + gly[l] <=> h[c] + gly[c]	1	215335.1	-1000	1000		Transport, Lysosomal			
GLYt4	glycine transport via sodium symport	na1[e] + gly[e] -> na1[c] + gly[c]	0	105727.1 or 67760.1 or 69354.1 or 56774.1	0	1000	0	Transport, Extracellular			
GLYt7_211_r	glycine reversible transport via sodium and chloride symport (2:1:1)	2 na1[e] + gly[e] + cl[e] <=> 2 na1[c] + cl[c] + gly[c]	1	14664.1 or 14664.2	-1000	1000	2	Transport, Extracellular			

GLYt7_311_r	glycine reversible transport via sodium and chloride symport (3:1:1)	3 na1[e] + gly[e] + cl[e] <=> 3 na1[c] + cl[c] + gly[c]	1	104245.1	-1000	1000		Transport, Extracellular			
GLYtm	glycine passive transport to mitochondria	gly[c] <=> gly[m]	1		-1000	1000		Transport, Mitochondrial			
GLYtp	glycine passive transport to peroxisome	gly[c] <=> gly[x]	1		-1000	1000		Transport, Peroxisomal			
GMAND	GDP-D-mannose dehydratase	gdpmann[c] -> h2o[c] + gdpddman[c]	0	218138.1	0	1000		Fructose and Mannose Metabolism			
GMPR	GMP reductase	2 h[c] + nadph[c] + gmp[c] -> nh4[c] + nadp[c] + imp[c]	0	105446.1 or 105446.2 or 105446.3 or 66355.1	0	1000		Nucleotides			
GMPS2	GMP synthase	h2o[c] + atp[c] + gln-L[c] + xmp[c] -> 2 h[c] + glu-L[c] + amp[c] + ppi[c] + gmp[c]	0	229363.1	0	1000		Nucleotides			
GMPtg	GMP intracellular transport	gmp[c] <=> gmp[g]	1		-1000	1000		Transport, Golgi Apparatus			
GMPtn	GMP nuclear transport	gmp[c] <=> gmp[n]	1		-1000	1000		Transport, Nuclear			
GNCORE1t	gncore1 (mucin O-glycan) export	gncore1[g] -> gncore1[e]	0		0	1000	2	Transport, Extracellular	PMID: 10430883, PMID: 848954	Reaction that provides mucin O-glycans to gut microbiota, e.g. B. thetaiotaomicron. BT is well known to degrade mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis.	
GNCORE2t	gncore2 (mucin O-glycan) export	gncore2[g] -> gncore2[e]	0		0	1000	2	Transport, Extracellular	PMID: 10430883, PMID: 848954	Reaction that provides mucin O-glycans to gut microbiota, e.g. B. thetaiotaomicron. BT is well known to degrade mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis.	
GND	phosphogluconate dehydrogenase	nadp[c] + 6pgc[c] -> nadph[c] + co2[c] + ru5p-D[c]	0	110208.1	0	1000		Pentose Phosphate Pathway			
GNDer	phosphogluconate dehydrogenase, endoplasmic reticulum	nadp[r] + 6pgc[r] -> nadph[r] + co2[r] + ru5p-D[r]	0		0	1000		Pentose Phosphate Pathway			
GNMT	glycine N-methyltransferase	amet[c] + gly[c] -> h[c] + ahcys[c] + sarcs[c]	0	14711.1	0	1000		Glycine, Serine, and Threonine Metabolism			
GP1CALPHAte	gp1calpha_hs transport	gp1calpha_hs[c] <=> gp1calpha_hs[e]	1		-1000	1000		Transport, Extracellular			
GP1CALPHAtg	gp1calpha_hs intracellular transport	gp1calpha_hs[c] <=> gp1calpha_hs[g]	1		-1000	1000		Transport, Golgi Apparatus			
GP1Cte	gp1c_hs transport	gp1c_hs[c] <=> gp1c_hs[e]	1		-1000	1000		Transport, Extracellular			
GP1Ctg	gp1c_hs intracellular transport	gp1c_hs[c] <=> gp1c_hs[g]	1		-1000	1000		Transport, Golgi Apparatus			
GPAM_hs	glycerol-3-phosphate acyltransferase	Rtotalcoa[c] + glyc3p[c] -> coa[c] + alpa_hs[c]	0	14732.1	0	1000		Triacylglycerol Synthesis			
GPAMm_hs	glycerol-3-phosphate acyltransferase	Rtotalcoa[m] + glyc3p[m] -> coa[m] + alpa_hs[m]	0	14732.1	0	1000		Triacylglycerol Synthesis			
GPDDA1	Glycerophosphodiester phosphodiesterase (Glycerophosphocholine)	h2o[c] + g3pc[c] -> h[c] + chol[c] + glyc3p[c]	0		0	1000		Glycerophospholipid Metabolism			
GPIAT	glucosaminylphosphatidyl inositol acetyltransferase	gpail_hs[c] + pmtcoa[c] -> coa[c] + gacpail_hs[c]	0	70325.1	0	1000		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
GPIDA2er	glycophosphatidylinositol (GPI) deacylase, endoplasmic reticulum	h2o[r] + em2emgacpail_prot_hs[r] -> h[r] + dem2emgacpail_prot_hs[r] + hdca[r]	0	241062.1	0	1000		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
GPIDAer	glycophosphatidylinositol (GPI) deacylase, endoplasmic reticulum	h2o[r] + gpi_prot_hs[r] -> h[r] + dgpi_prot_hs[r] + hdca[r]	0	241062.1	0	1000		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
GPIMTer_L	GlcN-acylPI mannosyltransferase, endoplasmic reticulum	0.1 dolmanp_L[r] + gacpail_hs[r] -> 0.1 dolp_L[r] + h[r] + mgacpail_hs[r]	0	67556.1 or 72084.1	0	1000		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
GPIMTer_U	GlcN-acylPI mannosyltransferase, endoplasmic reticulum	0.1 dolmanp_U[r] + gacpail_hs[r] -> h[r] + 0.1 dolp_U[r] + mgacpail_hs[r]	0	67556.1 or 72084.1	0	1000		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
GQ1BALPHAte	gq1balpha_hs transport	gq1balpha_hs[c] <=> gq1balpha_hs[e]	1		-1000	1000		Transport, Extracellular			
GQ1BALPHAtg	gq1balpha_hs intracellular transport	gq1balpha_hs[c] <=> gq1balpha_hs[g]	1		-1000	1000		Transport, Golgi Apparatus			
GQ1Bte	gq1b_hs transport	gq1b_hs[c] <=> gq1b_hs[e]	1		-1000	1000		Transport, Extracellular			
GQ1Btg	gq1b_hs intracellular transport	gq1b_hs[c] <=> gq1b_hs[g]	1		-1000	1000		Transport, Golgi Apparatus			
GRTT	geranyltranstransferase	ipdp[c] + grdp[c] -> ppi[c] + frdp[c]	0	14593.1	0	1000		Cholesterol Metabolism			
GRTTx	geranyltranstransferase	ipdp[x] + grdp[x] -> ppi[x] + frdp[x]	0	110196.1	0	1000		Cholesterol Metabolism			
GSNKm	guanosine kinase (mitochondrial)	atp[m] + gsn[m] -> h[m] + adp[m] + gmp[m]	0		0	1000		Nucleotides			
GSNt	guanosine facilated transport in cytosol	gsn[e] <=> gsn[c]	1	13340.1 or 63959.1	-1000	1000		Transport, Extracellular			
GSNt4	guanosine transport in via sodium symport	na1[e] + gsn[e] -> na1[c] + gsn[c]	0	114304.1 or 269346.1	0	1000		Transport, Extracellular			
GSNt5	guanosine transport in via sodium (1:2) symport	2 na1[e] + gsn[e] -> 2 na1[c] + gsn[c]	0	114304.1	0	1000		Transport, Extracellular			
GSNtl	guanosine facilated transport from lysosome	gsn[l] <=> gsn[c]	1	71279.1	-1000	1000		Transport, Lysosomal			
GSNtm	guanosine facilated transport in mitochondria	gsn[c] <=> gsn[m]	1	63959.1	-1000	1000		Transport, Mitochondrial			
GT1Ate	gt1a_hs transport	gt1a_hs[c] <=> gt1a_hs[e]	1		-1000	1000		Transport, Extracellular			
GT1Atg	gt1a_hs intracellular transport	gt1a_hs[c] <=> gt1a_hs[g]	1		-1000	1000		Transport, Golgi Apparatus			
GTHDH	Glutathione dehydrogenase (dehydroascorbate reductase)	dhdascb[c] + 2 gthrd[c] -> ascb-L[c] + gthox[c]	0		0	1000		Ascorbate and Aldarate Metabolism			
GTHO	glutathione oxidoreductase	h[c] + nadph[c] + gthox[c] -> nadp[c] + 2 gthrd[c]	0	14782.1	0	1000		Glutamate metabolism			
GTHOm	glutathione oxidoreductase	h[m] + nadph[m] + gthox[m] -> nadp[m] + 2 gthrd[m]	0	14782.1	0	1000		Glutamate metabolism			
GTHP	glutathione peridoxase	h2o2[c] + 2 gthrd[c] <=> 2 h2o[c] + gthox[c]	1	14776.1 or 14775.1 or 18477.1 or 21672.1 or 21672.2 or 18477.2 or 625249.1 or 18477.3 or 14775.2 or 21672.3	-1000	1000		Glutathione Metabolism			
GTHPe	glutathione peroxidase (e)	2 gthrd[e] + h2o2[e] <=> 2 h2o[e] + gthox[e]	1	75512.1 or 14778.1	-1000	1000		Glutathione Metabolism			
GTHPm	glutathione peroxidase, mitochondria	h2o2[m] + 2 gthrd[m] <=> 2 h2o[m] + gthox[m]	1	625249.1 or 11757.1 or 11757.2	-1000	1000		Glutathione Metabolism			
GTHRDt	Glutathione transport into mitochondria	h2o[c] + atp[c] + gthrd[c] <=> adp[c] + h[c] + pi[c] + gthrd[m]	1		-1000	1000		Glutathione Metabolism			
GTHRDtr	glutathione transport via diffusion	gthrd[c] <=> gthrd[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
GTHS	glutathione synthetase	atp[c] + gly[c] + glucys[c] -> adp[c] + h[c] + pi[c] + gthrd[c]	0	14854.1	0	1000		Glutathione Metabolism			
GTMLTe	g-glutamyltransferase (e)	ala-L[c] + gthrd[c] -> cgly[e] + gluala[e]	0	14598.1 or 14598.2 or 14598.3	0	1000		Glutathione Metabolism			
GTPCI	GTP cyclohydrolase I	h2o[c] + gtp[c] -> h[c] + for[c] + ahdt[c]	0	14528.1	0	1000		Tetrahydrobiopterin			
GTPCIn	GTP cyclohydrolase I, nuclear	h2o[n] + gtp[n] -> h[n] + for[n] + ahdt[n]	0	14528.1	0	1000		Tetrahydrobiopterin			
GTPtn	GTP diffusion in nucleus	gtp[c] <=> gtp[n]	1		-1000	1000		Transport, Nuclear			
GUACYC	guanylate cyclase	gtp[c] -> 35cgmp[c] + ppi[c]	0	(230103.1 or (60596.1 and 239134.1) or 234889.1 and 239134.1 or 14917.1 or (54195.1 and 234889.1) or 14919.1 or 230103.2 or 245650.1 or 18160.1 or (54195.1 and 60596.1))	0	1000		Nucleotides			
GUAD	guanine deaminase	h2o[c] + h[c] + gua[c] -> nh4[c] + xan[c]	0	14544.1	0	1000		Purine Catabolism			
GUAPRT	guanine phosphoribosyltransferase	prpp[c] + gua[c] -> ppi[c] + gmp[c]	0	15452.1	0	1000		Salvage Pathway			
GUAt	Guanine transport	gua[e] <=> gua[c]	1	13340.1	-1000	1000		Transport, Extracellular			
GULLACter	gulonolactone endoplasmic reticular transport	gullac[c] -> gullac[r]	0		0	1000		Transport, Endoplasmic Reticular			
GULN3D	L-gulonate 3-dehydrogenase	nad[c] + guln[c] <=> h[c] + nadh[c] + 3dhguln[c]	1		-1000	1000		Pentose and Glucuronate Interconversions			
GULNDer	gulonate dehydrogenase, endoplasmic reticulum	h[r] + nadph[r] + glcur[r] <=> nadp[r] + guln[r]	1		-1000	1000		Pentose and Glucuronate Interconversions			
GULNter	L-gulonate endoplasmic reticular export	guln[r] -> guln[c]	0		0	1000		Transport, Endoplasmic Reticular			
GUMDCHAe	binding of guar gums with deoxyxholic acid in the intestinal lumen, reducing serum cholsterol levels.	gum[u] + dchac[u] -> gumdchac[u]	0		0	1000	3	Food processing, Lumen	PMID: 21611850, PMID: 7825524, McFadzean B, Dicks P, Groenmeyer G, Harris P, O'Connor C. (2011). Minerals Engineering 24: 463-9, T.Pandolf and F.M. Clydesdale (1992) Journal of food science, vol.57, no.5, 1242-1245.	guar gum binds bile acids and leads to enhanced excretion, there by the 7-alpha hydroxylase pathway is activated laeding to increased cholesterol catabolism for synthesis of more bile acids (regulates cholesterol metabolism). however the decreased serum cholesterol levels are brought about by many other cumulative effects (water unstirred action of dieatary fibres, glycemic role etc) (PMID: 18302966, Gunness P, Gidley MJ. (2010). Food & Function 1: 149-55).	
GUMDCHAt	binding of guar gums with deoxycholic acid transport	h[e] + gumdchac[e] <=> h[c] + gumdchac[c]	1		-1000	1000	1	Transport, Extracellular		Needed to provide this metabolite for reaction GUMDCHAe in joint model.	
GUMGCHLe	binding of guar gums with glycocholate in the intestinal lumen, reducing serum cholsterol levels.	gchola[u] + gum[u] -> gumgchol[u]	0		0	1000	3	Food processing, Lumen	PMID: 21611850, PMID: 7825524, McFadzean B, Dicks P, Groenmeyer G, Harris P, O'Connor C. (2011). Minerals Engineering 24: 463-9, T.Pandolf and F.M. Clydesdale (1992) Journal of food science, vol.57, no.5, 1242-1245.	guar gum binds bile acids and leads to enhanced excretion, there by the 7-alpha hydroxylase pathway is activated laeding to increased cholesterol catabolism for synthesis of more bile acids (regulates cholesterol metabolism). however the decreased serum cholesterol levels are brought about by many other cumulative effects (water unstirred action of dieatary fibres, glycemic role etc) (PMID: 18302966, Gunness P, Gidley MJ. (2010). Food & Function 1: 149-55).	
GUMGCHLt	binding of guar gums with glycocholate transport	h[e] + gumgchol[e] <=> h[c] + gumgchol[c]	1		-1000	1000	1	Transport, Extracellular		Needed to provide this metabolite for reaction GUMGCHLe in joint model.	
GUMTCHOLe	binding of guar gums with taurocholate in the intestinal lumen, reducing serum cholsterol levels.	tchola[u] + gum[u] -> gumtchol[u]	0		0	1000	3	Food processing, Lumen	PMID: 21611850, PMID: 7825524, McFadzean B, Dicks P, Groenmeyer G, Harris P, O'Connor C. (2011). Minerals Engineering 24: 463-9, T.Pandolf and F.M. Clydesdale (1992) Journal of food science, vol.57, no.5, 1242-1245.	guar gum binds bile acids and leads to enhanced excretion, there by the 7-alpha hydroxylase pathway is activated laeding to increased cholesterol catabolism for synthesis of more bile acids (regulates cholesterol metabolism). however the decreased serum cholesterol levels are brought about by many other cumulative effects (water unstirred action of dieatary fibres, glycemic role etc) (PMID: 18302966, Gunness P, Gidley MJ. (2010). Food & Function 1: 149-55).	
GUMTCHOLt	binding of guar gums with taurocholate transport	h[e] + gumtchol[e] <=> h[c] + gumtchol[c]	1		-1000	1000	1	Transport, Extracellular		Needed to provide this metabolite for reaction GUMTCHOLe in joint model.	
GUMt	Guar gum transport	h[e] + gum[e] <=> h[c] + gum[c]	1		-1000	1000	1	Transport, Extracellular		Needed to provide this metabolite for reaction GUMDCHAe, GUMGCHLe and GUMTCHOLe in joint model.	
GUR1PP	Glucuronate 1-phosphate phosphatase	h2o[c] + glcur1p[c] -> pi[c] + glcur[c]	0		0	1000		Pentose and Glucuronate Interconversions			
GluForTx	Glutamate formimidoyltransferase	h[c] + thf[c] + forglu[c] -> glu-L[c] + 5forthf[c]	0	14317.1 or 14317.2	0	1000		Histidine Metabolism			
H2CO3D	carboxylic acid dissociation	h2o[c] + co2[c] <=> h2co3[c]	1	12354.1 or 76459.2 or 76459.1 or 12349.1 or 12351.1 or 12350.1 or 12346.1 or 71934.1 or 12354.2 or 23831.1 or 230099.1	-1000	1000		Miscellaneous			
H2CO3D2	carboxylic acid dissociation	h[c] + hco3[c] <=> h2co3[c]	1		-1000	1000		Miscellaneous			
H2CO3D2m	carboxylic acid dissociation, mitochondrial	h[m] + hco3[m] <=> h2co3[m]	1		-1000	1000		Miscellaneous			
H2CO3Dm	carboxylic acid dissociation	h2o[m] + co2[m] <=> h2co3[m]	1	12352.1 or 56078.1	-1000	1000		Miscellaneous			
H2ETer	H2 phosphoethanolaminyl transferase, endoplasmic reticulum	mgacpail_hs[r] + pe_hs[r] -> dag_hs[r] + emgacpail_hs[r]	0	27392.1 or 27392.2	0	1000		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
H2MTer_L	H2 mannosyltransferase, endoplasmic reticulum	0.1 dolmanp_L[r] + mgacpail_hs[r] -> 0.1 dolp_L[r] + h[r] + m2gacpail_hs[r]	0	230801.1	0	1000		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
H2MTer_U	H2 mannosyltransferase, endoplasmic reticulum	0.1 dolmanp_U[r] + mgacpail_hs[r] -> h[r] + 0.1 dolp_U[r] + m2gacpail_hs[r]	0	230801.1	0	1000		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
H2O2syn	Hydrogen peroxide synthesis (NADPH dependent)	o2[c] + h[c] + nadph[c] -> h2o2[c] + nadp[c]	0	99439.1 or 99439.2 or 214593.1	0	1000		Tyrosine metabolism			
H2O2t	hydrogen peroxide transport via diffusion	h2o2[e] <=> h2o2[c]	1		-1000	1000		Transport, Extracellular			
H2O2tly	hydrogen peroxide lysosomal transport via diffusion	h2o2[c] <=> h2o2[l]	1		-1000	1000		Transport, Lysosomal			
H2O2tm	hydrogen peroxide mitochondrial transport	h2o2[c] <=> h2o2[m]	1		-1000	1000		Transport, Mitochondrial			
H2O2tn	hydrogen peroxide nuclear transport	h2o2[c] <=> h2o2[n]	1		-1000	1000		Transport, Nuclear			
H2O2tp	hydrogen peroxide peroxisomal transport via diffusion	h2o2[c] <=> h2o2[x]	1		-1000	1000		Transport, Peroxisomal			
H2Ot	H2O transport via diffusion	h2o[e] <=> h2o[c]	1	20537.1	-1000	1000		Transport, Extracellular			
H2Oter	H2O endoplasmic reticulum transport	h2o[c] <=> h2o[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
H2Otg	H2O transport, Golgi apparatus	h2o[c] <=> h2o[g]	1		-1000	1000		Transport, Golgi Apparatus			
H2Otly	H2O transport, lysosomal	h2o[c] <=> h2o[l]	1		-1000	1000		Transport, Lysosomal			
H2Otm	H2O transport, mitochondrial	h2o[c] <=> h2o[m]	1	11833.1	-1000	1000		Transport, Mitochondrial			

H2Ote	H2O transport, nucleur	h2o[n] <=> h2o[c]	1		-1000	1000		Transport, Nuclear			
H2Op	H2O transport, peroxisomal	h2o[c] <=> h2o[x]	1		-1000	1000		Transport, Peroxisomal			
H3ETer	H3 phosphoethanolaminyl transferase, endoplasmic reticulum	pe_hs[r] + ms2gecpail_hs[r] -> mensgecpail_hs[r] + dag_hs[r]	0	27392.1 or 27392.2	0	1000		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
H3MTer_L	H3 mannosyltransferase, endoplasmic reticulum	0.1 dolmanp_L[r] + ms2gecpail_hs[r] -> 0.1 dolp_L[r] + h[c] + ms2mecpail_hs[r]	0	55981.1	0	1000		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
H3MTer_U	H3 mannosyltransferase, endoplasmic reticulum	0.1 dolmanp_L[r] + ms2gecpail_hs[r] -> h[r] + 0.1 dolp_L[r] + ms2mecpail_hs[r]	0	55981.1	0	1000		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
H4ETer	H4 phosphoethanolaminyl transferase, endoplasmic reticulum	pe_hs[r] + ms2gecpail_hs[r] -> dag_hs[r] + ens2engecpail_hs[r]	0	56703.1 or 18701.1 or 18701.2 or 56703.2	0	1000		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
H4ETer	H4 phosphoethanolaminyl transferase, endoplasmic reticulum	pe_hs[r] + ms2gecpail_hs[r] -> ens2engecpail_hs[r] + dag_hs[r]	0	27392.1 or 27392.2	0	1000		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
H5MTer_L	H5 mannosyltransferase, endoplasmic reticulum	0.1 dolmanp_L[r] + ensgecpail_hs[r] -> mensgecpail_hs[r] + 0.1 dolp_L[r] + h[r]	0	230801.1	0	1000		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
H5MTer_U	H5 mannosyltransferase, endoplasmic reticulum	dolmanp_L[r] + ensgecpail_hs[r] -> mensgecpail_hs[r] + 2 h[r] + dolp_L[r]	0	230801.1	0	1000	2	Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
H6ETer	H6 phosphoethanolaminyl transferase, endoplasmic reticulum	ms2engecpail_hs[r] + pe_hs[r] -> dag_hs[r] + ens2engecpail_hs[r]	0	56703.1 or 18701.1 or 18701.2 or 56703.2	0	1000	2	Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
H6MTer_L	H6 mannosyltransferase, endoplasmic reticulum	0.1 dolmanp_L[r] + ms2engecpail_hs[r] -> 0.1 dolp_L[r] + h[c] + ms3mngecpail_hs[r]	0	239827.1	0	1000		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
H6MTer_U	H6 mannosyltransferase, endoplasmic reticulum	ms2engecpail_hs[r] + 0.1 dolmanp_L[r] -> h[r] + 0.1 dolp_L[r] + ms3mngecpail_hs[r]	0	239827.1	0	1000		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
H6_ET2er	H6 phosphoethanolaminyl transferase, endoplasmic reticulum	pe_hs[r] + ens3gecpail_hs[r] -> dag_hs[r] + ensen2gecpail_hs[r]	0	18701.1 or 433931.1 or 18701.2	0	1000		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
H6_ETer	H6 phosphoethanolaminyl transferase, endoplasmic reticulum	pe_hs[r] + ens3gecpail_hs[r] -> dag_hs[r] + ens2engecpail_hs[r]	0	27392.1 or 27392.2	0	1000		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
H7ET2er	H7 phosphoethanolaminyl transferase, endoplasmic reticulum	pe_hs[r] + ens2ensgecpail_hs[r] -> dag_hs[r] + gpi_hs[r]	0	18701.1 or 433931.1 or 18701.2	0	1000	2	Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
H7MTer_L	H7 mannosyltransferase, endoplasmic reticulum	0.1 dolmanp_L[r] + ens2ensgecpail_hs[r] -> 0.1 dolp_L[r] + h[r] + ensen2ensecpail_hs[r]	0	239827.1	0	1000		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
H7MTer_U	H7 mannosyltransferase, endoplasmic reticulum	dolmanp_L[r] + ens2ensgecpail_hs[r] -> 2 h[r] + dolp_L[r] + ensen2ensgecpail_hs[r]	0	239827.1	0	1000	2	Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
H7_ETer	H7 phosphoethanolaminyl transferase, endoplasmic reticulum	pe_hs[r] + ensen2gecpail_hs[r] -> dag_hs[r] + gpi_hs[r]	0	27392.1 or 27392.2	0	1000		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
H7_TAer	H7 transamidase, endoplasmic reticulum	ens2engecpail_hs[r] + prot_prot[r] -> gpi_sig[r] + ens2engecpail_prot_hs[r]	0	276846.1 or 78928.1 or 228812.2 or 14731.1 or 329777.1	0	1000		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
H8MTer_L	H8 mannosyltransferase, endoplasmic reticulum	0.1 dolmanp_L[r] + gpi_hs[r] -> 0.1 dolp_L[r] + h[r] + ns4ensl3gecpail_hs[r]	0	239827.1	0	1000		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
H8MTer_U	H8 mannosyltransferase, endoplasmic reticulum	0.1 dolmanp_L[r] + gpi_hs[r] -> h[r] + 0.1 dolp_L[r] + ns4ensl3gecpail_hs[r]	0	239827.1	0	1000		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
H8TAer	H8 transamidase, endoplasmic reticulum	gpi_hs[r] + prot_prot[r] -> gpi_sig[r] + gpi_prot_hs[r]	0	276846.1 or 78928.1 or 228812.2 or 14731.1 or 329777.1	0	1000		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
HACD1m	3-hydroxyacyl-CoA dehydrogenase (acetoacetyl-CoA) (mitochondria)	h[m] + nadh[m] + aacoa[m] <=> nad[m] + 3hbcoa[m]	1	15107.1 or 231086.1 or 97212.1 or 15108.1	-1000	1000		Tryptophan metabolism			
HACD1x	3-hydroxyacyl-CoA dehydrogenase (acetoacetyl-CoA) (mitochondria)	h[x] + nadh[x] + aacoa[x] <=> nad[x] + 3hbcoa[x]	1	74147.1 or 15488.1	-1000	1000		Tryptophan metabolism			
HACD9m	3-hydroxyacyl-CoA dehydrogenase (2-Methylacetoacetyl-CoA), mitochondrial	nad[m] + 3hmbcoa[m] <=> h[m] + nadh[m] + 2maacoa[m]	1	15108.1	-1000	1000		Valine, Leucine, and Isoleucine Metabolism			
HAS1	hyaluronan synthase	uacgam[c] + udpg[cur] -> 2 h[c] + 2 udp[c] + ha_pre1[e]	0	15118.1 or 15116.1 or 15117.1 or 15118.2	0	1000		Hyaluronan Metabolism			
HAS2	hyaluronan synthase	ha_pre1[e] + uacgam[c] + udpglcur[c] -> 2 h[c] + 2 udp[c] + ha[e]	0	15118.1 or 15116.1 or 15117.1 or 15118.2	0	1000		Hyaluronan Metabolism			
HAdy	hyaluronan transport, extracellular to lysosome	ha[e] -> ha[l]	0		0	1000		Transport, Lysosomal			
HBZOPT10m	Hydroxybenzoate Decaprenyltransferase	4hbz[m] + decdp[m] -> 3dphb[m] + ppi[m]	0	71883.1	0	1000	2	Ubiquinone Biosynthesis			
HCO3_CLt	bicarbonate transport (Cl-/HCO3- exchange)	hco3[e] + cl[c] <=> hco3[c] + cl[e]	1	20533.1 or 20535.1 or 20536.1 or 240215.1 or 20536.2	-1000	1000		Transport, Extracellular			
HCO3_NAt	bicarbonate transport (Na/HCO3 cotransport)	hco3[e] + na1[e] <=> hco3[c] + na1[c]	1	218756.1	-1000	1000		Transport, Extracellular			
HCOLMARINte	xenobiotic transport	hcoumarin[e] <=> hcoumarin[c]	1		-1000	1000		Transport, Extracellular			
HDCAter	palmitate ER export	hdca[r] -> hdca[c]	0		0	1000		Transport, Endoplasmic Reticular			
HDCAtr	fatty acid transport via diffusion	hdca[e] <=> hdca[c]	1		-1000	1000		Transport, Extracellular			
HDCEAtr	fatty acid transport via diffusion	hdcea[e] <=> hdcea[c]	1		-1000	1000		Transport, Extracellular			
HDD2COAtx	hdd2coa intracellular transport	hdd2coa[c] <=> hdd2coa[x]	1		-1000	1000		Transport, Peroxisomal			
HESTRATRIOLte	hydroxylated estrogen derivative transport	hestratriol[c] <=> hestratriol[e]	1		-1000	1000		Transport, Extracellular			
HESTRATRIOLtr	hydroxylated estrogen derivative transport	hestratriol[c] <=> hestratriol[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
HEX1	hexokinase (D-glucose:ATP)	atp[c] + glc-D[c] -> adp[c] + h[c] + g6p[c]	0	15275.1 or 212032.1 or 103988.1 or 15275.2 or 15277.1 or 15275.3 or 103988.2 or 103988.3 or 15275.4 or 216019.1 or 15275.5	0	1000		Glycolysis/Gluconeogenesis			
HEX10	hexokinase (D-glucosamine:ATP)	atp[c] + gam[c] -> adp[c] + h[c] + gam6p[c]	0	15275.1 or 212032.1 or 103988.1 or 15275.2 or 15277.1 or 15275.3 or 103988.2 or 103988.3 or 15275.4 or 216019.1 or 15275.5	0	1000		Aminosugar Metabolism			
HEX4	hexokinase (D-mannose:ATP)	atp[c] + man[c] -> adp[c] + h[c] + man6p[c]	0	15275.1 or 212032.1 or 103988.1 or 15275.2 or 15277.1 or 15275.3 or 103988.2 or 103988.3 or 15275.4 or 216019.1 or 15275.5	0	1000		Fructose and Mannose Metabolism			
HEX7	hexokinase (D-fructose:ATP)	atp[c] + fru[c] -> adp[c] + h[c] + f6p[c]	0	15275.1 or 212032.1 or 103988.1 or 15275.2 or 15277.1 or 15275.3 or 103988.2 or 103988.3 or 15275.4 or 216019.1 or 15275.5	0	1000		Fructose and Mannose Metabolism			
HEXCCOAtx	fatty acid intracellular transport	hexccoa[c] <=> hexccoa[x]	1		-1000	1000		Transport, Peroxisomal			
HEXCCPT1	carnitine O-palmitoyltransferase	crn[c] + hexccoa[c] -> coa[c] + hexccrn[c]	0	12895.4 or 12894.1 or 78670.1 or 12895.2 or 12895.3 or 12895.1	0	1000		Carnitine shuttle			
HEXCCPT2	carnitine transferase	coa[m] + hexccrn[m] -> crn[m] + hexccoa[m]	0	12896.1	0	1000		Carnitine shuttle			
HEXCCRNt	transport into the mitochondria (carnitine)	hexccrn[c] -> hexccrn[m]	0	57279.1	0	1000		Carnitine shuttle			
HEXI2	fatty acid transport via diffusion	hexc[e] <=> hexc[c]	1		-1000	1000		Transport, Extracellular			
HGNTOR	Homogentisate: oxygen 1,2-oxidoreductase (decyclizing)	o2[c] + hgntst[c] -> h[c] + 4mlacac[c]	0	15233.1	0	1000		Tyrosine metabolism			
HIBDm	3-hydroxyisobutyrate dehydrogenase, mitochondrial	nad[m] + 3hmp[m] <=> h[m] + nadh[m] + 2mop[m]	1	58875.1	-1000	1000		Valine, Leucine, and Isoleucine Metabolism			
HISCAT1	transport of L-Histidine by y+ transporter	his-L[c] <=> his-L[p]	1	11987.1	-1000	1000	3	Transport, Extracellular	PMID: 14770310, PMID: 12501630, PMID: 17494634,PMID:18195088.	ubiquitously expressed y+ transport system, mediates uniport transport of arginine, lysine, ornithine and histidine. (PMID:18195088). Located on the basolateral surface, mediates a bidirectional uniport transport of actionic amino acid and is Na+ independent (PMID: 17494634). Recon 1 contains the reactions but with irreversible form.	
HISD	histidase	his-L[c] -> nh4[c] + urcan[c]	0	15109.1	0	1000		Histidine Metabolism			
HISDC	histidine decarboxylase	h[c] + his-L[c] -> co2[c] + hista[c]	0	15186.1 or 13195.1	0	1000		Histidine Metabolism			
HISILELAT2tc	transport of L-Histidine into the cell and efflux of L-Isoleucine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	ile-L[c] + his-L[e] -> ile-L[e] + his-L[c]	0	(20539.1 and 17254.1)	0	1000	3	Transport, Extracellular	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	litger affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the mebrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274).	
HISLAT1tc	transport of L-Histidine by LAT1 in association with 4F2hc, across the apical surface of the membranes.	leu-L[c] + his-L[u] -> leu-L[u] + his-L[c]	0	(20539.1 and 17254.1)	0	1000	4	Transport, Lumen	Hans Gerhard Vogel, Franz J. Hock, Jochen Maas, Dieter Mayer (2006), Drug discovery and evaluation: Safety and pharmacokinetic assays, Springer publication, Chapter II D, page 456, table 3, PMID: 15035298, PMID: 12634921, European Journal of Pharmacology 441 (2002) 127–132. Am J Physiol Cell Physiol 281:C1077-C1093, 2001. Amino Acids (2005) 29: 229–233 DOI 10.1007/s00726-005-0221-x, PMID: 11901210	leucine is the only amino acid tested for efflux. Expressed in ovary, placenta, brain, spleen, testis, activated lymphocytes and some tumor cells. Functions as a antiport transport system (DOI 10.1016/j.ceil.2009.01.02), requires heterodimerization with glycoprotein CD98 (Pflugers Arch-Eur J Physiol (2000) 440:503-512, DOI 10.1007/s004240000274, PMID: 10958334).	
HISPHELAT2tc	transport of L-Histidine into the cell and efflux of L-Phenylalanine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	phe-L[c] + his-L[e] -> phe-L[e] + his-L[c]	0	(20539.1 and 17254.1)	0	1000	3	Transport, Extracellular	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	litger affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the mebrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274).	
HISSNAT5tc	transport of L-Histidine into the cell coupled with co-transport with Sodium and counter transport with proton by SNAT5 transporter.	h[c] + na1[u] + his-L[u] <=> na1[c] + h[u] + his-L[c]	1	209837.1	-1000	1000	3	Transport, Lumen	PMID: 12845534, PMCID: PMC1665133, PMID:18195088	SNAT5 performs both symport with sodium and antiport with proton, for the net transport of neutral amino acid into the cell. Cellular localization has been reported in stomach, brain, liver, lung, small intestine, spleen, colon and kidney. (PMID: 12845534)	
HISTASE	Histaminase	h2o[c] + n2[c] + hista[c] -> h2o2[c] + nh4[c] + imeacr[c]	0	237940.1 or 237940.2 or 76507.1	0	1000		Histidine Metabolism			
HISTAVESSEC	Histamine secretion via secretory vesicle (ATP dircon)	2 h2o[c] + 2 atp[c] + 3 hista[c] -> 2 adp[c] + 2 h[c] + 2 n[c] + 3 hista[e]	0	214084.1 or 110877.1	0	1000		Transport, Extracellular			

HISTAtu	Histamine uniport	hista[e] <=> hista[c]	1	20518.1 or 20519.1 or 20518.2	-1000	1000		Transport, Extracellular			
HISabPTc	transport of L-Histidine by hPT3 or hPT4 peptide transporters.	h[l] + his-L[l] -> h[c] + his-L[c]	0	(65221.1 or 100561.1)	0	1000	3	Transport, Lysosomal	PMID: 16289537, PMID: 12905028, PMID: 17681807	hPT3 (human peptide transporter 3) transports histidine and di-peptides from the lysosomes into the cytosol. Co-transports proton, expressed in lung, thymus, spleen and faintly in brain, placenta, liver, adrenal gland and heart (PMID: 12905028). hPT4 expressed in brain, placenta and retina. Transports carnosine and histidine in a proton symport mechanism. (PMID: 12905028)	
HISt4	L-histidine transport in via sodium symport	na1[e] + his-L[e] -> na1[c] + his-L[c]	0	67760.1 or 56774.1	0	1000		Transport, Extracellular			
HISttNi	Histidine transport (Na, H coupled)	h[e] + 2 na1[e] + his-L[e] <=> h[e] + 2 na1[c] + his-L[c]	1	76257.1	-1000	1000		Transport, Extracellular			
HISttiDF	L-histidine transport via diffusion (extracellular to cytosol)	his-L[e] -> his-L[c]	0	69354.1	0	1000		Transport, Extracellular			
HISyLATtc	transport of L-Histidine by y+LAT1 or y+LAT2 transporters in small intestine and kidney	na1[e] + arg-L[c] + his-L[e] -> na1[c] + arg-L[e] + his-L[c]	0	(20540.1 or (330836.1 and 17254.1))	0	1000	3	Transport, Extracellular	PMID: 11546643, PMID:18195088	y+LAT1 and y+LAT2 transporters requires CD98 for sequesterization to the plasma membrane. Acts as an amino acid exchanger, with influx of neutral aminoa acids and efflux of cationic amino acid, requires Na+ for optimal activity. Can also operate with H+ in absence of Na+ (PMID: 11546643).	
HISyLATtbc	transport of Histidine by y+LAT1 or y+LAT2 with co-transporter of h in small intestine and kidney	h[e] + arg-L[c] + his-L[e] -> h[c] + arg-L[e] + his-L[c]	0	(20540.1 or (330836.1 and 17254.1))	0	1000	3	Transport, Extracellular	PMID: 11546643, PMID:18195088	y+LAT1 and y+LAT2 transporters requires CD98 for sequesterization to the plasma membrane. Acts as an amino acid exchanger, with influx of neutral aminoa acids and efflux of cationic amino acid, requires Na+ for optimal activity. Can also operate with H+ in absence of Na+ (PMID: 11546643).	
HKYNH	3-Hydroxy-L-kynurenine hydrolase	h2o[c] + 3hkynt[c] -> 3humbenz[c] + ala-L[c]	0	70789.1	0	1000		Tryptophan metabolism			
HKt	H+/K+ gastric/non-gastric P-ATPase and ABC ATPase	h2o[c] + atp[c] + k[e] -> adp[c] + pi[c] + h[e] + k[c]	0	11945.1 and 11944.1	0	1000		Transport, Extracellular			
HMBS	hydroxymethylbilane synthase	h2o[c] + 4 ptrhmb[c] -> 4 ohmb[c] + hmbil[c]	0	15288.1	0	1000		Heme Biosynthesis			
HMGCOAR	Hydroxymethylglutaryl CoA reductase (ir)	2 h[c] + 2 nadph[c] + hmgcoa[r] -> 2 nadp[c] + coa[r] + mev-R[r]	0	15357.1	0	1000		Cholesterol Metabolism			
HMGCOARx	Hydroxymethylglutaryl CoA reductase (ir)	2 h[x] + hmgcoa[x] + 2 nadph[x] -> coa[x] + mev-R[x] + 2 nadp[x]	0	15357.1	0	1000		Cholesterol Metabolism			
HMGCOASi	Hydroxymethylglutaryl CoA synthase (ir)	h2o[c] + aacoa[c] + accoa[c] -> h[c] + coa[c] + hmgcoa[c]	0	20871.1 or 20871.2	0	1000		Cholesterol Metabolism			
HMGCOASim	Hydroxymethylglutaryl CoA synthase (ir)	h2o[m] + accoa[m] + aacoa[m] -> h[m] + coa[m] + hmarcoa[m]	0	15360.1	0	1000		Cholesterol Metabolism			
HMGCOAtm	Hydroxymethylglutaryl-CoA reversible mitochondrial transport	hmgcoa[c] <=> hmgcoa[m]	1		-1000	1000		Transport, Mitochondrial			
HMGCOAtx	Hydroxymethylglutaryl-CoA reversible peroxisomal transport	hmgcoa[c] <=> hmgcoa[x]	1		-1000	1000		Transport, Peroxisomal			
HMGLm	hydroxymethylglutaryl-CoA lyase	hmgcoa[m] -> accoa[m] + acac[m]	0	208982.1 or 15356.1	0	1000		Cholesterol Metabolism			
HMGLx	hydroxymethylglutaryl-CoA lyase	hmgcoa[x] -> accoa[x] + acac[x]	0	15356.1	0	1000		Cholesterol Metabolism			
HOhb4	L-homoserine via sodium symport	na1[e] + hom-L[e] -> na1[c] + hom-L[c]	0	11988.1 or 11988.1 or 11987.1	0	1000		Transport, Extracellular			
HOXG	Heme oxygenase 1	3 o2[c] + 5 h[c] + 3 nadph[c] + pheme[c] -> 3 h2o[c] + 3 nadp[c] + biliverdin[c] + co[c] + fe2+[c]	0	15368.1 or 15369.1	0	1000		Heme Degradation			
HPACtr	hydroxyphenylacetate transport via diffusion	4hphac[c] <=> 4hphac[e]	1		-1000	1000		Transport, Extracellular			
HPCLx	2-hydroxyphytanoyl-CoA lyase	4 h[x] + phyt2oilxcoa[x] -> formcoa[x] + pristanal[x]	0		0	1000		Fatty Acid Metabolism			
HPDCACRNCPT1	carnitine fatty-acyl transferase	crn[c] + hpdcacoa[c] -> coa[c] + hpdcacrn[c]	0	12894.1 or 78070.1 or 12895.1 or 12895.2 or 12895.3	0	1000		Carnitine shuttle			
HPDCACRNCPT2	heptadecanoate transport into the mitochondria	coa[m] + hpdcacrn[m] -> crn[m] + hpdcacoa[m]	0	12896.1	0	1000		Carnitine shuttle			
HPDCACRNt	heptadecanoate transport into the mitochondria	hpdcacrn[c] -> hpdcacrn[m]	0	57279.1	0	1000		Carnitine shuttle			
HPDCAt	fatty acid transport via diffusion	hpdca[e] <=> hpdca[c]	1		-1000	1000		Transport, Extracellular			
HPETFABP1tc	transport of 5-HPETE into the enterocytes	2 5HPET[c] <=> 2 5HPET[r]	1	14080.1	-1000	1000	3	Transport, Endoplasmic Reticular	PMID: 9555061, PMCID: PMC2821027, PMID: 9054409, PMID: 9082452, PMCID: PMC2670630, http://rmss.3.libraries.rutgers.edu/dlr/TMP/rutgers-lib_26338-PDF-1.pdf	crystal structure of LFAB revealed 2 binding sites (in contrast to IFAB which has 1:1 stoichiometry) for oleate (PMID: 9054409). LFAB is expressed in liver, kidney, intestine, pancreas, stomach and lung (PMCID: PMC2670630). Once the long chain fatty acids enter the enterocytes, bind to the FABP reversibly, for transport into the E.R. to reconstitute triacylglycerols (PMID: 20522896, PMID: 19280719).	
HPRROhm	L-hydroxyproline dehydrogenase (NAD), mitochondrial	nad[m] + 4hpro-LT[m] -> 2 h[m] + nadh[m] + 1p3h5c[m]	0	212647.1 or 212647.2	0	1000		Arginine and Proline Metabolism			
HPYRDC	hydroxypyruvate decarboxylase	h[c] + hpyr[c] -> co2[c] + gcald[c]	0		0	1000		Glyoxylate and Dicarboxylate Metabolism			
HPYRDCm	hydroxypyruvate decarboxylase, mitochondria	h[m] + hpyr[m] -> co2[m] + gcald[m]	0		0	1000		Glyoxylate and Dicarboxylate Metabolism			
HPYRR2x	hydroxypyruvate reductase (NADH)	h[c] + nadh[c] + hpyr[c] -> nad[c] + glyc-S[c]	0	16833.1 or 16832.1 or 106357.1 or 16833.2 or 16832.1 and 16828.1 or 52815.1 or 16828.1 or 52815.2	0	1000		Glyoxylate and Dicarboxylate Metabolism			
HPYRR3y	Hydroxypyruvate reductase (NADPH)	h[c] + nadph[c] + hpyr[c] -> nadp[c] + glyc-R[c]	0	76238.1	0	1000		Glyoxylate and Dicarboxylate Metabolism			
HPYRtp	hydroxypyruvate transport, peroxisomal	hpyr[x] <=> hpyr[x]	1		-1000	1000		Transport, Peroxisomal			
HRETNtn	4-hydroxyretinoic acid transport, Nuclear	hretn[c] <=> hretn[n]	1		-1000	1000		Transport, Nuclear			
HS1ly	heparan-N-sulfatase, lysosomal	h2o[l] + hs_deg[l] -> h[l] + so4[l] + hs_deg2[l]	0	27029.1	0	1000		Heparan sulfate degradation			
HS2ly	heparan-N-sulfatase, lysosomal	h2o[l] + hs_deg6[l] -> h[l] + so4[l] + hs_deg7[l]	0	27029.1	0	1000		Heparan sulfate degradation			
HS3ly	heparan-N-sulfatase, lysosomal	h2o[l] + hs_deg12[l] -> h[l] + so4[l] + hs_deg13[l]	0	27029.1	0	1000		Heparan sulfate degradation			
HS4ly	heparan-N-sulfatase, lysosomal	h2o[l] + hs_deg18[l] -> h[l] + so4[l] + hs_deg19[l]	0	27029.1	0	1000		Heparan sulfate degradation			
HSAT1ly	heparan-glucosaminide N-acetyltransferase, lysosomal	accoa[c] + hs_deg2[l] -> coa[c] + h[l] + hs_deg3[l]	0		0	1000		Heparan sulfate degradation			
HSAT2ly	heparan-glucosaminide N-acetyltransferase, lysosomal	accoa[c] + hs_deg7[l] -> coa[c] + h[l] + hs_deg8[l]	0		0	1000		Heparan sulfate degradation			
HSAT3ly	heparan-glucosaminide N-acetyltransferase, lysosomal	accoa[c] + hs_deg13[l] -> coa[c] + h[l] + hs_deg14[l]	0		0	1000		Heparan sulfate degradation			
HSAT4ly	heparan-glucosaminide N-acetyltransferase, lysosomal	accoa[c] + hs_deg19[l] -> coa[c] + h[l] + hs_deg20[l]	0		0	1000		Heparan sulfate degradation			
HSD1-1B1r	11-beta-hydroxysteroid dehydrogenase type 1	h[r] + nadph[r] + cortsn[r] <=> nadp[r] + crtsl[r]	1	15483.1 or 15483.2	-1000	1000		Steroid Metabolism			
HSD1-1B2r	11-beta-hydroxysteroid dehydrogenase type 2	h[r] + nadh[r] + cortsn[r] <=> nad[r] + crtsl[r]	1	15484.1	-1000	1000		Steroid Metabolism			
HSD17B1	testicular 17-beta-hydroxysteroid dehydrogenase	h[c] + nadph[c] + estrone[c] <=> nadp[c] + estradiol[c]	1	14979.1 or 15485.1	-1000	1000		Steroid Metabolism			
HSD17B2r	17-beta-hydroxysteroid dehydrogenase	h[r] + nad[r] + androstenol[r] -> nadh[r] + testerone[r]	0	15486.1	0	1000		Steroid Metabolism			
HSD17B3r	testicular 17-beta-hydroxysteroid dehydrogenase	h[r] + nadph[r] + androstenol[r] -> nadp[r] + testerone[r]	0	15487.1	0	1000		Steroid Metabolism			
HSD17B42x	hydroxysteroid (17-beta) dehydrogenase 4	h[x] + o2[x] + dhcholoylcoa[x] + nadph[x] -> 2 h2o[x] + nad[x] + dhocholoylcoa[x]	0	15488.1	0	1000		Bile Acid Biosynthesis			
HSD17B4x	hydroxysteroid (17-beta) dehydrogenase 4	h[x] + o2[x] + cholcoa[x] + nadph[x] -> h2o[x] + nad[x] + dhtcoa[x]	0	15488.1	0	1000		Bile Acid Biosynthesis			
HSD17B7r	testicular 17-beta-hydroxysteroid dehydrogenase	h[r] + nadph[r] + estrone[r] -> nadp[r] + estradiol[r]	0	15490.1	0	1000		Steroid Metabolism			
HSD17B8r	17-beta-hydroxysteroid dehydrogenase	h[r] + nadh[r] + estrone[r] -> nad[r] + estradiol[r]	0	15486.1	0	1000		Steroid Metabolism			
HSD17B9r	17-beta-hydroxysteroid dehydrogenase (type 7)	1.5 o2[r] + androstenol[r] + h[r] + nadph[r] -> 2 h2o[r] + nadp[r] + androsterone[r]	0	15490.1	0	1000		Steroid Metabolism			
HSD3A1r	3 alpha-hydroxysteroid dehydrogenase (type 3)	h[r] + nadh[r] + androstandrs[r] <=> androstn[r] + nad[r]	1	83702.1	-1000	1000		Steroid Metabolism			
HSD3A2r	3 alpha-hydroxysteroid dehydrogenase (type 3)	h[r] + nadph[r] + androstandrs[r] <=> androstn[r] + nadp[r]	1	83702.1	-1000	1000		Steroid Metabolism			
HSD3B11	3 beta-hydroxysteroid dehydrogenase/delta 5--4-isomerase type 1	nad[c] + pregnlone[c] -> h[c] + nadh[c] + prgsrn[c]	0	15493.1	0	1000		Steroid Metabolism			
HSD3B11r	3 beta-hydroxysteroid dehydrogenase/delta 5--4-isomerase type 1	nad[r] + pregnlone[r] -> h[r] + nadh[r] + prgsrn[r]	0	15492.1	0	1000		Steroid Metabolism			
HSD3B12r	3 beta-hydroxysteroid dehydrogenase/delta 5--4-isomerase type 1	nad[r] + dhea[r] -> h[r] + nadh[r] + androstnd[r]	0	15492.1	0	1000		Steroid Metabolism			
HSD3B13	3 beta-hydroxysteroid dehydrogenase/delta 5--4-isomerase type 1	nad[c] + 17ahpregnlone[c] -> h[c] + nadh[c] + 17ahpprgsrn[c]	0	15493.1	0	1000		Steroid Metabolism			
HSD3B13r	3 beta-hydroxysteroid dehydrogenase/delta 5--4-isomerase type 1	nad[r] + 17ahpregnlone[r] -> h[r] + nadh[r] + 17ahpprgsrn[r]	0	15492.1	0	1000		Steroid Metabolism			
HSD3B2r	3 beta-hydroxysteroid dehydrogenase type 1	h[r] + nadh[r] + androstenol[r] -> h2o[r] + nad[r] + androstandrs[r]	0	15492.1	0	1000		Steroid Metabolism			
HSD3B3r	3 beta-hydroxysteroid dehydrogenase type 1	h[r] + nadph[r] + androstenol[r] -> h2o[r] + nadp[r] + androstandrs[r]	0	15492.1	0	1000		Steroid Metabolism			
HSD3B7	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	nad[r] + sol7a1[r] -> h[r] + nadh[r] + sol7aone[r]	0	101502.1	0	1000		Bile Acid Biosynthesis			
HSD3B7P	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	nadp[r] + sol7a1[r] -> h[r] + nadph[r] + sol7aone[r]	0	101502.1	0	1000		Bile Acid Biosynthesis			
HSPASEly	heparan sulfate proteoglycan protease, lysosome (endosome)	h2o[l] + hspg[l] -> Ser_Gly_Ala_X_G[s][1] + hs[l]	0		0	1000		Heparan sulfate degradation			
HSPGt	heparan sulfate transport, golgi to extracellular	hspg[g] -> hspg[e]	0		0	1000		Transport, Extracellular			
HSPGly	heparan sulfate transport, extracellular to lysosome	hspg[e] -> hspg[l]	0		0	1000		Transport, Lysosomal			
HTAXOLte	xenobiotic transport	hxsol[e] <=> hxsol[c]	1		-1000	1000		Transport, Extracellular			
HXANd	hypoxanthine facilated transport from lysosome	hxan[l] <=> hxan[c]	1	71279.1	-1000	1000		Transport, Lysosomal			
HXANtx	hypoxanthine diffusion in peroxisome	hxan[c] -> hxan[x]	0		0	1000		Transport, Peroxisomal			
HXPRT	hypoxanthine phosphoribosyltransferase (Hypoxanthine)	prpp[c] + hxan[c] -> ppi[c] + imp[c]	0	15452.1	0	1000		Salvage Pathway			
HYPOE	hypothetical enzyme	h2o[c] + pyam5p[c] -> pi[c] + pydam[c]	0	57028.1	0	1000		Vitamin B6 Metabolism			
HYPTROX	Hypotaurine oxidase	o2[c] + 2 h[c] + 2 hyptaur[c] -> 2 taur[c]	0		0	1000		Taurine and hypotaurine metabolism			
HYXNt	Hypoxanthine transport	hxan[e] <=> hxan[c]	1	13340.1	-1000	1000		Transport, Extracellular			
Hyg	Proton intracellular transport	h[g] <=> h[c]	1		-1000	1000		Transport, Golgi Apparatus			
Hm	Uncoupling protein	h[c] -> h[m]	0	22229.1 or 74011.1 or 22229.2 or 22228.1 or 22227.1 or 20523.1 or 20523.2	0	1000		Transport, Mitochondrial			
Hr	H transporter, endoplasmic reticulum	h[c] <=> h[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
Hx	H transporter, peroxisome	h[c] <=> h[x]	1		-1000	1000		Transport, Peroxisomal			
ICDHxm	Isocitrate dehydrogenase (NAD+)	nad[m] + icit[m] -> akg[m] + co2[m] + nadh[m]	0	15929.1 and 67834.1 and 170718.1 or 15929.1 and 67834.1 and 170718.2 or 15929.1 and 67834.1 and 170718.3 or 67834.1 and 170718.1 and 15929.2 or 67834.1 and 15929.2 and 170718.2 or 15929.2 and 67834.1 and 170718.3	0	1000		Citric Acid Cycle			
ICDHy	Isocitrate dehydrogenase (NADP)	nadp[c] + icit[c] -> nadph[c] + akg[c] + co2[c]	0	15926.1	0	1000		Citric Acid Cycle			
ICDHyp	Isocitrate dehydrogenase (NADP+)	nadp[x] + icit[x] -> akg[x] + co2[x] + nadph[x]	0	15926.1	0	1000		Citric Acid Cycle			
ICDHyrm	Isocitrate dehydrogenase (NADP+)	nadp[m] + icit[m] <=> nadph[m] + akg[m] + co2[m]	1	269951.1	-1000	1000		Citric Acid Cycle			

IDHPOXOX2b	Iodide:hydrogen-peroxide oxidoreductase 2	3tyr-L[c] + iodine[c] -> h[c] + i[c] + 35iotatyr[c]	0	22018.1 or 22018.2 or 22018.3 or 22018.4 or 22018.5	0	1000		Tyrosine metabolism			
IDHPOXOX3	Iodide:hydrogen-peroxide oxidoreductase 3	h2o2[c] + 3tyr-L[c] + 35iotatyr[c] -> 2 h2o[c] + 2amac[c] + triiodthy[c]	0	22018.1 or 22018.2 or 22018.3 or 22018.4 or 22018.5	0	1000		Tyrosine metabolism			
IDHPOXOX4	Iodide:hydrogen-peroxide oxidoreductase 4	h2o2[c] + 2 35iotatyr[c] -> 2 h2o[c] + 2amac[c] + thyox-L[c]	0	22018.1 or 22018.2 or 22018.3 or 22018.4 or 22018.5	0	1000		Tyrosine metabolism			
IDHPOXOXb	Iodide:hydrogen-peroxide oxidoreductase	iodine[c] + tyr-L[c] -> h[c] + i[c] + 3tyr-L[c]	0	22018.1 or 22018.2 or 22018.3 or 22018.4 or 22018.5	0	1000		Tyrosine metabolism			
IDOAASE1ly	alpha-L-iduronidase, lysosomal	h2o[l] + hs_dog4[l] -> hs_dog2[l] + idour[l]	0	15932.1	0	1000		Heparan sulfate degradation			
IDOAASE2ly	alpha-L-iduronidase, lysosomal	h2o[l] + hs_dog1[l] -> idour[l] + hs_dog3[l]	0	15932.1	0	1000		Heparan sulfate degradation			
IDOAASE3ly	alpha-L-iduronidase, lysosomal	h2o[l] + hs_dog2[l] -> idour[l] + hs_dog1'E[l]	0	15932.1	0	1000		Heparan sulfate degradation			
IDOAASE4ly	alpha-L-iduronidase, lysosomal	h2o[l] + cs_b_dog3[l] -> cs_a_dog3[l] + idour[l]	0	15932.1	0	1000		Chondroitin sulfate degradation			
IDOURly	iduronate transport into lysosome	h[c] + idour[c] <=> h[l] + idour[l]	1	23550d.1	-1000	1000		Transport, Lysosomal			
IDPtn	IDP nuclear transport	idp[c] <=> idp[n]	1		-1000	1000		Transport, Nuclear			
ILEATB0tc	transport of L-Isoleucine into the intestinal cells by ATB0 transporter	2 na1[u] + cl[u] + ile-L[e] -> 2 na1[c] + cl[c] + ile-L[c]	0	56774.1	0	1000	3	Transport, Lumen	PMID:18195088	ATB0 is both sodium and chloride coupled, with reaction stoichiometry 2Na+:1cl:1amino acid. The transporter is located in the intestine, has a broad substrate specificity (both neutral and cationic amino acids), but is not involved in the transport of aspartate, glutamate and proline (PMID:18195088).	
ILEB0AT1c	transport of L-Isoleucine by the apical neutral amino acid transporters B(0)AT1 or B(0)AT2 to kidney, intestine or brain	na1[u] + ile-L[u] -> na1[c] + ile-L[c]	0	(70008.1 or (74338.1 and 57394.1))	0	1000	3	Transport, Lumen	PMID: 19472175, PMID: 15804236, PMID: 18400692, PMID: 16185194, PMID: 18195088	B(0)AT1 transports all the neutral amino acids with preference for methionine, leucine and valine. Reaction stoichiometry is 1:1. Requires heterodimerization with collectrin protein for increased affinity. Found in kidney and intestine, however also reported to be expressed in skin. Requires association with ACE2 for expression in intestine but with collectrin for expression in kidney. The localization of the B(0)AT2 transporter has been studied in brain tissue but data from the kidney have not been reported (PMID: 18195088)	3.4.17.23
ILELAT1tc	transport of L-Isoleucine by LAT1 in association with 4F2hc, across the apical surface of the membranes.	leu-L[c] + ile-L[u] -> leu-L[u] + ile-L[c]	0	(20539.1 and 17254.1)	0	1000	3	Transport, Lumen	Hans Gerhard Vogel, Franz J. Hock, Jochen Maas, Dieter Mayer (2006). Drug discovery and evaluation: Safety and pharmacokinetic assays, Springer publication, Chapter II D, page 456, table 3, PMID: 19035290, PMID: 12634921, European Journal of Pharmacology 441 (2002) 127-132. Am J Physiol Cell Physiol 281:C1077-C1093, 2001. Amino Acids (2005) 29: 229–233 DOI 10.1007/s00726-005-0221-x. PMID 11901210	leucine is the only amino acid tested for efflux. Expressed in ovary, placenta, brain, spleen, testis, activated lymphocytes and some tumor cells. Functions as a antiport transport system (DOI 10.1016/j.ceb.2009.01.02), requires heterodimerization with glycoprotein CD98 (Pflugers Arch-Eur J Physiol (2000) 440:503-512, DOI 10.1007/s004240000274, PMID: 10958334).	
ILELPHELAT2tc	transport of L-Isoleucine into the cell and efflux of L-Phenylalanine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	ile-L[e] + phe-L[c] -> ile-L[c] + phe-L[e]	0	(20539.1 and 17254.1)	0	1000	3	Transport, Extracellular	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-x, PMID: 10195088, Am J Physiol (2001) 281:C1077-C1093.	biger affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the mebrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274).	
ILETA	isoleucine transaminase	akgt[c] + ile-L[c] <=> glu-L[c] + 3mop[c]	1	12035.1	-1000	1000		Valine, Leucine, and Isoleucine Metabolism			
ILETAm	isoleucine transaminase, mitochondrial	akgt[m] + ile-L[m] <=> glu-L[m] + 3mop[m]	1	12036.1	-1000	1000		Valine, Leucine, and Isoleucine Metabolism			
ILEt4	L-isoleucine transport in via sodium symport	na1[e] + ile-L[e] -> na1[c] + ile-L[c]	0	56774.1	0	1000		Transport, Extracellular			
ILEt5m	Isoleucine mitochondrial transport	ile-L[c] <=> ile-L[m]	1		-1000	1000		Transport, Mitochondrial			
ILEtec	L-isoleucine transport via diffusion (extracellular to cytosol)	ile-L[e] <=> ile-L[c]	1	21511.3.1 or 72401.1	-1000	1000		Transport, Extracellular			
IMACTD	Imidazole acetaldehyde dehydrogenase	h2o[c] + nad[c] + imeacc[c] -> 2 h[c] + nadh[c] + imeacc[c]	0	19378.1 or 56752.1 or 110695.1 or 11668.1 or 11671.1 or 19378.2 or 19378.3	0	1000		Histidine Metabolism			
IMACTD_m	Imidazole acetaldehyde dehydrogenase (mito)	h2o[m] + nad[m] + imeacc[m] -> 2 h[m] + nadh[m] + imeacc[m]	0	11668.1 or 212647.1 or 212647.2 or 72535.1	0	1000		Histidine Metabolism			
IMPC	IMP cyclohydrolase	h2o[c] + imp[c] <=> fprica[c]	1	10814?.1	-1000	1000		IMP Biosynthesis			
IMPD	IMP dehydrogenase	h2o[c] + nad[c] + imp[c] -> h[c] + nadh[c] + xmp[c]	0	23917.1 or 23918.1 or 23912.2	0	1000		Nucleotides			
INOSTO	inositol oxygenase	o2[c] + inost[c] -> h2o[c] + h[c] + glcur[c]	0	56727.1	0	1000		Inositol Phosphate Metabolism			
INSKin	inosine kinase, mitochondrial	atp[m] + ins[m] -> h[m] + adp[m] + imp[m]	0		0	1000		Nucleotides			
INSTt2r	inositol transport in via proton symport	h[e] + inost[e] <=> h[c] + inost[c]	1	239606.1	-1000	1000		Transport, Extracellular			
INSTt4	inositol transport via sodium symport	na1[e] + inost[e] <=> na1[c] + inost[c]	1	53881.1	-1000	1000		Transport, Extracellular			
INSTt4_2	inositol transport via sodium symport	2 na1[e] + inost[e] <=> 2 na1[c] + inost[c]	1	233836.1	-1000	1000		Transport, Extracellular			
INSt	Inosine transport (diffusion)	ins[e] <=> ins[c]	1	133461.1 or 63959.1	-1000	1000		Transport, Extracellular			
INSt4	inosine transport in via sodium symport	na1[e] + ins[e] -> na1[c] + ins[c]	0	114304.1 or 269346.1	0	1000		Transport, Extracellular			
INSt5	inosine transport in via sodium (1:2) symport	2 na1[e] + ins[e] -> 2 na1[c] + ins[c]	0	114304.1	0	1000		Transport, Extracellular			
INStf	inosine facilated transport from lysosome	ins[l] <=> ins[c]	1	71279.1	-1000	1000		Transport, Lysosomal			
INStm	inosine facilated transport in mitochondria	ins[c] <=> ins[m]	1	63959.1	-1000	1000		Transport, Mitochondrial			
IPDDIx	isopentenyl-diphosphate D-isomerase	ipdp[x] <=> dmpp[x]	1	319554.1 or 320581.1	-1000	1000		Cholesterol Metabolism			
IPDItr	IPDP intracellular transport	ipdp[r] <=> ipdp[c]	1		-1000	1000		Transport, Endoplasmic Reticular			
IPDPtx	IPDP intracellular transport	ipdp[x] <=> ipdp[c]	1		-1000	1000		Transport, Peroxisomal			
ITCOAL1m	Itaconate--CoA ligase (GDP-forming), mitochondrial	cos[m] + gtp[m] + itacon[m] <=> pi[m] + gdp[m] + itaconi[m]	1	20917.1 and 56451.1	-1000	1000		C5-Branched dibasic acid metabolism			
ITCOAL1m	Itaconate--CoA ligase (ADP-forming), mitochondrial	cos[m] + atp[m] + itacon[m] <=> adp[m] + pi[m] + itaconi[m]	1	56451.1 and 20916.1	-1000	1000		C5-Branched dibasic acid metabolism			
ITPtn	ITP nuclear transport	itp[c] <=> itp[n]	1		-1000	1000		Transport, Nuclear			
IZPN	imidazolonepropionase	h2o[c] + 4izp[c] -> h[c] + 4oxgla[c]	0		0	1000		Histidine Metabolism			
Ic	Iodide uniport	i[e] <=> i[c]	1	216225.1	-1000	1000		Transport, Extracellular			
KAS8	b-ketoacyl synthetase (palmitate, n-C16:0)	20 h[c] + 14 malcoa[c] + accoa[c] + 7 malcoa[c] -> 6 h2o[c] + 14 nadp[c] + 7 co2[c] + 8 coa[c] + hdca[c]	0	14104.1	0	1000		Fatty acid elongation			
KCC2t	K+-Cl- cotransporter (N864+)	rb4[e] + cl[e] <=> rb4[c] + cl[c]	1	107723.1 or 20499.1 or 20498.1	-1000	1000		Transport, Extracellular			
KCCt	K+-Cl- cotransport	k[e] + cl[e] <=> cl[c] + k[c]	1	107723.1 or 20499.1 or 57138.1 or 20498.1	-1000	1000		Transport, Extracellular			
KDNH	2-keto-3deoxy-D-glycero-D-galactonoic acid phosphohydrolase	h2o[c] + kdnp[c] -> pi[c] + kdn[c]	0		0	1000		Aminosugar Metabolism			
KHK	ketohexokinase	atp[c] + fru[c] -> adp[c] + h[c] + f1p[c]	0	16548.1 or 16548.2	0	1000		Fructose and Mannose Metabolism			
KHK2	ketohexokinase (D-xylulose)	atp[c] + xylu-D[c] -> adp[c] + h[c] + xu1p-D[c]	0	16548.1 or 16548.2	0	1000		Glyoxylate and Dicarboxylate Metabolism			
KHK3	ketohexokinase (D-tagatose)	atp[c] + tagat-D[c] -> adp[c] + h[c] + tag1p-D[c]	0	16548.1 or 16548.2	0	1000		Galactose metabolism			
KSII_CORE2t	keratan sulfate II (core2) transport, golgi to extracellular	ksii_core2[g] -> ksii_core2[e]	0		0	1000		Transport, Extracellular			
KSII_CORE2tly	keratan sulfate II (core 2) transport, extracellular to lysosome	ksii_core2[e] -> ksii_core2[l]	0		0	1000		Transport, Lysosomal			
KSII_CORE4t	keratan sulfate II (core4) transport, golgi to extracellular	ksii_core4[g] -> ksii_core4[e]	0		0	1000		Transport, Extracellular			
KSII_CORE4tly	keratan sulfate II (core 4) transport, extracellular to lysosome	ksii_core4[e] -> ksii_core4[l]	0		0	1000		Transport, Lysosomal			
KSIt	keratan sulfate I transport, golgi to extracellular	ksi[g] -> ksi[e]	0		0	1000		Transport, Extracellular			
KSItly	keratan sulfate I transport, extracellular to lysosome	ksi[e] -> ksi[l]	0		0	1000		Transport, Lysosomal			
KYN	kynureninase	h2o[c] + l-kynr[c] -> h[c] + ala-L[c] + anth[c]	0	70789.1	0	1000		Tryptophan metabolism			
KYNO3OX	kynurenine 3-monooxygenase	o2[c] + h[c] + nadph[c] + l-kynr[c] -> h2o[c] + nadp[c] + hkynr[c]	0	98256.1	0	1000		Tryptophan metabolism			
KYNAKGAT	L-Kynurenine:2-oxoglutarate aminotransferase	akg[c] + l-kynr[c] -> glu-L[c] + 4aphdoh[c]	0	23923.1 or 70266.1 or 23923.2	0	1000		Tryptophan metabolism			
KYNATESYN	4-(2-Aminophenyl)-2,4-dioxobutanoate dehydratase	4aphdoh[c] -> h2o[c] + kynate[c]	0		0	1000		Tryptophan metabolism			
Kt3g	potassium transport via proton antiport	h[g] + k[c] <=> h[c] + k[g]	1	236727.1 or 77031.1	-1000	1000		Transport, Golgi Apparatus			
LAC2e	b-galactosidase, extracellular	h2o[e] + lcts[e] -> glc-D[e] + gal[e]	0	22643.1	0	1000		Galactose metabolism			
LAC2ly	b-galactosidase,lysosomal	h2o[l] + lcts[l] -> gal[l] + glc-D[l]	0	50917.1 or 19025.1 or 12091.1 or 18010.1	0	1000		Galactose metabolism			
LALDD	D-lactaldehyde dehydrogenase	nadp[c] + lald-D[c] <=> h[c] + nadph[c] + mthgxl[c]	1	76238.1	-1000	1000		Pyruvate Metabolism			
LALDO	D-Lactaldehyde:NAD+ oxidoreductase (glutathione-formulation)	nad[c] + gthrd[c] + lald-D[c] <=> h[c] + nadh[c] + lgt-S[c]	1	11532.1	-1000	1000		Pyruvate Metabolism			
LALDO2	D-Lactaldehyde:NADP+ 1-oxidoreductase	h[c] + nadph[c] + mthgxl[c] -> nadp[c] + lald-D[c]	0	110198.1 or 58810.2 or 11677.1 or 58810.1	0	1000		Pyruvate Metabolism			
LALDO2x	D-Lactaldehyde:NADP+ 1-oxidoreductase	h[c] + nadh[c] + mthgxl[c] -> nad[c] + lald-D[c]	0	110198.1	0	1000		Pyruvate Metabolism			
LAPCOAl	lysosomal acid phosphorylase (CoA)	h2o[l] + coa[l] -> pi[l] + dpcoa[l]	0	11432.1	0	1000		CoA Catabolism			
LCADt	lactaldehyde dehydrogenase	h2o[c] + nad[c] + lald-L[c] -> 2 h[c] + nadh[c] + lac-L[c]	0	19378.1 or 56752.1 or 11670.1 or 110695.1 or 67689.1 or 56847.1 or 11668.1 or 11671.1 or 19378.2 or 19378.3	0	1000		Pyruvate Metabolism			
LCADt_D	lactaldehyde dehydrogenase	h2o[c] + nad[c] + lald-D[c] -> 2 h[c] + nadh[c] + lac-D[c]	0	19378.1 or 56752.1 or 11670.1 or 110695.1 or 67689.1 or 56847.1 or 11668.1 or 11671.1 or 19378.2 or 19378.3	0	1000		Pyruvate Metabolism			
LCADt_Dm	lactaldehyde dehydrogenase, mitochondrial	h2o[m] + nad[m] + lald-D[m] -> 2 h[m] + nadh[m] + lac-D[m]	0	(10477?.1 or 11669.1 or 212647.1 or 214579.1 or 56454.1 or 214579.2 or 212647.2 or 72535.1)	0	1000		Pyruvate Metabolism			
LCADtm	lactaldehyde dehydrogenase, mitochondrial	h2o[m] + nad[m] + lald-L[m] -> 2 h[m] + nadh[m] + lac-L[m]	0	(10477?.1 or 11669.1 or 212647.1 or 214579.1 or 56454.1 or 214579.2 or 212647.2 or 72535.1)	0	1000		Pyruvate Metabolism			
LCAT1e	Lecithin-cholesterol acyltransferase	chsterol[e] + pchol_hs[e] -> lpchol_hs[e] + xolest2_hs[e]	0	16816.1	0	1000		Fatty Acid Metabolism			

LCTSig	lactase transport from Golgi to extracellular (via vesicle)	lctn[g] -> lctn[e]	0		0	1000		Transport, Extracellular			
LCTSil	lactase transport from cytosol to lysosome (via autophagocytosis)	lctn[c] -> lctn[l]	0		0	1000		Transport, Lysosomal			
LCYSTAT	L-Cysteate:2-oxoglutarate aminotransferase	Lcyst[c] + akg[c] <=> glu-L[c] + 3opyr[c]	1	14718.1	-1000	1000		Cysteine Metabolism			
LCYSTATm	L-Cysteate:2-oxoglutarate aminotransferase, mitochondrial	akg[m] + Lcyst[m] <=> glu-L[m] + 3opyr[m]	1	14719.1	-1000	1000		Cysteine Metabolism			
LCYSTCBOXL	3-Sulfoalanine carboxy-lyase	h[c] + Lcyst[c] -> cys2[c] + taur[c]	0	246277.1 or 14415.1 or 14417.1 or 14415.2	0	1000		Taurine and hypotaurine metabolism			
LDH_D	D-lactate dehydrogenase	nad[c] + lac-D[c] <=> h[c] + pyr[c] + nadh[c]	1	52815.1 or 52815.2	-1000	1000		Pyruvate Metabolism			
LDH_Lm	L-lactate dehydrogenase	nad[m] + lac-L[m] <=> h[m] + nadh[m] + pyr[m]	1	16828.1	-1000	1000		Pyruvate Metabolism			
LEUATB0tc	transport of L-Leucine into the intestinal cells by ATB0 transporter	leu-L[u] + 2 na1[u] + cl[u] -> 2 na1[c] + leu-L[c] + cl[c]	0	56774.1	0	1000	3	Transport, Lumen	PMID:18195088	ATB0 is both sodium and chloride coupled, with reaction stoichiometry 2Na+:1cl:1amino acid. The transporter is localized in the intestine, has a broad substrate specificity (both neutral and cationic amino acids), but is not involved in the transport of aspartate, glutamate and proline (PMID:18195088).	
LEUB0ATic	transport of L-Leucine by the apical neutral amino acid transporters B(0)AT1 or B(0)AT2 in kidney, intestine or brain	leu-L[u] + na1[u] -> na1[c] + leu-L[c]	0	(70008.1 or (74338.1 and 57394.1))	0	1000	3	Transport, Lumen	PMID: 19472175, PMID: 15804236, PMID: 18408692, PMID: 16181594, PMID: 18195088	transports all the neutral amino acids with preference for methionine, leucine and valine. Reaction stoichiometry is 1:1. Requires heterodimerization with collectrin protein for increased affinity. Found in kidney and intestine, however also reported to be expressed in skin. Requires association with ACE2 for expression in intestine but with collectrin for expression in kidney. The localization of the B(0)AT2 transporter has been studied in brain tissue but data from the kidney have not been reported (PMID: 18195088).	3.4.17.23
LEUGLYHYc	hydrolysis of leucylglycine	h2o[c] + leuglyc[c] <=> leu-L[c] + gly[c]	1		-1000	1000	1	Dipeptide Degradation		renot probable reaction.	
LEUGLYPEPT1tc	transport of Leucylglycine by the apical PEPT1 amino acid transporters across the brush border colls of the enterocytes of the intestine and renal cells	h[u] + leuglyu[u] -> h[c] + leuglyc[c]	0	215335.1	0	1000	3	Transport, Lumen	PMID: 7858848, PMID: 14965252, PMID: 14977407, PMID: 10330047	PEPT1 appears to transport all di- and tri- peptides across the brush border of the intestinal cells (Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Advanced nutrition and human metabolism. Wadsworth cengage learning, 5th edition, page 193). PEPT1 is expressed highly in intestinal cells where as PEPT2 is localized to renal cells (PMID: 10330047).	
LEUGLYt	L-Leucylglycine transport via proton symport	h[e] + leuglyu[e] -> h[c] + leuglyc[c]	0		0	1000	1	Transport, Extracellular		Needed to provide this metabolite for reaction LEUGLYHYc in joint model.	
LEUILELAT2tc	transport of L-Leucine into the cell and efflux of L-Isoleucine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	ile-L[c] + leu-L[e] <=> leu-L[c] + ile-L[e]	1	(20539.1 and 17254.1)	-1000	1000	3	Transport, Extracellular	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID 18195088, Am J Physiol (2001) 281:C1077-C1093.	linger affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274), LAT2 carries both influx and efflux of phenylalanine, leucine and isoleucine, hence such reactions are reversible.	
LEUKTRA4t	leukotriene A4 transmembrane (homo sapiens) transport	leukrtA4[e] <=> leukrtA4[c]	1		-1000	1000		Transport, Extracellular			
LEUKTRA4tr	leukotriene intracellular transport	leukrtA4[c] <=> leukrtA4[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
LEUKTRB4t	leukotriene B4 transmembrane (homo sapiens) transport	leukrtB4[e] <=> leukrtB4[c]	1		-1000	1000		Transport, Extracellular			
LEUKTRB4tr	leukotriene intracellular transport	leukrtB4[c] <=> leukrtB4[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
LEUKTRD4t	leukotriene D4 transmembrane (homo sapiens) transport	leukrtD4[e] <=> leukrtD4[c]	1		-1000	1000		Transport, Extracellular			
LEUKTRD4tr	leukotriene intracellular transport	leukrtD4[c] <=> leukrtD4[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
LEUKTRE4t	leukotriene E4 transmembrane (homo sapiens) transport	leukrtE4[e] <=> leukrtE4[c]	1		-1000	1000		Transport, Extracellular			
LEUKTRF4t	leukotrieneF4 transmembrane (homo sapiens) transport	leukrtF4[e] <=> leukrtF4[c]	1		-1000	1000		Transport, Extracellular			
LEULELALAPc	hydrolysis of Leucylleucine in the small intestine for cellular uptake	h2o[c] + leuleu[c] <=> 2 leu-L[c]	1	66988.1	-1000	1000	4	Dipeptide Degradation	PMID: 1908238, PMID: 1931152	both pig(E.C. 3.4.11.5) and human (3.4.11.1) amino peptidase have similar amino acid sequence and catalytic properties (PMID: 1908238)	3.4.11.1
LEULEUPEPT1tc	transport of Leucylleucine by the apical PEPT1 amino acid transporters across the brush border colls of the enterocytes of the intestine and renal cells	h[u] + leuleuu[u] -> h[c] + leuleuc[c]	0	215335.1	0	1000	3	Transport, Lumen	PMID: 7858848, PMID: 14965252, PMID: 14977407, PMID: 10330047	PEPT1 appears to transport all di- and tri- peptides across the brush border of the intestinal cells (Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Advanced nutrition and human metabolism. Wadsworth cengage learning, 5th edition, page 193). PEPT1 is expressed highly in intestinal cells where as PEPT2 is localized to renal cells (PMID: 10330047).	
LEULELt	L-leucyl-L-leucine transport via proton symport	h[e] + leuleue[e] -> h[c] + leuleuc[c]	0		0	1000	1	Transport, Extracellular		Needed to provide this metabolite for reaction LEULELALAPc in joint model.	
LEUPHELAT2tc	transport of L-Leucine into the cell and efflux of L-Phenylalanine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	phe-L[c] + leu-L[e] <=> leu-L[c] + phe-L[e]	1	(20539.1 and 17254.1)	-1000	1000	3	Transport, Extracellular	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID 18195088, Am J Physiol (2001) 281:C1077-C1093.	linger affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274), LAT2 carries both influx and efflux of phenylalanine, leucine and isoleucine, hence such reactions are reversible.	
LEUTA	leucine transaminase	akg[c] + leu-L[c] <=> glu-L[c] + 4mop[c]	1	12035.1	-1000	1000		Valine, Leucine, and Isoleucine Metabolism			
LEUTAm	leucine transaminase, mitochondrial	akg[m] + leu-L[m] <=> glu-L[m] + 4mop[m]	1	12036.1	-1000	1000		Valine, Leucine, and Isoleucine Metabolism			
LEUt4	L-leucine transport in via sodium symport	na1[e] + leu-L[e] -> na1[c] + leu-L[c]	0	105727.1 or 67760.1 or 69354.1 or 56774.1 or 115691.1 or 11988.1 or 11987.1	0	1000		Transport, Extracellular			
LEUt5m	leucine mitochondrial transport	leu-L[c] <=> leu-L[m]	1		-1000	1000		Transport, Mitochondrial			
LEUtec	L-leucine transport via diffusion (extracellular to cytosol)	leu-L[e] <=> leu-L[c]	1	215113.1 or 72401.1	-1000	1000		Transport, Extracellular			
LEUyLATbc	transport of Leucine by y+LAT1 or y+LAT2 with co-transporter of h in small intestine and kidney	h[e] + arg-L[c] + leu-L[e] -> h[c] + leu-L[c] + arg-L[e]	0	(20540.1 or (330836.1 and 17254.1))	0	1000	3	Transport, Extracellular	PMID: 11546643, PMID:18195088	y+LAT1 and y+LAT2 transporters requires CD98 for sequesterization to the plasma membrane. Acts as an amino acid exchanger, with influx of neutral aminoa acids and efflux of cationic amino acid, requires Na+ for optimal activity. Can also operate with H+ in absence of Na+ (PMID: 11546643).	
LEUyLATic	transport of Leucine by y+LAT1 or y+LAT2 transporters in small intestine and kidney	na1[e] + arg-L[c] + leu-L[e] -> na1[c] + leu-L[c] + arg-L[e]	0	(20540.1 or (330836.1 and 17254.1))	0	1000	3	Transport, Extracellular	PMID: 11546643, PMID:18195088	y+LAT1 and y+LAT2 transporters requires CD98 for sequesterization to the plasma membrane. Acts as an amino acid exchanger, with influx of neutral aminoa acids and efflux of cationic amino acid, requires Na+ for optimal activity. Can also operate with H+ in absence of Na+ (PMID: 11546643).	
LFORKYNHYD	L-Formylkynurenine hydrolase	h2o[c] + Lfmkynr[c] -> h[c] + ala-L[c] + aformanth[c]	0	70789.1	0	1000		Tryptophan metabolism			
LGNCCOAtx	fatty acid intracellular transport	lgnccoa[c] <=> lgnccoa[x]	1		-1000	1000		Transport, Peroxisomal			
LGNCCPT1	carnitine O-palmitoyltransferase	crn[c] + lgnccoa[c] -> coa[c] + lgnccrn[c]	0	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	0	1000		Carnitine shuttle			
LGNCCPT2	transport into the mitochondria (carnitine)	coa[m] + lgnccrn[m] -> crn[m] + lgnccoa[m]	0	12896.1	0	1000		Carnitine shuttle			
LGNCCRNt	transport into the mitochondria (carnitine)	lgnccrn[c] -> lgnccrn[m]	0	57279.1	0	1000		Carnitine shuttle			
LGNCt	fatty acid transport via diffusion	lgnc[e] <=> lgnc[c]	1		-1000	1000		Transport, Extracellular			
LGTHL	lactoylglutathione lyase	mthgxl[c] + gthrd[c] -> lgt-S[c]	0	109801.1	0	1000		Pyruvate Metabolism			
LIMNENte	xenobiotic transport	limnen[e] <=> limnen[c]	1		-1000	1000		Transport, Extracellular			
LINKDEG1ly	degradation of proteoglycan linkage region, lysosomal	3 h2o[l] + hs_deg2[l] -> 2 gal[l] + glcur[l] + xyl-D[l]	0		0	1000		Heparan sulfate degradation			
LINKDEG2ly	degradation of proteoglycan linkage region, lysosomal	4 h2o[l] + cs_x_deg[l] -> h[l] + so4[l] + 2 gal[l] + glcur[l] + xyl-D[l]	0		0	1000		Chondroitin sulfate degradation			
LINKDEG3ly	degradation of proteoglycan linkage region, lysosomal	4 h2o[l] + cs_x_deg5[l] -> h[l] + so4[l] + 2 gal[l] + glcur[l] + xyl-IS[l]	0		0	1000		Chondroitin sulfate degradation			
LINKDEG4ly	degradation of proteoglycan linkage region, lysosomal	5 h2o[l] + cs_x_deg7[l] -> 2 h[l] + 2 so4[l] + 2 gal[l] + glcur[l] + xyl-DI[l]	0		0	1000		Chondroitin sulfate degradation			
LINOFABPpmtc	uptake of linolenic acid by the enterocytes	lnlc[u] -> lnlc[c]	0	(14719.1 or 12491.1)	0	1000	3	Transport, Lumen	PMID: 20086080, PMID: 10617989, PMID: 8717442, Progress in Lipid Research Volume 48, Issue 2, March 2009, Pages 101-115	GOT2 encodes FABPpm that may either act alone or in co-ordination with CD36, for the uptake of long chain fatty acids (exhibits a selective preference for long chain PUFA and essential fatty acids over non-essential fatty acids). The fatty acids alternatively can undergo passive diffusion. once inside the cell, they bind to the cytoplasmic fatty acid binding protein (FABPc) and thereby undergo activation or esterification. Additionally, a minority of fatty acids are thought to be transported by FATP1 and rapidly activated by plasma membrane acyl-CoA synthetase (ACS1) to form acyl-Co esters. (PMID: 20086080)	
LINOFATPtc	uptake of linolenic acid by the enterocytes	atp[c] + coa[c] + lnlc[u] -> amp[c] + ppi[c] + lnlccoa[c]	0	26569.1	0	1000	3	Transport, Lumen	PMID: 12518211, PMID: 20086080, PMID: 12856180, Inmen., Endoc. & Metab. Agents in Med. Chem., 2009, 9, 11-17,	major intestinal fatty acid transport protein, may also act in co-ordination with acyl co-A synthetase. The transport is ATP driven, further the transporter itself has fatty acid activating enzymtic properties (PMID: 12856180).	6.2.1.-
LIPOt	Lipoate transport via sodium symport	h2o[c] + atp[c] + 2 na1[e] + lipoate[e] -> adp[c] + h[c] + nil[c] + 2 na1[c] + lipoate[c]	0	330064.1	0	1000		Transport, Extracellular			
LNELDCCPT1c	production of Linoelaidyl carnitine	crn[c] + lneldccoa[c] <=> coa[c] + lneldccrn[c]	1	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	-1000	1000	4	Carnitine shuttle	Biochem. J. (1989) 263 (867–873)		2.3.1.21
LNELDCCPT2	carnitine transferase	coa[m] + lneldccrn[m] -> crn[m] + lneldccoa[m]	0	12896.1	0	1000		Carnitine shuttle			
LNELDCCRNt	transport into the mitochondria (carnitine)	lneldccrn[c] -> lneldccrn[m]	0	57279.1	0	1000		Carnitine shuttle			
LNELDCt	fatty acid transport via diffusion	lneldc[e] <=> lneldc[c]	1		-1000	1000		Transport, Extracellular			
LNLCCPT1	carnitine O-palmitoyltransferase	crn[c] + lnlccoa[c] -> coa[c] + lnlccrn[c]	0	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	0	1000		Carnitine shuttle			
LNLCCPT2	carnitine transferase	coa[m] + lnlccrn[m] -> crn[m] + lnlccoa[m]	0	12896.1	0	1000		Carnitine shuttle			
LNLCCRNt	transport into the mitochondria (carnitine)	lnlccrn[c] -> lnlccrn[m]	0	57279.1	0	1000		Carnitine shuttle			
LNLCt	Linoleic acid (n-C18:2) transport in via diffusion	lnlc[e] <=> lnlc[c]	1		-1000	1000		Transport, Extracellular			
LNLNCACPT1	carnitine O-palmitoyltransferase	crn[c] + lnlncacoa[c] -> coa[c] + lnlncacrn[c]	0	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	0	1000		Carnitine shuttle			
LNLNCACPT2	carnitine transferase	coa[m] + lnlncacrn[m] -> crn[m] + lnlncacoa[m]	0	12896.1	0	1000		Carnitine shuttle			
LNLNCACRNt	transport into the mitochondria (carnitine)	lnlncacrn[c] -> lnlncacrn[m]	0	57279.1	0	1000		Carnitine shuttle			
LNLNCAt	fatty acid transport via diffusion	lnlnca[e] <=> lnlnca[c]	1		-1000	1000		Transport, Extracellular			
LNLNCGCPT1	carnitine O-palmitoyltransferase	crn[c] + lnlncgcoa[c] -> coa[c] + lnlncgcrn[c]	0	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	0	1000		Carnitine shuttle			
LNLNCGCPT2	carnitine transferase	coa[m] + lnlncgcrn[m] -> crn[m] + lnlncgcoa[m]	0	12896.1	0	1000		Carnitine shuttle			
LNLNCGCRNt	transport into the mitochondria (carnitine)	lnlncgcrn[c] -> lnlncgcrn[m]	0	57279.1	0	1000		Carnitine shuttle			
LNLNCGt	fatty acid transport via diffusion	lnlncg[e] <=> lnlncg[c]	1		-1000	1000		Transport, Extracellular			
LNS14DM	cytochrome P450 lanosterol 14-alpha-demethylase (NADP)	3 o2[c] + 2 h[c] + 3 nadph[c] + lanost[c] -> 4 h2o[c] + 3 nadp[c] + fuf[c] + 4dmzym[c]	0	208285.1	0	1000		Cholesterol Metabolism			
LNS14DMr	cytochrome P450 lanosterol 14-alpha-demethylase	3 o2[r] + 2 h[r] + 3 nadph[r] + lanost[r] -> 4 h2o[r] + 4dmzym[r] + 3 nadp[r] + fuf[r]	0	13121.1	0	1000		Cholesterol Metabolism			
LNSTLSr	lanosterol synthase	Sxg23epx[r] -> lanost[r]	0	16987.1	0	1000		Cholesterol Metabolism			
LPCHOLTDlu	diffusion of lysophosphatidylcholine accross the brush border membrane	lpchol_hs[u] <=> lpchol_hs[c]	1		-1000	1000	2	Transport, Lumen	Sareen S. Gropper, jack L. Smith, James L. Groff (2009) Wadsworth cengage learning, Advanced nutrition and human metabolism, 5th edition, page 142-144.		
LPCHOLt	lysophosphatidylcholine (homo sapiens) transport	lpchol_hs[e] <=> lpchol_hs[c]	1		-1000	1000		Transport, Extracellular			
LPCOXp	L-pipecolate oxidase, peroxisomal	Lpipecol[x] + o2[x] -> h[x] + h2o2[x] + thp2c[x]	0	19193.1	0	1000		Lysine Metabolism			

LPS	lipase	h2o[c] + tag_hs[c] -> h[c] + Rtotal3[c] + dag_hs[c]	0	16956.1	0	1000		Triacylglycerol Synthesis			
LPS2	lipase	h2o[c] + dag_hs[c] -> h[c] + Rtotal[c] + mag_hs[c]	0	16956.1	0	1000		Triacylglycerol Synthesis			
LPS2e	lipase, extracellular	h2o[e] + dag_hs[e] -> h[e] + Rtotal[e] + mag_hs[e]	0	15450.1	0	1000		Fatty Acid Metabolism			
LPS3	lipase	h2o[c] + mag_hs[c] -> h[c] + Rtotal2[c] + glyc[c]	0	23945.1 or 23945.2	0	1000		Triacylglycerol Synthesis			
LPS3e	lipase, extracellular	h2o[e] + mag_hs[e] -> h[e] + Rtotal2[e] + glyc[e]	0	15450.1	0	1000		Fatty Acid Metabolism			
LPS4e	phospholipase	h2o[e] + pglyc_hs[e] -> h[e] + 1glyc_hs[e] + Rtotal2[e]	0	237625.1	0	1000		Triacylglycerol Synthesis			
LPSe	lipase	h2o[e] + tag_hs[e] -> h[e] + dag_hs[e] + Rtotal3[e]	0	16891.1 or 67717.1 or 69060.1 or 18946.1 or 15450.1 or 18947.1	0	1000		Triacylglycerol Synthesis			
LRAT	Lecithin retinol acyltransferase	pchol_hs[c] + retinol[c] -> lpchol_hs[c] + retfa[c]	0	79235.1	0	1000		Vitamin A Metabolism			
LRAT1	Lecithin retinol acyltransferase (11-cis)	pchol_hs[c] + retinol-cis-11[c] -> lpchol_hs[c] + 11-cis-retfa[c]	0		0	1000		Vitamin A Metabolism			
LRAT2	Lecithin retinol acyltransferase (9-cis)	pchol_hs[c] + retinol-9-cis[c] -> lpchol_hs[c] + 9-cis-retfa[c]	0		0	1000		Vitamin A Metabolism			
LS3	Lumisterol 3 formation	pd3[c] <=> lum3[c]	1		-1000	1000		Vitamin D			
LSTO1r	Lathosterol oxidase	o2[r] + h[r] + nadph[r] + chlstol[r] -> 2 h2o[r] + nadp[r] + ddsmsterol[r]	0	235293.1	0	1000		Cholesterol Metabolism			
LSTO2r	Lathosterol oxidase	o2[r] + h[r] + nadph[r] + lthstrl[r] -> 7dhchsterol[r] + 2 h2o[r] + nadp[r]	0	235293.1	0	1000		Cholesterol Metabolism			
LTA4H	Leukotriene A-4 hydrolase	h2o[c] + leuktrA4[c] -> leuktrB4[c]	0	16993.1	0	1000		Eicosanoid Metabolism			
LTC4CP	Leukotriene C4 carboxypeptidase	h2o[c] + leuktrC4[c] <=> gly[c] + leuktrF4[c]	1		-1000	1000		Eicosanoid Metabolism			
LTC4Sr	Leukotriene C4 synthase	gthrd[r] + leuktrA4[r] -> leuktrC4[r]	0	17001.1 or 17001.2 or 211666.1 or 66447.1	0	1000		Eicosanoid Metabolism			
LTD4DP	Leukotriene D4 dipeptidase	h2o[c] + leuktrD4[c] <=> gly[c] + leuktrE4[c]	1		-1000	1000		Eicosanoid Metabolism			
LTDCL	L-Tryptophan decarboxy-lyase	h[c] + trp-L[c] -> co2[c] + trypta[c]	0	13195.1	0	1000		Tryptophan metabolism			
LYSALArBATtc	transport of L-Lysine into the cell in exchange for L-Alanine by b0,+AT transporter at the apical surfaces of the membranes of small intestine and renal cells.	ala-L[c] + lys-L[u] -> ala-L[u] + lys-L[c]	0	(30962.1 and 20532.1)	0	1000	3	Transport, Lumen	PMID: 10958334, PMID: 19184091, PMID: 18195088, PMID: 11546643	sodium independant antiport transport system, exchanges di-basic amino acids into the cells and neutral amino acids out of the cell. Located on the apical surfaces of transporting epithelia. Cellular localization being small intestine, kidney (proximal tubule), lung, placenta, brain and thymus. Requires the heterodimerization with rBAT glycoprotein. (PMID: 10958334).	
LYSATB0tc	transport of L-Lysine into the intestinal cells by ATB0 transporter	2 na1[u] + cl[u] + lys-L[u] -> 2 na1[c] + cl[c] + lys-L[c]	0	56774.1	0	1000	3	Transport, Lumen	PMID:18195088	ATB0 is both sodium and chloride coupled, with reaction stoichiometry 2Na+:1cl:1amino acid. The transporter is localted in the intestine, has a broad substrate specificity (both neutral and cationic amino acids), but is not involved in the transport of aspartate, glutamate and proline (PMID:18195088).	
LYSLEUrBATtc	transport of L-Lysine into the cell in exchange for L-Leucine by b0,+AT transporter at the apical surfaces of the membranes of small intestine and renal cells.	leu-L[c] + lys-L[u] -> leu-L[u] + lys-L[c]	0	(30962.1 and 20532.1)	0	1000	3	Transport, Lumen	PMID: 10958334, PMID: 19184091, PMID: 18195088, PMID: 11546643	sodium independant antiport transport system, exchanges di-basic amino acids into the cells and neutral amino acids out of the cell. Located on the apical surfaces of transporting epithelia. Cellular localization being small intestine, kidney (proximal tubule), lung, placenta, brain and thymus. Requires the heterodimerization with rBAT glycoprotein. (PMID: 10958334).	
LYSMTF1n	histone-lysine N-methyltransferase, nuclear	amet[n] + peplys[n] -> ahcys[n] + Nmelys[n]	0	239122.1 or 77683.1 or 110147.1 or 231051.1 or 67956.1 or 73251.1 or 64707.1 or 110147.2 or 208266.1 or 84505.1 or 231051.2 or 20937.1	0	1000		Lysine Metabolism			
LYSMTF2n	histone-lysine N-methyltransferase, nuclear	amet[n] + Nmelys[n] -> ahcys[n] + Ndmelys[n]	0	239122.1 or 77683.1 or 110147.1 or 231051.1 or 67956.1 or 73251.1 or 64707.1 or 110147.2 or 208266.1 or 84505.1 or 231051.2 or 20937.1	0	1000		Lysine Metabolism			
LYSMTF3n	histone-lysine N-methyltransferase, nuclear	amet[n] + Ndmelys[n] -> ahcys[n] + Ntmelys[n]	0	239122.1 or 77683.1 or 110147.1 or 231051.1 or 67956.1 or 73251.1 or 64707.1 or 110147.2 or 208266.1 or 84505.1 or 231051.2 or 20937.1	0	1000		Lysine Metabolism			
LYSOXp	L-lysine oxidase, peroxisomal	o2[x] + h2o[x] + lys-L[x] -> h2o2[x] + nh4[x] + 6a2ohxnt[x]	0		0	1000		Lysine Metabolism			
LYSt4	L-lysine transport in via sodium symport	na1[e] + lys-L[e] -> na1[c] + lys-L[c]	0	56774.1 or 20520.1	0	1000		Transport, Extracellular			
LYSt5r	L-lysine transport via diffusion	lys-L[e] <=> lys-L[c]	1	11987.1	-1000	1000	2	Transport, Extracellular			
LYStiDF	L-lysine transport via diffusion (extracellular to cytosol)	lys-L[e] -> lys-L[c]	0	69354.1 or 11989.1 or 11988.1 or 11987.1	0	1000		Transport, Extracellular			
LYStip	L-lysine transport, peroxisomal (irreversible)	lys-L[c] -> lys-L[x]	0		0	1000		Transport, Peroxisomal			
LYStm	Lysine mitochondrial transport via ornithine carrier	h[m] + lys-L[c] <=> h[c] + lys-L[m]	1	18408.1 or 83885.1	-1000	1000		Transport, Mitochondrial			
LYStn	L-lysine transport, nuclear	lys-L[c] <=> lys-L[n]	1		-1000	1000		Transport, Nuclear			
L_LACDcm	L-Lactate dehydrogenase, cytosolic/mitochondrial	2 ficytC[m] + lac-L[c] -> 2 h[c] + pyr[c] + 2 focytC[m]	0	626571.1	0	1000		Pyruvate Metabolism			
L_LACt2r	L-lactate reversible transport via proton symport	h[e] + lac-L[e] <=> h[c] + lac-L[c]	1	20503.1 or 80879.1 or 20501.1 or 57274.1	-1000	1000		Transport, Extracellular			
L_LACt4r	L-lactate reversible transport via sodium symport	na1[e] + lac-L[e] <=> na1[c] + lac-L[c]	1		-1000	1000		Transport, Extracellular			
L_LACtcm	L-lactate transport via diffusion (cytosol to mitochondria)	lac-L[c] -> lac-L[m]	0	64008.1	0	0		Transport, Mitochondrial			
L_LACtm	L-lactate transport, mitochondrial	h[c] + lac-L[c] <=> h[m] + lac-L[m]	1	20501.1	0	0		Transport, Mitochondrial			
M1316Mg	mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase	2 h2o[g] + nm4masn[g] -> 2 man[g] + nm2masn[g]	0	17158.1 or 140481.1	0	1000		N-Glycan Biosynthesis			
M13N2Tg	alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase	uacgam[g] + m4masn[g] -> h[g] + udp[g] + nm4masn[g]	0	17308.1	0	1000		N-Glycan Biosynthesis			
M13N4Tg	alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase	uacgam[g] + n2m2masn[g] -> h[g] + udp[g] + n3m2masn[g]	0	103534.1 or 269181.1 or 103534.2	0	1000		N-Glycan Biosynthesis			
M14NTg	beta-1,4-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase	uacgam[g] + n2m2masn[g] -> h[g] + udp[g] + n2m2nmasn[g]	0	17309.1	0	1000		N-Glycan Biosynthesis			
M16N4Tg	alpha-1,6-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase	uacgam[g] + n4m2masn[g] -> h[g] + udp[g] + n5m2masn[g]	0		0	1000		N-Glycan Biosynthesis			
M16N6Tg	alpha-1,6-mannosyl-glycoprotein 6-beta-N-acetylglucosaminyltransferase	uacgam[g] + n3m2masn[g] -> h[g] + udp[g] + n4m2masn[g]	0	107895.1	0	1000		N-Glycan Biosynthesis			
M16NTg	alpha-1,6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase	uacgam[g] + nm2masn[g] -> h[g] + udp[g] + n2m2masn[g]	0	217664.1	0	1000		N-Glycan Biosynthesis			
M4ATAer	M4A transamidase, endoplasmic reticulum	pre_prot[r] + m[em]3gacpail_hs[r] -> gpi_sig[r] + m[em]3gacpail_prot_hs[r]	0	276846.1 or 228812.1 or 14731.1 or 329777.1	0	1000		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
M4BET2er	M4B phosphoethanolaminyl transferase, endoplasmic reticulum	pe_hs[r] + mem2emgacpail_hs[r] -> dag_hs[r] + m[em]3gacpail_hs[r]	0	18701.1 or 433931.1 or 18701.2	0	1000		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
M4BTAer	M4B transamidase, endoplasmic reticulum	mem2emgacpail_hs[r] + pre_prot[r] -> gpi_sig[r] + mem2emgacpail_prot_hs[r]	0	276846.1 or 78928.1 or 228812.1 or 14731.1 or 329777.1	0	1000		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
M4CET3er	M4C phosphoethanolaminyl transferase, endoplasmic reticulum	pe_hs[r] + m3emgacpail_hs[r] -> dag_hs[r] + mem2emgacpail_hs[r]	0	56703.1 or 18701.1 or 18701.2 or 56703.2	0	1000		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
M4MPDOL_Lter	m4mpdol flippase	m4mpdol_L[c] -> m4mpdol_L[r]	0		0	1000		N-Glycan Biosynthesis			
M4MPDOL_Uter	m4mpdol flippase	m4mpdol_U[c] -> m4mpdol_U[r]	0		0	1000		N-Glycan Biosynthesis			
M7MASNBterg	m7masnB transport from endoplasmic reticulum to Golgi apparatus	m7masnB[r] -> m7masnB[g]	0		0	1000		N-Glycan Biosynthesis			
M8MASNterg	m8masn transport from ER to Golgi apparatus	m8masn[r] -> m8masn[g]	0		0	1000		N-Glycan Biosynthesis			
MACACI	maleylacetoacetate isomerase	4mlacac[c] -> 4fumacac[c]	0	14874.2 or 14874.3 or 14874.1	0	1000		Tyrosine metabolism			
MACOXO	3-Methylimidazole acetaldehyde:NAD+ oxidoreductase	h2o[c] + nad[c] + 3mldz[c] -> 2 h[c] + nadh[c] + 3mlda[c]	0	109731.1 or 11670.1 or 67689.1 or 56847.1	0	1000		Histidine Metabolism			
MAGHSTDlu	difussion of mono-acyl glycerol accross the brush border membrane	mag_hs[u] <=> mag_hs[c]	1		-1000	1000	2	Transport, Lumen	Sareen S. Gropper, jack L. Smith, James L. Groff (2009) Wadaworth cengage learning, Advanced nutrition and human metabolism, 5th edition, page 142-144.		
MAGt	monoacylglycerol 2 (homo sapiens) transport	mag_hs[e] <=> mag_hs[c]	1		-1000	1000		Transport, Extracellular			
MALSO3tm	Malate:sulfite antiport, mitochondrial	so3[m] + mal-L[c] <=> so3[c] + mal-L[m]	1	27376.1	-1000	1000		Transport, Mitochondrial			
MALSO4tm	Malate:sulfate antiport, mitochondrial	mal-L[c] + so4[m] <=> mal-L[m] + so4[c]	1	27376.1	-1000	1000		Transport, Mitochondrial			
MALT	alpha-glucosidase	h2o[c] + malt[c] -> 2 glc-D[c]	0	76051.1	0	1000		Starch and Sucrose Metabolism			
MALTSULtm	Malate:thiosulfate antiport, mitochondrial	mal-L[c] + tsul[m] <=> mal-L[m] + tsul[c]	1	27376.1	-1000	1000		Transport, Mitochondrial			
MALTe	alpha-glucosidase, extracellular	h2o[e] + malt[e] -> 2 glc-D[e]	0	232714.1	0	1000		Starch and Sucrose Metabolism			
MALTly	alpha-glucosidase, lysosomal	h2o[l] + malt[l] -> 2 glc-D[l]	0	14387.1	0	1000		Starch and Sucrose Metabolism			
MALTt1r	maltose transport (uniport)	malt[e] <=> malt[c]	1	20527.1	-1000	1000		Transport, Extracellular			
MALtm	malate transport, mitochondrial	pi[m] + mal-L[c] <=> pi[c] + mal-L[m]	1	27376.1	-1000	1000		Transport, Mitochondrial			
MAN1PT2	mannose-1-phosphate guanylyltransferase (GDP)	h[c] + gdp[c] + man1p[c] -> pi[c] + gdpmann[c]	0	331026.1 or 331026.2 or 69080.1 or 69080.2	0	1000		Fructose and Mannose Metabolism			
MAN1_6B1er	mannosidase I, endoplasmic reticulum (g1m6masnB1-producing)	h2o[r] + g1m7masnC[r] -> g1m6masnB1[r] + man[r]	0	227619.1	0	1000		N-Glycan Biosynthesis			
MAN1_7Ber	mannosidase I, endoplasmic reticulum (g1m7masnB-producing)	h2o[r] + g1m8masn[r] -> g1m7masnB[r] + man[r]	0	227619.1	0	1000		N-Glycan Biosynthesis			
MAN2_6B1er	mannosidase II, endoplasmic reticulum (g1m6masnB1-producing)	h2o[r] + g1m7masnB[r] -> g1m6masnB1[r] + man[r]	0		0	1000		N-Glycan Biosynthesis			
MAN2_7Cer	mannosidase II, endoplasmic reticulum (g1m7masnC-producing)	h2o[r] + g1m8masn[r] -> g1m7masnC[r] + man[r]	0		0	1000		N-Glycan Biosynthesis			
MAN6PI	mannose-6-phosphate isomerase	man6p[c] <=> f6p[c]	1	110119.1	-1000	1000		Fructose and Mannose Metabolism			
MANt1r	mannose transport (uniport)	man[e] <=> man[c]	1	20527.1 or 20525.1 or 20526.1	-1000	1000		Transport, Extracellular			
MANt4	D-mannose transport via sodium cotransport	na1[e] + man[e] <=> na1[c] + man[c]	1	230612.1	-1000	1000		Transport, Extracellular			
MANter	mannose efflux from endoplasmic reticulum	man[r] -> man[c]	0		0	1000		Transport, Endoplasmic Reticular			
MANtg	mannose efflux from Golgi apparatus	man[g] -> man[c]	0		0	1000		Transport, Golgi Apparatus			
MANtly	mannose efflux from lysosome	man[l] -> man[c]	0		0	1000		Transport, Lysosomal			
MAOLNOR	monoamine oxidase (L-Normetanephrine)	h2o[c] + o2[c] + normete-L[c] -> h2o2[c] + nh4[c] + 3m4hpga[c]	0	109731.1 or 17161.1	0	1000		Tyrosine metabolism			

MAOX	Methylamine oxidase	h2o[c] + o2[c] + mma[c] -> h2o2[c] + nh4[c] + fald[c]	0	237940.1 or 237940.2 or 11754.1 or 76507.1	0	1000		Tyrosine metabolism			
MCCCrm	methylcrotonoyl-CoA carboxylase, mitochondrial	atp[m] + hco3[m] + 3mb2coa[m] <=> h[m] + adp[m] + pi[m] + 3mgcoa[m]	1	72039.1 and 78038.1	-1000	1000		Valine, Leucine, and Isoleucine Metabolism			
MCD	Malonyl-CoA Decarboxylase cytoplasmic	h[c] + malcoa[c] -> co2[c] + accoa[c]	0	56690.1	0	1000		Fatty Acid Metabolism			
MCDm	Malonyl-CoA Decarboxylase, mitochondrial	h[m] + malcoa[m] -> co2[m] + accoa[m]	0	56690.1	0	1000		Fatty Acid Metabolism			
MCDp	Malonyl-CoA Decarboxylase peroxisomal	h[x] + malcoa[x] -> accoa[x] + co2[x]	0	56690.1	0	1000		Fatty Acid Metabolism			
MCITS	2-methylcitrate synthase	h2o[c] + ppcoa[c] + oaa[c] -> h[c] + 2mcit[c] + coa[c]	0		0	1000		Propanoate Metabolism			
MCLACCYSR	3-mercaptolactate:cysteine reductase	nad[c] + cys-L[c] + mercplac[c] -> h[c] + nadh[c] + mercplaccys[c]	0		0	1000		Cysteine Metabolism			
MCOATA	Malonyl-CoA-ACP transacylase	malcoa[c] + ACP[c] <=> coa[c] + malACP[c]	1	14104.1	-1000	1000		Fatty Acid Metabolism			
MCOATAm	Malonyl-CoA-ACP transacylase, mitochondrial	malcoa[m] + ACP[m] <=> coa[m] + malACP[m]	1	223722.1 or 223722.2	-1000	1000		Fatty Acid Metabolism			
MCPST	3-mercaptopyruvate sulfurtransferase	cyan[c] + mercppyr[c] -> h[c] + pyr[c] + tcynt[c]	0	246221.1	0	1000		Cysteine Metabolism			
MDH	malate dehydrogenase	nad[c] + mal-L[c] <=> h[c] + nadh[c] + oaa[c]	1	76668.1 or 17449.1	-1000	1000		Citric Acid Cycle			
MDHm	malate dehydrogenase, mitochondrial	nad[m] + mal-L[m] <=> h[m] + nadh[m] + oaa[m]	1	17448.1	-1000	1000		Citric Acid Cycle			
MDRPD	5-Methylthio-5-deoxy-D-ribulose 1-phosphate dehydratase	5mdru1p[c] -> h2o[c] + dkmpp[c]	0		0	1000		Arginine and Proline Metabolism			
ME1m	malic enzyme (NAD), mitochondrial	nad[m] + mal-L[m] -> co2[m] + nadh[m] + pyr[m]	0	107029.1	0	1000		Pyruvate Metabolism			
ME2	malic enzyme (NADP)	nadp[c] + mal-L[c] -> pyr[c] + nadph[c] + co2[c]	0	17436.1	0	1000		Pyruvate Metabolism			
ME2m	malic enzyme (NADP), mitochondrial	nadp[m] + mal-L[m] -> nadph[m] + co2[m] + pyr[m]	0	107029.1 or 109264.1	0	1000		Pyruvate Metabolism			
MECOALm	mesaconate--CoA ligase (ADP-forming), mitochondrial	coa[m] + atp[m] + mescon[m] <=> adp[m] + pi[m] + mescoa[m]	1	56451.1 and 20916.1	-1000	1000		C5-Branched dibasic acid metabolism			
MECOAS1m	mesaconate--CoA ligase (GDP-forming)	coa[m] + gtp[m] + mescon[m] <=> pi[m] + gdp[m] + mescoa[m]	1	20917.1 and 56451.1	-1000	1000		C5-Branched dibasic acid metabolism			
MELATN23DOX	Melatonin:oxygen 2,3-dioxygenase (indole-decyclizing)	o2[c] + melatn[c] -> fna5moxam[c]	0	15930.1	0	1000		Tryptophan metabolism			
MELATNOX	Melatonin:NADP oxidoreductase	o2[c] + h[c] + nadph[c] + melatn[c] -> h2o[c] + nadp[c] + 6hoxmelatn[c]	0	404195.1 or 13078.1 or 13077.1 or 13076.1	0	1000		Tryptophan metabolism			
MEOHt2	Methanol diffusion	meoh[e] <=> meoh[c]	1		-1000	1000		Transport, Extracellular			
MEOHtly	Methanol transporter, lysosome	meoh[c] <=> meoh[l]	1		-1000	1000		Transport, Lysosomal			
MEOHtr	Methanol transporter, endoplasmic reticulum	meoh[c] <=> meoh[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
MEPIVESSte	metanephrine secretion via secretory vesicle (ATP driven)	2 h2o[c] + 2 atp[c] + 3 mepi[c] -> 2 adp[c] + 2 h[c] + 2 pi[c] + 3 mepi[e]	0		0	1000		Transport, Extracellular			
MERCPLACCYSt	3-mercaptolactate-cysteine disulfide transport, extracellular	mercplaccys[c] -> mercplaccys[e]	0		0	1000		Transport, Extracellular			
MESCOALm	Mesaconyl-CoA pyruvate-lyase	h2o[m] + mescoa[m] -> pyr[m] + accoa[m]	0		0	1000		C5-Branched dibasic acid metabolism			
METAT	methionine adenosyltransferase	h2o[c] + atp[c] + met-L[c] -> pi[c] + amet[c] + ppi[c]	0	((232087.1 and 108645.1) or (108645.2 and 232087.1) or 11720.1)	0	1000		Methionine Metabolism			
METATB0tc	transport of L-Methionine into the intestinal cells by ATB0 transporter	2 na1[u] + cl[u] + met-L[u] -> 2 na1[c] + cl[c] + met-L[c]	0	56774.1	0	1000	3	Transport, Lumen	PMID:18195088	ATB0 is both sodium and chloride coupled, with reaction stoichiometry 2Na+:1cl:1amino acid. The transporter is localted in the intestine, has a broad substrate specificity (both neutral and cationic amino acids), but is not involved in the transport of aspartate, glutamate and proline (PMID:18195088).	
METB0ATAtc	transport of L-Methionine by the apical neutral amino acid transporter B(0)AT1 or B(0)AT2 in kidney, intestine or brain	na1[u] + met-L[u] -> na1[c] + met-L[c]	0	(70008.1 or (74338.1 and 57394.1))	0	1000	3	Transport, Lumen	PMID: 19472175, PMID: 15804236, PMID: 18400692, PMID: 16185194, PMID: 18195088	B(0)AT1 transports all the neutral amino acids with preference for methionine, leucine and valine. Reaction stoichiometry is 1:1. Requires heterodimerization with collectrin protein for increased affinity. Found in kidney and intestine, however also reported to be expressed in skin. Requires association with ACE2 for expression in intestine but with collectrin for expression in kidney. The localization of the B(0)AT2 transporter has been studied in brain tissue but data from the kidney have not been reported (PMID: 18195088). also catalyzed by system A transporter (SLC38A4).	3.4.17.23
METILELAT2tc	transport of L-Methionine into the cell and efflux of L-Isoleucine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	ile-L[c] + met-L[e] -> ile-L[e] + met-L[c]	0	(20539.1 and 17254.1)	0	1000	3	Transport, Extracellular	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s00420000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	higer affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of memebranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for traficking of the complex to the mebrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s00420000274).	
METLAT1tc	transport of L-Methionine by LAT1 in association with 4F2hc, across the apical surface of the memebranes.	leu-L[c] + met-L[u] -> leu-L[u] + met-L[c]	0	(20539.1 and 17254.1)	0	1000	3	Transport, Lumen	Hans Gerhard Vogel, Franz J. Hock, Jochen Maas, Dieter Mayer (2006), Drug discovery and evaluation: Safety and pharmacokinetic assays, Springer publication, Chapter II D, page 456, table 3, PMID: 19035290, PMID: 12634921, European Journal of Pharmacology 441 (2002) 127-132. Am J Physiol Cell Physiol 281:C1077-C1093, 2001. Amino Acids (2005) 29: 229–233 DOI 10.1007/s00726-005-0221-x. PMID: 11901210	leucine is the only amino acid tested for efflux. Expressed in ovary, placenta, brain, spleen, testis, activated lymphocytes and some tumor cells. Functions as a antiport transport system (DOI 10.1016/j.cell.2009.01.02), requires heterodimerization with glycoprotein CD98 (Pflugers Arch-Eur J Physiol (2000) 440:503-512, DOI 10.1007/s004240000274, PMID: 10958334).	
METLEUex	Methionine/Leucine exchange (Met in)	leu-L[c] + met-L[e] -> met-L[c] + leu-L[e]	0	17254.1 and 20539.1	0	1000		Transport, Extracellular			
METPHELAT2tc	transport of L-Methionine into the cell and efflux of L-Phenylalanine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	phe-L[c] + met-L[e] -> phe-L[e] + met-L[c]	0	(20539.1 and 17254.1)	0	1000	3	Transport, Extracellular	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s00420000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	higer affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of memebranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for traficking of the complex to the mebrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s00420000274).	
METS	methionine synthase	5mthf[c] + hcys-L[c] -> h[c] + thf[c] + met-L[c]	0	238505.1	0	1000		Methionine Metabolism			
METt4	L-methionine transport in via sodium symport	na1[e] + met-L[e] -> na1[c] + met-L[c]	0	105727.1 or 67760.1 or 56774.1 or 20520.1	0	1000		Transport, Extracellular			
METtec	L-methionine transport via diffusion (extracellular to cytosol)	met-L[e] <=> met-L[c]	1	215113.1 or 72401.1	-1000	1000		Transport, Extracellular			
METyLATtc	transport of L-Methionine by y+LAT1 or y+LAT2 transporters in small intestine and kidney	na1[e] + arg-L[c] + met-L[e] -> na1[c] + arg-L[e] + met-L[c]	0	(20540.1 or (330836.1 and 17254.1))	0	1000	3	Transport, Extracellular	PMID: 11546643, PMID:18195088	y+LAT1 and y+LAT2 transporters requires CD98 for sequesterization to the plasma membrane. Acts as an amino acid exchanger, with influx of neutral aminoa acids and efflux of cationic amino acid, requires Na+ for optimal activity. Can also operate with H+ in absence of Na+ (PMID: 11546643).	
METyLATthc	transport of Methionine by y+LAT1 or y+LAT2 with co-transporter of h in small intestine and kidney	h[e] + arg-L[c] + met-L[e] -> h[c] + arg-L[e] + met-L[c]	0	(20540.1 or (330836.1 and 17254.1))	0	1000	3	Transport, Extracellular	PMID: 11546643, PMID:18195088	y+LAT1 and y+LAT2 transporters requires CD98 for sequesterization to the plasma membrane. Acts as an amino acid exchanger, with influx of neutral aminoa acids and efflux of cationic amino acid, requires Na+ for optimal activity. Can also operate with H+ in absence of Na+ (PMID: 11546643).	
MEVK1x	mevalonate kinase (atp)	atp[x] + mev-R[x] -> h[x] + adp[x] + 5pmev[x]	0	17855.1	0	1000		Cholesterol Metabolism			
MG1er	mannosyl-oligosaccharide glucosidase, endoplasmic reticulum	h2o[r] + g3m8masn[r] -> glc-D[r] + g2m8masn[r]	0	57377.1	0	1000		N-Glycan Biosynthesis			
MG2er	mannosyl-oligosaccharide glucosidase, endoplasmic reticulum	h2o[r] + g2m8masn[r] -> glc-D[r] + g1m8masn[r]	0		0	1000		N-Glycan Biosynthesis			
MG3er	mannosyl-oligosaccharide glucosidase, endoplasmic reticulum	h2o[r] + g1m8masn[r] -> glc-D[r] + m8masn[r]	0		0	1000		N-Glycan Biosynthesis			
MGACONm	methylglutaconase, mitochondrial	citmcoa-L[m] <=> h2o[m] + mescoa[m]	1		-1000	1000		C5-Branched dibasic acid metabolism			
MGCHrm	methylglutaconyl-CoA hydratase (reversible), mitochondrial	h2o[m] + 3mgcoa[m] <=> hmgcoa[m]	1	11992.1	-1000	1000		Valine, Leucine, and Isoleucine Metabolism			
MGSA	methylglyoxal synthase	dhap[c] -> pi[c] + mthgxl[c]	0		0	1000		Pyruvate Metabolism			
MGSA2	methyglyoxylate synthase 2 (from g3p)	g3p[c] -> pi[c] + mthgxl[c]	0		0	1000		Pyruvate Metabolism			
MHISOR	N-Methylhistamine:oxygen oxidoreductase (deaminating)	h2o[c] + o2[c] + mhista[c] -> h2o2[c] + nh4[c] + 3mldz[c]	0	237940.1 or 237940.2 or 11754.1 or 76507.1	0	1000		Histidine Metabolism			
MI13456PK	inositol-1,3,4,5,6-pentakisphosphate 2-kinase	atp[c] + mi13456p[c] -> adp[c] + h[c] + minohp[c]	0		0	1000		Inositol Phosphate Metabolism			
MI13456Ptn	inositol 1,3,4,5,6-pentakisphosphate nuclear transport (diffusion)	mi13456p[c] <=> mi13456p[n]	1		-1000	1000		Transport, Nuclear			
MI1345PKn	inositol-1,3,4,5-triphosphate 6-kinase, nucleus	atp[n] + mi1345p[n] -> h[n] + adp[n] + mi13456p[n]	0	69718.1	0	1000		Inositol Phosphate Metabolism			
MI1345PP	inositol-1,3,4,5-trisphosphate 5-phosphatase	h2o[c] + mi1345p[c] -> pi[c] + mi134p[c]	0	104015.1 or 170835.1 or 170835.1 or 16331.1 or 212111.1 or 64436.1 or 16330.1 or 16332.1 or 104015.2	0	1000		Inositol Phosphate Metabolism			
MI1346PKn	inositol-1,3,4,6-tetrakisphosphate 5-kinase, nucleus	atp[n] + mi1346p[n] -> h[n] + adp[n] + mi13456p[n]	0	69718.1	0	1000		Inositol Phosphate Metabolism			
MI1346Ptn	1D-myo-Inositol 1,3,4,6-tetrakisphosphate nuclear transport (diffusion)	mi1346p[c] <=> mi1346p[n]	1		-1000	1000		Transport, Nuclear			
MI134P4P	inositol-1,3,4-trisphosphate 4-phosphatase	h2o[c] + mi134p[c] -> pi[c] + mi13p[c]	0		0	1000		Inositol Phosphate Metabolism			
MI134PK	inositol-1,3,4-trisphosphate 6-kinase	atp[c] + mi134p[c] -> adp[c] + h[c] + mi1346p[c]	0		0	1000		Inositol Phosphate Metabolism			
MI134PP	inositol-1,3,4-trisphosphate 1-phosphatase	h2o[c] + mi134p[c] -> pi[c] + mi34p[c]	0	16329.1	0	1000		Inositol Phosphate Metabolism			
MI13PP	inositol-1,3-bisphosphate 3-phosphatase	h2o[c] + mi13p[c] -> pi[c] + mi1p-D[c]	0		0	1000		Inositol Phosphate Metabolism			
MI1456PKn	inositol-1,4,5,6- tetrakisphosphate 3-kinase, nucleus	atp[n] + mi1456p[n] -> h[n] + adp[n] + mi13456p[n]	0	69718.1	0	1000		Inositol Phosphate Metabolism			
MI145P6Kn	inositol-1,4,5-triphosphate 6-kinase, nucleus	atp[n] + mi145p[n] -> h[n] + adp[n] + mi1456p[n]	0	69718.1	0	1000		Inositol Phosphate Metabolism			
MI145PK	inositol-1,4,5-trisphosphate 3-kinase	atp[c] + mi145p[c] -> adp[c] + h[c] + mi1345p[c]	0	228550.1 or 233011.1 or 320404.1	0	1000		Inositol Phosphate Metabolism			
MI145PKn	inositol-1,4,5-trisphosphate 3-kinase, nucleus	atp[n] + mi145p[n] -> h[n] + adp[n] + mi1345p[n]	0	69718.1	0	1000		Inositol Phosphate Metabolism			
MI145PP	inositol-1,4,5-trisphosphate 5-phosphatase	h2o[c] + mi145p[c] -> pi[c] + mi14p[c]	0	104015.1 or 170835.1 or 170835.1 or 16331.1 or 212111.1 or 64436.1 or 16330.1 or 16332.1 or 104015.2	0	1000		Inositol Phosphate Metabolism			
MI14P4P	inositol-1,4-bisphosphate 4-phosphatase	h2o[c] + mi14p[c] -> pi[c] + mi1p-D[c]	0		0	1000		Inositol Phosphate Metabolism			
MI14PP	inositol-1,4-bisphosphate 1-phosphatase	h2o[c] + mi14p[c] -> pi[c] + mi4p-D[c]	0	16329.1	0	1000		Inositol Phosphate Metabolism			
MI14Ptn	inositol 1,4-bisphosphate nuclear transport (diffusion)	mi14p[c] <=> mi14p[n]	1		-1000	1000		Transport, Nuclear			

MI1PP	myo-inositol 1-phosphatase	h2o[c] + mi1p-D[c] -> pi[c] + inost[c]	0	114663.1 or 55980.1	0	1000		Inositol Phosphate Metabolism			
MI1PS	myo-inositol-1-phosphate synthase	g6p[c] -> mi1p-D[c]	0	71780.1	0	1000		Inositol Phosphate Metabolism			
MI1P_Dm	inositol 1-phosphate nuclear transport (diffusion)	mi1p-D[c] <=> mi1p-D[n]	1		-1000	1000		Transport, Nuclear			
MI345PK	inositol-3,4,5,6-tetrakisphosphate 1-kinase	atp[c] + mi1345p[c] -> adp[c] + h[c] + mi13456p[c]	0		0	1000		Inositol Phosphate Metabolism			
MI34PP	inositol-3,4-bisphosphate 4-phosphatase	h2o[c] + mi134p[c] -> pi[c] + mi13p-D[c]	0	234515.1 or 269180.1 or 269180.2	0	1000		Inositol Phosphate Metabolism			
MI3PP	myo-inositol 3-phosphatase	h2o[c] + mi13p-D[c] -> pi[c] + inost[c]	0	114663.1 or 55980.1	0	1000		Inositol Phosphate Metabolism			
MI4PP	myo-inositol 4-phosphatase	h2o[c] + mi4p-D[c] -> pi[c] + inost[c]	0	114663.1 or 55980.1	0	1000		Inositol Phosphate Metabolism			
MICITDr	2-methylisocitrate dehydratase	h2o[c] + 2mecan[c] <=> micit[c]	1		-1000	1000		Propanoate Metabolism			
MINOHPtn	inositol hexakisphosphate nuclear transport (diffusion)	minohp[c] <=> minohp[n]	1		-1000	1000		Transport, Nuclear			
MK10t	Menaquinone secretion/ uptake (menaquinone 10)	mqn10[c] <=> mqn10[e]	1		-1000	1000	2	Transport, Extracellular	PMID: 18841274	Gut microbiota, in-particular Bacteroides, produce menaquinone, which contributes to host vitamin K homeostasis. The human liver contains 90% menaquinone/ 10% phylloquinone. AH	
MK11t	Menaquinone secretion/ uptake (menaquinone 11)	mqn11[c] <=> mqn11[e]	1		-1000	1000	2	Transport, Extracellular	PMID: 18841274	Gut microbiota, in-particular Bacteroides, produce menaquinone, which contributes to host vitamin K homeostasis. The human liver contains 90% menaquinone/ 10% phylloquinone. AH	
MK7t	Menaquinone secretion/ uptake (menaquinone 7)	mqn7[c] <=> mqn7[e]	1		-1000	1000	2	Transport, Extracellular	PMID: 18841274	Gut microbiota, in-particular Bacteroides, produce menaquinone, which contributes to host vitamin K homeostasis. The human liver contains 90% menaquinone/ 10% phylloquinone. AH	
MK8t	Menaquinone secretion/ uptake (menaquinone 8)	mqn8[c] <=> mqn8[e]	1		-1000	1000	2	Transport, Extracellular	PMID: 18841274	Gut microbiota, in-particular Bacteroides, produce menaquinone, which contributes to host vitamin K homeostasis. The human liver contains 90% menaquinone/ 10% phylloquinone. AH	
MK9t	Menaquinone secretion/ uptake (menaquinone 9)	mqn9[c] <=> mqn9[e]	1		-1000	1000	2	Transport, Extracellular	PMID: 18841274	Gut microbiota, in-particular Bacteroides, produce menaquinone, which contributes to host vitamin K homeostasis. The human liver contains 90% menaquinone/ 10% phylloquinone. AH	
MLTG1	Maltodextrin glucosidase (maltriotose)	h2o[c] + malttr1[c] -> glc-D[c] + malt[c]	0	76851.1	0	1000		Starch and Sucrose Metabolism			
MLTG1e	Maltodextrin glucosidase (maltriotose), extracellular	h2o[e] + malttr1[e] -> glc-D[e] + malt[e]	0	23271.4.1	0	1000		Starch and Sucrose Metabolism			
MLTG1ly	Maltodextrin glucosidase (maltriotose), lysosome	h2o[l] + malttr1[l] -> glc-D[l] + malt[l]	0	14387.1	0	1000		Starch and Sucrose Metabolism			
MM5ag	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus	h2o[g] + m5masoC[g] -> man[g] + m4masoC[g]	0	17156.1 or 230815.1 or 17155.1	0	1000		N-Glycan Biosynthesis			
MM5bg	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus	h2o[g] + m5masoB1[g] -> man[g] + m4masoB[g]	0	17156.1 or 230815.1 or 17155.1	0	1000		N-Glycan Biosynthesis			
MM5cg	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus	h2o[g] + m5masoB2[g] -> man[g] + m4masoA[g]	0	17156.1 or 230815.1 or 17155.1	0	1000		N-Glycan Biosynthesis			
MM6B1ag	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus	h2o[g] + m6masoB1[g] -> m5masoB1[g] + man[g]	0	17156.1 or 230815.1 or 17155.1	0	1000		N-Glycan Biosynthesis			
MM6B1bg	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus	h2o[g] + m6masoB2[g] -> m5masoB1[g] + man[g]	0	17156.1 or 230815.1 or 17155.1	0	1000		N-Glycan Biosynthesis			
MM6B2g	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus	h2o[g] + m6masoB2[g] -> man[g] + m5masoB2[g]	0	17156.1 or 230815.1 or 17155.1	0	1000		N-Glycan Biosynthesis			
MM6ag	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus	h2o[g] + m6masoA[g] -> man[g] + m5masoC[g]	0	230815.1	0	1000		N-Glycan Biosynthesis			
MM6bg	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus	h2o[g] + m6masoC[g] -> man[g] + m5masoC[g]	0	17156.1 or 230815.1 or 17155.1	0	1000		N-Glycan Biosynthesis			
MM7Ag	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus	h2o[g] + m7masoA[g] -> man[g] + m6masoA[g]	0	230815.1	0	1000		N-Glycan Biosynthesis			
MM7B1g	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus	h2o[g] + m7masoB[g] -> man[g] + m6masoB1[g]	0	17156.1 or 230815.1 or 17155.1	0	1000		N-Glycan Biosynthesis			
MM7B2g	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus	h2o[g] + m7masoB[g] -> m6masoB2[g] + man[g]	0	17156.1 or 230815.1 or 17155.1	0	1000		N-Glycan Biosynthesis			
MM7Cag	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus	h2o[g] + m7masoA[g] -> m6masoC[g] + man[g]	0	17156.1 or 230815.1 or 17155.1	0	1000		N-Glycan Biosynthesis			
MM7Cbg	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus	h2o[g] + m7masoC[g] -> m6masoC[g] + man[g]	0	17156.1 or 230815.1 or 17155.1	0	1000		N-Glycan Biosynthesis			
MM8Ag	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus	h2o[g] + m8masoI[g] -> m7masoA[g] + man[g]	0	17156.1 or 230815.1 or 17155.1	0	1000		N-Glycan Biosynthesis			
MM8Ber	mannosyl-oligosaccharide 1,2-alpha-mannosidase, endoplasmic reticulum	h2o[r] + m8masoI[r] -> m7masoB[r] + man[r]	0	227619.1	0	1000		N-Glycan Biosynthesis			
MM8Cg	mannosyl-oligosaccharide 1,2-alpha-mannosidase, Golgi apparatus	h2o[g] + m8masoI[g] -> man[g] + m7masoC[g]	0	17156.1 or 230815.1 or 17155.1	0	1000		N-Glycan Biosynthesis			
MMCD	Methylmalonyl-CoA decarboxylase	h[c] + mmcoa-S[c] -> co2[c] + ppcoa[c]	0	56690.1	0	1000		Valine, Leucine, and Isoleucine Metabolism			
MMCDm	Methylmalonyl-CoA decarboxylase, mitochondrial	h[m] + mmcoa-S[m] -> co2[m] + ppcoa[m]	0	56690.1	0	1000		Valine, Leucine, and Isoleucine Metabolism			
MMCDp	Methylmalonyl-CoA decarboxylase, peroxisomal	h[x] + mmcoa-S[x] -> co2[x] + ppcoa[x]	0	56690.1	0	1000		Valine, Leucine, and Isoleucine Metabolism			
MMEm	methylmalonyl-CoA epimerase/racemase	mmcoa-R[m] <=> mmcoa-S[m]	1	73724.1	-1000	1000		Valine, Leucine, and Isoleucine Metabolism			
MMMm	methylmalonyl-CoA mutase	mmcoa-R[m] <=> succoa[m]	1	17850.1	-1000	1000		Valine, Leucine, and Isoleucine Metabolism			
MMSADIm	methylmalonate-semialdehyde dehydrogenase	co2[m] + nad[m] + 2mop[m] -> co2[m] + nadh[m] + pptcoa[m]	0	104776.1	0	1000		Valine, Leucine, and Isoleucine Metabolism			
MMSADIm	methylmalonate-semialdehyde dehydrogenase (malonic semialdehyde), mitochondrial	co2[m] + nad[m] + msa[m] -> co2[m] + nadh[m] + accoa[m]	0	104776.1	0	1000		Propanoate Metabolism			
MMTSADm	malonate-semialdehyde dehydrogenase (acetylating), mitochondrial	co2[m] + nad[m] + 2mop[m] -> h[m] + nadh[m] + mmcoa-R[m]	0		0	1000		Valine, Leucine, and Isoleucine Metabolism			
MOGAT	monoacylglycerol acyltransferase	Rtotal.co2[c] + mag_hs[c] -> co2[c] + dag_hs[c]	0	233549.1 or 68393.1	0	1000		Triacylglycerol Synthesis			
MTAP	5'-methylthioadenosine phosphorylase	pi[c] + 5mta[c] -> ade[c] + 5mdr1p[c]	0	66902.1	0	1000		Arginine and Proline Metabolism			
MTHFC	methenyltetrahydrofolate cyclohydrolase	h2o[c] + methf[c] <=> 10fthf[c] + h[c]	1	108156.1	-1000	1000		Folate Metabolism			
MTHFCm	methenyltetrahydrofolate cyclohydrolase, mitochondrial	h2o[m] + methf[m] <=> 10fthf[m] + h[m]	1	177681.1 or 270685.1	-1000	1000		Folate Metabolism			
MTHFD	methylenetetrahydrofolate dehydrogenase (NADP)	nadp[c] + mlthf[c] <=> nadph[c] + methf[c]	1	108156.1	-1000	1000		Folate Metabolism			
MTHFD2	methylenetetrahydrofolate dehydrogenase (NAD)	nad[c] + mlthf[c] <=> nadh[c] + methf[c]	1		-1000	1000		Folate Metabolism			
MTHFD2m	methylenetetrahydrofolate dehydrogenase (NAD), mitochondrial	nad[m] + mlthf[m] <=> nadh[m] + methf[m]	1	177681.1	-1000	1000		Folate Metabolism			
MTHFDm	methylenetetrahydrofolate dehydrogenase (NADP), mitochondrial	nadp[m] + mlthf[m] <=> nadph[m] + methf[m]	1	177681.1 or 270685.1	-1000	1000		Folate Metabolism			
MTHFR3	5,10-methylenetetrahydrofolatereductase (NADPH)	2 h[c] + nadph[c] + mlthf[c] -> nadp[c] + 5mthf[c]	0	17769.1	0	1000		Folate Metabolism			
MTHFTe	transport of THF into the protal blood	5mthf[c] -> 5mthf[e]	0		0	1000	2	Transport, Extracellular	Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Advanced nutrition and human metabolism, Wadsworth cengage learning, 5th edition, page 350, G.F.M. Ball (2006) Vitamins their role in the human body, Blackwell publishing, chapter 17, page 351-354.	5-methylfolate is found in the portal circulation, so this reaction was added as folate exit from the enterocytes. The transport is carrier protein-mediated, Na+ independent and electro-neutral.	
MTHGXLt	Methylglyoxal transport (cytosol to extracellular)	mthgxl[c] -> mthgxl[e]	0		0	1000		Transport, Extracellular			
MTRI	5-methylthioribose-1-phosphate isomerase	5mdr1p[c] <=> 5mdru1p[c]	1		-1000	1000		Arginine and Proline Metabolism			
N2M2NMASNt	n2m2nmasn transport, Golgi to extracellular	n2m2nmasn[g] -> n2m2nmasn[e]	0		0	1000		Transport, Extracellular			
N2M2NMASNtly	n2m2nmasn transport, extracellular to lysosome	n2m2nmasn[e] -> n2m2nmasn[l]	0		0	1000		Transport, Lysosomal			
NTTg	N-acetylgalactosamine 3-beta-galactosyltransferase, Golgi annexamin	udpgal[g] + Tn_antigen[g] -> h[g] + udp[g] + T_antigen[g]	0	94192.1	0	1000		O-Glycan Biosynthesis			
N4TTg	N-acetylgalactosamine 4-beta-galactosyltransferase, Golgi appaxonin	udpgal[g] + core6[g] -> h[g] + udp[g] + f1a[g]	0		0	1000		O-Glycan Biosynthesis			
NABTNO	N4-Acetylaminobutanal:NAD+ oxidoreductase	h2o[c] + nad[c] + n4abutn[c] -> 2 h[c] + nadh[c] + 4aabutn[c]	0	19378.1 or 56752.1 or 110695.1 or 11668.1 or 11671.1 or 19378.2 or 19379.3	0	1000		Arginine and Proline Metabolism			
NABTNOm	N4-Acetylaminobutanal:NAD+ oxidoreductase (mt)	h2o[m] + nad[m] + n4abutn[m] -> 2 h[m] + nadh[m] + 4aabutn[m]	0	212647.1 or 11668.1 or 72535.1	0	1000		Arginine and Proline Metabolism			
NACASPAH	N-Acetyl-L-aspartate amidohydrolase	h2o[c] + Nacasp[c] -> asp-L[c] + ac[c]	0	11484.1 or 71670.1	0	1000		Alanine and Aspartate Metabolism			
NACASPtm	N-acetyl-L-aspartate transport (mitochondria to cytosol)	Nacasp[m] -> Nacasp[c]	0		0	1000		Transport, Mitochondrial			
NACDe	release of nicotinate at the basolateral surface	nac[c] -> nac[e]	0		0	1000	1	Transport, Extracellular	PMID: 21749321.	diffusion process. Hypothetically created. Nothing much is known about nicain exit from the enterocytes.	
NACHEX10ly	beta-N-acetylhexosaminidase, lysosomal	2 h2o[l] + lsxi_dreg7[l] -> 2 acgam[l] + lsxi_dreg8[l]	0	(15211.1 or 15212.1 or (15212.1 and 15211.1))	0	1000		Keratan sulfate degradation			
NACHEX11ly	beta-N-acetylhexosaminidase, lysosomal	h2o[l] + lsxi_dreg10[l] -> acgam[l] + lsxi_dreg11[l]	0	(15211.1 or 15212.1 or (15212.1 and 15211.1))	0	1000		Keratan sulfate degradation			
NACHEX12ly	beta-N-acetylhexosaminidase, lysosomal	h2o[l] + lsxi_dreg13[l] -> acgam[l] + lsxi_dreg14[l]	0	(15211.1 or 15212.1 or (15212.1 and 15211.1))	0	1000		Keratan sulfate degradation			
NACHEX13ly	beta-N-acetylhexosaminidase, lysosomal	h2o[l] + lsxi_dreg16[l] -> acgam[l] + lsxi_dreg17[l]	0	(15211.1 or 15212.1 or (15212.1 and 15211.1))	0	1000		Keratan sulfate degradation			
NACHEX14ly	beta-N-acetylhexosaminidase, lysosomal	h2o[l] + lsxi_dreg19[l] -> acgam[l] + lsxi_dreg20[l]	0	(15211.1 or 15212.1 or (15212.1 and 15211.1))	0	1000		Keratan sulfate degradation			
NACHEX15ly	beta-N-acetylhexosaminidase, lysosomal	h2o[l] + lsxi_dreg22[l] -> acgam[l] + lsxi_dreg23[l]	0	(15211.1 or 15212.1 or (15212.1 and 15211.1))	0	1000		Keratan sulfate degradation			
NACHEX16ly	beta-N-acetylhexosaminidase, lysosomal	h2o[l] + lsxi_dreg25[l] -> acgam[l] + lsxi_dreg26[l]	0	(15211.1 or 15212.1 or (15212.1 and 15211.1))	0	1000		Keratan sulfate degradation			
NACHEX17ly	beta-N-acetylhexosaminidase, lysosomal	h2o[l] + lsxi_dreg28[l] -> acgam[l] + lsxi_dreg29[l]	0	(15211.1 or 15212.1 or (15212.1 and 15211.1))	0	1000		Keratan sulfate degradation			
NACHEX18ly	beta-N-acetylhexosaminidase, lysosomal	h2o[l] + lsxi_dreg31[l] -> acgam[l] + lsxi_dreg32[l]	0	(15211.1 or 15212.1 or (15212.1 and 15211.1))	0	1000		Keratan sulfate degradation			
NACHEX19ly	beta-N-acetylhexosaminidase, lysosomal	h2o[l] + lsxi_dreg34[l] -> acgam[l] + lsxi_dreg35[l]	0	(15211.1 or 15212.1 or (15212.1 and 15211.1))	0	1000		Keratan sulfate degradation			

NACHEX1ly	beta-N-acetylhexosaminidase, lysosomal	h2o[l] + cs_a_deg[l] -> acgal[l] + cs_a_deg2[l]	0	(15211.1 or 15212.1 or (15212.1 and 15211.1))	0	1000		Chondroitin sulfate degradation			
NACHEX20ly	beta-N-acetylhexosaminidase, lysosomal	h2o[l] + ksii_deg37[l] -> acgam[l] + ksii_deg38[l]	0	(15211.1 or 15212.1 or (15212.1 and 15211.1))	0	1000		Keratan sulfate degradation			
NACHEX21ly	beta-N-acetylhexosaminidase, lysosomal	h2o[l] + ksii_deg39[l] -> acgam[l] + ksii_deg40[l]	0	(15211.1 or 15212.1 or (15212.1 and 15211.1))	0	1000		Keratan sulfate degradation			
NACHEX22ly	beta-N-acetylhexosaminidase, lysosomal	h2o[l] + ksii_deg41[l] -> acgam[l] + m2mal[l]	0	(15211.1 or 15212.1 or (15212.1 and 15211.1))	0	1000		Keratan sulfate degradation			
NACHEX23ly	beta-N-acetylhexosaminidase, lysosomal	h2o[l] + ksii_core2_deg6[l] -> acgam[l] + ksii_core2_deg5[l]	0	(15211.1 or 15212.1 or (15212.1 and 15211.1))	0	1000		Keratan sulfate degradation			
NACHEX24ly	beta-N-acetylhexosaminidase, lysosomal	h2o[l] + ksii_core2_deg7[l] -> acgam[l] + ksii_core2_deg8[l]	0	(15211.1 or 15212.1 or (15212.1 and 15211.1))	0	1000		Keratan sulfate degradation			
NACHEX25ly	beta-N-acetylhexosaminidase, lysosomal	h2o[l] + ksii_core2_deg9[l] -> acgam[l] + f1a[l]	0	(15211.1 or 15212.1 or (15212.1 and 15211.1))	0	1000		Keratan sulfate degradation			
NACHEX26ly	beta-N-acetylhexosaminidase, lysosomal	2 h2o[l] + ksii_core4_deg4[l] -> 2 acgam[l] + ksii_core2_deg5[l]	0	(15211.1 or 15212.1 or (15212.1 and 15211.1))	0	1000		Keratan sulfate degradation			
NACHEX27ly	beta-N-acetylhexosaminidase, lysosomal	h2o[l] + ha_deg1[l] -> acgam[l] + ha_prot1[l]	0	(15211.1 or 15212.1 or (15212.1 and 15211.1))	0	1000		Hyaluronan Metabolism			
NACHEX2ly	beta-N-acetylhexosaminidase, lysosomal	h2o[l] + cs_a_deg4[l] -> acgal[l] + cs_a_deg5[l]	0	(15211.1 or 15212.1 or (15212.1 and 15211.1))	0	1000		Chondroitin sulfate degradation			
NACHEX3ly	beta-N-acetylhexosaminidase, lysosomal	h2o[l] + cs_b_deg1[l] -> acgal[l] + cs_b_deg2[l]	0	(15211.1 or 15212.1 or (15212.1 and 15211.1))	0	1000		Chondroitin sulfate degradation			
NACHEX4ly	beta-N-acetylhexosaminidase, lysosomal	h2o[l] + cs_c_deg1[l] -> acgal[l] + cs_c_deg2[l]	0	(15211.1 or 15212.1 or (15212.1 and 15211.1))	0	1000		Chondroitin sulfate degradation			
NACHEX5ly	beta-N-acetylhexosaminidase, lysosomal	h2o[l] + cs_c_deg4[l] -> acgal[l] + cs_c_deg5[l]	0	(15211.1 or 15212.1 or (15212.1 and 15211.1))	0	1000		Chondroitin sulfate degradation			
NACHEX6ly	beta-N-acetylhexosaminidase, lysosomal	h2o[l] + cs_d_deg1[l] -> acgal[l] + cs_d_deg2[l]	0	(15211.1 or 15212.1 or (15212.1 and 15211.1))	0	1000		Chondroitin sulfate degradation			
NACHEX7ly	beta-N-acetylhexosaminidase, lysosomal	h2o[l] + cs_d_deg5[l] -> acgal[l] + cs_d_deg6[l]	0	(15211.1 or 15212.1 or (15212.1 and 15211.1))	0	1000		Chondroitin sulfate degradation			
NACHEX8ly	beta-N-acetylhexosaminidase, lysosomal	h2o[l] + cs_e_deg2[l] -> acgal[l] + cs_e_deg3[l]	0	(15211.1 or 15212.1 or (15212.1 and 15211.1))	0	1000		Chondroitin sulfate degradation			
NACHEX9ly	beta-N-acetylhexosaminidase, lysosomal	h2o[l] + cs_e_deg6[l] -> acgal[l] + cs_e_deg7[l]	0	(15211.1 or 15212.1 or (15212.1 and 15211.1))	0	1000		Chondroitin sulfate degradation			
NACHEXA10ly	beta-N-acetylhexosaminidase A, lysosomal	2 h2o[l] + ksii_deg8[l] -> h[l] + acgam[l] + so4[l] + ksii_deg11[l]	0	(15211.1 or (15212.1 and 15211.1))	0	1000		Keratan sulfate degradation			
NACHEXA11ly	beta-N-acetylhexosaminidase A, lysosomal	2 h2o[l] + ksii_deg12[l] -> h[l] + acgam[l] + so4[l] + ksii_deg14[l]	0	(15211.1 or (15212.1 and 15211.1))	0	1000		Keratan sulfate degradation			
NACHEXA12ly	beta-N-acetylhexosaminidase A, lysosomal	2 h2o[l] + ksii_deg15[l] -> h[l] + acgam[l] + so4[l] + ksii_deg17[l]	0	(15211.1 or (15212.1 and 15211.1))	0	1000		Keratan sulfate degradation			
NACHEXA13ly	beta-N-acetylhexosaminidase A, lysosomal	2 h2o[l] + ksii_deg18[l] -> h[l] + acgam[l] + so4[l] + ksii_deg20[l]	0	(15211.1 or (15212.1 and 15211.1))	0	1000		Keratan sulfate degradation			
NACHEXA14ly	beta-N-acetylhexosaminidase A, lysosomal	2 h2o[l] + ksii_deg21[l] -> h[l] + acgam[l] + so4[l] + ksii_deg23[l]	0	(15211.1 or (15212.1 and 15211.1))	0	1000		Keratan sulfate degradation			
NACHEXA15ly	beta-N-acetylhexosaminidase A, lysosomal	2 h2o[l] + ksii_deg24[l] -> h[l] + acgam[l] + so4[l] + ksii_deg26[l]	0	(15211.1 or (15212.1 and 15211.1))	0	1000		Keratan sulfate degradation			
NACHEXA16ly	beta-N-acetylhexosaminidase A, lysosomal	2 h2o[l] + ksii_deg27[l] -> h[l] + acgam[l] + so4[l] + ksii_deg29[l]	0	(15211.1 or (15212.1 and 15211.1))	0	1000		Keratan sulfate degradation			
NACHEXA17ly	beta-N-acetylhexosaminidase A, lysosomal	2 h2o[l] + ksii_deg30[l] -> h[l] + acgam[l] + so4[l] + ksii_deg32[l]	0	(15211.1 or (15212.1 and 15211.1))	0	1000		Keratan sulfate degradation			
NACHEXA18ly	beta-N-acetylhexosaminidase A, lysosomal	2 h2o[l] + ksii_deg33[l] -> h[l] + acgam[l] + so4[l] + ksii_deg35[l]	0	(15211.1 or (15212.1 and 15211.1))	0	1000		Keratan sulfate degradation			
NACHEXA19ly	beta-N-acetylhexosaminidase A, lysosomal	2 h2o[l] + ksii_deg36[l] -> h[l] + acgam[l] + so4[l] + ksii_deg38[l]	0	(15211.1 or (15212.1 and 15211.1))	0	1000		Keratan sulfate degradation			
NACHEXA1ly	beta-N-acetylhexosaminidase A, lysosomal	2 h2o[l] + cs_a6[l] -> h[l] + acgal[l] + so4[l] + cs_a_deg2[l]	0	(15211.1 or (15212.1 and 15211.1))	0	1000		Chondroitin sulfate degradation			
NACHEXA20ly	beta-N-acetylhexosaminidase A, lysosomal	2 h2o[l] + ksii_core2_deg5[l] -> h[l] + acgam[l] + so4[l] + ksii_core2_deg5[l]	0	(15211.1 or (15212.1 and 15211.1))	0	1000		Keratan sulfate degradation			
NACHEXA21ly	beta-N-acetylhexosaminidase A, lysosomal	2 h2o[l] + ksii_core2_deg6[l] -> h[l] + acgam[l] + so4[l] + ksii_core2_deg8[l]	0	(15211.1 or (15212.1 and 15211.1))	0	1000		Keratan sulfate degradation			
NACHEXA22ly	beta-N-acetylhexosaminidase A, lysosomal	3 h2o[l] + ksii_core4_deg3[l] -> h[l] + 2 acgam[l] + so4[l] + ksii_core2_deg5[l]	0	(15211.1 or (15212.1 and 15211.1))	0	1000		Keratan sulfate degradation			
NACHEXA2ly	beta-N-acetylhexosaminidase A, lysosomal	2 h2o[l] + cs_b[l] -> h[l] + acgal[l] + so4[l] + cs_b_deg2[l]	0	(15211.1 or (15212.1 and 15211.1))	0	1000		Chondroitin sulfate degradation			
NACHEXA3ly	beta-N-acetylhexosaminidase A, lysosomal	2 h2o[l] + cs_c[l] -> h[l] + acgal[l] + so4[l] + cs_c_deg2[l]	0	(15211.1 or (15212.1 and 15211.1))	0	1000		Chondroitin sulfate degradation			
NACHEXA4ly	beta-N-acetylhexosaminidase A, lysosomal	2 h2o[l] + cs_c_deg5[l] -> h[l] + acgal[l] + so4[l] + cs_c_deg5[l]	0	(15211.1 or (15212.1 and 15211.1))	0	1000		Chondroitin sulfate degradation			
NACHEXA5ly	beta-N-acetylhexosaminidase A, lysosomal	2 h2o[l] + cs_d[l] -> h[l] + acgal[l] + so4[l] + cs_d_deg6[l]	0	(15211.1 or (15212.1 and 15211.1))	0	1000		Chondroitin sulfate degradation			
NACHEXA6ly	beta-N-acetylhexosaminidase A, lysosomal	2 h2o[l] + cs_d_deg6[l] -> h[l] + acgal[l] + so4[l] + cs_d_deg6[l]	0	(15211.1 or (15212.1 and 15211.1))	0	1000		Chondroitin sulfate degradation			
NACHEXA7ly	beta-N-acetylhexosaminidase A, lysosomal	3 h2o[l] + cs_e[l] -> 2 h[l] + acgal[l] + 2 so4[l] + cs_e_deg5[l]	0	(15211.1 or (15212.1 and 15211.1))	0	1000		Chondroitin sulfate degradation			
NACHEXA8ly	beta-N-acetylhexosaminidase A, lysosomal	3 h2o[l] + cs_e_deg4[l] -> 2 h[l] + acgal[l] + 2 so4[l] + cs_e_deg7[l]	0	(15211.1 or (15212.1 and 15211.1))	0	1000		Chondroitin sulfate degradation			
NACHEXA9ly	beta-N-acetylhexosaminidase A, lysosomal	3 h2o[l] + ksii_deg8[l] -> h[l] + 2 acgam[l] + so4[l] + ksii_deg8[l]	0	(15211.1 or (15212.1 and 15211.1))	0	1000		Keratan sulfate degradation			
NACHORCTL3ta	absorption of nicotinate at the brush border of enterocytes	h[sn] + nac[sn] -> h[c] + nac[c]	0	102570.1	0	1000	2	Transport, Lumen	PMID: 18411268, PMID: 15728713	nicotinate is essential for life expansion, needs to be re-absorbed. Can be either obtainedfrom diet, from tryptophan or breakdown of proteins. Low pH is required for an efficient uptake. The orphan transporter is highly operative in PCT eg kidneys. Some authors have also suggested involvement of SLC5A8 in niacin uptake when niacin is administered at high pharmacological doses (PMID: 21749321).	
NACUP	Nicotinic acid uptake	nac[e] -> nac[c]	0		0	1000		Transport, Extracellular			
NADH2_u10m	NADH dehydrogenase, mitochondrial	5 h[m] + nadh[m] + q10[m] -> 4 h[c] + nad[m] + q10h2[m]	0	179992.1 or 664095.1 or 662318.1 or 179993.1 or 683442.1 or 783360.1 or 663771.1 or 671844.1 or 179991.1 or 723000.1 or 661488.1 or 69875.1 or 100043472.1 or 544005.1 or 230075.2 or 666951.1 or 754086.1 or 672273.1 or 80286.2 or 660446.1 or 783130.2 or 665916.1 or 681598.1 or 225887.1 or 2271971.1 or 68349.1 or 230075.1 or 227197.1 or 664416.1 or 68375.1 or 2266446.1 or 80286.1 or 407785.1 or 179995.1 or 681971.1 or 595136.1 or 664144.1 or 6730.1 or 67264.1 or 68202.1 or 68194.1	0	1000		Oxidative Phosphorylation			
NADH6pu	NADH transporter, peroxisome	nadh[c] -> nadh[x]	0		0	1000		Transport, Peroxisomal			
NADH6ru	NADH transporter, endoplasmic reticulum	nadh[c] -> nadh[r]	0		0	1000		Transport, Endoplasmic Reticular			
NADK	NAD kinase	atp[c] + nad[c] -> adp[c] + h[c] + nadp[c]	0	1921855.1	0	1000		NAD Metabolism			
NADN	NAD nucleosidase	h2o[c] + nad[c] -> h[c] + adprib[c] + ncam[c]	0		0	1000		NAD Metabolism			
NADNe	NAD nucleosidase,extracellular	h2o[e] + nad[e] -> h[e] + adprib[e] + ncam[e]	0	12494.1	0	1000		NAD Metabolism			
NADPH6ru	NADPH transporter, endoplasmic reticulum	nadph[c] -> nadph[r]	0		0	1000		Transport, Endoplasmic Reticular			
NADPH6xu	NADPH transporter, peroxisome	nadph[c] -> nadph[x]	0		0	1000		Transport, Peroxisomal			
NADPN	NADP nucleosidase	h2o[c] + nadp[c] -> h[c] + ncam[c] + adprbp[c]	0		0	1000		NAD Metabolism			
NADPNe	NADP nucleosidase,extracellular	h2o[e] + nadp[e] -> h[e] + adprbp[e] + ncam[e]	0	12494.1	0	1000		NAD Metabolism			
NADPtru	NADP transporter, endoplasmic reticulum	nadp[r] -> nadp[c]	0		0	1000		Transport, Endoplasmic Reticular			
NADPtxu	NADP transporter, peroxisome	nadp[x] -> nadp[c]	0		0	1000		Transport, Peroxisomal			
NADS2	NAD synthase (glutamine-hydrolysing)	h2o[c] + atp[c] + gln-L[c] + dnad[c] -> h[c] + nad[c] + glu-L[c] + amet[c] + ppi[c]	0	7894.1	0	1000		NAD Metabolism			
NADtn	NAD transport, nuclear through pores	nad[n] <=> nad[c]	1		-1000	1000		Transport, Nuclear			
NADtpu	NAD transporter, peroxisome	nad[x] -> nad[c]	0		0	1000		Transport, Peroxisomal			
NADtru	NAD transporter, endoplasmic reticulum	nad[r] -> nad[c]	0		0	1000		Transport, Endoplasmic Reticular			

NAGA2ly	N-acetylgalactosaminidase, alpha-	h[l] + Tn_antigen[l] + salp[l] -> Ser_Thr[l] + salpacgal[l]	0	17939.1	0	1000		Keratan sulfate degradation			
NAGAlby	N-acetylgalactosaminidase, beta-	h[l] + acghgbside_ba[l] + salp[l] -> gbside_ba[l] + salpacgal[l]	0		0	1000		Sphingolipid Metabolism			
NAGAly	N-acetylgalactosaminidase, alpha-	h[l] + acghgbside_ba[l] + salp[l] -> gbside_ba[l] + salpacgal[l]	0	17939.1	0	1000		Sphingolipid Metabolism			
NAGLCAly	N-acetylglucosaminidase, lysosomal	h2o[l] + cmreb[l] -> acgam[l] + Tn_antigen[l]	0		0	1000		Keratan sulfate degradation			
NAHCO3_HCLt	bicarbonate transport (HCl/NaHCO3 exchange)	h[c] + hco3[e] + na1[e] + cl[c] <=> h[e] + hco3[c] + na1[c] + cl[e]	1	94229.1 or 59033.1	-1000	1000		Transport, Extracellular			
NAit	Na+ / iodide cotransport	2 na1[e] + i[e] <=> 2 na1[c] + i[c]	1	114479.1	-1000	1000		Transport, Extracellular			
NAt	sodium transport (antiport)	na1[e] <=> na1[c]	1	53881.1 or 205137.1 or 114479.1	-1000	1000		Transport, Extracellular			
NAt3_1	sodium:proton antiporter (H:NA in 1:1)	h[e] + na1[c] <=> h[c] + na1[e]	1	277973.1 or 105243.1 or 226999.1 or 205544.1 or 110895.1	-1000	1000		Transport, Extracellular			
NAt3_1g	sodium:proton antiporter (H:NA in 1:1)	na1[c] + h[g] <=> h[c] + na1[g]	1	236727.1 or 77831.1	-1000	1000		Transport, Golgi Apparatus			
NAt5	sodium/ammonium proton antiporter	na1[c] + nh4[e] <=> nh4[c] + na1[e]	1	105243.1 or 226999.1 or 28544.1	-1000	1000		Transport, Extracellular			
NAtx	sodium transport via diffusion (peroxisome)	na1[c] <=> na1[x]	1		-1000	1000		Transport, Peroxisomal			
NBAHH_ir	Nalpha-(beta-alanyl)-L-histidine hydrolase IR	h2o[c] + carn[c] -> ala-B[c] + his-L[c]	0	338403.1	0	1000		beta-Alanine metabolism			
NCAMDe	release of nicotinamide at the basolateral surface	ncam[c] -> ncam[e]	0		0	1000	1	Transport, Extracellular	PMID: 21749321.	diffusion process. Hypothetically created. Nothing much is known about nicain exit from the enterocytes.	
NCAMLIP	Nicotinamide acid uptake	ncam[e] -> ncam[c]	0		0	1000		Transport, Extracellular			
NCCt	Na+-Cl- cotransport	na1[e] + cl[e] -> na1[c] + cl[c]	0	20497.1	0	1000		Transport, Extracellular			
NCKt	Na+/Ca2+-K+ exchange	4 na1[c] + k[e] + ca2[e] <=> 4 na1[e] + k[c] + ca2[c]	1	238384.1 or 214111.1 or 238384.2 or 238384.3 or 76376.1 or 94249.1	-1000	1000		Transport, Extracellular			
NCNt	Na+/Ca2+-NH4+ exchange	4 na1[c] + nh4[e] + ca2[e] <=> nh4[c] + 4 na1[e] + ca2[c]	1	214111.1 or 76376.1	-1000	1000		Transport, Extracellular			
NDP10ex	nucleoside-diphosphatase (IDP), extracellular	h2o[e] + idp[e] -> h[e] + pi[e] + imp[e]	0	76025.1	0	1000		Nucleotides			
NDP3ex	nucleoside-diphosphatase (GDP), extracellular	h2o[e] + gdp[e] -> h[e] + pi[e] + gmp[e]	0	76025.1	0	1000		Nucleotides			
NDP6	nucleoside-diphosphatase (dCDP)	h2o[c] + dcdp[c] -> h[c] + pi[c] + dcmp[c]	0		0	1000		Nucleotides			
NDP7er	nucleoside-diphosphatase (UDP), endoplasmic reticulum	h2o[r] + udp[r] -> h[r] + pi[r] + ump[r]	0		0	1000		Nucleotides			
NDP7ex	nucleoside-diphosphatase (UDP), extracellular	h2o[e] + udp[e] -> h[e] + pi[e] + ump[e]	0	76025.1	0	1000		Nucleotides			
NDP7g	nucleoside-diphosphatase (UDP), Golgi apparatus	udp[g] + h2o[g] -> h[g] + pi[g] + ump[g]	0	67464.1	0	1000		Nucleotides			
NDP8	nucleoside-diphosphatase (dUDP)	h2o[c] + dudp[c] -> h[c] + pi[c] + dump[c]	0	21915.1	0	1000		Nucleotides			
NDP9ex	nucleoside-diphosphatase (UTP), extracellular	h2o[e] + utp[e] -> h[e] + pi[e] + udp[e]	0	76025.1	0	1000		Nucleotides			
NDPK1	nucleoside-diphosphate kinase (ATP:GDP)	atp[c] + gdp[c] <=> adp[c] + gtp[c]	1	18103.1 and 18102.2 or 18102.1 and 18103.1 or 171567.1 or 54369.1 or 79059.1 or 171567.2	-1000	1000		Nucleotides			
NDPK10	nucleoside-diphosphate kinase (ATP:dIDP)	atp[c] + didp[c] <=> adp[c] + didp[c]	1	18103.1 and 18102.2 or 18102.1 and 18103.1 or 171567.1 or 54369.1 or 79059.1 or 171567.2	-1000	1000		Nucleotides			
NDPK10m	nucleoside-diphosphate kinase (ATP:dIDP), mitochondrial	atp[m] + didp[m] <=> adp[m] + didp[m]	1	56520.1	-1000	1000		Nucleotides			
NDPK10n	nucleoside-diphosphate kinase (ATP:dIDP), nuclear	atp[n] + didp[n] <=> adp[n] + didp[n]	1	18102.1 and 18103.1 or 18103.1 and 18102.2	-1000	1000		Nucleotides			
NDPK1m	nucleoside-diphosphate kinase (ATP:GDP), mitochondrial	atp[m] + gdp[m] <=> adp[m] + gtp[m]	1	56520.1	-1000	1000		Nucleotides			
NDPK1n	nucleoside-diphosphate kinase (ATP:GDP), nuclear	atp[n] + gdp[n] <=> adp[n] + gtp[n]	1	18102.1 and 18103.1 or 18103.1 and 18102.2	-1000	1000		Nucleotides			
NDPK2	nucleoside-diphosphate kinase (ATP:UDP)	atp[c] + udp[c] <=> adp[c] + utp[c]	1	18103.1 and 18102.2 or 18102.1 and 18103.1 or 171567.1 or 54369.1 or 79059.1 or 171567.2	-1000	1000		Nucleotides			
NDPK2m	nucleoside-diphosphate kinase (ATP:UDP), mitochondrial	atp[m] + udp[m] <=> adp[m] + utp[m]	1	56520.1	-1000	1000		Nucleotides			
NDPK2n	nucleoside-diphosphate kinase (ATP:UDP), nuclear	atp[n] + udp[n] <=> utp[n] + adp[n]	1	18102.1 and 18103.1 or 18103.1 and 18102.2	-1000	1000		Nucleotides			
NDPK3	nucleoside-diphosphate kinase (ATP:CDP)	atp[c] + cdp[c] <=> adp[c] + ctp[c]	1	18103.1 and 18102.2 or 18102.1 and 18103.1 or 171567.1 or 54369.1 or 79059.1 or 171567.2	-1000	1000		Nucleotides			
NDPK3m	nucleoside-diphosphate kinase (ATP:CDP), mitochondrial	atp[m] + cdp[m] <=> adp[m] + ctp[m]	1	56520.1	-1000	1000		Nucleotides			
NDPK3n	nucleoside-diphosphate kinase (ATP:CDP), nuclear	atp[n] + cdp[n] <=> ctp[n] + adp[n]	1	18102.1 and 18103.1 or 18103.1 and 18102.2	-1000	1000		Nucleotides			
NDPK4	nucleoside-diphosphate kinase (ATP:dTDP)	atp[c] + dtdp[c] <=> adp[c] + dttp[c]	1	18103.1 and 18102.2 or 18102.1 and 18103.1 or 171567.1 or 54369.1 or 79059.1 or 171567.2	-1000	1000		Nucleotides			
NDPK4m	nucleoside-diphosphate kinase (ATP:dTDP), mitochondrial	atp[m] + dtdp[m] <=> adp[m] + dttp[m]	1	56520.1	-1000	1000		Nucleotides			
NDPK4n	nucleoside-diphosphate kinase (ATP:dTDP), nuclear	atp[n] + dtdp[n] <=> adp[n] + dttp[n]	1	18102.1 and 18103.1 or 18103.1 and 18102.2	-1000	1000		Nucleotides			
NDPK5	nucleoside-diphosphate kinase (ATP:dGDP)	atp[c] + dgdp[c] <=> adp[c] + dgtp[c]	1	18103.1 and 18102.2 or 18102.1 and 18103.1 or 171567.1 or 54369.1 or 79059.1 or 171567.2	-1000	1000		Nucleotides			
NDPK5m	nucleoside-diphosphate kinase (ATP:dGDP), mitochondrial	atp[m] + dgdp[m] <=> adp[m] + dgtp[m]	1	56520.1	-1000	1000		Nucleotides			
NDPK5n	nucleoside-diphosphate kinase (ATP:dGDP), nuclear	atp[n] + dgdp[n] <=> dgtp[n] + adp[n]	1	18102.1 and 18103.1 or 18103.1 and 18102.2	-1000	1000		Nucleotides			
NDPK6	nucleoside-diphosphate kinase (ATP:dUDP)	atp[c] + dudp[c] <=> adp[c] + dump[c]	1	18103.1 and 18102.2 or 18102.1 and 18103.1 or 171567.1 or 54369.1 or 79059.1 or 171567.2	-1000	1000		Nucleotides			
NDPK6m	nucleoside-diphosphate kinase (ATP:dUDP), mitochondrial	atp[m] + dudp[m] <=> adp[m] + dump[m]	1	56520.1	-1000	1000		Nucleotides			
NDPK6n	nucleoside-diphosphate kinase (ATP:dUDP), nuclear	atp[n] + dudp[n] <=> adp[n] + dump[n]	1	18102.1 and 18103.1 or 18103.1 and 18102.2	-1000	1000		Nucleotides			
NDPK7	nucleoside-diphosphate kinase (ATP:dCDP)	atp[c] + dcdp[c] <=> adp[c] + dctp[c]	1	18103.1 and 18102.2 or 18102.1 and 18103.1 or 171567.1 or 54369.1 or 79059.1 or 171567.2	-1000	1000		Nucleotides			
NDPK7m	nucleoside-diphosphate kinase (ATP:dCDP), mitochondrial	atp[m] + dcdp[m] <=> adp[m] + dctp[m]	1	56520.1	-1000	1000		Nucleotides			
NDPK7n	nucleoside-diphosphate kinase (ATP:dCDP), nuclear	atp[n] + dcdp[n] <=> dctp[n] + adp[n]	1	18102.1 and 18103.1 or 18103.1 and 18102.2	-1000	1000		Nucleotides			
NDPK8	nucleoside-diphosphate kinase (ATP:dADP)	atp[c] + dadp[c] <=> adp[c] + datp[c]	1	18103.1 and 18102.2 or 18102.1 and 18103.1 or 171567.1 or 54369.1 or 79059.1 or 171567.2	-1000	1000		Nucleotides			
NDPK8m	nucleoside-diphosphate kinase (ATP:dADP), mitochondrial	atp[m] + dadp[m] <=> adp[m] + datp[m]	1	56520.1	-1000	1000		Nucleotides			
NDPK8n	nucleoside-diphosphate kinase (ATP:dADP), nuclear	atp[n] + dadp[n] <=> datp[n] + adp[n]	1	18102.1 and 18103.1 or 18103.1 and 18102.2	-1000	1000		Nucleotides			
NDPK9	nucleoside-diphosphate kinase (ATP:IDP)	atp[c] + idp[c] <=> adp[c] + itp[c]	1	18103.1 and 18102.2 or 18102.1 and 18103.1 or 171567.1 or 54369.1 or 79059.1 or 171567.2	-1000	1000		Nucleotides			
NDPK9m	nucleoside-diphosphate kinase (ATP:IDP), mitochondrial	atp[m] + idp[m] <=> adp[m] + itp[m]	1	56520.1	-1000	1000		Nucleotides			
NDPK9n	nucleoside-diphosphate kinase (ATP:IDP), nuclear	atp[n] + idp[n] <=> adp[n] + itp[n]	1	18102.1 and 18103.1 or 18103.1 and 18102.2	-1000	1000		Nucleotides			
NH4t3r	ammonia transport via proton antiport	nh4[c] + h[e] <=> h[c] + nh4[e]	1	19743.1 or 58176.1	-1000	1000		Transport, Extracellular			
NH4tn	ammonia nuclear transport	nh4[c] <=> nh4[n]	1		-1000	1000		Transport, Nuclear			
NH4tp	ammonia peroxisomal transport	nh4[c] <=> nh4[x]	1		-1000	1000		Transport, Peroxisomal			
NICRNS	NICRNS	atp[c] + nicrnm[c] -> adp[c] + h[c] + nicrnt[c]	0		0	1000		NAD Metabolism			
NICRNTtn	NICRNT transport, nuclear trhough pore	nicrnt[c] <=> nicrnt[n]	1		-1000	1000		Transport, Nuclear			
NIFEDIPINEte	xenobiotic transport	nifedipine[e] <=> nifedipine[c]	1		-1000	1000		Transport, Extracellular			
NKCC2t	Na+-K+-Cl- cotransport (NH4+)	na1[e] + nh4[e] + 2 cl[e] <=> nh4[c] + na1[c] + 2 cl[c]	1	20495.1 or 20496.1	-1000	1000		Transport, Extracellular			
NKCCt	Na+-K+-Cl- cotransport	na1[e] + k[e] + 2 cl[e] <=> na1[c] + 2 cl[c] + k[c]	1	20495.1 or 20496.1	-1000	1000		Transport, Extracellular			
NMNATm	nicotinamide-nucleotide adenylyltransferase, mitochondrial	h[m] + atp[m] + nmn[m] -> nad[m] + ppi[m]	0	74080.1	0	1000		NAD Metabolism			
NMNATn	nicotinamide-nucleotide adenylyltransferase	atp[n] + h[n] + nmn[n] -> ppi[n] + nad[n]	0	66454.1	0	1000		NAD Metabolism			
NMNATr	nicotinamide-nucleotide adenylyltransferase	atp[c] + h[c] + nmn[c] <=> nad[c] + ppi[c]	1	226518.1 or 226518.2 or 74080.1	-1000	1000		NAD Metabolism			
NMNS	NMN synthetase	h[c] + prpp[c] + ncam[c] -> ppi[c] + nmn[c]	0		0	1000		NAD Metabolism			
NMNtn	NMN transport, nuclear through pore	nmn[c] <=> nmn[n]	1		-1000	1000		Transport, Nuclear			
NMPTRCOX	N-Methylputrescine:oxygen oxidoreductase (deaminating)	o2[c] + mmptrc[c] -> h2o2[c] + nbd[c] + 3mpyr[c]	0	237940.1 or 237940.2 or 11754.1 or 76507.1	0	1000		Alkaloid biosynthesis II			
NNAT	nicotinate-nucleotide adenylyltransferase	atp[c] + h[c] + nicrnt[c] -> ppi[c] + dnad[c]	0	18605.1 or 18606.1 or 209558.1	0	1000		NAD Metabolism			
NNATm	nicotinate-nucleotide adenylyltransferase, mitochondrial	h[m] + atp[m] + nicrnt[m] -> ppi[m] + dnad[m]	0	74080.1	0	1000		NAD Metabolism			
NNATn	nicotinate-nucleotide adenylyltransferase	atp[n] + h[n] + nicrnt[n] -> ppi[n] + dnad[n]	0	66454.1	0	1000		NAD Metabolism			

NNATr	nicotinate-nucleotide adenylyltransferase	atp[c] + h[c] + nicrnt[c] <=> ppi[c] + dnad[c]	1	226518.1 or 226518.2 or 74080.1	-1000	1000		NAD Metabolism			
NNDPR	nicotinate-nucleotide diphosphorylase (carboxylating)	2 h[c] + prpp[c] + quln[c] -> co2[c] + ppi[c] + nicrnt[c]	0	67375.1	0	1000		NAD Metabolism			
NNMT	Nicotinamide N-methyltransferase	amet[c] + nicamt[c] -> 1mncamt[c] + ahcys[c]	0	18113.1	0	1000		NAD Metabolism			
NORANMT	noradrenaline N-methyltransferase	amet[c] + nrpphe[c] -> h[c] + ahcys[c] + adrnl[c]	0	18948.1	0	1000		Tyrosine metabolism			
NOS1	Nitric Oxide Synthase (intermediate forming)	o2[c] + h[c] + nadph[c] + arg-L[c] -> h2o[c] + nadp[c] + nwharg[c]	0	18125.1 or 18126.1 or 18126.2 or 18127.1	0	1000		Arginine and Proline Metabolism			
NOS2	Nitric Oxide Synthase (NO forming)	2 o2[c] + nadph[c] + 2 nwharg[c] -> 2 h2o[c] + h[c] + nadp[c] + 2 citr-L[c] + 2 no[c]	0	18125.1 or 18126.1 or 18126.2 or 18127.1	0	1000		Arginine and Proline Metabolism			
NOt	NO transport (diffusion)	no[e] <=> no[c]	1		-1000	1000		Transport, Extracellular			
NP1	nucleotide phosphatase	h[c] + nac[c] + r1p[c] -> pi[c] + nicrnt[c]	0	667034.1	0	1000		NAD Metabolism			
NPTHLte	xenobiotic transport	npth[e] <=> npth[c]	1		-1000	1000		Transport, Extracellular			
NRPPHRSFt	norepinephrine sulfate transport (diffusion)	nrpphres[c] -> nrpphres[e]	0		0	1000		Transport, Extracellular			
NRPPHRVESSEC	Noradrenaline secretion via secretory vesicle (ATP driven)	h2o[c] + atp[c] + nrpphe[c] -> adp[c] + 2 h[c] + pi[c] + nrenphe[e]	0	214084.1 or 110877.1	0	1000	2	Transport, Extracellular			
NRPPHRt4_2_r	Norepinephrine reversible transport in via sodium symport (1:2)	2 na1[e] + nrpphe[e] <=> 2 na1[c] + nrpphe[c]	1	20538.1 or 13162.1	-1000	1000		Transport, Extracellular			
NRPPHRto	Norepinephrine antiport	nrpphe[e] <=> nrpphe[c]	1	20518.1 or 20519.1 or 20518.2	-1000	1000		Transport, Extracellular			
NRVNCCOAtx	fatty acid intracellular transport	nrvnccoa[c] <=> nrvnccoa[x]	1		-1000	1000		Transport, Peroxisomal			
NRVNCCPT1	carnitine O-palmitoyltransferase	crn[c] + nrvnccoa[c] -> coa[c] + nrvnccrn[c]	0	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	0	1000		Carnitine shuttle			
NRVNCCPT2	carnitine transferase	coa[m] + nrvnccrn[m] -> crn[m] + nrvnccoa[m]	0	12896.1	0	1000		Carnitine shuttle			
NRVNCCRNt	transport into the mitochondria (carnitine)	nrvnccrn[c] -> nrvnccrn[m]	0	57279.1	0	1000		Carnitine shuttle			
NRVNCt	fatty acid transport via diffusion	nrvn[e] <=> nrvn[c]	1		-1000	1000		Transport, Extracellular			
NS26T2g	alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase	cmpacna[g] + sT_antigen[g] -> h[g] + cmp[g] + dsT_antigen[g]	0	20445.1	0	1000		O-Glycan Biosynthesis			
NS26Tg	alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase	cmpacna[g] + Tn_antigen[g] -> h[g] + cmp[g] + sTn_antigen[g]	0	20445.1	0	1000		O-Glycan Biosynthesis			
NTSC	5'-nucleotidase	h2o[c] + nicrnt[c] -> pi[c] + nicrn[c]	0	76952.1	0	1000		NAD Metabolism			
NTD1	5'-nucleotidase (dUMP)	h2o[c] + dump[c] -> pi[c] + duri[c]	0	50773.1	0	1000		Pyrimidine Catabolism			
NTD10	5'-nucleotidase (XMP)	h2o[c] + xmp[c] -> pi[c] + xtsin[c]	0	76952.1	0	1000		Nucleotides			
NTD12	5'-nucleotidase (dIMP)	h2o[c] + dimp[c] -> pi[c] + idsin[c]	0	50773.1	0	1000		Nucleotides			
NTD1m	5'-nucleotidase (dUMP), mitochondrial	h2o[m] + dump[m] -> pi[m] + duri[m]	0	103850.1	0	1000		Nucleotides			
NTD2	5'-nucleotidase (UMP)	h2o[c] + ump[c] -> pi[c] + uri[c]	0	107569.1	0	1000		Pyrimidine Catabolism			
NTD2e	5'-nucleotidase (UMP), extracellular	h2o[e] + ump[e] -> pi[e] + uri[e]	0	23959.1	0	1000		Nucleotides			
NTD2l	5'-nucleotidase (UMP), lysosome	h2o[l] + ump[l] -> pi[l] + uri[l]	0	11432.1	0	1000		Nucleic acid degradation			
NTD2m	5'-nucleotidase (UMP), mitochondrial	h2o[m] + ump[m] -> pi[m] + uri[m]	0	103850.1	0	1000		Nucleotides			
NTD3l	5'-nucleotidase (dCMP), lysosomal	h2o[l] + dcmp[l] -> pi[l] + dcyd[l]	0	11432.1	0	1000		Nucleic acid degradation			
NTD4	5'-nucleotidase (CMP)	h2o[c] + cmp[c] -> pi[c] + cytd[c]	0	107569.1	0	1000		Pyrimidine Catabolism			
NTD4e	5'-nucleotidase (CMP), extracellular	h2o[e] + cmp[e] -> pi[e] + cytd[e]	0	23959.1	0	1000		Nucleotides			
NTD4l	5'-nucleotidase (CMP), lysosome	h2o[l] + cmp[l] -> pi[l] + cytd[l]	0	11432.1	0	1000		Nucleic acid degradation			
NTD5	5'-nucleotidase (dTMP)	h2o[c] + dtmp[c] -> pi[c] + thymd[c]	0	50773.1	0	1000		Pyrimidine Catabolism			
NTD5l	5'-nucleotidase (dTMP), lysosomal	h2o[l] + dtmp[l] -> pi[l] + thymd[l]	0	11432.1	0	1000		Nucleic acid degradation			
NTD5m	5'-nucleotidase (dTMP), mitochondrial	h2o[m] + dtmp[m] -> pi[m] + thymd[m]	0	103850.1	0	1000		Nucleotides			
NTD6	5'-nucleotidase (dAMP)	h2o[c] + damp[c] -> pi[c] + dad-2[c]	0	76952.1	0	1000		Nucleotides			
NTD6l	5'-nucleotidase (dAMP), lysosome	h2o[l] + damp[l] -> pi[l] + dad-2[l]	0	11432.1	0	1000		Nucleic acid degradation			
NTD7e	5'-nucleotidase (AMP), extracellular	h2o[e] + amp[e] -> adn[e] + pi[e]	0	23959.1	0	1000		Nucleotides			
NTD7l	5'-nucleotidase (AMP), lysosome	h2o[l] + amp[l] -> adn[l] + pi[l]	0	11432.1	0	1000		Nucleic acid degradation			
NTD8	5'-nucleotidase (dGMP)	h2o[c] + dgmp[c] -> pi[c] + dgsr[c]	0	50773.1 or 76952.1	0	1000		Nucleotides			
NTD8l	5'-nucleotidase (dGMP), lysosomal	h2o[l] + dgmp[l] -> pi[l] + dgsr[l]	0	11432.1	0	1000		Nucleic acid degradation			
NTD9	5'-nucleotidase (GMP)	h2o[c] + gmp[c] -> pi[c] + gsn[c]	0	76952.1	0	1000		Nucleotides			
NTD9e	5'-nucleotidase (GMP), extracellular	h2o[e] + gmp[e] -> pi[e] + gsn[e]	0	23959.1	0	1000		Nucleotides			
NTD9l	5'-nucleotidase (GMP), lysosome	h2o[l] + gmp[l] -> pi[l] + gsn[l]	0	11432.1	0	1000		Nucleic acid degradation			
NTMELYSmer	protein trimethyl lysine transport (nucleus to ER)	Nmelys[n] -> Nmelys[r]	0		0	1000		Transport, Nuclear			
NTP3e	nucleoside-triphosphatase (GTP)	h2o[e] + gtp[e] -> h[e] + pi[e] + gdp[e]	0	76025.1	0	1000		Nucleotides			
NTPP10	Nucleoside triphosphate pyrophosphorylase (dttp)	h2o[c] + dttp[c] -> h[c] + ppi[c] + dttmp[c]	0	16434.1 or 16434.2	0	1000		Nucleotides			
NTPPT11	Nucleoside triphosphate pyrophosphorylase (utp)	h2o[c] + utp[c] -> h[c] + ppi[c] + ump[c]	0	16434.1 or 16434.2	0	1000		Nucleotides			
NTPP9	Nucleoside triphosphate pyrophosphorylase (itp)	h2o[c] + itp[c] -> h[c] + ppi[c] + imp[c]	0	16434.1 or 16434.2	0	1000		Nucleotides			
O16G1e	oligo-1,6-glucosidase (glygn4 -> glygn5), extracellular	h2o[e] + glygn4[e] -> glc-D[e] + glygn5[e]	0	69983.1	0	1000		Starch and Sucrose Metabolism			
O16G2e	oligo-1,6-glucosidase (strch2 ->strch3), extracellular	h2o[e] + strch2[e] -> glc-D[e] + malt[e]	0	69983.1	0	1000		Starch and Sucrose Metabolism			
O2St	superoxide anion transport via diffusion (extracellular)	o2s[c] <=> o2s[e]	1		-1000	1000		Transport, Extracellular			
O2Stm	superoxide anion transport via diffusion (mitochondria)	o2s[c] <=> o2s[m]	1		-1000	1000		Transport, Mitochondrial			
O2Stn	superoxide anion transport via diffusion (nucleus)	o2s[c] <=> o2s[n]	1		-1000	1000		Transport, Nuclear			
O2Stx	superoxide anion transport via diffusion (peroxisome)	o2s[c] <=> o2s[x]	1		-1000	1000		Transport, Peroxisomal			
O2t	o2 transport (diffusion)	o2[e] <=> o2[c]	1		-1000	1000		Transport, Extracellular			
O2ter	O2 transport, endoplasmic reticulum	o2[c] <=> o2[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
O2tm	O2 transport (diffusion)	o2[c] <=> o2[m]	1		-1000	1000		Transport, Mitochondrial			
O2tn	O2 nuclear transport	o2[c] <=> o2[n]	1		-1000	1000		Transport, Nuclear			
O2tp	O2 transport, peroxisomal	o2[c] <=> o2[x]	1		-1000	1000		Transport, Peroxisomal			
OAGt3e	oagt3_bs transport	oagt3_bs[c] <=> oagt3_bs[e]	1		-1000	1000		Transport, Extracellular			
OAGt3g	oagt3_bs intracellular transport	oagt3_bs[c] <=> oagt3_bs[g]	1		-1000	1000		Transport, Golgi Apparatus			
OAGT3e	oagt3_bs transport	oagt3_bs[c] <=> oagt3_bs[e]	1		-1000	1000		Transport, Extracellular			
OAGT3g	oagt3_bs intracellular transport	oagt3_bs[c] <=> oagt3_bs[g]	1		-1000	1000		Transport, Golgi Apparatus			
OBDHc	2-Oxobutanoate dehydrogenase, cytosolic	nad[c] + coa[c] + 2obut[c] -> nadh[c] + co2[c] + ppcoa[c]	0		0	1000		Glycine, Serine, and Threonine Metabolism			
OCBTm	ornithine carbamoyltransferase, irreversible	orn[m] + cbp[m] -> h[m] + pi[m] + citr-L[m]	0	18416.1	0	1000		Urea cycle/amino group metabolism			
OCCOAtm	Octanoyl-CoA transport, diffusion	occoa[c] -> occoa[m]	0		0	1000		Transport, Mitochondrial			
OCCOAtx	fatty acid intracellular transport	occoa[c] <=> occoa[x]	1		-1000	1000		Transport, Peroxisomal			
OCDCAte	fatty acid transport via diffusion	ocdca[e] <=> ocdca[c]	1		-1000	1000		Transport, Extracellular			
OCDCEAte	fatty acid transport via diffusion	ocdcea[e] <=> ocdcea[c]	1		-1000	1000		Transport, Extracellular			
OCDEAFABPtc	transport of octadecenoyl coA into the enterocytes	2 ocdcea[c] <=> 2 ocdcea[r]	1	14080.1	-1000	1000	3	Transport, Endoplasmic Reticular	PMID: 9555061, PMCID: PMC2821027, PMID: 9054409, PMID: 9082452, PMCID: PMC2670638, http://rna13.libraries.rutgers.edu/dlr/TMP/rogers-lib_26338-PDF-1.pdf	crystal structure of LFAB revealed 2 binding sites (in contrast to IFAB which has 1:1 stoichiometry) for oleate (PMID: 9054409). LFAB is expressed in liver, kidney, intestine, pancreas, stomach and lung (PMCID: PMC2670638). Once the long chain fatty acids enter the enterocytes, bind to the FABP reversibly, for transport into the E.R. to reconstitute triacylglycerols (PMID: 20522896, PMID: 19280719).	
OCDCAFATPtc	uptake of octadecenoate by the enterocytes	atp[c] + coa[c] + ocdcea[a] -> amp[c] + ppi[c] + odecoa[c]	0	26569.1	0	1000	3	Transport, Lumen	PMID: 10518211, PMID: 20086080, PMID: 12856180, Immun., Endoc. & Metab. Agents in Med. Chem., 2009, 9, 11-17,	major intestinal fatty acid transport protein, may also act in co-ordination with acyl co-A synthetase. The transport is ATP driven, further the transporter itself has fatty acid activating enzymic properties (PMID: 12856180).	6.2.1.-
OMEPRAZOLEte	xenobiotic transport	omeprazole[e] <=> omeprazole[c]	1		-1000	1000		Transport, Extracellular			
OMPDC	orotidine-5'-phosphate decarboxylase	h[c] + orotP[c] -> co2[c] + ump[c]	0	22247.1	0	1000		Pyrimidine Biosynthesis			
ONPTHLte	xenobiotic transport	onpth[e] <=> onpth[c]	1		-1000	1000		Transport, Extracellular			
OPAHir	5-Oxoproline amidohydrolase (ATP-hydrolysing) (ir)	2 h2o[c] + atp[c] + 5oxpro[c] -> adp[c] + h[c] + pi[c] + glu-L[c]	0	75475.1	0	1000		Glutathione Metabolism			
ORETNF	4-oxo-retinoic acid formation (oxidation)	o2[c] + 2 rretol[c] -> 2 orntl[c]	0		0	1000		Vitamin A Metabolism			
ORETNF2	13-cis-4-oxo-retinoic acid formation (oxidation)	o2[c] + 2 13-cis-rretol[c] -> 2 13-cis-orntl[c]	0		0	1000		Vitamin A Metabolism			
ORETNtn	4-oxo-retinoic acid transport, Nuclear	orntl[c] <=> orntl[n]	1		-1000	1000		Transport, Nuclear			
ORETNtn2	13-cis-4-oxo-retinoic acid transport, Nuclear	13-cis-orntl[c] <=> 13-cis-orntl[n]	1		-1000	1000		Transport, Nuclear			
ORNALArBATtc	transport of L-Ornithine into the cell in exchange for L-Alanine by hL+AT transporter at the apical surfaces of the membranes of small intestine and renal cells.	ala-L[c] + orn[a] -> orn[c] + ala-L[a]	0	(30962.1 and 20532.1)	0	1000	3	Transport, Lumen	PMID: 10958334, PMID: 19184091, PMID: 18195088, PMID: 11546643	sodium-independant antiport transport system; exchanges zi-basic amino acids into the cells and neutral amino acids out of the cell. Located on the apical surfaces of transporting epithelia. Cellular localization being small intestine, kidney (proximal tubule), lung, placenta, brain and thymus. Requires the heterodimerization with rBAT glycoprotein. (PMID: 10958334).	
ORNDC	Ornithine Decarboxylase	h[c] + orn[c] -> co2[c] + ptrc[c]	0	18263.1	0	1000		Urea cycle/amino group metabolism			
ORNLEUtBATtc	transport of L-Ornithine into the cell in exchange for L-Leucine by hL+AT transporter at the apical surfaces of the membranes of small intestine and renal cells.	leu-L[c] + orn[a] -> leu-L[a] + orn[c]	0	(30962.1 and 20532.1)	0	1000	3	Transport, Lumen	PMID: 10958334, PMID: 19184091, PMID: 18195088, PMID: 11546643	sodium-independant antiport transport system; exchanges zi-basic amino acids into the cells and neutral amino acids out of the cell. Located on the apical surfaces of transporting epithelia. Cellular localization being small intestine, kidney (proximal tubule), lung, placenta, brain and thymus. Requires the heterodimerization with rBAT glycoprotein. (PMID: 10958334).	
ORNTArm	ornithine transaminase reversible (m)	akg[m] + orn[m] <=> glu-L[m] + glu5sa[m]	1	18242.1	-1000	1000		Urea cycle/amino group metabolism			
ORNt	ornithine transport via diffusion (extracellular to cytosol)	orn[e] <=> orn[c]	1	11987.1	-1000	1000	2	Transport, Extracellular			
ORNt3m	ornithine mitochondrial transport via proton antiport	h[c] + orn[m] <=> h[m] + orn[c]	1	18408.1 or 83885.1	-1000	1000		Transport, Mitochondrial			
ORNt4m	ornithine mitochondrial transport exchange with citrulline	h[c] + orn[m] + citr-L[c] <=> h[m] + orn[c] + citr-L[m]	1	18408.1 or 83885.1	-1000	1000		Transport, Mitochondrial			
ORNtiDF	ornithine transport via diffusion (extracellular to cytosol)	orn[e] -> orn[c]	0	11988.1 or 11988.6 or 11987.1	0	1000		Transport, Extracellular			
ORPT	orotate phosphoribosyltransferase	prpp[c] + orotP[c] <=> ppcp[c] + orot[c]	1	22247.1	-1000	1000		Pyrimidine Biosynthesis			
OXAHCOtex	oxalate transport via bicarbonate countertransport	2 hco3[c] + oxa[e] -> 2 hco3[e] + oxa[c]	0	13487.1 or 231583.1 or 13521.1 or 231583.2 or 231583.3	0	1000		Transport, Extracellular			
OXAtp	oxalate transport out of peroxisome	oxa[x] -> oxa[c]	0		0	1000		Transport, Peroxisomal			
P4501A1tm	Cytochrome P450 11A1, mitochondrial [Pancreas]	h[m] + nadph[m] + 2 o2[m] + chsterol[m] -> 2 h2o[m] + nadp[m] + 4aspn5[m] + pregnlone[m]	0	13070.1	0	1000		Steroid Metabolism			
P4501B1tm	Steroid 11-beta-hydroxylase	11docrstrn[m] + h[m] + nadph[m] + o2[m] -> h2o[m] + nadp[m] + crtsterol[m]	0	110115.1	0	1000		Steroid Metabolism			

P45011B12m	Steroid 11-beta-hydroxylase	11docrtsl[m] + h[m] + nadph[m] + o2[m] -> h2o[m] + nadp[m] + crtsl[m]	0	110115.1	0	1000		Steroid Metabolism			
P45011B21m	Steroid 11-beta-hydroxylase	11docrtstrn[m] + h[m] + nadph[m] + 2 o2[m] -> 2 h2o[m] + nadp[m] + aldstrn[m]	0	13072.1	0	1000		Steroid Metabolism			
P45017A1r	Cytochrome P450 17A1	o2[r] + h[r] + nadph[r] + prgnlone[r] -> h2o[r] + nadp[r] + 17ahprgnlone[r]	0	13074.1	0	1000		Steroid Metabolism			
P45017A2r	Cytochrome P450 17A1	0.5 o2[r] + h[r] + nadph[r] + 17ahprgnlone[r] -> acald[r] + h2o[r] + nadp[r] + dhea[r]	0	13074.1	0	1000		Steroid Metabolism			
P45017A3r	Cytochrome P450 17A1	o2[r] + h[r] + nadph[r] + prgstrn[r] -> h2o[r] + nadp[r] + 17ahprgstrn[r]	0	13074.1	0	1000		Steroid Metabolism			
P45017A4r	Cytochrome P450 17A1	0.5 o2[r] + h[r] + nadph[r] + 17ahprgstrn[r] -> acald[r] + h2o[r] + nadp[r] + andrstndn[r]	0	13074.1	0	1000		Steroid Metabolism			
P45019A1r	aromatase	2 o2[r] + nadph[r] + andrstndn[r] -> 2 h2o[r] + nadp[r] + estrone[r] + for[r]	0	13075.1 or 13075.2	0	1000		Steroid Metabolism			
P45019A2r	aromatase	2 o2[r] + nadph[r] + tststerone[r] -> 2 h2o[r] + nadp[r] + estradiol[r] + for[r]	0	13075.1 or 13075.2	0	1000		Steroid Metabolism			
P4501B1r	cytochrome P450 1B1	o2[r] + h[r] + nadph[r] + estradiol[r] -> h2o[r] + nadp[r] + hestratriol[r]	0	13078.1	0	1000		Steroid Metabolism			
P45021A1r	Steroid 21-hydroxylase	o2[r] + h[r] + nadph[r] + prgstrn[r] -> 11docrtstrn[r] + h2o[r] + nadp[r]	0	13079.1	0	1000		Steroid Metabolism			
P45021A2r	Steroid 21-hydroxylase	o2[r] + h[r] + nadph[r] + 17ahprgstrn[r] -> 11docrtsl[r] + h2o[r] + nadp[r]	0	13079.1	0	1000		Steroid Metabolism			
P45027A11m	5-beta-cholestane-3-alpha,7-alpha,12-alpha-triol 27-hydroxylase	h[m] + nadph[m] + o2[m] + xoltriol[m] -> h2o[m] + nadp[m] + xoltetrol[m]	0	104086.1	0	1000		Bile Acid Biosynthesis			
P45027A12m	5-beta-cholestane-3-alpha,7-alpha,12-alpha-triol 27-hydroxylase	nadp[m] + xoltetrol[m] -> h[m] + nadph[m] + thcholst[m]	0	104086.1	0	1000		Bile Acid Biosynthesis			
P45027A13m	5-beta-cholestane-3-alpha,7-alpha,12-alpha-triol 27-hydroxylase	nadph[m] + o2[m] + thcholst[m] -> h2o[m] + nadp[m] + thcholstoic[m]	0	104086.1	0	1000		Bile Acid Biosynthesis			
P45027A14m	5-beta-cytochrome P450, family 27, subfamily A, polypeptide 1	h[m] + nadph[m] + o2[m] + xol7ah2[m] -> h2o[m] + nadp[m] + xol7ah3[m]	0	104086.1	0	1000		Bile Acid Biosynthesis			
P45027A15m	5-beta-cytochrome P450, family 27, subfamily A, polypeptide 1	h[m] + nadph[m] + o2[m] + xol7ah3[m] -> 2 h2o[m] + nadp[m] + xol7ah2al[m]	0	104086.1	0	1000		Bile Acid Biosynthesis			
P45027A16m	Cytochrome P450 27	nadph[m] + o2[m] + xol7ah2al[m] -> h2o[m] + nadp[m] + dhcholestanate[m]	0	104086.1	0	1000		Bile Acid Biosynthesis			
P45027A1m	Cytochrome P450 27	h[m] + nadph[m] + o2[m] + chsterol[m] -> h2o[m] + nadp[m] + xol27oh[m]	0	104086.1	0	1000		Bile Acid Biosynthesis			
P4502C18	cytochrome P450 2C18	0.5 o2[c] + h[c] + nadph[c] + antipyrene[c] -> nadp[c] + dmantipyrine[c] + meoh[c]	0	72082.1	0	1000		CYP Metabolism			
P4502C19	cytochrome P450 2C19	o2[c] + h[c] + nadph[c] + omeprazole[c] -> h2o[c] + nadp[c] + 5homeprazole[c]	0	404195.1	0	1000		CYP Metabolism			
P4502C8	cytochrome P450 2C8	o2[c] + h[c] + nadph[c] + taxol[c] -> h2o[c] + nadp[c] + htaxol[c]	0	69888.1 or 69888.2	0	1000		CYP Metabolism			
P4502D6	cytochrome P450 2D6	o2[c] + h[c] + nadph[c] + debrisoquine[c] -> h2o[c] + nadp[c] + 4hdebrisoquine[c]	0	56448.1	0	1000		CYP Metabolism			
P4502E1	cytochrome P450 2E1	o2[c] + h[c] + nadph[c] + 4nph[c] -> h2o[c] + 24nph[c] + nadp[c]	0	13106.1	0	1000		CYP Metabolism			
P4502F1	cytochrome P450 2F1	o2[c] + h[c] + nadph[c] + npthl[c] -> h2o[c] + nadp[c] + onpthl[c]	0	13107.1	0	1000		CYP Metabolism			
P45039A1r	oxysterol 7-alpha-hydroxylase	o2[r] + h[r] + nadph[r] + xol24oh[r] -> h2o[r] + nadp[r] + xoltri24[r]	0	56050.1	0	1000		Bile Acid Biosynthesis			
P4503A4	cytochrome P450 3A4	o2[c] + h[c] + nadph[c] + nifedipine[c] -> h2o[c] + nadp[c] + hnifedipine[c]	0	100041375.1	0	1000		CYP Metabolism			
P4503A43r	cytochrome p450 P450 3A43	o2[r] + h[r] + nadph[r] + tststerone[r] -> h2o[r] + nadp[r] + whtststerone[r]	0	56388.1 or 56388.2 or 56388.3	0	1000		Steroid Metabolism			
P4503A5	cytochrome P450 3A5	o2[c] + h[c] + nadph[c] + aflatoxin[c] -> h2o[c] + nadp[c] + eaflatoxin[c]	0		0	1000		CYP Metabolism			
P4503A7r	cytochrome p450 P450 3A7	o2[r] + h[r] + nadph[r] + tststerone[r] -> 6htststerone[r] + h2o[r] + nadp[r]	0	13113.1	0	1000		Steroid Metabolism			
P45046A1r	cytochrome P450, family 46, subfamily A, polypeptide 1	o2[r] + h[r] + nadph[r] + chsterol[r] -> h2o[r] + nadp[r] + xol24oh[r]	0	13116.1	0	1000		Bile Acid Biosynthesis			
P4504B1r	cytochrome P450 4B1	o2[r] + arachd[r] + h[r] + nadph[r] -> h2o[r] + nadp[r] + 12harachd[r]	0	13107.1	0	1000		Eicosanoid Metabolism			
P4504F121r	cytochrome p450 4F12/4F2	o2[r] + arachd[r] + h[r] + nadph[r] -> h2o[r] + nadp[r] + wharachd[r]	0	64385.1	0	1000		Eicosanoid Metabolism			
P4504F122r	cytochrome p450 4F12/4F2	o2[r] + h[r] + nadph[r] + leuktrB4[r] -> h2o[r] + nadp[r] + leuktrB4woh[r]	0	106648.1 or 64385.1 or 72054.1	0	1000		Eicosanoid Metabolism			
P4504F123r	cytochrome p450 4F12/4F2	o2[r] + h[r] + nadph[r] + ebastine[r] -> h2o[r] + nadp[r] + ebastineoh[r]	0	64385.1	0	1000		CYP Metabolism			
P4504F81r	cytochrome p450 4F8	o2[r] + arachd[r] + h[r] + nadph[r] -> h2o[r] + nadp[r] + 18harachd[r]	0	208285.1	0	1000		Eicosanoid Metabolism			
P4507A1r	cytochrome P450, family 7, subfamily A, polypeptide 1	o2[r] + h[r] + nadph[r] + chsterol[r] -> h2o[r] + nadp[r] + xol7a[r]	0	13122.1	0	1000		Bile Acid Biosynthesis			
P4507B11r	oxysterol 7alpha-hydroxylase	o2[r] + h[r] + nadph[r] + xol25oh[r] -> h2o[r] + nadp[r] + xoltri25[r]	0	13123.1	0	1000		Bile Acid Biosynthesis			
P4507B12r	oxysterol 7alpha-hydroxylase	o2[r] + h[r] + nadph[r] + xol27oh[r] -> h2o[r] + nadp[r] + xoltri27[r]	0	13123.1	0	1000		Bile Acid Biosynthesis			
P4508B11r	sterol 12-alpha-hydroxylase	o2[r] + h[r] + nadph[r] + xol7aone[r] -> h2o[r] + nadp[r] + xoldiolone[r]	0	13124.1	0	1000		Bile Acid Biosynthesis			
P4508B13r	sterol 12-alpha-hydroxylase (nadh)	o2[r] + h[r] + nadh[r] + xol7aone[r] -> h2o[r] + nad[r] + xoldiolone[r]	0	13124.1	0	1000		Bile Acid Biosynthesis			
P450LTB4r	cytochrome p450 leukotriene B4	1.5 o2[r] + nadph[r] + leuktrB4woh[r] -> 2 h2o[r] + nadp[r] + leuktrB4wcooh[r]	0		0	1000		Eicosanoid Metabolism			
P450SCC1m	cholesterol monooxygenase	h[m] + nadph[m] + o2[m] + chsterol[m] <=> h2o[m] + nadp[m] + 20ahchsterol[m]	1		-1000	1000		Cholesterol Metabolism			
P5CDm	1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	2 h2o[m] + nad[m] + 1pyr5c[m] -> h[m] + nadh[m] + glu-L[m]	0	212647.1 or 212647.2	0	1000		Glutamate metabolism			
P5CR	pyrroline-5-carboxylate reductase	2 h[c] + nadph[c] + 1pyr5c[c] -> nadp[c] + pro-L[c]	0	69051.1 or 66194.1	0	1000		Urea cycle/amino group metabolism			
P5CRm	pyrroline-5-carboxylate reductase (m)	2 h[m] + nadph[m] + 1pyr5c[m] -> nadp[m] + pro-L[m]	0	209027.1 or 209027.2	0	1000		Arginine and Proline Metabolism			
P5CRx	pyrroline-5-carboxylate reductase	2 h[c] + nadh[c] + 1pyr5c[c] -> nad[c] + pro-L[c]	0	69051.1 or 66194.1	0	1000		Urea cycle/amino group metabolism			
P5CRxm	pyrroline-5-carboxylate reductase (m)	2 h[m] + nadh[m] + 1pyr5c[m] -> nad[m] + pro-L[m]	0	209027.1 or 209027.2	0	1000		Arginine and Proline Metabolism			
PACCOAL	phenylacetate-CoA ligase	atp[c] + coa[c] + pac[c] -> amp[c] + ppi[c] + phaccoa[c]	0		0	1000		Phenylalanine metabolism			
PAFH	Platelet-activating factor acetylhydrolase	h2o[c] + paf_hs[c] -> h[c] + ac[c] + ak2lgchol_hs[c]	0	18476.1 and 18475.1 or 18472.1 and 18476.1 and 18475.1 or 100163.1	0	1000		Glycerophospholipid Metabolism			
PAFHe	Platelet-activating factor acetylhydrolase	h2o[e] + paf_hs[e] -> h[e] + ac[e] + ak2lgchol_hs[e]	0	27226.1	0	1000		Glycerophospholipid Metabolism			
PAFS	alkyl glycerol phosphocholine acetyl transferase	accoa[c] + ak2lgchol_hs[c] -> coa[c] + paf_hs[c]	0		0	1000		Glycerophospholipid Metabolism			
PAFt	Platelet activating factor transmembrane (homo sapiens) transport	paf_hs[e] <=> paf_hs[c]	1		-1000	1000		Transport, Extracellular			
PAIL45P_HStn	phosphatidylinositol 4,5-bisphosphate nuclear transport (diffusion)	pail45p_hs[c] <=> pail45p_hs[n]	1		-1000	1000		Transport, Nuclear			
PAIL4P_HStn	phosphatidylinositol 4-phosphate nuclear transport (diffusion)	pail4p_hs[c] <=> pail4p_hs[n]	1		-1000	1000		Transport, Nuclear			
PAIL_HStn	phosphatidylinositol nuclear transport (diffusion)	pail_hs[c] <=> pail_hs[n]	1		-1000	1000		Transport, Nuclear			
PALFATPtc	uptake of Hexadecanoate by the enterocytes	atp[c] + coa[c] + hdca[u] -> amp[c] + ppi[c] + pmtcoa[c]	0	26569.1	0	1000	3	Transport, Lumen	PMID: 10518211, PMID: 20086080, PMID: 12856180, Immun., Endoc. & Metab. Agents in Med. Chem., 2009, 9, 11-17,	major intestinal fatty acid transport protein, may also act in co-ordination with acyl co-A synthetase. The transport is ATP driven, further the transporter itself has fatty acid activating enzymic properties (PMID: 12856180).	6.2.1.-
PAN4PP	phosphatase (pan4p)	h2o[c] + pan4p[c] -> pi[c] + ptth[c]	0		0	1000		CoA Catabolism			
PAPStg	3'-Phosphoadenylyl sufate Golgi transport	paps[c] <=> paps[g]	1	73836.1	-1000	1000		Transport, Golgi Apparatus			
PAPtg	adenosine 3',5'-bisphosphate Golgi transport	pap[g] -> pap[c]	0		0	1000		Transport, Golgi Apparatus			
PA_HSter	phosphatidate scramblase	pa_hs[c] <=> pa_hs[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
PA_HStg	phosphatidate scramblase	pa_hs[c] <=> pa_hs[g]	1		-1000	1000		Transport, Golgi Apparatus			
PA_HStn	phosphatidate transport, nuclear	pa_hs[c] <=> pa_hs[n]	1		-1000	1000		Transport, Nuclear			
PCFLOPm	phosphatidylcholine flippase	h2o[c] + atp[c] + pchol_hs[m] -> adp[c] + h[c] + pi[c] + pchol_hs[c]	0	11982.1	0	1000		Transport, Mitochondrial			
PCHOLHSTDe	Transport, extracellular	pchol_hs[c] -> pchol_hs[e]	0		0	1000	2	Transport, Extracellular	Sareen S. Gropper, jack L. Smith, James L. Groff (2009) Wadaworth cengage learning, Advanced nutrition and human metabolism, 5th edition, page 142-148.	transported in chylomicrons into lymph	
PCHOLP_hs	choline phosphatase	h2o[c] + pchol_hs[c] -> h[c] + pa_hs[c] + chol[c]	0	18806.1	0	1000		Glycerophospholipid Metabolism			
PCHOLPg_hs	choline phosphatase	h2o[g] + pchol_hs[g] -> h[g] + chol[g] + pa_hs[g]	0	18805.1	0	1000		Glycerophospholipid Metabolism			
PCHOLPm_hs	choline phosphatase	h2o[m] + pchol_hs[m] -> h[m] + pa_hs[m] + chol[m]	0	18805.1	0	1000		Glycerophospholipid Metabolism			
PCHOLPr_hs	choline phosphatase	h2o[r] + pchol_hs[r] -> h[r] + chol[r] + pa_hs[r]	0	18805.1	0	1000		Glycerophospholipid Metabolism			
PCHOL_HSter	phosphatidylcholine scramblase	pchol_hs[c] <=> pchol_hs[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
PCHOL_HStg	phosphatidylcholine scramblase	pchol_hs[c] <=> pchol_hs[g]	1		-1000	1000		Transport, Golgi Apparatus			
PCLAD	picolinic acid decarboxylase	h[c] + cmusa[c] -> co2[c] + am6sa[c]	0	266645.1	0	1000		Tryptophan metabolism			
PCLYSOX	Procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase	o2[c] + akg[c] + pcollglys[c] -> co2[c] + succ[c] + pcollg5hlys[c]	0	26432.1 or 18822.1 or 26432.2 or 26433.1	0	1000		Lysine Metabolism			
PCREATtmdiffir	Phosphocreatine transport to/from mitochondria via diffusion	pcreat[m] -> pcreat[c]	0		0	1000		Urea cycle/amino group metabolism			
PCRNtc	transport into the cytosol from peroxisome (carnitine)	pcrn[x] -> pcrn[c]	0		0	1000		Carnitine shuttle			
PCRNtm	transport into the mitochondria from cytosol (carnitine)	pcrn[c] -> pcrn[m]	0		0	1000		Carnitine shuttle			
PCm	pyruvate carboxylase	pyr[m] + atp[m] + hco3[m] -> h[m] + adp[m] + pi[m] + oaa[m]	0	18563.1 or 18563.2	0	1000		Pyruvate Metabolism			
PCt	phosphatidylcholine transporter	h2o[c] + atp[c] + pchol_hs[c] <=> adp[c] + h[c] + pi[c] + pchol_hs[e]	1	18670.1 or 18670.2 or 18670.3	-1000	1000		Transport, Extracellular			
PDE1	3',5'-cyclic-nucleotide phosphodiesterase	h2o[c] + camp[c] -> h[c] + amp[c]	0	18576.1 or 18584.1 or 18578.1 or 18584.2 or 18583.1 or 18584.3 or 18584.4 or 23984.1 or 241489.1 or 207728.1 or 110385.1 or 18577.1 or 54611.1 or 18576.2 or 29863.1 or 18574.1 or 18573.2 or 18575.1 or 218461.1 or 18584.5 or 238871.1 or 18583.2 or 18573.1	0	1000		Nucleotides			
PDE1g	3',5'-cyclic-nucleotide phosphodiesterase,Golgi	h2o[g] + camp[g] -> h[g] + amp[g]	0	23984.1	0	1000		Nucleotides			

PDE4	3',5'-cyclic-nucleotide phosphodiesterase	h2o[c] + 35cgmp[c] -> h[c] + gmp[c]	0	225600.1 and 78600.1 and 18587.1 or 18576.1 or 110855.1 or 18585.1 or 18585.2 or 18585.3 or 18585.4 or 18585.5 or 241489.1 or 207728.1 or 18585.6 or 18585.7 or 18585.8 or 18585.9 or 54611.1 or 18576.1 or 18585.10 or 18574.1 or 18588.1 and 225600.1 and 18582.1 and 110855.1 and 18587.1 or 18573.1 or 18585.11 or 18585.12 or 18585.13 or 18585.14 or 23984.1 or 242202.3 or 18585.15 or 18585.16 or 242202.2 or 242202.1 or 18573.1 or 18575.1 or 18585.17 or 18585.18 or 18585.19	0	1000		Nucleotides			
PDE4g	3',5'-cyclic-nucleotide phosphodiesterase, Golgi	h2o[g] + 35cgmp[g] -> h[g] + gmp[g]	0	23984.1	0	1000		Nucleotides			
PDHm	pyruvate dehydrogenase	coa[m] + nad[m] + pyr[m] -> co2[m] + nadh[m] + accoa[m]	0	18597.1 and 68263.1 or 27402.1 and 13382.1 or 68263.1 and 18598.1 or 235339.1	0	1000		Glycolysis/Gluconeogenesis			
PDX5PO	pyridoxine 5'-phosphate oxidase	o2[c] + pdx5p[c] <=> h2o2[c] + pydx5p[c]	1	103711.1	-1000	1000		Vitamin B6 Metabolism			
PDXPP	Pyridoxine 5-phosphate phosphatase	h2o[c] + pdx5p[c] -> pi[c] + pydxn[c]	0	57028.1	0	1000		Vitamin B6 Metabolism			
PEAMNO	Phenethylamine oxidase	h2o[c] + o2[c] + peamn[c] -> h2o2[c] + nh4[c] + pacald[c]	0	109731.1 or 237940.1 or 17161.1 or 237940.2 or 76507.1	0	1000		Phenylalanine metabolism			
PECDCHe	binding of pectins with deoxycholic acid in the intestinal lumen, reducing serum cholsterol levels.	h[u] + pect[u] + dchac[u] -> pectindchac[u]	0		0	1000	3	Food processing, Lumen	PMID: 16925468, PMID: 12537466, PMID: 9808647, T.Pandolf and F.M. Clydesdale (1992) Journal of food science, vol.57, no.5, 1242-1245.	pectin binds bile acids and leads to enhanced excretion, there by the 7-alpha hydroxylase pathway is activated laeding to increased cholesterol catabolism for synthesis of more bile acids (regulates cholesterol metabolism). however the decreased serum cholesterol levels are brought about by many other cumulative effects (water unstirred action of dieatary fibres, glycemic role etc) (PMID: 18302966, Gunness P, Gidley MJ. (2010). Food & Function 1: 149-55). pectin also binds more effeciently cholic acid. one proton added to reactants for elemental balancing.	
PECDCHt	binding of pectins with deoxycholic acid transport	h[e] + pectindchac[e] <=> h[c] + pectindchac[c]	1		-1000	1000	1	Transport, Extracellular		Needed to provide this metabolite for reaction PECDCHe in joint model.	
PECGCHLe	binding of pectins with glycocholate in the intestinal lumen, reducing serum cholsterol levels.	h[u] + gchola[u] + pect[u] -> pectingchol[u]	0		0	1000	3	Food processing, Lumen	PMID: 16925468, PMID: 12537466, PMID: 9808647, T.Pandolf and F.M. Clydesdale (1992) Journal of food science, vol.57, no.5, 1242-1245.	pectin binds bile acids and leads to enhanced excretion, there by the 7-alpha hydroxylase pathway is activated laeding to increased cholesterol catabolism for synthesis of more bile acids (regulates cholesterol metabolism). however the decreased serum cholesterol levels are brought about by many other cumulative effects (water unstirred action of dieatary fibres, glycemic role etc) (PMID: 18302966, Gunness P, Gidley MJ. (2010). Food & Function 1: 149-55). pectin also binds more effeciently cholic acid. one proton added to reactants for elemental balancing.	
PECGCHLt	binding of pectins with glycocholate transport	h[e] + pectingchol[e] <=> h[c] + pectingchol[c]	1		-1000	1000	1	Transport, Extracellular		Needed to provide this metabolite for reaction PECGCHLe in joint model.	
PECGONCOATr	Pseudoecgonine CoA transferase (ER)	atp[r] + h[r] + coa[r] + pecgon[r] -> amp[r] + ppi[r] + pecgoncoa[r]	0		0	1000		Alkaloid biosynthesis II			
PECTCHLe	binding of pectins with taurocholate in the intestinal lumen, reducing serum cholsterol levels.	h[u] + tchola[u] + pect[u] -> pectintchol[u]	0		0	1000	3	Food processing, Lumen	PMID: 16925468, PMID: 12537466, PMID: 9808647, T.Pandolf and F.M. Clydesdale (1992) Journal of food science, vol.57, no.5, 1242-1245.	pectin binds bile acids and leads to enhanced excretion, there by the 7-alpha hydroxylase pathway is activated laeding to increased cholesterol catabolism for synthesis of more bile acids (regulates cholesterol metabolism). however the decreased serum cholesterol levels are brought about by many other cumulative effects (water unstirred action of dieatary fibres, glycemic role etc) (PMID: 18302966, Gunness P, Gidley MJ. (2010). Food & Function 1: 149-55). pectin also binds more effeciently cholic acid. one proton added to reactants for elemental balancing.	
PECTCHLt	binding of pectins with taurocholate transport	h[e] + pectintchol[e] <=> h[c] + pectintchol[c]	1		-1000	1000	1	Transport, Extracellular		Needed to provide this metabolite for reaction PECTCHLe in joint model.	
PECTt	Pectins transport	h[e] + pect[e] <=> h[c] + pect[c]	1		-1000	1000	1	Transport, Extracellular		Needed to provide this metabolite for reaction PECDCHe, PECGCHLe and PECTCHLe in joint model.	
PEFLIP	phosphatidylethanolamine flippase	h2o[c] + atp[c] + pe_hs[e] -> adp[c] + h[c] + pi[c] + pe_hs[c]	0	11982.1 or 11980.1	0	1000		Transport, Extracellular			
PEFLIPm	phosphatidylethanolamine flippase	h2o[c] + atp[c] + pe_hs[c] -> adp[c] + h[c] + pi[c] + pe_hs[m]	0	11982.1 or 11980.1	0	1000		Transport, Mitochondrial			
PEHSFABPe	transport of lysophosphatidylethanolamine into the enterocytes	2 pe_hs[c] <=> 2 pe_hs[r]	1	14080.1	-1000	1000	3	Transport, Endoplasmic Reticular	PMID: 9555061, PMCID: PMC2821027, PMID: 9054409, PMID: 9082452, PMCID: PMC2670638, http://mss3.libraries.rutgers.edu/dlr/TMP/rutgers-lib_26338-PDF-1.pdf	crystal structure of LFAB revealed 2 binding sites (in contrast to IFAB which has 1:1 stoichiometry) for oleate (PMID: 9054409). LFAB is expressed in liver, kidney, intestine, pancreas, stomach and lung (PMCID: PMC2670638). Once the long chain fatty acids enter the enterocytes, bind to the FABP reversibly, for transport into the E.R. to reconstitute triacylglycerols (PMID: 20522896, PMID: 19280719).	
PEPCK	Phosphoenolpyruvate carboxykinase (GTP)	oaa[c] + gtp[c] -> co2[c] + pep[c] + gdp[c]	0	18534.1	0	1000		Glycolysis/Gluconeogenesis			
PEPCKm	Phosphoenolpyruvate carboxykinase (GTP)	gtp[m] + oaa[m] -> co2[m] + gdp[m] + pep[m]	0	74551.1	0	1000		Glycolysis/Gluconeogenesis			
PEPLYStn	peptide (lysine) nuclear transport via diffusion	peplys[e] <=> peplys[n]	1		-1000	1000		Transport, Nuclear			
PERILLYLte	xenobiotic transport	perillyl[e] <=> perillyl[c]	1		-1000	1000		Transport, Extracellular			
PEROXx	peroxisomal lumped long chain fatty acid oxidation	3 nad[x] + 3 coa[x] + 2 o2[x] + 3 h2o[x] + pristcoa[x] -> 3 h[x] + 3 nadh[x] + accoa[x] + 2 h2o2[x] + dmnoncoa[x] + 2 ppcoa[x]	0	74147.1 and 80911.1 and 113868.1 and 15488.1	0	1000		Fatty acid oxidation, peroxisome			
PETHCT	phosphoethanolamine cytidyltransferase	h[c] + ctp[c] + ethamp[c] -> ppi[c] + cdpea[c]	0	68671.1	0	1000		Glycerophospholipid Metabolism			
PETOHMm_hs	phosphatidylethanolamine N-methyltransferase	3 amet[m] + pe_hs[m] -> 3 h[m] + 3 ahcys[m] + pchol_hs[m]	0	18618.1 or 18618.2 or 18618.3	0	1000		Glycerophospholipid Metabolism			
PETOHMr_hs	phosphatidylethanolamine N-methyltransferase	3 amet[r] + pe_hs[r] -> 3 ahcys[r] + 3 h[r] + pchol_hs[r]	0	18618.1 or 18618.2 or 18618.3	0	1000		Glycerophospholipid Metabolism			
PE_HSter	phosphatidylethanolamine scramblase	pe_hs[c] <=> pe_hs[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
PE_HStg	phosphatidylethanolamine scramblase	pe_hs[c] <=> pe_hs[g]	1		-1000	1000		Transport, Golgi Apparatus			
PE_HStm	phosphatidylethanolamine scramblase	pe_hs[c] <=> pe_hs[m]	1		-1000	1000		Transport, Mitochondrial			
PEt	phosphatidylethanolamin (homo sapiens) transport	pe_hs[e] <=> pe_hs[c]	1		-1000	1000		Transport, Extracellular			
PFK	phosphofructokinase	atp[c] + f6p[c] -> adp[c] + h[c] + fdp[c]	0	56421.1 or 18641.1 and 18642.1 or 18642.1 and 18641.2 or 18641.1 or 56421.1 and 18642.1 or 18642.1 or 56421.1 and 18641.1 or 18641.2 or 56421.1 and 18641.2	0	1000		Glycolysis/Gluconeogenesis			
PFK26	6-phosphofructo-2-kinase	atp[c] + f6p[c] -> adp[c] + h[c] + f26bp[c]	0	18639.1 or 18640.1 or 270198.1 or 170768.1	0	1000		Fructose and Mannose Metabolism			
PGCD	phosphoglycerate dehydrogenase	nad[c] + 3pg[c] -> h[c] + nadh[c] + 3php[c]	0	236539.1	0	1000		Glycine, Serine, and Threonine Metabolism			
PGDI	Prostaglandin-H2 D-isomerase [Precursor]	prostgh2[c] <=> prostgd2[c]	1	54486.1 or 19215.1	-1000	1000		Eicosanoid Metabolism			
PGDIr	Prostaglandin-H2 D-isomerase [Precursor]	prostgh2[r] <=> prostgd2[r]	1	54486.1 or 19215.1	-1000	1000		Eicosanoid Metabolism			
PGESr	Prostaglandin E synthase	prostgh2[r] <=> prostge2[r]	1	96979.1 or 96979.2 or 64292.1 or 96979.3 or 64292.2 or 96979.4	-1000	1000		Eicosanoid Metabolism			
PGI	glucose-6-phosphate isomerase	g6p[c] <=> f6p[c]	1	14751.1	-1000	1000		Glycolysis/Gluconeogenesis			
PGISr	Prostaglandin I2 synthase	prostgh2[r] <=> prostgi2[r]	1	19223.1	-1000	1000		Eicosanoid Metabolism			
PGK	phosphoglycerate kinase	atp[c] + 3pg[c] <=> adp[c] + 13dpg[c]	1	18663.1 or 18655.1	-1000	1000		Glycolysis/Gluconeogenesis			
PGL	6-phosphogluconolactonase	h2o[c] + 6pgl[c] -> h[c] + 6pgc[c]	0	66171.1	0	1000		Pentose Phosphate Pathway			
PGLYCP	Phosphoglycolate phosphatase	h2o[c] + 2pglyc[c] -> pi[c] + glyclt[c]	0	67078.1	0	1000		Glyoxylate and Dicarboxylate Metabolism			
PGLYCt	phosphatidylglycerol (homo sapiens) transport	pglyc_hs[e] <=> pglyc_hs[c]	1		-1000	1000		Transport, Extracellular			
PGLer	6-phosphogluconolactonase, endoplasmic reticulum	h2o[r] + 6pgl[r] -> h[r] + 6pgc[r]	0	100198.1	0	1000		Pentose Phosphate Pathway			
PGM	phosphoglycerate mutase	2pg[c] <=> 3pg[c]	1	12183.1 or 56012.1 or 18648.1 or 12183.2 or 56012.2	-1000	1000		Glycolysis/Gluconeogenesis			
PGMT	phosphoglucomutase	g1p[c] <=> g6p[c]	1	72157.1 or 66681.1	-1000	1000		Glycolysis/Gluconeogenesis			
PGPPT	phosphatidyl-CMP: glycerophosphate phosphatidyltransferase	cdpdag_hs[c] + glyc3p[c] -> h[c] + cmp[c] + pgp_hs[c]	0	74451.1	0	1000		Glycerophospholipid Metabolism			
PGPP_hs	Phosphatidylglycerol phosphate phosphatase (homo sapiens)	h2o[c] + pgp_hs[c] -> pi[c] + pglyc_hs[c]	0		0	1000		Glycerophospholipid Metabolism			
PGS	Prostaglandin G/H synthase	2 o2[c] + h[c] + nadph[c] + arachd[c] -> h2o[c] + nadp[c] + prostgh2[c]	0	19225.1 or 19224.1	0	1000		Eicosanoid Metabolism			
PGSr	Prostaglandin G/H synthase	2 o2[r] + arachd[r] + h[r] + nadph[r] -> h2o[r] + nadp[r] + prostgh2[r]	0	19225.1 or 19224.1	0	1000		Eicosanoid Metabolism			
PHACCOAGLNAC	Phenylacetyl-CoA:L-glutamine alpha-N-phenylacetyltransferase	gln-L[c] + phaccoa[c] -> coa[c] + pheacgln[c]	0		0	1000		Phenylalanine metabolism			
PHCDm	L-1-pyrroline-3-hydroxy-5-carboxylate dehydrogenase	2 h2o[m] + nad[m] + 1p3h5c[m] -> h[m] + nadh[m] + e4hglu[m]	0	212647.1 or 212647.2	0	1000		Arginine and Proline Metabolism			
PHCHGSm	L-1-Pyrroline-3-hydroxy-5-carboxylate spontaneous conversion to L-4-Hydroxyglutamate semialdehyde, mitochondrial	h[m] + h2o[m] + 1p3h5c[m] <=> 4hglusa[m]	1		-1000	1000		Arginine and Proline Metabolism			
PHEACGLNt	PHEACGLN extracellular transport via diffusion	pheacgln[c] <=> pheacgln[e]	1		-1000	1000		Transport, Extracellular			
PHEATB0tc	transport of L-Phenylalanine into the intestinal cells by ATB0 transporter	2 na1[u] + cl[u] + phe-L[u] -> 2 na1[c] + cl[c] + phe-L[c]	0	56774.1	0	1000	3	Transport, Lumen	PMID:18195088	ATB0 is both sodium and chloride coupled, with reaction stoichiometry 2Na+:1cl:1amino acid. The transporter is localted in the intestine, has a broad substrate specificity (both neutral and cationic amino acids), but is not involved in the transport of aspartate, glutamate and proline (PMID:18195088).	
PHEB0AT1tc	transport of L-Phenylalanine by the apical neutral amino acid transporters in kidney and intestine	na1[u] + phe-L[u] -> na1[c] + phe-L[c]	0	(70008.1 or (74338.1 and 57394.1))	0	1000	3	Transport, Lumen	PMID: 19472175, PMID: 15804236, PMID: 18400692	transports all the neutral amino acids with preference for methionine, leucine and valine. Reaction stoichiometry is 1:1. Requires heterodimerization with collectrin protein for increased affinity. Found in kidney and intestine, however also reported to be expressed in skin. Requires association with ACE2 for expression in intestine but with collectrin for expression in kidney.	3.4.17.23
PHEILELAT2tc	transport of L-Phenylalanine into the cell and efflux of L-Isoleucine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	ile-L[c] + phe-L[e] <=> ile-L[e] + phe-L[c]	1	(20539.1 and 17254.1)	-1000	1000	3	Transport, Extracellular	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s00420000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	higer affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of memebranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for traficking of the complex to the mebrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s00420000274). LAT2 carries both influx and efflux of phenylalanine, leucine and isoleucine, hence such reactions are reversible.	

PHELAT1tc	transport of L-Phenylalanine by LAT1 in association with 4F2hc, across the apical surface of the memebranes.	leu-L[c] + phe-L[u] -> leu-L[u] + phe-L[c]	0	(20539.1 and 17254.1)	0	1000	3	Transport, Lumen	Hans Gerhard Vogel, Franz J. Hock, Jochen Maas, Dieter Mayer (2006), Drug discovery and evaluation: Safety and pharmacokinetic assays, Springer publication, Chapter II D, page 456, table 3, PMID: 19035290, PMID: 12634921, European Journal of Pharmacology 441 (2002) 127-132. Am J Physiol Cell Physiol 281:C1077-C1093, 2001. Amino Acids (2005) 29: 229–233 DOI 10.1007/s00726-005-0221-x. PMID: 11901210	leucine is the only amino acid tested for efflux. Expressed in ovary, placenta, brain, spleen, testis, activated lymphocytes and some tumor cells. Functions as a antiport transport system (DOI 10.1016/j.cell.2009.01.02), requires heterodimerization with glycoprotein CD98 (Pflugers Arch-Eur J Physiol (2000) 440:503-512, DOI 10.1007/s004240000274, PMID: 10958334).	
PHELAT3tc	transport of phenylalanine by LAT3 inintestinal cells	phe-L[u] <=> phe-L[c]	1	72401.1	-1000	1000	3	Transport, Lumen	PMCID: PMC1864869, PMID: 12930836, PMID: 18195088	LAT3 transports neutral amino acids and is Na+ independant. The transport mechanism is facilitated diffusion (PMID: 12930836). The substrate specificty is for leucine, isoleucine, methionine and phenylalanine (PMID: 18195088).	
PHEMEt	heme transport	pheme[e] -> pheme[c]	0	52466.1	0	1000		Transport, Extracellular			
PHEMEtm	Heme transport to cytosol	pheme[m] <=> pheme[c]	1		-1000	1000		Transport, Mitochondrial			
PHETA1	phenylalanine transaminase	akg[c] + phe-L[c] <=> glu-L[c] + phpyr[c]	1	14718.1	-1000	1000		Phenylalanine metabolism			
PHETA1m	phenylalanine transaminase (m)	akg[m] + phe-L[m] <=> glu-L[m] + phpyr[m]	1	234724.1 or 14719.1	-1000	1000		Phenylalanine metabolism			
PHETHPTOX2	L-Phenylalanine,tetrahydrobiopterin:oxygen oxidoreductase (4-hydroxylating)	o2[c] + phe-L[c] + thbpt[c] -> tyr-L[c] + thbpt4acam[c]	0	18478.1	0	1000		Tyr, Phe, Trp Biosynthesis			
PHEt4	L-phenylalanine transport in via sodium symport	na1[e] + phe-L[e] -> na1[c] + phe-L[c]	0	105727.1 or 67760.1 or 69354.1 or 56774.1 or 11989.1 or 11988.1 or 11987.1	0	1000		Transport, Extracellular			
PHEyLATtc	transport of L-Phenylalanine by y+LAT1 or y+LAT2 transporters in small intestine and kidney	na1[e] + phe-L[e] + arg-L[c] -> na1[c] + phe-L[c] + arg-L[e]	0	(20540.1 or (330836.1 and 17254.1))	0	1000	3	Transport, Extracellular	PMID: 11546643, PMID:18195088	y+LAT1 and y+LAT2 transporters requires CD98 for sequesterization to the plasma membrane. Acts as an amino acid exchanger, with influx of neutral aminoa acids and efflux of cationic amino acid, requires Na+ for optimal activity. Can also operate with H+ in absence of Na+ (PMID: 11546643).	
PHEyLATthc	transport of Phenylalanine by y+LAT1 or y+LAT2 with co-transporter of h in small intestine and kidney	h[e] + phe-L[e] + arg-L[c] -> h[c] + phe-L[c] + arg-L[e]	0	(20540.1 or (330836.1 and 17254.1))	0	1000	3	Transport, Extracellular	PMID: 11546643, PMID:18195088	y+LAT1 and y+LAT2 transporters requires CD98 for sequesterization to the plasma membrane. Acts as an amino acid exchanger, with influx of neutral aminoa acids and efflux of cationic amino acid, requires Na+ for optimal activity. Can also operate with H+ in absence of Na+ (PMID: 11546643).	
PHYCBOXL	L-Phenylalanine carboxy-lyase	h[c] + phe-L[c] -> co2[c] + peamn[c]	0	13195.1	0	1000		Phenylalanine metabolism			
PHYHx	Phytanoyl-CoA dioxygenase, peroxisomal	o2[x] + akg[x] + phytcoa[x] -> co2[x] + phyt2ohcoa[x] + succ[x]	0	16922.1	0	1000		Fatty acid oxidation, peroxisome			
PHYQt	Phylloquinone transport	h2o[c] + atp[c] + phyQ[e] -> adp[c] + h[c] + pi[c] + phyQ[c]	0		0	1000		Transport, Extracellular			
PHYTt	fatty acid transport via diffusion	phyt[e] <=> phyt[c]	1		-1000	1000		Transport, Extracellular			
PI345P3P	phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase	h2o[c] + pail345p_hs[c] -> pi[c] + pail45p_hs[c]	0	19211.1	0	1000		Inositol Phosphate Metabolism			
PI345P3Pn	phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase, nuclear	h2o[n] + pail345p_hs[n] -> pail45p_hs[n] + pi[n]	0	19211.1	0	1000		Inositol Phosphate Metabolism			
PI345P5Pn	phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase, nuclear	h2o[n] + pail345p_hs[n] -> pi[n] + pail34p_hs[n]	0		0	1000		Inositol Phosphate Metabolism			
PI34P3Pn	phosphatidylinositol-3,4-bisphosphate 3-phosphatase, nuclear	h2o[n] + pail34p_hs[n] -> pail4p_hs[n] + pi[n]	0		0	1000		Inositol Phosphate Metabolism			
PI34P4Pn	phosphatidylinositol-3,4-bisphosphate 4-phosphatase, nuclear	h2o[n] + pail34p_hs[n] -> pi[n] + pail3p_hs[n]	0		0	1000		Inositol Phosphate Metabolism			
PI34P5K	phosphatidylinositol 3,4-bisphosphate 5-kinase	atp[c] + pail34p_hs[c] -> adp[c] + h[c] + pail345p_hs[c]	0	18719.1 or 18717.1 or 18720.1	0	1000		Inositol Phosphate Metabolism			
PI34P5Kn	phosphatidylinositol 3,4-bisphosphate 5-kinase, nuclear	atp[n] + pail34p_hs[n] -> h[n] + adp[n] + pail345p_hs[n]	0		0	1000		Inositol Phosphate Metabolism			
PI35P3P	phosphatidylinositol-3,5-bisphosphate 3-phosphatase	h2o[c] + pail35p_hs[c] -> pi[c] + pail5p_hs[c]	0	74302.1 or 74302.2 or 74302.3	0	1000		Inositol Phosphate Metabolism			
PI3P3Pn	phosphatidylinositol-3-phosphate 3-phosphatase, nuclear	h2o[n] + pail3p_hs[n] -> pail_hs[n] + pi[n]	0		0	1000		Inositol Phosphate Metabolism			
PI3P4K	phosphatidylinositol 3-phosphate 4-kinase	atp[c] + pail3p_hs[c] -> adp[c] + h[c] + pail34p_hs[c]	0	107650.1 or 18719.1 or 224020.1 or 18717.1 or 18720.1 or 84095.1	0	1000		Inositol Phosphate Metabolism			
PI3P4Kn	phosphatidylinositol 3-phosphate 4-kinase, nuclear	atp[n] + pail3p_hs[n] -> h[n] + adp[n] + pail34p_hs[n]	0		0	1000		Inositol Phosphate Metabolism			
PI3P5K	phosphatidylinositol 3-phosphate 5-kinase	atp[c] + pail3p_hs[c] -> adp[c] + h[c] + pail35p_hs[c]	0	18719.1 or 18717.1 or 18720.1	0	1000		Inositol Phosphate Metabolism			
PI3PP	phosphatidylinositol-3-phosphate 3-phosphatase	h2o[c] + pail3p_hs[c] -> pi[c] + pail_hs[c]	0	74302.1 or 74302.2 or 74302.3	0	1000		Inositol Phosphate Metabolism			
PI45P3K	phosphatidylinositol 4,5-bisphosphate 3-kinase	atp[c] + pail45p_hs[c] -> adp[c] + h[c] + pail345p_hs[c]	0	18710.1 and 18707.1 or 18709.1 and 18706.1 or 74769.1 and 18710.1 or 18708.3 and 18706.1 or 320207.1 and 30955.1 or 18706.1 and 18710.1 or 18709.1 and 74769.1 or 74769.1 and 18708.1 or 18708.3 and 18707.1 or 30955.1 and 23900.1 or 18709.1 and 18707.1 or 18708.2 and 74769.1 or 18708.1 and 18707.1 or 18708.1 and 74769.1 or 18708.3 and 18706.1 or 18708.2 and 18707.1 or 18706.1 and 18708.1	0	1000		Inositol Phosphate Metabolism			
PI45P3Kn	phosphatidylinositol 4,5-bisphosphate 3-kinase, nuclear	atp[n] + pail45p_hs[n] -> h[n] + adp[n] + pail345p_hs[n]	0		0	1000		Inositol Phosphate Metabolism			
PI45P4P	phosphatidylinositol-4,5-bisphosphate 4-phosphatase	h2o[c] + pail45p_hs[c] -> pi[c] + pail5p_hs[c]	0		0	1000		Inositol Phosphate Metabolism			
PI45P5P	phosphatidylinositol-4,5-bisphosphate 5-phosphatase	h2o[c] + pail45p_hs[c] -> pi[c] + pail4p_hs[c]	0	320634.1 or 104015.1 or 320634.2 or 64436.1 or 20975.1 or 16330.1 or 104015.2	0	1000		Inositol Phosphate Metabolism			
PI45P5Pn	phosphatidylinositol-4,5-bisphosphate 5-phosphatase, nuclear	h2o[n] + pail45p_hs[n] -> pail4p_hs[n] + pi[n]	0		0	1000		Inositol Phosphate Metabolism			
PI45PLC	phosphatidylinositol 4,5-bisphosphate phospholipase C	h2o[c] + pail45p_hs[c] -> h[c] + dag_hs[c] + mi145p[c]	0	433022.1 or 18797.1 or 18795.1 or 114875.1 or 74055.1 or 227120.1 or 18803.1 or 18798.1 or 18799.1 or 18798.2 or 18803.2 or 18802.1 or 72469.1 or 18796.1 or 269615.1 or 234779.1 or 269437.1 or 18795.2	0	1000		Inositol Phosphate Metabolism			
PI45PLCn	phosphatidylinositol 4,5-bisphosphate phospholipase C, nucleus	h2o[n] + pail45p_hs[n] -> h[n] + dag_hs[n] + mi145p[n]	0	18795.1 or 18795.2	0	1000		Inositol Phosphate Metabolism			
PI4P3K	phosphatidylinositol 4-phosphate 3-kinase	atp[c] + pail4p_hs[c] -> adp[c] + h[c] + pail34p_hs[c]	0	18710.1 and 18707.1 or 18709.1 and 18706.1 or 74769.1 and 18710.1 or 18708.3 and 18706.1 or 320207.1 and 30955.1 or 18705.1 or 18706.1 and 18710.1 or 18709.1 and 74769.1 or 74769.1 and 18708.1 or 18708.3 and 18707.1 or 30955.1 and 23900.1 or 18709.1 and 18707.1 or 18704.1 or 18708.2 and 74769.1 or 18708.1 and 18707.1 or 18708.1 and 74769.1 or 18708.1 and 18710.1 and 18707.1 or 18709.1 and 18706.1 or 74769.1 and 18710.1 or 18708.3 and 18706.1 or 320207.1 and 30955.1 or 18705.1 or 18706.1 and 18710.1 or 18709.1 and 74769.1 or 74769.1 and 18708.1 or 18708.3 and 18707.1 or 30955.1 and 23900.1 or 18709.1 and 18707.1 or 18704.1 or 18708.2 and 74769.1 or 18708.1 and 18707.1 or 18708.1 and 74769.1 or 18708.3 and 18706.1 or 240752.1 or 18708.2 and 18707.1 or 18706.1 and 18708.3 and 18706.1 or 240752.1 or 18708.2 and 18707.1 or 18706.1 and 18708.1	0	1000		Inositol Phosphate Metabolism			
PI4P3Ker	phosphatidylinositol 4-phosphate 3-kinase, endoplasmic reticulum	atp[r] + pail4p_hs[r] -> adp[r] + h[r] + pail34p_hs[r]	0	240752.1	0	1000		Inositol Phosphate Metabolism			
PI4P3Kn	phosphatidylinositol 4-phosphate 3-kinase, nuclear	atp[n] + pail4p_hs[n] -> h[n] + adp[n] + pail34p_hs[n]	0		0	1000		Inositol Phosphate Metabolism			
PI4P4Pn	phosphatidylinositol-4-phosphate 4-phosphatase, nuclear	h2o[n] + pail4p_hs[n] -> pail_hs[n] + pi[n]	0		0	1000		Inositol Phosphate Metabolism			
PI4P5K	phosphatidylinositol 4-phosphate 5-kinase	atp[c] + pail4p_hs[c] -> adp[c] + h[c] + pail45p_hs[c]	0	108083.1 or 18718.1 or 18719.1 or 18717.1 or 18711.1 or 18711.2 or 18711.3 or 18720.1 or 108083.2 or 117150.1	0	1000		Glycerophospholipid Metabolism			
PI4P5Kn	phosphatidylinositol 4-phosphate 5-kinase, nuclear	atp[n] + pail4p_hs[n] -> h[n] + adp[n] + pail45p_hs[n]	0		0	1000		Inositol Phosphate Metabolism			
PI4PLCn	phosphatidylinositol 4-phosphate phospholipase C, nucleus	h2o[n] + pail4p_hs[n] -> h[n] + dag_hs[n] + mi14p[n]	0	18795.1 or 18795.2	0	1000		Inositol Phosphate Metabolism			
PI4PP	phosphatidylinositol-4-phosphate 4-phosphatase	h2o[c] + pail4p_hs[c] -> pi[c] + pail_hs[c]	0		0	1000		Inositol Phosphate Metabolism			

PI5P3K	phosphatidylinositol-5-phosphate 3-kinase	atp[c] + pail5p_hs[c] -> adp[c] + h[c] + pail35p_hs[c]	0	18710.1 and 18707.1 or 18709.1 and 18706.1 or 74769.1 and 18710.1 or 18708.1 and 18706.1 or 320207.1 and 30955.1 or 18705.1 or 18706.1 and 18710.1 or 18709.1 and 74769.1 or 225326.1 or 74769.1 and 18708.1 or 18708.1 and 18707.1 or 30955.1 and 23900.1 or 18709.1 and 18707.1 or 18704.1 or 18708.1 and 74769.1 or 18708.1 and 18707.1 or 18708.1 and 74769.1 or 18708.1 and 18706.1 or 240752.1 or 18708.1 and 18707.1 or 18706.1 and 18708.1	0	1000		Inositol Phosphate Metabolism			
PI5P3Ker	phosphatidylinositol-5-phosphate 3-kinase, endoplasmic reticulum	atp[r] + pail5p_hs[r] -> adp[r] + h[r] + pail35p_hs[r]	0	240752.1	0	1000		Inositol Phosphate Metabolism			
PI5P4K	phosphatidylinositol-5-phosphate 4-kinase	atp[c] + pail5p_hs[c] -> adp[c] + h[c] + pail45p_hs[c]	0	107650.1 or 224020.1 or 84095.1	0	1000		Inositol Phosphate Metabolism			
PI5P4Kn	phosphatidylinositol-5-phosphate 4-kinase, nuclear	atp[n] + pail5p_hs[n] -> h[n] + adp[n] + pail45p_hs[n]	0		0	1000		Inositol Phosphate Metabolism			
PIACGT	phosphatidylinositol N-acetylglucosaminyltransferase	pail_hs[c] + uacgam[c] -> h[c] + udp[c] + acgpail_hs[c]	0	18700.1 or 13481.1 or 56176.2 or 18700.2 or 67292.1 or 13481.2 or 56176.3 or 67292.2 or 56176.1 or 110417.1 or 14755.2 or 18700.3 or 14755.1	0	1000		Glycosylphosphatidylinositol (GPI)-anchor biosynthesis			
PIK3	phosphatidylinositol 3-kinase	atp[c] + pail_hs[c] -> adp[c] + h[c] + pail3p_hs[c]	0	18710.1 and 18707.1 or 18709.1 and 18706.1 or 74769.1 and 18710.1 or 18708.1 and 18706.1 or 320207.1 and 30955.1 or 18705.1 or 18706.1 and 18710.1 or 18709.1 and 74769.1 or 225326.1 or 74769.1 and 18708.1 or 18708.1 and 18707.1 or 30955.1 and 23900.1 or 18709.1 and 18707.1 or 18704.1 or 18708.1 and 74769.1 or 18708.1 and 18707.1 or 18708.1 and 74769.1 or 18708.1 and 18706.1 or 240752.1 or 18708.1 and 18707.1 or 18706.1 and 18708.1	0	1000		Inositol Phosphate Metabolism			
PIK3er	phosphatidylinositol 3-kinase, endoplasmic reticulum	atp[r] + pail_hs[r] -> adp[r] + h[r] + pail3p_hs[r]	0	240752.1	0	1000		Inositol Phosphate Metabolism			
PIK3n	phosphatidylinositol 3-kinase, nuclear	atp[n] + pail_hs[n] -> h[n] + adp[n] + pail3p_hs[n]	0		0	1000		Inositol Phosphate Metabolism			
PIK4	phosphatidylinositol 4-kinase	atp[c] + pail_hs[c] -> adp[c] + h[c] + pail4p_hs[c]	0	107650.1 or 224020.1 or 84095.1	0	1000		Glycerophospholipid Metabolism			
PIK4n	phosphatidylinositol 4-kinase, nuclear	atp[n] + pail_hs[n] -> h[n] + adp[n] + pail4p_hs[n]	0		0	1000		Inositol Phosphate Metabolism			
PIK5	phosphatidylinositol 5-kinase	atp[c] + pail_hs[c] -> adp[c] + h[c] + pail5p_hs[c]	0	18719.1 or 18717.1 or 18720.1	0	1000		Inositol Phosphate Metabolism			
PIK5n	phosphatidylinositol 5-kinase, nuclear	atp[n] + pail_hs[n] -> h[n] + adp[n] + pail5p_hs[n]	0		0	1000		Inositol Phosphate Metabolism			
PIPLCn	phosphatidylinositol phospholipase C, nucleus	h2o[n] + pail_hs[n] -> h[n] + dag_hs[n] + mi1p-D[n]	0	18795.1 or 18795.2	0	1000		Inositol Phosphate Metabolism			
PIt2m	phosphate transporter, mitochondrial	h[c] + pi[c] <=> h[m] + pi[m]	1	18674.1 or 18674.2 or 18674.3 or 18674.4	0	0		Transport, Mitochondrial			
PIt2m_2	phosphate transporter, mitochondrial	2 h[c] + pi[c] <=> 2 h[m] + pi[m]	1		-1000	1000		Transport, Mitochondrial			
PIt7	phosphate transport in/out via three Na+ symporter	3 na1[e] + pi[e] <=> pi[c] + 3 na1[c]	1	20505.1 or 20531.1	-1000	1000		Transport, Extracellular			
PIt7ir	phosphate transport in/out via three Na+ symporter (irreversible)	3 na1[e] + pi[e] -> pi[c] + 3 na1[c]	0	105355.1 or 218103.1 or 319848.1 or 20504.1	0	1000		Transport, Extracellular			
PIt8	phosphate transport in/out via Na+ symporter	1.5 na1[e] + pi[e] <=> pi[c] + 1.5 na1[c]	1	20516.1 or 20515.1	-1000	1000		Transport, Extracellular			
PIt9	phosphate transport in/out via two Na+ symporter	2 na1[e] + pi[e] <=> pi[c] + 2 na1[c]	1	142681.1	-1000	1000		Transport, Extracellular			
PIter	phosphate transport, endoplasmic reticulum	pi[r] <=> pi[c]	1		-1000	1000		Transport, Endoplasmic Reticular			
PItg	phosphate transport, Golgi apparatus	pi[g] -> pi[c]	0		0	1000		Transport, Golgi Apparatus			
PItn	phosphate transport, nuclear	pi[n] <=> pi[c]	1		-1000	1000		Transport, Nuclear			
PItx	Phosphate transporter, peroxisome	pi[c] <=> pi[x]	1		-1000	1000		Transport, Peroxisomal			
PLA2	phospholipase A2	h2o[c] + ak2gchol_hs[c] -> h[c] + Rtotal2[c] + ak2lgchol_hs[c]	0		0	1000		Glycerophospholipid Metabolism			
PLYSPSer	protein lysine peptidase (endoplasmic reticulum)	h2o[r] + Ntmelys[r] -> pepslys[r] + tmlys[r]	0	56529.1 or 66624.1 or 66286.1 or 76687.1 or 69019.1	0	1000		Lysine Metabolism			
PMANM	phosphomannomutase	man1p[c] <=> man6p[c]	1	54128.1 or 66681.1 or 29858.1	-1000	1000		Fructose and Mannose Metabolism			
PMEVKx	phosphomevalonate kinase	atp[x] + 5pmev[x] -> adp[x] + 5dpmev[x]	0	68603.1	0	1000		Cholesterol Metabolism			
PMI12346PH	5-diphosphoinositol-1,2,3,4,6-pentakisphosphate diphosphohydrolase	h2o[c] + ppmi12346p[c] -> h[c] + pi[c] + minohp[c]	0	27399.2 or 271424.1 or 27399.1	0	1000		Inositol Phosphate Metabolism			
PMI12346PHn	5-diphosphoinositol-1,2,3,4,6-pentakisphosphate diphosphohydrolase, nuclear	h2o[n] + ppmi12346p[n] -> h[n] + minohp[n] + pi[n]	0	76500.1 or 76500.2 or 27399.1 or 76500.3 or 76500.4 or 271424.1 or 27399.2 or 76500.5 or 76500.6	0	1000		Inositol Phosphate Metabolism			
PMI1346PH	diphosphoinositol-1,3,4,6-tetrakisphosphate diphosphohydrolase	h2o[c] + ppmi1346p[c] -> h[c] + pi[c] + mi13456p[c]	0	27399.2 or 271424.1 or 27399.1	0	1000		Inositol Phosphate Metabolism			
PMI1346PHn	diphosphoinositol-1,3,4,6-tetrakisphosphate diphosphohydrolase, nucleus	h2o[n] + ppmi1346p[n] -> h[n] + mi13456p[n] + pi[n]	0	76500.1 or 76500.2 or 27399.1 or 76500.3 or 76500.4 or 271424.1 or 27399.2 or 76500.5 or 76500.6	0	1000		Inositol Phosphate Metabolism			
PMTCOAFABP1tc	transport of palmitoyl coA into the enterocytes	2 pmtcoa[c] <=> 2 pmtcoa[r]	1	14080.1	-1000	1000	3	Transport, Endoplasmic Reticular	PMID: 9555061, PMCID: PMC2821027, PMID: 9054409, PMID: 9082452, PMCID: PMC2670638, http://mss3.libraries.rutgers.edu/dlr/TMP/rutgers-lib_26338-PDF-1.pdf	crystal structure of LFAB revealed 2 binding sites (in contrast to IFAB which has 1:1 stoichiometry) for oleate (PMID: 9054409). LFAB is expressed in liver, kidney, intestine, pancreas, stomach and lung (PMCID: PMC2670638). Once the long chain fatty acids enter the enterocytes, bind to the FABP reversibly, for transport into the E.R. to reconstitute triacylglycerols (PMID: 20522896, PMID: 19280719).	
PMTCOAtx	fatty acid intracellular transport	pmtcoa[c] <=> pmtcoa[x]	1		-1000	1000		Transport, Peroxisomal			
PNP	purine-nucleoside phosphorylase	pi[c] + rnam[c] <=> h[c] + ncam[c] + r1p[c]	1	667034.1	-1000	1000		NAD Metabolism			
PNTEH	Hydrolase Class (RXN R02973)	h2o[c] + ptth[c] -> cysam[c] + pnto-R[c]	0	26464.1 or 26464.2 or 56752.1	0	1000		CoA Catabolism			
PNTK	pantothenate kinase	atp[c] + pnto-R[c] -> adp[c] + h[c] + 4ppan[c]	0	75735.1 or 269614.1 or 74450.1 or 74450.2 or 75735.2 or 74450.3 or 74450.4 or 75735.3 or 211347.1	0	1000		CoA Biosynthesis			
PNTKm	pantothenate kinase (mitochondrial)	atp[m] + pnto-R[m] -> h[m] + adp[m] + 4ppan[m]	0	74450.5	0	1000		CoA Biosynthesis			
PNTORDe	release of pantothenate across the basolatral membrane	pnto-R[c] -> pnto-R[e]	0		0	1000	1	Transport, Extracellular	PMID: 21749321	not much is known about the pantothenic acid exit across the basolateral membrane. Diffusion reaction is hypothetical. However, uptake of pantothenate by RBCs takes place by simple diffusion (G.F.M. Ball (2006) Vitamins their role in the human body, Blackwell publishing, chapter 15, page 329.).	
PNTOt5	Pantothenate sodium symporter II	h2o[c] + atp[c] + 2 na1[e] + pnto-R[e] -> adp[c] + h[c] + pi[c] + 2 na1[c] + pnto-R[c]	0	330064.1	0	1000		Transport, Extracellular			
PPA	inorganic diphosphatase	h2o[c] + ppi[c] -> h[c] + 2 pi[c]	0	67895.1	0	1000		Oxidative Phosphorylation			
PPA2	inorganic triphosphatase	h2o[c] + pppi[c] -> h[c] + pi[c] + ppi[c]	0		0	1000		Others			
PPA2m	inorganic triphosphatase, mitochondrial	h2o[m] + pppi[m] -> h[m] + pi[m] + ppi[m]	0		0	1000		Others			
PPAP	phosphatidic acid phosphatase	h2o[c] + pa_hs[c] -> pi[c] + dag_hs[c]	0	67916.1 or 19012.1 or 50784.1 or 19012.2	0	1000		Triacylglycerol Synthesis			
PPAer	inorganic diphosphatase, endoplasmic reticulum	h2o[r] + ppi[r] -> h[r] + 2 pi[r]	0	14378.1 or 14377.1 or 68401.1	0	1000		Miscellaneous			
PPAm	inorganic diphosphatase	h2o[m] + ppi[m] -> h[m] + 2 pi[m]	0	74776.1 or 74776.2 or 74776.3 or 74776.4	0	1000		Oxidative Phosphorylation			
PPAn	inorganic diphosphatase, nuclear	h2o[n] + ppi[n] -> h[n] + 2 pi[n]	0		0	1000		Miscellaneous			
PPAt	Propionate transport, diffusion	ppa[e] -> ppa[c]	0		0	1000		Transport, Extracellular			
PPAtm	Propionate transport, diffusion	ppa[c] -> ppa[m]	0		0	1000		Transport, Mitochondrial			
PPBNGS	porphobilinogen synthase	2 5aop[c] -> 2 h2o[c] + h[c] + ppbng[c]	0	17025.1 or 17025.2	0	1000		Heme Biosynthesis			
PPCDC	phosphopantothenoylcysteine decarboxylase	h[c] + 4ppcys[c] -> co2[c] + pan4p[c]	0	66812.1	0	1000		CoA Biosynthesis			
PPCOACm	Propionyl-CoA carboxylase, mitochondrial	ppcoa[m] + atp[m] + hco3[m] -> h[m] + adp[m] + pi[m] + mmcoa-S[m]	0	66904.1 and 110821.1	0	1000		Valine, Leucine, and Isoleucine Metabolism			
PPCOAOm	Propanoyl-CoA:FAD 2,3-oxidoreductase, mitochondrial	ppcoa[m] + fad[m] -> fadh2[m] + prpncoa[m]	0	102632.1 or 66948.1 or 11364.1 or 66885.1 or 11409.1 or 71985.1 or 229211.1	0	1000		Propanoate Metabolism			
PPD2CSPp	PPD2CSPp	6a2ohxnt[x] -> 1pipdn2c[x] + h2o[x]	0		0	1000		Lysine Metabolism			
PPDOx	Propane-1,2-diol:NAD+ 1-oxidoreductase	h[c] + nadh[c] + lald-D[c] -> nad[c] + 12ppd-R[c]	0	110198.1	0	1000		Pyruvate Metabolism			
PPDOy	Propane-1,2-diol:NADP+ 1-oxidoreductase	h[c] + nadph[c] + lald-D[c] -> nadp[c] + 12ppd-R[c]	0	110198.1 or 58810.2 or 11677.1 or 58810.1	0	1000		Pyruvate Metabolism			

PPIer	Diphosphate transporter, endoplasmic reticulum	ppi[c] <=> ppi[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
PPIx	Diphosphate transporter, peroxisome	ppi[c] <=> ppi[x]	1		-1000	1000		Transport, Peroxisomal			
PPM	phosphopentomutase	r1p[c] <=> r5p[c]	1	72157.1	-1000	1000		Pentose Phosphate Pathway			
PPMI12346Pm	5-diphosphatidylinositol pentakisphosphate nuclear transport (diffusion)	ppmi12346p[c] <=> ppmi12346p[n]	1		-1000	1000		Transport, Nuclear			
PPMI1346Pm	diphosphatidylinositol tetrakisphosphate nuclear transport (diffusion)	ppmi1346p[c] <=> ppmi1346p[n]	1		-1000	1000		Transport, Nuclear			
PPNCL3	phosphopantothenate-cysteine ligase	atp[c] + cys-L[c] + 4ppan[c] -> h[c] + amp[c] + ppi[c] + 4ppcys[c]	0	106564.1	0	1000		CoA Biosynthesis			
PPOR	Phenylpyruvate oxygen oxidoreductase (hydroxylating,decarboxylating)	o2[c] + phpyr[c] -> co2[c] + 2hyoxpla[c]	0	15445.1	0	1000		Phenylalanine metabolism			
PPPGOm	protoporphyrinogen IX mitochondrial transport	pppg9[c] <=> pppg9[m]	1		-1000	1000		Heme Biosynthesis			
PPPGOm	protoporphyrinogen oxidase, mitochondrial	3 o2[m] + 2 pppg9[m] -> 6 h2o[m] + 2 ppp9[m]	0	19044.1	0	1000		Heme Biosynthesis			
PPPIm	Inorganic triphosphate transport through nuclear pore	pppi[c] <=> pppi[n]	1		-1000	1000		Transport, Nuclear			
PRAGSr	phosphoribosylglycinamide synthase	atp[c] + gly[c] + prasn[c] <=> adp[c] + h[c] + pi[c] + gar[c]	1	14450.1 or 14450.2	-1000	1000		IMP Biosynthesis			
PRAIS	phosphoribosylaminoimidazole synthase	atp[c] + fgeam[c] -> adp[c] + 2 h[c] + pi[c] + air[c]	0	14450.1 or 14450.2	0	1000		IMP Biosynthesis			
PRASCS	phosphoribosylaminoimidazolesuccinocarboxamide synthase	atp[c] + asp-L[c] + 5aizc[c] <=> adp[c] + h[c] + pi[c] + 25aics[c]	1	67054.1	-1000	1000		IMP Biosynthesis			
PRDX	Peroxidase (multiple substrates)	h2o2[c] + mso3[c] -> 2 h2o[c] + fald[c]	0	13861.1	0	1000		Miscellaneous			
PRDXI	Peroxidase (multiple substrates)	h2o2[i] + mso3[i] -> 2 h2o[i] + fald[i]	0	17523.1	0	1000		Miscellaneous			
PRFGS	phosphoribosylformylglycinamidine synthase	h2o[c] + atp[c] + gln-L[c] + fgam[c] -> adp[c] + h[c] + pi[c] + glu-L[c] + fpram[c]	0	23782.1	0	1000		IMP Biosynthesis			
PRGNLONESULT	steroid sulfotransferase	pregn[c] + pregnlone[c] -> h[c] + pap[c] + pregnlonesul[c]	0	20859.1 or 54200.2	0	1000		Steroid Metabolism			
PRGNLONEtm	pregnenolone intracellular transport	pregnlone[c] <=> pregnlone[m]	1		-1000	1000		Transport, Mitochondrial			
PRGNLONEtr	pregnenolone intracellular transport	pregnlone[c] <=> pregnlone[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
PRGSTRNt	progesterone transmembrane (homo sapiens) transport	progest[e] <=> progest[c]	1		-1000	1000		Transport, Extracellular			
PRISTANAtx	pristanal peroxisomal transport	pristanal[c] <=> pristanal[x]	1		-1000	1000		Transport, Peroxisomal			
PRISTCOAtx	pristcoa peroxisomal transport	pristcoa[c] <=> pristcoa[x]	1		-1000	1000		Transport, Peroxisomal			
PRISTtx	prist peroxisomal transport	prist[c] <=> prist[x]	1		-1000	1000		Transport, Peroxisomal			
PRO1x	proline oxidase (L-proline, NAD)	nad[c] + pro-L[c] -> 2 h[c] + nadh[c] + 1pyr5c[c]	0	56189.1	0	1000		Arginine and Proline Metabolism			
PRO1xm	proline oxidase (NAD), mitochondrial	nad[m] + pro-L[m] -> 2 h[m] + nadh[m] + 1pyr5c[m]	0	19125.1	0	1000		Arginine and Proline Metabolism			
PROAKGOX1r	L-Proline,2-oxoglutarate:oxygen oxidoreductase (4-hydroxylating) (ER)	o2[r] + akg[r] + pro-L[r] -> co2[r] + 4hpro-LT[r] + succ[r]	0	18453.1 or 18452.1 or 18451.1	0	1000		Arginine and Proline Metabolism			
PROB0ATtc	transport of L-Proline by the apical neutral amino acid transporters B(0)AT1 or B(0)AT2 in kidney, intestine or brain	na1[u] + pro-L[u] -> na1[c] + pro-L[c]	0	(70088.1 or (74338.1 and 57394.1))	0	1000	3	Transport, Lumen	PMID: 19472175, PMID: 15804236, PMID: 18406692, PMID: 16185194, PMID: 18195088	B(0)AT1 transports all the neutral amino acids with preference for methionine, leucine and valine. Reaction stoichiometry is 1:1. Requires heteredimerization with collectin protein for increased affinity. Found in kidney and intestine, however also reported to be expressed in skin. Requires association with ACE2 for expression in intestine but with collectrin for expression in kidney. The the localization of the B(0)AT2 transporter has been studied in brain tissue but data from the kidney have not been reported (PMID: 18195088).	3.4.17.23
PROD2	Proline dehydrogenase	fad[c] + pro-L[c] -> h[c] + fadh2[c] + 1pyr5c[c]	0	56189.1	0	1000		Arginine and Proline Metabolism			
PROD2m	Proline dehydrogenase (m)	fad[m] + pro-L[m] -> h[m] + fadh2[m] + 1pyr5c[m]	0	19125.1	0	1000		Arginine and Proline Metabolism			
PRODPATtc	transport of D-Proline by the apical PAT2 or PAT1 amino acid transporters in kidney and intestine	h[u] + pro-D[u] -> h[c] + pro-D[c]	0	215335.1	0	1000	3	Transport, Lumen	PMID:18195088, PMID:18406692, PMID: 15345686, PMID: 17123464, PMCID: PMC34647	PAT2 is strongly expressed in heart and lung and more weakly in kidney and muscle (PMID:18406692). PAT2 doest not strongly discriminate between L and D isomers (PMID: 18406692). PAT1 proton-amino acid co-transporter with 1:1 stoichiometry, does not discriminate between L and D isomers, located on the apical membrane of kidney and intestine (PMID: 18406692, PMID: 18195088).	
PRODt2r	D-proline reversible transport via proton symport	h[e] + pro-D[e] <=> h[c] + pro-D[c]	1	215335.1	-1000	1000		Transport, Extracellular			
PRODt2rL	D-proline reversible transport via proton symport (lysosome)	h[l] + pro-D[l] <=> h[c] + pro-D[c]	1	215335.1	-1000	1000		Transport, Lysosomal			
PROGLYPEPT1tc	transport of Prolylglycine by the apical PEPT1 amino acid transporters across the brush border cells of the enterocytes of the intestine and renal cells	h[u] + prolylgly[u] -> h[c] + prolylgly[c]	0	215335.1	0	1000	3	Transport, Lumen	PMID: 7858848, PMID: 14965252, PMID: 14977407, PMID: 10330047	PEPT1 appears to transport all di- and tri- peptides across the brush border of the intestinal cells (Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Advanced nutrition and human metabolism, Wadsworth cengage learning, 5th edition, page 103). PEPT1 is expressed highly in intestinal cells where as PEPT2 is localized to renal cells (PMID: 10330047).	
PROGLYPROTr	hydrolysis of glycylproline in the small intestine for cellular uptake	h2o[c] + prolylgly[c] <=> gly[c] + pro-L[c]	1	18624.1	-1000	1000	3	Dipeptide Degradation	PMID: 15552267		3.4.13.9
PROGLYt	L-prolylglycine transport via proton symport	h[e] + prolylgly[e] -> h[c] + prolylgly[c]	0		0	1000	1	Transport, Extracellular		Needed to provide this metabolite for reaction PROGLYPEPTtc in joint model.	
PROIMINOtc	transport of L-Proline by the apical IMINO amino acid transporters in kidney and intestine	2 na1[u] + cl[u] + pro-L[u] -> 2 na1[c] + cl[c] + pro-L[c]	0	(102680.1 and 57394.1)	0	1000	3	Transport, Lumen	PMID: 19057969, PMID: 15632147, PMID: 18195088, PMID: 18400692	IMINO transporter is suggested to be a candidate for intinoglycinuria (PMID: 16052352). Associted with collectrin in kidney.	
PROLPATtc	transport of L-Proline by the apical PAT2 or PAT1 amino acid transporters in kidney and intestine	h[u] + pro-L[u] -> h[c] + pro-L[c]	0	215335.1	0	1000	3	Transport, Lumen	PMID:18195088, PMID:18406692, PMID: 15345686, PMID: 17123464, PMCID: PMC34647	PAT2 is strongly expressed in heart and lung and more weakly in kidney and muscle (PMID:18406692). PAT2 doest not strongly discriminate between L and D isomers (PMID: 18406692). PAT1 proton-amino acid co-transporter with 1:1 stoichiometry, does not discriminate between L and D isomers, located on the apical membrane of kidney and intestine (PMID: 18406692, PMID: 18195088).	
PROSTGD2t	prostaglandin transport via bicarbonate countertransport	hco3[c] + prostgd2[e] <=> hco3[e] + prostgd2[c]	1	24059.1	-1000	1000		Transport, Extracellular			
PROSTGE1t	prostaglandin transport via bicarbonate countertransport	hco3[c] + prostge1[e] <=> hco3[e] + prostge1[c]	1	24059.1	-1000	1000		Transport, Extracellular			
PROSTGE1t3	prostaglandine E1 transport (ATP-dependent)	h2o[c] + atp[c] + prostge1[c] -> adp[c] + h[c] + pi[c] + prostate1[e]	0	239273.1	0	1000		Transport, Extracellular			
PROSTGE2t	prostaglandin transport via bicarbonate countertransport	hco3[c] + prostge2[e] <=> hco3[e] + prostge2[c]	1	108116.1 or 108115.1 or 24059.1 or 28250.1	-1000	1000		Transport, Extracellular			
PROSTGE2t2	prostaglandin uniport	prostge2[e] <=> prostge2[c]	1	28518.1 or 28517.1 or 28518.2	-1000	1000		Transport, Extracellular			
PROSTGE2t3	prostaglandine E2 transport (ATP-dependent)	h2o[c] + atp[c] + prostge2[c] -> adp[c] + h[c] + pi[c] + prostate2[e]	0	239273.1	0	1000		Transport, Extracellular			
PROSTGF2t	prostaglandin uniport	prostgf2[e] <=> prostgf2[c]	1	28518.1 or 28517.1 or 28518.1	-1000	1000		Transport, Extracellular			
PROSTGH2t	prostaglandin transport via bicarbonate countertransport	hco3[c] + prostgh2[e] <=> hco3[e] + prostgh2[c]	1		-1000	1000		Transport, Extracellular			
PROSTGI2t	prostaglandin transport via bicarbonate countertransport	hco3[c] + prostgi2[e] <=> hco3[e] + prostgi2[c]	1		-1000	1000		Transport, Extracellular			
PROSTGI2tr	Prostaglandin I2 intracellular transport	prostgi2[c] <=> prostgi2[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
PROt2r	L-proline reversible transport via proton symport	h[e] + pro-L[e] <=> h[c] + pro-L[c]	1	215335.1	-1000	1000		Transport, Extracellular			
PROt2rL	L-proline reversible transport via proton symport (lysosome)	h[l] + pro-L[l] <=> h[c] + pro-L[c]	1	215335.1	-1000	1000		Transport, Lysosomal			
PROt4	Na+/Proline-L symporter	na1[e] + pro-L[e] -> na1[c] + pro-L[c]	0	105727.1 or 67760.1 or 69354.1	0	1000		Transport, Extracellular			
PROt4t2r	Proline transport (sodium symport) (2:1)	2 na1[e] + pro-L[e] <=> 2 na1[c] + pro-L[c]	1	240332.1	-1000	1000		Transport, Extracellular			
PROtm	L-proline transport, mitochondrial	pro-L[c] <=> pro-L[m]	1		-1000	1000		Transport, Mitochondrial			
PRPNCOAHYDm	Propenoyl-CoA hydrolase (m)	h2o[m] + prpncoa[m] -> 3hpcoa[m]	0	11992.1 or 231086.1 or 97212.1 or 93747.1	0	1000		beta-Alanine metabolism			
PRPNCOAHYDx	Propenoyl-CoA hydrolase (x)	h2o[x] + prpncoa[x] -> 3hpcoa[x]	0	74147.1	0	1000		beta-Alanine metabolism			
PRPPS	phosphoribosylpyrophosphate synthetase	atp[c] + r5p[c] <=> h[c] + amp[c] + prpp[c]	1	75456.1 or 75456.2 or 19139.1 or 110639.1	-1000	1000		Pentose Phosphate Pathway			
PSDm_ln	Phosphatidylserine decarboxylase	h[m] + ps_ln[m] -> co2[m] + pe_ln[m]	0	320951.1	0	1000		Glycerophospholipid Metabolism			
PSERT	phosphoserine transaminase	glu-L[c] + 3php[c] -> akg[c] + pser-L[c]	0	107272.1 or 107272.2	0	1000		Glycine, Serine, and Threonine Metabolism			
PSFLIP	phosphatidylserine flippase	h2o[c] + atp[c] + ps_ln[e] -> adp[c] + h[c] + pi[c] + ps_ln[c]	0	11982.1 or 11980.1	0	1000		Transport, Extracellular			
PSFLIPm	phosphatidylserine flippase	h2o[c] + atp[c] + ps_ln[c] -> adp[c] + h[c] + pi[c] + ps_ln[m]	0	11982.1 or 11980.1	0	1000		Transport, Mitochondrial			
PSP_L	phosphoserine phosphatase (L-serine)	h2o[c] + pser-L[c] -> pi[c] + ser-L[c]	0	100678.1	0	1000		Glycine, Serine, and Threonine Metabolism			
PSSA1_ln	Phosphatidylserine synthase homo sapiens	ser-L[c] + pchol_ln[c] <=> chol[c] + ps_ln[c]	1	19210.1	-1000	1000		Glycerophospholipid Metabolism			
PSSA2_ln	Phosphatidylserine synthase homo sapiens	ser-L[c] + pe_ln[c] <=> etha[c] + ps_ln[c]	1	27388.1	-1000	1000		Glycerophospholipid Metabolism			
PSYGCHe	binding of psyllium with glycocholate in the intestinal lumen, reducing serum cholesterol levels.	gchola[u] + psyl[u] -> psylchola[u]	0		0	1000	3	Food processing, Lumen	Zacherl C, Eisner P, Engel K-H. (2011). Food Chemistry 126: 423-8, Dongewski G. (2007). Food Chemistry 104: 390-7	psyllium consists of two parts- arabinoxylan, which is a hemi-cellulose and beta-sitosterol. Psyllium binds bile acids and leads to enhanced excretion, there by the 7-alpha hydroxylase pathway is activated leading to increased cholesterol catabolism for synthesis of more bile acids (regulates cholesterol metabolism). however the decreased serum cholesterol levels are brought about by many other cumulative effects (water unstirred action of dieatary fibres, glycemic rule etc) (PMID: 18302966, Gunness P, Gidley MJ. (2010). Food & Function 1: 149-55).	
PSYGCHt	binding of psyllium with glycocholate transport	h[e] + psylchola[e] <=> h[c] + psylchola[c]	1		-1000	1000	1	Transport, Extracellular		Needed to provide this metabolite for reaction PSYGCHe in joint model.	
PSYLt	Psyllium transport	h[e] + psyl[e] <=> h[c] + psyl[c]	1		-1000	1000	1	Transport, Extracellular		Needed to provide this metabolite for reaction PSYTDECHe, PSYGCHe and PSYTCHe in joint model.	
PSYTCHe	binding of psyllium with taurocholate in the intestinal lumen, reducing serum cholesterol levels.	tchola[u] + psyl[u] -> psylchola[u]	0		0	1000	3	Food processing, Lumen	Zacherl C, Eisner P, Engel K-H. (2011). Food Chemistry 126: 423-8, Dongewski G. (2007). Food Chemistry 104: 390-7	psyllium consists of two parts- arabinoxylan, which is a hemi-cellulose and beta-sitosterol. Psyllium binds bile acids and leads to enhanced excretion, there by the 7-alpha hydroxylase pathway is activated leading to increased cholesterol catabolism for synthesis of more bile acids (regulates cholesterol metabolism). however the decreased serum cholesterol levels are brought about by many other cumulative effects (water unstirred action of dieatary fibres, glycemic rule etc) (PMID: 18302966, Gunness P, Gidley MJ. (2010). Food & Function 1: 149-55).	
PSYTCHt	binding of psyllium with taurocholate transport	h[e] + psylchola[e] <=> h[c] + psylchola[c]	1		-1000	1000	1	Transport, Extracellular		Needed to provide this metabolite for reaction PSYTCHe in joint model.	
PSYTDECHe	binding of psyllium with taurodeoxycholate in the intestinal lumen, reducing serum cholesterol levels.	tdechola[u] + psyl[u] -> psyltdechola[u]	0		0	1000	3	Food processing, Lumen	Zacherl C, Eisner P, Engel K-H. (2011). Food Chemistry 126: 423-8, Dongewski G. (2007). Food Chemistry 104: 390-7	psyllium consists of two parts- arabinoxylan, which is a hemi-cellulose and beta-sitosterol. Psyllium binds bile acids and leads to enhanced excretion, there by the 7-alpha hydroxylase pathway is activated leading to increased cholesterol catabolism for synthesis of more bile acids (regulates cholesterol metabolism). however the decreased serum cholesterol levels are brought about by many other cumulative effects (water unstirred action of dieatary fibres, glycemic rule etc) (PMID: 18302966, Gunness P, Gidley MJ. (2010). Food & Function 1: 149-55). Deoxycholic acid is a secondary bile salt formed by decarjugation and further 7-alpha-dehydroxylation by the bacterial action in the gut (Harper's illustrated biochemistry, 28th edition, page 229-231). Taurodeoxy-cholic acid may be formed by the conjugation of taurine with deoxycholic acid (no evidence found for suc hreaction but the metabolite Taurodeoxycholic acid has been estimated in human blood and bile in trave amounts (HMDB00896)).	
PSYTDECHt	binding of psyllium with taurodeoxycholate transport	h[e] + psylchola[e] <=> h[c] + psylchola[c]	1		-1000	1000	1	Transport, Extracellular		Needed to provide this metabolite for reaction PSYTDECHe in joint model.	
PS_HSter	phosphatidylserine scramblase	ps_ln[c] <=> ps_ln[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
PS_HSg	phosphatidylserine scramblase	ps_ln[c] <=> ps_ln[g]	1		-1000	1000		Transport, Golgi Apparatus			
PSt3	phosphatidylserine (homo sapiens) transport	ps_ln[e] <=> ps_ln[c]	1		-1000	1000		Transport, Extracellular			
PTDCACRNCPT1	carnitine fatty-acyl transferase	crn[c] + ptdcacoa[c] -> coa[c] + ptdcacrn[c]	0	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	0	1000		Carnitine shuttle			
PTDCACRNCPT2	pentadecanoate transport into the mitochondria	coa[m] + ptdcacrn[m] -> crn[m] + ptdcacoa[m]	0	12896.1	0	1000		Carnitine shuttle			
PTDCACRNt	pentadecanoate transport into the mitochondria	ptdcacrn[c] -> ptdcacrn[m]	0	57279.1	0	1000		Carnitine shuttle			
PTDCAt	fatty acid transport via diffusion	ptdca[e] <=> ptdca[c]	1		-1000	1000		Transport, Extracellular			
PTE2x	peroxisomal acyl-CoA thioesterase	pmtcoa[x] + h2o[x] -> h[x] + coa[x] + hdca[x]	0	170789.1 or 171210.1 or 170789.2 or 170789.3	0	1000		Fatty Acid Metabolism			

PTE3x	peroxisomal acyl-CoA thioesterase	h2o[x] + pristcoa[x] -> h[x] + coa[x] + pristc[x]	0	171210.1	0	1000		Fatty Acid Metabolism			
PTE4x	peroxisomal acyl-CoA thioesterase	h2o[x] + phytcoa[x] -> h[x] + coa[x] + phyt[x]	0	171210.1	0	1000		Fatty Acid Metabolism			
PTE5x	peroxisomal acyl-CoA thioesterase	h2o[x] + adrncoa[x] -> h[x] + coa[x] + adrn[x]	0	171210.1	0	1000		Fatty Acid Metabolism			
PTHPS	6-pyruvoyltetrahydropterin synthase	ahdt[c] -> pypt[c] + fpthp[c]	0	19286.1	0	1000		Tetrahydrobiopterin			
PTHPSn	6-pyruvoyltetrahydropterin synthase, nuclear	ahdt[n] -> pypt[n] + fpthp[n]	0	19286.1	0	1000		Tetrahydrobiopterin			
PTPAT	pantetheine-phosphate adenylyltransferase	atp[c] + h[c] + pant6p[c] <=> ppi[c] + dpcoa[c]	1	71743.1	-1000	1000		CoA Biosynthesis			
PTRCAT1	Putrescine acetyltransferase	accoa[c] + ptrc[c] -> h[c] + coa[c] + aptrc[c]	0	69215.1 or 20229.1	0	1000		Arginine and Proline Metabolism			
PTRCOX1	Putrescine:oxygen oxidoreductase (deaminating)	h2o[c] + o2[c] + ptrc[c] -> h2o2[c] + nh4[c] + 4abutn[c]	0	237940.1 or 237940.2 or 11754.1 or 76507.1	0	1000		Arginine and Proline Metabolism			
PUNP1	purine-nucleoside phosphorylase (Adenosine)	pi[c] + adn[c] <=> ade[c] + r1p[c]	1	667034.1	-1000	1000		Nucleotides			
PUNP2	purine-nucleoside phosphorylase (Deoxyadenosine)	pi[c] + dadn_2[c] <=> 2dr1p[c] + ade[c]	1	667034.1	-1000	1000		Purine Catabolism			
PUNP3	purine-nucleoside phosphorylase (Guanosine)	pi[c] + gsn[c] <=> gua[c] + r1p[c]	1	667034.1	-1000	1000		Purine Catabolism			
PUNP4	purine-nucleoside phosphorylase (Deoxyguanosine)	pi[c] + dgsn[c] <=> 2dr1p[c] + gua[c]	1	667034.1	-1000	1000		Purine Catabolism			
PUNP5	purine-nucleoside phosphorylase (Inosine)	pi[c] + ins[c] <=> hxan[c] + r1p[c]	1	667034.1	-1000	1000		Purine Catabolism			
PUNP6	purine-nucleoside phosphorylase (Deoxyinosine)	pi[c] + dins[c] <=> 2dr1p[c] + hxan[c]	1	667034.1	-1000	1000		Purine Catabolism			
PUNP7	purine-nucleoside phosphorylase (Xanthosine)	pi[c] + xtsn[c] <=> xan[c] + r1p[c]	1	667034.1	-1000	1000		Nucleotides			
PVD3	Provitamin D3 formation	7dhchstrol[c] <=> pvd3[c]	1		-1000	1000		Vitamin D			
PVAM5POr	pyridoxamine 5'-phosphate oxidase	h2o[c] + o2[c] + pyam5p[c] <=> h2o2[c] + nh4[c] + pydx5p[c]	1	103711.1	-1000	1000		Vitamin B6 Metabolism			
PVAM5Ptm	Pyridoxamine 5'-phosphate transport via diffusion, mitochondrial	pyam5p[c] <=> pyam5p[m]	1		-1000	1000		Transport, Mitochondrial			
PVDAMK	pyridoxamine kinase	atp[c] + pydam[c] -> adp[c] + h[c] + pyam5p[c]	0	216134.1	0	1000		Vitamin B6 Metabolism			
PVDAMtr	pyridoxamine transport via diffusion	pydam[e] <=> pydam[c]	1		-1000	1000		Transport, Extracellular			
PVDX5Ptm	Pyridoxal 5'-phosphate transport via diffusion, mitochondrial	pydx5p[c] <=> pydx5p[m]	1		-1000	1000		Transport, Mitochondrial			
PVDXDH	pyridoxal dehydrogenase	h2o[c] + o2[c] + pydx[c] -> h2o2[c] + 4pyrdx[c]	0	11761.1	0	1000		Vitamin B6 Metabolism			
PVDXK	pyridoxal kinase	atp[c] + pydx[c] -> adp[c] + h[c] + pydx5p[c]	0	216134.1	0	1000		Vitamin B6 Metabolism			
PVDXNK	pyridoxine kinase	atp[c] + pydxn[c] -> adp[c] + h[c] + pdx5p[c]	0	216134.1	0	1000		Vitamin B6 Metabolism			
PVDXNtr	pyridoxine transport via diffusion	pydxn[e] <=> pydxn[c]	1		-1000	1000		Transport, Extracellular			
PVDXP	Pyridoxal 5-phosphate phosphatase	h2o[c] + pydx5p[c] -> pi[c] + pydx[c]	0	57028.1	0	1000		Vitamin B6 Metabolism			
PVDXtr	pyridoxal transport via diffusion	pydx[e] <=> pydx[c]	1		-1000	1000		Transport, Extracellular			
PYK	pyruvate kinase	adp[c] + h[c] + pep[c] -> atp[c] + pyr[c]	0	18746.1 or 66260.1 or 18770.1 or 18746.2 or 18770.2 or 18746.3	0	1000		Glycolysis/Gluconeogenesis			
PYLALDOX	Perillyl aldehyde:NAD+ oxidoreductase	h2o[c] + nad[c] + pylald[c] -> 2 h[c] + nadh[c] + peracd[c]	0	19378.1 or 56752.1 or 110695.1 or 11668.1 or 11671.1 or 19378.2 or 19378.3	0	1000		Limonene and pinene degradation			
PYLALDOXm	Perillyl aldehyde:NAD+ oxidoreductase (m)	h2o[m] + nad[m] + pylald[m] -> 2 h[m] + nadh[m] + peracd[m]	0	11668.1 or 212647.1 or 212647.2 or 72535.1	0	1000		Limonene and pinene degradation			
PYNP2r	pyrimidine-nucleoside phosphorylase (uracil)	pi[c] + ura[c] <=> ura[c] + r1p[c]	1	22271.1 or 22271.2 or 76654.1	-1000	1000		Pyrimidine Catabolism			
PYRt2m	pyruvate mitochondrial transport via proton symport	h[c] + pyr[c] <=> h[m] + pyr[m]	1	20501.1	-1000	1000		Transport, Mitochondrial			
PYRt2p	pyruvate peroxisomal transport via proton symport	h[c] + pyr[c] <=> h[x] + pyr[x]	1	20503.1 or 20501.1	-1000	1000		D-alanine metabolism			
PYRt2r	pyruvate reversible transport via proton symport	h[e] + pyr[e] <=> h[c] + pyr[c]	1	20503.1 or 80879.1 or 20501.1	-1000	1000		Transport, Extracellular			
QUILSYN	Quinolinate Synthase (Eukaryotic)	cmusa[c] -> h2o[c] + h[c] + quln[c]	0		0	1000		Tryptophan metabolism			
RADH	retinal dehydrogenase	h2o[c] + nad[c] + retinal[c] <=> 2 h[c] + nadh[c] + rete[c]	1		-1000	1000		Vitamin A Metabolism			
RADH2	retinal dehydrogenase (NADPH)	h2o[c] + nadp[c] + retinal[c] <=> 2 h[c] + nadph[c] + rete[c]	1		0	1000		Vitamin A Metabolism			
RADH3	retinal dehydrogenase	h2o[c] + nad[c] + retinal-cis-13[c] <=> 2 h[c] + nadh[c] + 13-cis-rete[c]	1		-1000	1000		Vitamin A Metabolism			
RADH4	retinal dehydrogenase (NADPH)	h2o[c] + nadp[c] + retinal-cis-13[c] <=> 2 h[c] + nadph[c] + 13-cis-rete[c]	1		0	1000		Vitamin A Metabolism			
RAHY	retinoic acid hydroxylation (P450)	o2[c] + h[c] + nadph[c] + rete[c] -> h2o[c] + nadp[c] + hrete[c]	0		0	1000		Vitamin A Metabolism			
RAI1	retinal isomerase (11-cis)	retinal[c] <=> retinal-11-cis[c]	1		-1000	1000		Vitamin A Metabolism			
RAI2	retinal isomerase (9-cis)	retinal[c] <=> retinal-cis-9[c]	1		-1000	1000		Vitamin A Metabolism			
RAI3	13-cis-retinoic acid isomerase	rete[c] <=> 13-cis-rete[c]	1	14863.1 or 14863.2	-1000	1000		Vitamin A Metabolism			
RAI4	13-cis-4-oxo-retinoic acid isomerase	orete[c] <=> 13-cis-orete[c]	1		-1000	1000		Vitamin A Metabolism			
RAtn	Retinoate transport, nuclear	rete[c] <=> rete[n]	1		-1000	1000		Transport, Nuclear			
RAtn3	13-cis-retinoic acid transport, nuclear	13-cis-rete[c] <=> 13-cis-rete[n]	1		-1000	1000		Transport, Nuclear			
RBK	ribokinase	atp[c] + rib-D[c] -> adp[c] + h[c] + r5p[c]	0	71336.1	0	1000		Pentose Phosphate Pathway			
RBK_D	D-ribulokinase	atp[c] + rbl-D[c] -> adp[c] + h[c] + ru5p-D[c]	0		0	1000		Pentose and Glucuronate Interconversions			
RBTt	ribitol transport via passive diffusion	rbt[c] <-> rbt[e]	0		0	1000		Transport, Extracellular			
RDH1	retinol dehydrogenase (all-trans)	nad[c] + retinol[c] <=> h[c] + nadh[c] + retinal[c]	1	107605.1 or 19682.1	-1000	1000		Vitamin A Metabolism			
RDH1a	retinol dehydrogenase (all-trans,NADPH)	nadp[c] + retinol[c] <=> h[c] + nadph[c] + retinal[c]	1	105014.1 or 235033.1 or 98711.1 or 108841.1 or 242285.1 or 17252.1 or 77974.1	0	1000		Vitamin A Metabolism			
RDH2	retinol dehydrogenase (9-cis,NADH)	nad[c] + retinol-9-cis[c] <=> h[c] + nadh[c] + retinal-cis-9[c]	1	19682.1	-1000	1000		Vitamin A Metabolism			
RDH2a	retinol dehydrogenase (9-cis,NADPH)	nadp[c] + retinol-9-cis[c] <=> h[c] + nadph[c] + retinal-cis-9[c]	1	105014.1 or 235033.1 or 108841.1 or 242285.1 or 17252.1 or 77974.1	0	1000		Vitamin A Metabolism			
RDH3	retinol dehydrogenase (11-cis,NADH)	nad[c] + retinol-cis-11[c] <=> h[c] + nadh[c] + retinal-11-cis[c]	1	19682.1	-1000	1000		Vitamin A Metabolism			
RDH3a	retinol dehydrogenase (11-cis,NADPH)	nadp[c] + retinol-cis-11[c] <=> h[c] + nadph[c] + retinal-11-cis[c]	1	105014.1 or 108841.1 or 242285.1 or 17252.1 or 77974.1	0	1000		Vitamin A Metabolism			
RDH4	retinol dehydrogenase (13-cis,NADH)	nad[c] + retinol-cis-13[c] <=> h[c] + nadh[c] + retinal-cis-13[c]	1	19682.1	-1000	1000		Vitamin A Metabolism			
RE2666G	RE2666G	salpgal[g] + galside_bt[g] -> h[g] + salp[g] + digalside_bt[g]	0		0	1000	0	Sphingolipid Metabolism			
RETFA	retinol acyltransferase	Rtotal2coa[c] + retinol[c] -> coa[c] + retfa[c]	0		0	1000		Vitamin A Metabolism			
RETFAt	fatty acid retinol efflux	retfa[c] -> retfa[e]	0		0	1000		Transport, Extracellular			
RETFAt1	fatty acid retinol efflux (9-cis)	9-cis-retfa[c] -> 9-cis-retfa[e]	0		0	1000		Transport, Extracellular			
RETFAt2	fatty acid retinol efflux (11-cis)	11-cis-retfa[c] -> 11-cis-retfa[e]	0		0	1000		Transport, Extracellular			
RETH1	retinyl ester hydrolase (9-cis)	h2o[c] + 9-cis-retnlz[c] -> Rtotal2[c] + retinol-9-cis[c]	0		0	1000		Vitamin A Metabolism			
RETH1e	retinyl ester hydrolase (9-cis), extracellular	h2o[e] + 9-cis-retnlz[e] -> h[e] + Rtotal2[e] + retinol-9-cis[e]	0		0	1000		Vitamin A Metabolism			
RETH2	retinyl ester hydrolase (11-cis)	h2o[c] + 11-cis-retnlz[c] -> h[c] + Rtotal2[c] + retinol-cis-11[c]	0		0	1000		Vitamin A Metabolism			
RETH2e	retinyl ester hydrolase (11-cis), extracellular	h2o[e] + 11-cis-retnlz[e] -> h[e] + Rtotal2[e] + retinol-cis-11[e]	0		0	1000		Vitamin A Metabolism			
RETHe	retinyl ester hydrolase, extracellular	h2o[e] + retnlz[e] -> h[e] + Rtotal2[e] + retinol[e]	0		0	1000		Vitamin A Metabolism			
RETI1	retinol isomerase (11-cis)	retinol[c] <=> retinol-cis-11[c]	1		-1000	1000		Vitamin A Metabolism			
RETI2	retinol isomerase (9-cis)	retinol[c] <=> retinol-9-cis[c]	1		-1000	1000		Vitamin A Metabolism			
RETI3	retinol isomerase (13-cis)	retinol[c] <=> retinol-cis-13[c]	1		-1000	1000		Vitamin A Metabolism			
RETINOLte	transport of retinol into the intestine and liver cells	retinol[u] -> retinol[c]	0	(19660.1 or (19662.1 and 20897.1 and 19659.1))	0	1000	3	Transport, Lumen	PMID: 21482499, PMID: 21368206, PMID:16011460, Sureen S. Gropper, Jack L. Smith, James L. Groff (2009) Advanced nutrition and human metabolism, Wadsworth cengage learning, 5th edition, page 375-379	circulating retinol is bound to the retinol binding protein-4 with high affinity forming retinol-RBP complex, STRA6 acts as a transporter of this complex and further activates signalling cascades (PMID: 21368206). after entry into the enterocytes, the CRBP 1 and 2 play role in uptake of retinol into the liver cells and also enhance retinol absorption (PMID: 16011460).	
RETNCOA	Retinoyl CoA formation	atp[c] + coa[c] + rete[c] -> amp[c] + ppi[c] + retncoa[c]	0		0	1000		Vitamin A Metabolism			
RETNGLCt	retinoyl glucuronide efflux	retnglc[c] -> retnglc[e]	0		0	1000		Transport, Extracellular			
RETNGLCt2	retinoyl glucuronide efflux (13-cis)	13-cis-retnglc[c] -> 13-cis-retnglc[e]	0		0	1000		Transport, Extracellular			
RETNGLCt2r	retinoyl glucuronide efflux (13-cis) from ER	13-cis-retnglc[r] -> 13-cis-retnglc[c]	0		0	1000		Transport, Endoplasmic Reticular			
RETNGLCtr	retinoyl glucuronide efflux from ER	retnglc[r] -> retnglc[c]	0		0	1000		Transport, Endoplasmic Reticular			
RETNt	retinoic acid transport	rete[c] <=> rete[e]	1		-1000	1000		Transport, Extracellular			
RETNtr	retinoic acid transport in ER	rete[c] -> rete[r]	0		0	1000		Transport, Endoplasmic Reticular			
RETNtr2	retinoic acid transport in ER (13-cis)	13-cis-rete[c] -> 13-cis-rete[r]	0		0	1000		Transport, Endoplasmic Reticular			
RETt	Retinol transport via facilitated diffusion	retinol[e] -> retinol[c]	0		0	1000		Transport, Extracellular			
RIBFLVt	absorption of riboflavin by diffusion	ribflv[u] -> ribflv[c]	0		0	1000	2	Transport, Lumen	G.F.M. Ball (2006) Vitamins their role in the human body, Blackwell publishing, chapter 12, page 291.	absorption of riboflavin by simple diffusion at high concentration.	
RIBFLVt3	riboflavin transport (ATP dependent)	h2o[c] + atp[c] + ribflv[e] -> adp[c] + h[c] + pi[c] + ribflv[c]	0		0	1000		Transport, Extracellular			
RIBFLVte	release of riboflavin into the portal blood.	h2o[c] + atp[c] + ribflv[c] -> adp[c] + h[c] + pi[c] + ribflv[e]	0	52710.1	0	1000	2	Transport, Extracellular	G.F.M. Ball (2006) Vitamins their role in the human body, Blackwell publishing, chapter 12, page 291-292, PMID: 21854757, PMID 2046314?, Said HM, Hollander D, Mohammadkhani R. (1993). Biochimica et Biophysica Acta (BBA) - Biomembranes 1148: 263-8.	both entry and exit of riboflavin from the enterocytes in energy dependant and Na+ independant. Carrier protein mediated. In mice, no homolog of the human gene could be found.	
RIBt	ribose transport via diffusion	rib-D[e] <=> rib-D[c]	1		-1000	1000		Transport, Extracellular			
RIBt2	ribose transport in via proton symporter	h[e] + rib-D[e] -> h[c] + rib-D[c]	0		0	1000		Transport, Extracellular			
RNDR1	ribonucleoside-diphosphate reductase (ADP)	adp[c] + trdrd[c] -> h2o[c] + dadp[c] + trdox[c]	0	20135.1 and 20133.1	0	1000		Nucleotides			
RNDR2	ribonucleoside-diphosphate reductase (GDP)	gdp[c] + trdrd[c] -> h2o[c] + dgdp[c] + trdox[c]	0	20135.1 and 20133.1	0	1000		Nucleotides			
RNDR3	ribonucleoside-diphosphate reductase (CDP)	cdp[c] + trdrd[c] -> h2o[c] + dcdp[c] + trdox[c]	0	20135.1 and 20133.1	0	1000		Nucleotides			
RNDR4	ribonucleoside-diphosphate reductase (UDP)	udp[c] + trdrd[c] -> h2o[c] + dudp[c] + trdox[c]	0	20135.1 and 20133.1	0	1000		Nucleotides			
RNMK	ribosylnicotinamide kinase	atp[c] + rnam[c] -> adp[c] + h[c] + nmn[c]	0	225994.1	0	1000		NAD Metabolism			
RPE	ribulose 5-phosphate 3-epimerase	ru5p-D[c] <=> xu5p-D[c]	1	66646.1 or 66646.2	-1000	1000		Pentose Phosphate Pathway			
RPI	ribose-5-phosphate isomerase	r5p[c] <=> ru5p-D[c]	1	19895.1	-1000	1000		Pentose Phosphate Pathway			
RTOT1	R total flux	R1tcoa_bs[c] -> Rtotalcoa[c]	0		0	1000		R Group Synthesis			
RTOT2	R total flux	R2tcoa_bs[c] -> Rtotalcoa[c]	0		0	1000		R Group Synthesis			
RTOT3	R total flux	R3tcoa_bs[c] -> Rtotalcoa[c]	0		0	1000		R Group Synthesis			
RTOT4	R total flux	R4tcoa_bs[c] -> Rtotalcoa[c]	0		0	1000		R Group Synthesis			
RTOT5	R total flux	R5tcoa_bs[c] -> Rtotalcoa[c]	0		0	1000		R Group Synthesis			

RTOT6	R total flux	R6coa_hs[c] -> Rtotalcoa[c]	0		0	1000		R Group Synthesis			
RTOTAL2CRNCPT1	carnitine fatty-acyl transferase	crn[c] + Rtotal2coa[c] -> coa[c] + Rtotal2crn[c]	0	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	0	1000		Carnitine shuttle			
RTOTAL2CRNCPT2	R group transport into the mitochondria	coa[m] + Rtotal2crn[m] -> crn[m] + Rtotal2coa[m]	0	12896.1	0	1000		Carnitine shuttle			
RTOTAL2CRNt	R group transport into the mitochondria	Rtotal2crn[c] -> Rtotal2crn[m]	0	57279.1	0	1000		Carnitine shuttle			
RTOTAL2TDlu	difussion of fatty acid accross the brush border membrane	Rtotal2[u] <=> Rtotal2[c]	1		-1000	1000	2	Transport, Lumen	Sareen S. Gropper, jack L. Smith, James L. Groff (2009) Wadaworth cengage learning, Advanced nutrition and human metabolism, 5th edition, page 142-144.		
RTOTAL2t	fatty acid transmembrane transport	Rtotal2[e] <=> Rtotal2[c]	1		-1000	1000		Transport, Extracellular			
RTOTAL3CRNCPT1	carnitine fatty-acyl transferase	crn[c] + Rtotal3coa[c] -> coa[c] + Rtotal3crn[c]	0	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3	0	1000		Carnitine shuttle			
RTOTAL3CRNCPT2	R group transport into the mitochondria	coa[m] + Rtotal3crn[m] -> crn[m] + Rtotal3coa[m]	0	12896.1	0	1000		Carnitine shuttle			
RTOTAL3CRNt	R group transport into the mitochondria	Rtotal3crn[c] -> Rtotal3crn[m]	0	57279.1	0	1000		Carnitine shuttle			
RTOTAL3TDlu	difussion of fatty acid accross the brush border membrane	Rtotal3[u] <=> Rtotal3[c]	1		-1000	1000	2	Transport, Lumen	Sareen S. Gropper, jack L. Smith, James L. Groff (2009) Wadaworth cengage learning, Advanced nutrition and human metabolism, 5th edition, page 142-144.		
RTOTAL3t	fatty acid transmembrane transport	Rtotal3[e] <=> Rtotal3[c]	1		-1000	1000		Transport, Extracellular			
RTOTALCRNCPT1	carnitine fatty-acyl transferase	crn[c] + Rtotalcoa[c] -> coa[c] + Rtotalcrn[c]	0	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	0	1000		Carnitine shuttle			
RTOTALCRNCPT2	R group transport into the mitochondria	coa[m] + Rtotalcrn[m] -> crn[m] + Rtotalcoa[m]	0	12896.1	0	1000		Carnitine shuttle			
RTOTALCRNt	R group transport into the mitochondria	Rtotalcrn[c] -> Rtotalcrn[m]	0	57279.1	0	1000		Carnitine shuttle			
RTOTALDlu	difussion of fatty acid accross the brush border membrane	Rtotal[u] <=> Rtotal[c]	1		-1000	1000	2	Transport, Lumen	Sareen S. Gropper, jack L. Smith, James L. Groff (2009) Wadaworth cengage learning, Advanced nutrition and human metabolism, 5th edition, page 142-144.		
RTOTALt	fatty acid transmembrane transport	Rtotal[e] <=> Rtotal[c]	1		-1000	1000		Transport, Extracellular			
RTOT_2	R total flux 2 position	R2coa_hs[c] + R4coa_hs[c] -> 2 Rtotal2coa[c]	0		0	1000		R Group Synthesis			
RTOT_3	R total flux 3 position	R1coa_hs[c] + R2coa_hs[c] -> 2 Rtotal3coa[c]	0		0	1000		R Group Synthesis			
Rtotaltl	fatty acid intracellular transport	Rtotal[c] <=> Rtotal[l]	1		-1000	1000		Transport, Lysosomal			
Rtotaltp	fatty acid intracellular transport	Rtotal[c] <=> Rtotal[x]	1		-1000	1000		Transport, Peroxisomal			
S23T2g	beta-galactoside alpha-2,3-sialyltransferase (core 2)	core2[g] + cmpacna[g] -> h[g] + cmp[g] + ksii_core2_pre1[g]	0	20442.1 or 20444.1 or 20442.2 or 20443.1	0	1000		Keratan sulfate biosynthesis			
S23T3g	beta-galactoside alpha-2,3-sialyltransferase (complex N-glycan)	cmpacna[g] + l2fn2m2masn[g] -> h[g] + ksi_pre1[g] + cmp[g]	0	20441.1 or 20441.2 or 20441.3 or 20441.4 or 20441.5 or 20441.6 or 20441.7 or 20441.8 or 20441.9 or 20441.10 or 20441.11	0	1000		Keratan sulfate biosynthesis			
S23T4g	beta-galactoside alpha-2,3-sialyltransferase	cmpacna[g] + ksii_core4_pre1[g] -> h[g] + ksii_core4_pre2[g] + cmp[g]	0	20442.1 or 20444.1 or 20442.2 or 20443.1	0	1000		Keratan sulfate biosynthesis			
S23Tg	beta-galactoside alpha-2,3-sialyltransferase (T antigen)	T_antigen[g] + cmpacna[g] -> h[g] + cmp[g] + sT_antigen[g]	0	20442.1 or 20442.2	0	1000		O-Glycan Biosynthesis			
S26Tg	beta-galactoside alpha-2,6-sialyltransferase	2 cmpacna[g] + l2fn2m2masn[g] -> 2 h[g] + 2 cmp[g] + s2l2fn2m2masn[g]	0	20440.1 or 20440.2 or 20440.3	0	1000		N-Glycan Biosynthesis			
S2L2FN2M2MASNt	s2l2fn2m2masn transport, Golgi to extracellular	s2l2fn2m2masn[g] -> s2l2fn2m2masn[e]	0		0	1000		Transport, Extracellular			
S2L2FN2M2MASNtly	s2l2fn2m2masn transport, extracellular to lysosome	s2l2fn2m2masn[e] -> s2l2fn2m2masn[l]	0		0	1000		Transport, Lysosomal			
S2L2N2M2MASNtly	s2l2n2m2masn transport, extracellular to lysosome	s2l2n2m2masn[e] -> s2l2n2m2masn[l]	0		0	1000		Transport, Lysosomal			
S2L2N2M2Mt	de-Fuc form of PA6 (w/o peptide linkage) transport, lysosome to extracellular	s2l2n2m2m[l] <=> s2l2n2m2m[e]	1		-1000	1000	1	Transport, Extracellular			
S2T1g	chondroitin 2-sulfotransferase, Golgi	paps[g] + cs_c_d_e_pre1[g] -> h[g] + pap[g] + cs_d_pre2[g]	0	338362.1	0	1000		Chondroitin / heparan sulfate biosynthesis			
S2T2g	chondroitin 2-sulfotransferase, Golgi	paps[g] + cs_d_pre5[g] -> h[g] + cspg_d[g] + pap[g]	0	338362.1	0	1000		Chondroitin / heparan sulfate biosynthesis			
S2T3g	uronyl 2-sulfotransferase, Golgi	paps[g] + cs_b_pre5[g] -> h[g] + cspg_b[g] + pap[g]	0	338362.1	0	1000		Chondroitin / heparan sulfate biosynthesis			
S2T4g	uronyl 2-sulfotransferase, Golgi	2 paps[g] + hs_pre11[g] -> 2 h[g] + 2 pap[g] + hs_pre12[g]	0	23908.1	0	1000		Chondroitin / heparan sulfate biosynthesis			
S2TASE1ly	iduronate-2-sulfatase, lysosomal	h2o[l] + hs_deg15[l] -> h[l] + so4[l] + hs_deg16[l]	0	15931.1 or 15931.2	0	1000		Heparan sulfate degradation			
S2TASE2ly	iduronate-2-sulfatase, lysosomal	h2o[l] + hs_deg21[l] -> h[l] + so4[l] + hs_deg22[l]	0	15931.1 or 15931.2	0	1000		Heparan sulfate degradation			
S2TASE3ly	iduronate-2-sulfatase, lysosomal	h2o[l] + cs_b_deg2[l] -> h[l] + so4[l] + cs_b_deg3[l]	0	15931.1 or 15931.2	0	1000		Chondroitin sulfate degradation			
S2TASE4ly	glucuronate-2-sulfatase, lysosomal	h2o[l] + cs_d_deg2[l] -> h[l] + so4[l] + cs_d_deg3[l]	0		0	1000		Chondroitin sulfate degradation			
S2TASE5ly	glucuronate-2-sulfatase, lysosomal	h2o[l] + cs_d_deg6[l] -> h[l] + so4[l] + cs_c_deg5[l]	0		0	1000		Chondroitin sulfate degradation			
S3T1g	heparin-glucosamine 3-O-sulfotransferase	paps[g] + hs_pre13[g] -> h[g] + pap[g] + hs_pre14[g]	0	15476.1 or 628779.1 or 319415.1	0	1000		Chondroitin / heparan sulfate biosynthesis			
S3T2g	heparin-glucosamine 3-O-sulfotransferase	paps[g] + hs_pre14[g] -> h[g] + pap[g] + hs_pre15[g]	0	628779.1 or 319415.1 or 195646.1	0	1000		Chondroitin / heparan sulfate biosynthesis			
S3T3g	heparin-glucosamine 3-O-sulfotransferase	paps[g] + hs_pre15[g] -> h[g] + pap[g] + hspg[g]	0	15478.1 or 54710.1 or 328779.1 or 628779.1	0	1000		Chondroitin / heparan sulfate biosynthesis			
S3TASE1ly	N-acetylglucosamine-3-sulfatase, lysosomal	h2o[l] + hs_deg10[l] <=> h[l] + so4[l] + hs_deg11[l]	1		-1000	1000		Heparan sulfate degradation			
S3TASE2ly	N-acetylglucosamine-3-sulfatase, lysosomal	h2o[l] + hs_deg17[l] <=> h[l] + so4[l] + hs_deg18[l]	1		-1000	1000		Heparan sulfate degradation			
S3TASE3ly	N-acetylglucosamine-3-sulfatase, lysosomal	h2o[l] + hs_deg23[l] <=> h[l] + so4[l] + hs_deg24[l]	1		-1000	1000		Heparan sulfate degradation			
S4T1g	chondroitin 4-sulfotransferase, Golgi apparatus	2 paps[g] + cs_pre[g] -> 2 h[g] + 2 pap[g] + cs_a_b_e_pre1[g]	0	71797.1 or 58250.1 or 59031.1 or 72136.1	0	1000		Chondroitin / heparan sulfate biosynthesis			
S4T2g	chondroitin 4-sulfotransferase, Golgi apparatus	paps[g] + cs_a_b_pre3[g] -> h[g] + cspg_a[g] + pap[g]	0	71797.1 or 58250.1 or 59031.1 or 72136.1	0	1000		Chondroitin / heparan sulfate biosynthesis			
S4T3g	chondroitin 4-sulfotransferase, Golgi apparatus	paps[g] + cs_e_pre4[g] -> h[g] + pap[g] + cs_e_pre5a[g]	0	71797.1 or 58250.1 or 59031.1 or 72136.1	0	1000		Chondroitin / heparan sulfate biosynthesis			
S4T4g	chondroitin 4-sulfotransferase, Golgi apparatus	2 paps[g] + cs_c_d_e_pre1[g] -> 2 h[g] + 2 pap[g] + cs_e_pre2[g]	0		0	1000		Chondroitin / heparan sulfate biosynthesis			
S4T5g	chondroitin 4-sulfotransferase, Golgi apparatus	paps[g] + cs_e_pre5b[g] -> h[g] + cspg_e[g] + pap[g]	0		0	1000		Chondroitin / heparan sulfate biosynthesis			
S4T6g	chondroitin 4-sulfotransferase, Golgi apparatus	paps[g] + cs_b_pre4[g] -> h[g] + pap[g] + cs_b_pre5[g]	0	71797.1 or 58250.1 or 59031.1 or 72136.1	0	1000		Chondroitin / heparan sulfate biosynthesis			
S4TASE1ly	N-acetylgalactosamine-4-sulfatase, lysosomal	h2o[l] + cs_a[l] <=> h[l] + so4[l] + cs_a_deg1[l]	1	11881.1 or 11881.2	-1000	1000		Chondroitin sulfate degradation			
S4TASE2ly	N-acetylgalactosamine-4-sulfatase, lysosomal	h2o[l] + cs_a_deg3[l] <=> h[l] + so4[l] + cs_a_deg4[l]	1	11881.1 or 11881.2	-1000	1000		Chondroitin sulfate degradation			
S4TASE3ly	N-acetylgalactosamine-4-sulfatase, lysosomal	h2o[l] + cs_b[l] <=> h[l] + so4[l] + cs_b_deg1[l]	1	11881.1 or 11881.2	-1000	1000		Chondroitin sulfate degradation			
S4TASE4ly	N-acetylgalactosamine-4-sulfatase, lysosomal	h2o[l] + cs_e[l] <=> h[l] + so4[l] + cs_e_deg1[l]	1	11881.1 or 11881.2	-1000	1000		Chondroitin sulfate degradation			
S4TASE5ly	N-acetylgalactosamine-4-sulfatase, lysosomal	h2o[l] + cs_e_deg4[l] <=> h[l] + so4[l] + cs_e_deg5[l]	1	11881.1 or 11881.2	-1000	1000		Chondroitin sulfate degradation			
S6T10g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	ksi_pre22[g] + paps[g] -> h[g] + ksi_pre23[g] + pap[g]	0	26887.1 or 54371.1 or 56773.1 or 56773.2	0	1000		Keratan sulfate biosynthesis			
S6T11g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	ksi_pre25[g] + paps[g] -> h[g] + ksi_pre26[g] + pap[g]	0	26887.1 or 56773.1 or 54342.1 or 56773.1 or 56773.1	0	1000		Keratan sulfate biosynthesis			
S6T12g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	ksi_pre28[g] + paps[g] -> h[g] + ksi_pre29[g] + pap[g]	0	26887.1 or 56773.1 or 54342.1 or 56773.1 or 56773.1	0	1000		Keratan sulfate biosynthesis			
S6T13g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	ksi_pre31[g] + paps[g] -> h[g] + ksi_pre32[g] + pap[g]	0	26887.1 or 56773.1 or 54342.1 or 56773.1 or 56773.1	0	1000		Keratan sulfate biosynthesis			
S6T14g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	ksi_pre34[g] + paps[g] -> h[g] + ksi_pre35[g] + pap[g]	0	26887.1 or 56773.1 or 54342.1 or 56773.1 or 56773.1	0	1000		Keratan sulfate biosynthesis			
S6T15g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	ksi_pre36[g] + paps[g] -> h[g] + pap[g] + ksi[g]	0	53374.1 or 76969.1	0	1000		Keratan sulfate biosynthesis			
S6T16g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	ksii_core4_pre5[g] + paps[g] -> h[g] + ksii_core4_pre6[g] + pap[g]	0	26887.1 or 56773.1 or 54342.1 or 56773.1 or 56773.1	0	1000		Keratan sulfate biosynthesis			
S6T17g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	ksii_core4_pre8[g] + paps[g] -> h[g] + ksii_core4_pre9[g] + pap[g]	0	26887.1 or 56773.1 or 54342.1 or 56773.1 or 56773.1	0	1000		Keratan sulfate biosynthesis			
S6T18g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	ksii_core4_pre10[g] + paps[g] -> h[g] + pap[g] + ksii_core4[g]	0	53374.1 or 76969.1	0	1000		Keratan sulfate biosynthesis			
S6T19g	chondroitin 6-sulfotransferase, Golgi apparatus	2 paps[g] + cs_pre[g] -> 2 h[g] + 2 pap[g] + cs_c_d_e_pre1[g]	0	60322.1 or 53374.1	0	1000		Chondroitin / heparan sulfate biosynthesis			
S6T1g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	ksii_core2_pre5[g] + paps[g] -> h[g] + ksii_core2_pre6[g] + pap[g]	0	26887.1 or 56773.1 or 54342.1 or 56773.1 or 56773.1	0	1000		Keratan sulfate biosynthesis			
S6T20g	chondroitin 6-sulfotransferase, Golgi apparatus	paps[g] + cs_c_pre3[g] -> h[g] + cspg_c[g] + pap[g]	0	60322.1 or 53374.1	0	1000		Chondroitin / heparan sulfate biosynthesis			
S6T21g	chondroitin 6-sulfotransferase, Golgi apparatus	paps[g] + cs_d_pre4[g] -> h[g] + pap[g] + cs_d_pre5[g]	0	60322.1 or 53374.1	0	1000		Chondroitin / heparan sulfate biosynthesis			
S6T22g	chondroitin 6-sulfotransferase, Golgi apparatus	2 paps[g] + cs_a_b_e_pre1[g] -> 2 h[g] + 2 pap[g] + cs_e_pre2[g]	0	60322.1	0	1000		Chondroitin / heparan sulfate biosynthesis			
S6T23g	chondroitin 6-sulfotransferase, Golgi apparatus	paps[g] + cs_e_pre5a[g] -> h[g] + cspg_e[g] + pap[g]	0	60322.1	0	1000		Chondroitin / heparan sulfate biosynthesis			
S6T24g	chondroitin 6-sulfotransferase, Golgi apparatus	paps[g] + cs_e_pre4[g] -> h[g] + pap[g] + cs_e_pre5b[g]	0	60322.1 or 53374.1	0	1000		Chondroitin / heparan sulfate biosynthesis			
S6T25g	heparan sulfate 6-sulfotransferase, Golgi apparatus	3 paps[g] + hs_pre12[g] -> 3 h[g] + 3 pap[g] + hs_pre13[g]	0	50785.1 or 50787.1 or 50786.2 or 50786.1	0	1000		Chondroitin / heparan sulfate biosynthesis			
S6T2g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	ksii_core2_pre8[g] + paps[g] -> h[g] + ksii_core2_pre9[g] + pap[g]	0	26887.1 or 56773.1 or 54342.1 or 56773.1 or 56773.1	0	1000		Keratan sulfate biosynthesis			
S6T3g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	ksii_core2_pre10[g] + paps[g] -> h[g] + pap[g] + ksii_core2[g]	0	53374.1 or 76969.1	0	1000		Keratan sulfate biosynthesis			
S6T4g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	ksi_pre4[g] + paps[g] -> h[g] + ksi_pre5[g] + pap[g]	0	26887.1 or 56773.1 or 54342.1 or 56773.1 or 56773.1	0	1000		Keratan sulfate biosynthesis			
S6T5g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	ksi_pre7[g] + paps[g] -> h[g] + ksi_pre8[g] + pap[g]	0	26887.1 or 56773.1 or 54342.1 or 56773.1 or 56773.1	0	1000		Keratan sulfate biosynthesis			
S6T6g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	ksi_pre10[g] + paps[g] -> h[g] + ksi_pre11[g] + pap[g]	0	26887.1 or 56773.1 or 54342.1 or 56773.1 or 56773.1	0	1000		Keratan sulfate biosynthesis			

S6T7g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	ksi_pre13[g] + paps[g] -> h[g] + ksi_pre14[g] + pap[g]	0	26887.1 or 56773.1 or 54342.1 or 56773.1 or 56773.1	0	1000		Keratan sulfate biosynthesis			
S6T8g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	ksi_pre16[g] + paps[g] -> h[g] + ksi_pre17[g] + pap[g]	0	26887.1 or 56773.1 or 54342.1 or 56773.1 or 56773.1	0	1000		Keratan sulfate biosynthesis			
S6T9g	galactose/N-acetylglucosamine 6-O-sulfotransferase, Golgi apparatus	ksi_pre19[g] + paps[g] -> h[g] + ksi_pre20[g] + pap[g]	0	26887.1 or 56773.1 or 54342.1 or 56773.1 or 56773.1	0	1000		Keratan sulfate biosynthesis			
S6TASE10ly	galactose-6-sulfate sulfatase, lysosomal	h2o[l] + ksi_deg4[l] <=> h[l] + so4[l] + ksi_deg5[l]	1	50917.1 or 19025.1 or 12091.1 or 18010.1	-1000	1000		Keratan sulfate degradation			
S6TASE11ly	N-acetylglucosamine-6-sulfatase, lysosomal	h2o[l] + ksi_deg6[l] <=> h[l] + so4[l] + ksi_deg7[l]	1	75612.1	-1000	1000		Keratan sulfate degradation			
S6TASE12ly	N-acetylglucosamine-6-sulfatase, lysosomal	h2o[l] + ksi_deg9[l] <=> h[l] + so4[l] + ksi_deg10[l]	1	75612.1	-1000	1000		Keratan sulfate degradation			
S6TASE13ly	N-acetylglucosamine-6-sulfatase, lysosomal	h2o[l] + ksi_deg12[l] <=> h[l] + so4[l] + ksi_deg13[l]	1	75612.1	-1000	1000		Keratan sulfate degradation			
S6TASE14ly	N-acetylglucosamine-6-sulfatase, lysosomal	h2o[l] + ksi_deg15[l] <=> h[l] + so4[l] + ksi_deg16[l]	1	75612.1	-1000	1000		Keratan sulfate degradation			
S6TASE15ly	N-acetylglucosamine-6-sulfatase, lysosomal	h2o[l] + ksi_deg18[l] <=> h[l] + so4[l] + ksi_deg19[l]	1	75612.1	-1000	1000		Keratan sulfate degradation			
S6TASE16ly	N-acetylglucosamine-6-sulfatase, lysosomal	h2o[l] + ksi_deg21[l] <=> h[l] + so4[l] + ksi_deg22[l]	1	75612.1	-1000	1000		Keratan sulfate degradation			
S6TASE17ly	N-acetylglucosamine-6-sulfatase, lysosomal	h2o[l] + ksi_deg24[l] <=> h[l] + so4[l] + ksi_deg25[l]	1	75612.1	-1000	1000		Keratan sulfate degradation			
S6TASE18ly	N-acetylglucosamine-6-sulfatase, lysosomal	h2o[l] + ksi_deg27[l] <=> h[l] + so4[l] + ksi_deg28[l]	1	75612.1	-1000	1000		Keratan sulfate degradation			
S6TASE19ly	N-acetylglucosamine-6-sulfatase, lysosomal	h2o[l] + ksi_deg30[l] <=> h[l] + so4[l] + ksi_deg31[l]	1	75612.1	-1000	1000		Keratan sulfate degradation			
S6TASE1ly	N-acetylglucosamine-6-sulfatase, lysosomal	h2o[l] + hs[l] <=> h[l] + so4[l] + hs_deg1[l]	1	75612.1	-1000	1000		Heparan sulfate degradation			
S6TASE20ly	N-acetylglucosamine-6-sulfatase, lysosomal	h2o[l] + ksi_deg33[l] <=> h[l] + so4[l] + ksi_deg34[l]	1	75612.1	-1000	1000		Keratan sulfate degradation			
S6TASE21ly	N-acetylglucosamine-6-sulfatase, lysosomal	h2o[l] + ksi_deg36[l] <=> h[l] + so4[l] + ksi_deg37[l]	1	75612.1	-1000	1000		Keratan sulfate degradation			
S6TASE22ly	galactose-6-sulfate sulfatase, lysosomal	h2o[l] + ksii_core2_deg1[l] <=> h[l] + so4[l] + ksii_core2_deg2[l]	1	50917.1 or 19025.1 or 12091.1 or 18010.1	-1000	1000		Keratan sulfate degradation			
S6TASE23ly	N-acetylglucosamine-6-sulfatase, lysosomal	h2o[l] + ksii_core2_deg3[l] <=> h[l] + so4[l] + ksii_core2_deg4[l]	1	75612.1	-1000	1000		Keratan sulfate degradation			
S6TASE24ly	N-acetylglucosamine-6-sulfatase, lysosomal	h2o[l] + ksii_core2_deg6[l] <=> h[l] + so4[l] + ksii_core2_deg7[l]	1	75612.1	-1000	1000		Keratan sulfate degradation			
S6TASE25ly	galactose-6-sulfate sulfatase, lysosomal	h2o[l] + ksii_core4_deg1[l] <=> h[l] + so4[l] + ksii_core4_deg2[l]	1	50917.1 or 19025.1 or 12091.1 or 18010.1	-1000	1000		Keratan sulfate degradation			
S6TASE26ly	N-acetylglucosamine-6-sulfatase, lysosomal	h2o[l] + ksii_core4_deg3[l] <=> h[l] + so4[l] + ksii_core4_deg4[l]	1	75612.1	-1000	1000		Keratan sulfate degradation			
S6TASE2ly	N-acetylglucosamine-6-sulfatase, lysosomal	h2o[l] + hs_deg5[l] <=> h[l] + so4[l] + hs_deg6[l]	1	75612.1	-1000	1000		Heparan sulfate degradation			
S6TASE3ly	N-acetylglucosamine-6-sulfatase, lysosomal	h2o[l] + hs_deg11[l] <=> h[l] + so4[l] + hs_deg12[l]	1	75612.1	-1000	1000		Heparan sulfate degradation			
S6TASE4ly	N-acetylgalactosamine-6-sulfatase, lysosomal	h2o[l] + cs_c[l] <=> h[l] + so4[l] + cs_c_deg1[l]	1	50917.1 or 19025.1 or 12091.1 or 18010.1	-1000	1000		Chondroitin sulfate degradation			
S6TASE5ly	N-acetylgalactosamine-6-sulfatase, lysosomal	h2o[l] + cs_c_deg3[l] <=> h[l] + so4[l] + cs_c_deg4[l]	1	50917.1 or 19025.1 or 12091.1 or 18010.1	-1000	1000		Chondroitin sulfate degradation			
S6TASE6ly	N-acetylgalactosamine-6-sulfatase, lysosomal	h2o[l] + cs_d[l] <=> h[l] + so4[l] + cs_d_deg1[l]	1	50917.1 or 19025.1 or 12091.1 or 18010.1	-1000	1000		Chondroitin sulfate degradation			
S6TASE7ly	N-acetylgalactosamine-6-sulfatase, lysosomal	h2o[l] + cs_d_deg4[l] <=> h[l] + so4[l] + cs_d_deg5[l]	1	50917.1 or 19025.1 or 12091.1 or 18010.1	-1000	1000		Chondroitin sulfate degradation			
S6TASE8ly	N-acetylgalactosamine-6-sulfatase, lysosomal	h2o[l] + cs_e_deg1[l] <=> h[l] + so4[l] + cs_e_deg2[l]	1	50917.1 or 19025.1 or 12091.1 or 18010.1	-1000	1000		Chondroitin sulfate degradation			
S6TASE9ly	N-acetylgalactosamine-6-sulfatase, lysosomal	h2o[l] + cs_e_deg5[l] <=> h[l] + so4[l] + cs_e_deg6[l]	1	50917.1 or 19025.1 or 12091.1 or 18010.1	-1000	1000		Chondroitin sulfate degradation			
SACCD3m	saccharopine dehydrogenase (NADP, L-lysine forming), mitochondrial	h[m] + nadph[m] + akg[m] + lys-L[m] -> h2o[m] + nadp[m] + saccrp-L[m]	0	30956.1	0	1000		Lysine Metabolism			
SACCD4m	saccharopine dehydrogenase (NAD, L-glutamate forming), mitochondrial	h2o[m] + nadp[m] + saccrp-L[m] -> h[m] + nadph[m] + glu-L[m] + L2aadp6sa[m]	0	30956.1	0	1000		Lysine Metabolism			
SADT	sulfate adenylyltransferase	atp[c] + h[c] + so4[c] -> ppi[c] + aps[c]	0	23972.1 or 23971.1	0	1000		Nucleotides			
SALMCOM	S-Adenosyl-L-methionine:catechol O-methyltransferase	amet[c] + nrpphr[c] -> h[c] + ahcys[c] + normete-L[c]	0	12846.1 or 69156.1 or 12846.2	0	1000		Tyrosine metabolism			
SALMCOM2	S-Adenosyl-L-methionine:catechol O-methyltransferase	amet[c] + adrnl[c] -> h[c] + ahcys[c] + mepi[c]	0	69156.1	0	1000		Tyrosine metabolism			
SAMHISTA	S-Adenosyl-L-methionine:histamine N-tele-methyltransferase	amet[c] + hista[c] -> h[c] + ahcys[c] + mhista[c]	0	140483.1	0	1000		Histidine Metabolism			
SARCOXp	sarcosine oxidase, peroxisomal	o2[x] + h2o[x] + sarcs[x] -> h2o2[x] + gly[x] + fald[x]	0	19193.1	0	1000		Glycine, Serine, and Threonine Metabolism			
SARCStex	Sarcosine transport (extracellular to cytosol)	sarcs[e] -> sarcs[c]	0		0	1000		Transport, Extracellular			
SARCStm	Sarcosine transport (mitochondrial)	sarcs[c] -> sarcs[m]	0		0	1000		Transport, Mitochondrial			
SARCStp	Sarcosine transport (peroxisomal)	sarcs[c] -> sarcs[x]	0		0	1000		Transport, Peroxisomal			
SARDHm	Sarcosine dehydrogenase (m)	fad[m] + sarcs[m] + thf[m] -> fadh2[m] + gly[m] + mlthf[m]	0	192166.1	0	1000		Urea cycle/amino group metabolism			
SBPP1er	sphingoid base-phosphate phosphatase (sphinganine 1-phosphatase), endoplasmic reticulum	h2o[r] + sph1p[r] -> pi[r] + sphgn[r]	0	81535.1	0	1000		Sphingolipid Metabolism			
SBPP3er	sphingoid base-phosphate phosphatase (sphinganine 1-phosphatase), endoplasmic reticulum	h2o[r] + sphs1p[r] -> pi[r] + sphings[r]	0	81535.1	0	1000		Sphingolipid Metabolism			
SBTD_D2	D-sorbitol dehydrogenase (D-fructose producing)	nad[c] + sbt-D[c] -> h[c] + nadh[c] + fru[c]	0	20322.1	0	1000		Fructose and Mannose Metabolism			
SBTR	D-sorbitol reductase	h[c] + nadph[c] + glc-D[c] -> nadp[c] + sbt-D[c]	0	110198.1 or 58810.2 or 11677.1 or 58810.1	0	1000		Fructose and Mannose Metabolism			
SBTlu	diffusion of sorbitol into the enterocytes	sbt-D[u] -> sbt-D[c]	0		0	1000	3	Transport, Lumen	Sareen S. Gropper, jack L. Smith, James L. Groff (2009) Wadaworth cengage learning, Advanced nutrition and human metabolism, 5th edition, page 68-74. PMID: 20522896, William F. Ganong Review of medical physiology 12th edition Lange publication pages 384-393		
SBTt	D-sorbitol transport via diffusion (extracellular to cytosol)	sbt-D[e] <=> sbt-D[c]	1		-1000	1000	2	Transport, Extracellular	Sareen S. Gropper, jack L. Smith, James L. Groff (2009) Wadaworth cengage learning, Advanced nutrition and human metabolism, 5th edition, page 68-74. PMID: 20522896, William F. Ganong Review of medical physiology 12th edition Lange publication pages 384-393	Sorbitol is uptaken via diffusion in lumen	
SCP21x	Sterol carrier protein 2	phytcoa[c] <=> phytcoa[x]	1	20280.1	-1000	1000		Transport, Peroxisomal			
SCP22x	Sterol carrier protein 2	dmnoncoa[c] <=> dmnoncoa[x]	1	20280.1	-1000	1000		Transport, Peroxisomal			
SCP2x	peroxisomal thiolase 2	coa[x] + dhcholoylcoa[x] -> dgcholcoa[x] + ppcoa[x]	0	20280.1	0	1000		Bile Acid Biosynthesis			
SCP3x	peroxisomal thiolase 2	coa[x] + o2[x] + dhcholestancoa[x] -> h2o[x] + dcholcoa[x] + ppcoa[x]	0	20280.1	0	1000		Bile Acid Biosynthesis			
SCPx	peroxisomal thiolase 2	coa[x] + cholcoaone[x] -> cholcoa[x] + ppcoa[x]	0	20280.1	0	1000		Bile Acid Biosynthesis			
SEAHCYSHYD	Se-Adenosylselenohomocysteine hydrolase	h2o[c] + seahcys[c] -> adn[c] + selhcys[c]	0	74340.1 or 229709.1 or 229709.2 or 269378.1	0	1000		Selenoamino acid metabolism			
SEAHCYStn	Se-adenosyl-seleno-L-homocysteine nuclear transport	seahcys[c] <=> seahcys[n]	1		-1000	1000		Selenoamino acid metabolism			
SEASMETtn	Se-adenosyl-seleno-L-methionine nuclear transport	seasmet[c] <=> seasmet[n]	1		-1000	1000		Selenoamino acid metabolism			
SELADT	selenate adenylyltransferase	atp[c] + h[c] + sel[c] -> ppi[c] + adsel[c]	0	23972.1 or 23971.1	0	1000		Selenoamino acid metabolism			
SELCYSLY	selenocysteine lyase	dtt[c] + selcys[c] -> h[c] + ala-L[c] + dttOX[c] + seln[c]	0	50880.1	0	1000		Selenoamino acid metabolism			
SELCYSLY2	selenocysteine lyase	pdx5p[c] + selcys[c] -> h[c] + ala-L[c] + pydx5p[c] + seln[c]	0	50880.1	0	1000		Selenoamino acid metabolism			
SELCYSTGL	selanocystathionine g-lyase	h2o[c] + selcyst[c] -> nh4[c] + 2obut[c] + selcys[c]	0	107869.1 or 107869.2	0	1000		Selenoamino acid metabolism			
SELCYSTS	selanocystathionine beta-synthase	ser-L[c] + selhcys[c] -> h2o[c] + selcyst[c]	0	12411.1	0	1000		Selenoamino acid metabolism			
SELMETAT	selenomethionine adenosyltransferase	h2o[c] + atp[c] + selmeth[c] -> pi[c] + ppi[c] + seasmet[c]	0	232087.1 and 108645.1 or 108645.2 and 232087.1 or 11720.1	0	1000		Selenoamino acid metabolism			
SELNPS	Selenophosphate synthase	h2o[c] + atp[c] + seln[c] -> pi[c] + amp[c] + selnp[c]	0	109079.1 or 20768.1	0	1000		Selenoamino acid metabolism			
SELt4_3	selenate transport via sodium symport	3 na1[e] + sel[e] <=> 3 na1[c] + sel[c]	1	55961.1	-1000	1000		Transport, Extracellular			
SERALANaEx	L-alanine/L-serine Na-dependent exchange (Ser-L in)	na1[e] + ala-L[c] + ser-L[e] -> na1[c] + ala-L[e] + ser-L[c]	0	20514.1 or 55963.1	0	1000		Transport, Extracellular			
SERASNNaEx	L-serine/L-asparagine Na-dependent exchange (Ser-L in)	na1[e] + asn-L[c] + ser-L[e] -> na1[c] + asn-L[e] + ser-L[c]	0	20514.1	0	1000		Transport, Extracellular			
SERATB0tc	transport of L-Serine into the intestinal cells by ATB0 transporter	2 na1[u] + cl[u] + ser-L[u] -> 2 na1[c] + cl[c] + ser-L[c]	0	56774.1	0	1000	3	Transport, Lumen	PMID:18195088	ATB0 is both sodium and chloride coupled, with reaction stoichiometry 2Na+:1cl:1amino acid. The transporter is localted in the intestine, has a broad substrate specificity (both neutral and cationic amino acids), but is not involved in the transport of aspartate, glutamate and proline (PMID:18195088).	
SERB0AT1tc	transport of L-Serine by the apical neutral amino acid transporters in kidney and intestine	na1[u] + ser-L[u] -> na1[c] + ser-L[c]	0	(70008.1 or (74338.1 and 57394.1))	0	1000	3	Transport, Lumen	PMID: 19472175, PMID: 15804236, PMID: 18400692	transports all the neutral amino acids with preference for methionine, leucine and valine. Reaction stoichiometry is 1:1. Requires heterodimerization with collectrin protein for increased affinity. Found in kidney and intestine, however also reported to be expressed in skin. Requires association with ACE2 for expression in intestine but with collectrin for expression in kidney.	3.4.17.23
SERCYSNaEx	L-serine/L-cysteine Na-dependent exchange (Ser-L in)	na1[e] + cys-L[c] + ser-L[e] -> na1[c] + cys-L[e] + ser-L[c]	0	20514.1 or 55963.1	0	1000		Transport, Extracellular			
SERDGLNexR	D-Serine/Glutamine reversible exchange	gln-L[c] + ser-D[e] <=> gln-L[e] + ser-D[c]	1	53896.1 or 17254.1	-1000	1000		Transport, Extracellular			
SERDGLYexR	D-Serine/Glycine reversible exchange	gly[c] + ser-D[e] <=> gly[e] + ser-D[c]	1	53896.1 or 17254.1	-1000	1000		Transport, Extracellular			
SERGLNNaEx	L-serine/L-glutamine Na-dependent exchange (Ser-L in)	na1[e] + gln-L[c] + ser-L[e] -> na1[c] + gln-L[e] + ser-L[c]	0	20514.1	0	1000		Transport, Extracellular			
SERGLNexR	L-Serine/Glutamine reversible exchange	gln-L[c] + ser-L[e] <=> gln-L[e] + ser-L[c]	1	53896.1 or 17254.1	-1000	1000		Transport, Extracellular			
SERGLYALAGLYt	SERGLYALAGLYt	Ser_Gly_Ala_X_Gly[l] -> Ser_Gly_Ala_X_Gly[r]	0		0	1000	0	Transport, Endoplasmic Reticular			
SERGLYexR	L-Serine/Glycine reversible exchange	gly[c] + ser-L[e] <=> gly[e] + ser-L[c]	1	53896.1 or 17254.1	-1000	1000		Transport, Extracellular			
SERHL	L-Serine hydro-lyase	ser-L[c] -> h2o[c] + 2amac[c]	0	231691.1	0	1000		Glycine, Serine, and Threonine Metabolism			
SERILELAT2tc	transport of L-Serine into the cell and efflux of L-Isoleucine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	ile-L[c] + ser-L[e] -> ile-L[e] + ser-L[c]	0	(20539.1 and 17254.1)	0	1000	3	Transport, Extracellular	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s00420000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	higer affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of memebranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for traficking of the complex to the mebrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s00420000274).	
SERLYSNaex	Serine/Lysine Na-dependent exchange (Ser in)	na1[e] + ser-L[e] + lys-L[c] -> na1[c] + ser-L[c] + lys-L[e]	0	20540.1 and 20532.1	0	1000		Transport, Extracellular			

SERPHELAT2tc	transport of L-Serine into the cell and efflux of L-Phenylalanine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	phe-L[c] + ser-L[e] -> phe-L[e] + ser-L[c]	0	(20539.1 and 17254.1)	0	1000	3	Transport, Extracellular	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s00420000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	higer affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of memebranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for traficking of the complex to the mebrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s00420000274).	
SERPT	serine C-palmitoyltransferase	h[c] + ser-L[c] + pmtcoa[c] -> co2[c] + 3dsphgn[c] + coa[c]	0	20773.1 and 268656.1	0	1000		Sphingolipid Metabolism			
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]	0	20514.1 or 55963.1	0	1000		Transport, Extracellular			
SERt4	L-serine via sodium symport	na1[e] + ser-L[e] -> na1[c] + ser-L[c]	0	105727.1 or 67760.1 or 69354.1 or 56774.1	0	1000		Transport, Extracellular			
SERtN1	Serine transport (Na, H coupled)	h[c] + 2 na1[e] + ser-L[e] <=> h[e] + 2 na1[c] + ser-L[c]	1	209837.1	-1000	1000		Transport, Extracellular			
SERtp	L-serine transport, peroxisomal	ser-L[c] <=> ser-L[x]	1		-1000	1000		Transport, Peroxisomal			
SFGTH	S-Formylglutathione hydralase	h2o[c] + Sfglutth[c] <=> h[c] + for[c] + gthrd[c]	1	13885.1	-1000	1000		Tyrosine metabolism			
SGALSIDEtg	sgalside_hs intracellular transport	sgalside_hs[c] <=> sgalside_hs[g]	1		-1000	1000		Transport, Golgi Apparatus			
SGALSIDEtl	sgalside_hs intracellular transport	sgalside_hs[c] <=> sgalside_hs[l]	1		-1000	1000		Transport, Lysosomal			
SGPL11r	Sphingosine-1-phosphate lyase 1	sph1p[r] -> ethamp[r] + hxdcal[r]	0	20397.1	0	1000		Sphingolipid Metabolism			
SGPL12r	Sphingosine-1-phosphate lyase	h2o[r] + sphs1p[r] -> h[r] + ethamp[r] + hdca[r]	0	20397.1	0	1000		Sphingolipid Metabolism			
SIAASE	sialidase	2 h2o[c] + s2l2n2m2mn[c] -> 2 acnam[c] + l2n2m2mn[c]	0	241159.1 or 23956.1	0	1000		N-Glycan Degradation			
SIAASE2ly	sialidase, lysosomal	h2o[l] + ksi_deg3[l] -> acnam[l] + ksi_deg4[l]	0	50917.1 or 19025.1 or 12091.1 or 18010.1	0	1000		Keratan sulfate degradation			
SIAASE3ly	sialidase, lysosomal	h2o[l] + ksii_core2[l] -> acnam[l] + ksii_core2_deg1[l]	0	50917.1 or 19025.1 or 12091.1 or 18010.1	0	1000		Keratan sulfate degradation			
SIAASE4ly	sialidase, lysosomal	h2o[l] + ksii_core4[l] -> acnam[l] + ksii_core4_deg1[l]	0	50917.1 or 19025.1 or 12091.1 or 18010.1	0	1000		Keratan sulfate degradation			
SIAASEly	sialidase, lysosomal	2 h2o[l] + s2l2n2m2mn[l] -> 2 acnam[l] + l2n2m2mn[l]	0	50917.1 or 19025.1 or 12091.1 or 18010.1	0	1000		N-Glycan Degradation			
SIAT4Bg	Beta-galactoside alpha-2,3-sialyltransferase, Golgi apparatus	galgbside_hs[g] + cmpacna[g] -> h[g] + cmp[g] + acngalgbside_hs[g]	0	20444.1	0	1000		Sphingolipid Metabolism			
SIAT9g	Lactosylceramide alpha-2,3-sialyltransferase, Golgi apparatus	galgluside_hs[g] + cmpacna[g] -> h[g] + cmp[g] + gm3_hs[g]	0	20454.1	0	1000		Sphingolipid Metabolism			
SLCBK1	sphingolipid long chain base kinase (sphinganine)	atp[c] + sphgn[c] -> adp[c] + h[c] + sph1p[c]	0	56632.1	0	1000		Sphingolipid Metabolism			
SLDt	L-sulfolactate transport (cytosol to extracellular)	sl-L[c] -> sl-L[e]	0		0	1000		Cysteine Metabolism			
SLDx	L-sulfolactate dehydrogenase (NAD+)	nad[c] + sl-L[c] <=> h[c] + nadh[c] + 3spyr[c]	1	76668.1 or 17449.1	-1000	1000		Cysteine Metabolism			
SLDxm	L-sulfolactate dehydrogenase (NAD+), mitochondrial	nad[m] + sl-L[m] <=> h[m] + nadh[m] + 3spyr[m]	1	17448.1	-1000	1000		Cysteine Metabolism			
SMPD3g	sphingomyelin phosphodiesterase 3, neutral membrane (neutral sphingomyelinase II)	h2o[g] + sphmyln_hs[g] -> h[g] + crm_hs[g] + cholp[g]	0	58994.1 or 58994.2	0	1000		Sphingolipid Metabolism			
SMPD3l	sphingomyelin phosphodiesterase 3, neutral membrane (neutral sphingomyelinase II)	h2o[l] + sphmyln_hs[l] -> h[l] + crm_hs[l] + cholp[l]	0	58994.1 or 58994.2	0	1000		Sphingolipid Metabolism			
SMPD4	sphingomyelinase	h2o[c] + spc_hs[c] -> h[c] + cholp[c] + sphings[c]	0		0	1000		Sphingolipid Metabolism			
SMS	Sphingomyelin synthase (homo sapiens)	pchol_hs[c] + crm_hs[c] -> dag_hs[c] + sphmyln_hs[c]	0	208449.1	0	1000		Sphingolipid Metabolism			
SO4CLtex2	sulfate transport via chloride countertransport (2:1)	cl[c] + 2 so4[e] -> cl[e] + 2 so4[c]	0	171429.1 or 171429.2 or 171429.3	0	1000		Transport, Extracellular			
SO4HCOtex	sulfate transport via bicarbonate countertransport	2 hco3[c] + so4[e] -> 2 hco3[e] + so4[c]	0	13487.1 or 224661.1 or 231583.1 or 208890.1 or 224661.2 or 320718.1 or 13521.1 or 231583.2 or 208890.2 or 231583.3 or 268512.1 or 320718.2	0	1000		Transport, Extracellular			
SO4OXAtex2	sulfate transport via oxalate countertransport (2:1)	oxa[c] + 2 so4[e] -> oxa[e] + 2 so4[c]	0	171429.1 or 171429.2 or 171429.3	0	1000		Transport, Extracellular			
SO4t4_2	sulfate transport via sodium symport	2 na1[e] + so4[e] <=> 2 na1[c] + so4[c]	1	243755.1	-1000	1000		Transport, Extracellular			
SO4t4_3	sulfate transport via sodium symport	3 na1[e] + so4[e] <=> 3 na1[c] + so4[c]	1	55961.1	-1000	1000		Transport, Extracellular			
SO4tl	sulfate transport intracellular	so4[l] <=> so4[c]	1		-1000	1000		Transport, Lysosomal			
SOAT11	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1	R1coa_hs[c] + chsterol[c] -> coa[c] + xolest_hs[c]	0	20652.1	0	1000		Cholesterol Metabolism			
SOAT11r	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1	chsterol[r] + R1coa_hs[r] -> coa[r] + xolest_hs[r]	0	20652.1	0	1000		Cholesterol Metabolism			
SOAT12	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1	R2coa_hs[c] + chsterol[c] -> coa[c] + xolest_hs[c]	0	20652.1	0	1000		Cholesterol Metabolism			
SOAT12r	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1	chsterol[r] + R2coa_hs[r] -> coa[r] + xolest_hs[r]	0	20652.1	0	1000		Cholesterol Metabolism			
SOProd	SOProd	o2[m] + e-[m] -> o2s[m]	0		0	1000		Oxidative Phosphorylation			
SPC_HSt	sphingosylphosphorylcholine transport (diffusion)	spc_hs[c] <=> spc_hs[e]	1		-1000	1000		Transport, Extracellular			
SPH1Pte	sph1p transport	sph1p[c] <=> sph1p[e]	1		-1000	1000		Transport, Extracellular			
SPH1Ptr	sph1p intracellular transport	sph1p[c] <=> sph1p[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
SPHGNtr	sphinganine intracellular transport	sphgn[r] <=> sphgn[c]	1		-1000	1000		Transport, Endoplasmic Reticular			
SPHINGStl	sphingosine intracellular transport	sphings[c] <=> sphings[l]	1		-1000	1000		Transport, Lysosomal			
SPHINGStr	sphingosine intracellular transport	sphings[c] <=> sphings[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
SPHK21c	sphingosine kinase 2	atp[c] + sphings[c] -> adp[c] + h[c] + sphs1p[c]	0	56632.1	0	1000		Sphingolipid Metabolism			
SPHMDAc	sphingomyelin deacylase	h2o[c] + sphmyln_hs[c] -> Rtotal[c] + spc_hs[c]	0		0	1000		Sphingolipid Metabolism			
SPHMYLNtg	sphingomyelin intracellular transport	sphmyln_hs[c] <=> sphmyln_hs[g]	1		-1000	1000		Transport, Golgi Apparatus			
SPHMYLNtl	sphingomyelin intracellular transport	sphmyln_hs[c] <=> sphmyln_hs[l]	1		-1000	1000		Transport, Lysosomal			
SPHS1Pte	sphingosine-1-phosphate transport	sphs1p[c] <=> sphs1p[e]	1		-1000	1000		Transport, Extracellular			
SPHS1Ptr	sphingosine-1-phosphate transport	sphs1p[c] <=> sphs1p[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
SPMDOX	Spermidine:(acceptor) oxidoreductase	h2o[c] + o2[c] + spmd[c] -> 13dampp[c] + h2o2[c] + 4abutn[c]	0		0	1000		beta-Alanine metabolism			
SPMS	spermidine synthase	ametam[c] + ptrc[c] -> h[c] + 5mta[c] + spmd[c]	0	20810.1	0	1000		Urea cycle/amino group metabolism			
SPODM	superoxide dismutase	2 h[c] + 2 o2s[c] -> o2[c] + h2o2[c]	0	20655.1	0	1000		ROS Detoxification			
SPODMe	superoxide dismutase, extracellular	2 h[e] + 2 o2s[e] -> h2o2[e] + o2[e]	0	20657.1	0	1000		ROS Detoxification			
SPODMm	superoxide dismutase	2 h[m] + 2 o2s[m] -> o2[m] + h2o2[m]	0	20656.1	0	1000		ROS Detoxification			
SPODMn	superoxide dismutase, nuclear	2 h[n] + 2 o2s[n] -> h2o2[n] + o2[n]	0	20655.1	0	1000		ROS Detoxification			
SPODMx	superoxide dismutase, peroxisome	2 h[x] + 2 o2s[x] -> o2[x] + h2o2[x]	0	20655.1	0	1000		ROS Detoxification			
SPR	sepiapterin reductase	2 h[c] + 2 nadph[c] + 6pthp[c] -> 2 nadp[c] + thbpt[c]	0	20751.1	0	1000		Tetrahydrobiopterin			
SPRMS	spermine synthase	ametam[c] + spmd[c] -> h[c] + sprm[c] + 5mta[c]	0	20603.1	0	1000		Urea cycle/amino group metabolism			
SPRn	sepiapterin reductase, nuclear	2 h[n] + 6pthp[n] + 2 nadph[n] -> 2 nadp[n] + thbpt[n]	0	20751.1	0	1000		Tetrahydrobiopterin			
SPTix	serine-pyruvate aminotransferase (irreversible), peroxisomal	pyr[x] + ser-L[x] -> ala-L[x] + hpyr[x]	0	11611.1	0	1000		Glycine, Serine, and Threonine Metabolism			
SQLEr	Squalene epoxidase, endoplasmic reticular (NADP)	o2[r] + h[r] + nadph[r] + sql[r] -> h2o[r] + nadp[r] + Ssq23epx[r]	0	20775.1	0	1000		Cholesterol Metabolism			
SQLSr	Squalene synthase	h[r] + nadph[r] + 2 frdp[r] -> nadp[r] + 2 ppi[r] + sql[r]	0	14137.1	0	1000		Cholesterol Metabolism			
SR5AR2r	3-oxo-5-alpha-steroid 4-dehydrogenase	h[r] + nadph[r] + andrstndn[r] -> nadp[r] + andrstandn[r]	0	94224.1 or 78925.1	0	1000		Steroid Metabolism			
SR5ARr	3-oxo-5-alpha-steroid 4-dehydrogenase	h[r] + nadph[r] + tststerone[r] -> 5adtststerone[r] + nadp[r]	0	94224.1 or 78925.1	0	1000		Steroid Metabolism			
SRTN23OX	5-Hydroxytryptamine:oxygen 2,3-dioxygenase (indole-decyclizing)	o2[c] + srtn[c] -> f5hoxkyn[c]	0	15930.1	0	1000		Tryptophan metabolism			
SRTNACT	Acetyl-CoA:aralkylamine N-acetyltransferase	srtn[c] + accoa[c] -> h[c] + coa[c] + Nacsertn[c]	0	11298.1	0	1000		Tryptophan metabolism			
SRTNMTX	S-Adenosyl-L-methionine:amine N-methyltransferase (srtn)	amet[c] + srtn[c] -> h[c] + ahcys[c] + nmthsrtn[c]	0	21743.1	0	1000	2	Tryptophan metabolism			
SRTNt6_2_r	Serotonin reversible transport in via sodium symport/potassium antiport (1:2)	2 na1[e] + 2 k[c] + srtn[e] <=> 2 na1[c] + srtn[c] + 2 k[e]	1	15567.1	-1000	1000		Transport, Extracellular			
SRTNtu	Serotonin uniport	srtn[e] <=> srtn[c]	1	20518.1 or 20517.1 or 20518.2	-1000	1000		Transport, Extracellular			
SSALxm	succinate-semialdehyde dehydrogenase (NAD) reversible (mitochondrial)	h2o[m] + nad[m] + sucsal[m] -> 2 h[m] + nadh[m] + succ[m]	0	214579.1 or 214579.2	0	1000		Glutamate metabolism			
ST3GAL21g	CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransferase, Golgi apparatus	ga1_hs[g] + cmpacna[g] -> h[g] + cmp[g] + gm1b_hs[g]	0	20444.1	0	1000		Sphingolipid Metabolism			
ST3GAL22g	CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransferase, Golgi apparatus	gm1_hs[g] + cmpacna[g] -> h[g] + cmp[g] + gd1a_hs[g]	0	20444.1	0	1000		Sphingolipid Metabolism			
ST3GAL23g	CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransferase, Golgi apparatus	gd1b_hs[g] + cmpacna[g] -> h[g] + cmp[g] + gt1b_hs[g]	0	20444.1	0	1000		Sphingolipid Metabolism			
ST3GAL61g	Type 2 lactosamine alpha-2,3-sialyltransferase	gal14acglcgalgluside_hs[g] + cmpacna[g] -> h[g] + cmp[g] + acngal14acglcgalgluside_hs[g]	0	54613.1	0	1000		Blood Group Biosynthesis			
ST3GAL62g	Type 2 lactosamine alpha-2,3-sialyltransferase	galacglcgal14acglcgalgluside_hs[g] + cmpacna[g] -> h[g] + acngalacglcgal14acglcgalgluside_hs[g] + cmp[g]	0	54613.1	0	1000		Blood Group Biosynthesis			
ST6GALNAC21	Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	cmpacna[g] + acngalgbside_hs[g] -> h[g] + acn13acngalgbside_hs[g] + cmp[g]	0	20446.1	0	1000		Sphingolipid Metabolism			
ST6GALNAC22	Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	cmpacna[g] + acngalgbside_hs[g] -> h[g] + acn23acngalgbside_hs[g] + cmp[g]	0	20446.1	0	1000		Sphingolipid Metabolism			
ST6GALNAC23	Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	ga2_hs[g] + cmpacna[g] -> h[g] + gm2a_hs[g] + cmp[g]	0	20446.1	0	1000		Sphingolipid Metabolism			
ST6GALNAC24	Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	gm1a_hs[g] + cmpacna[g] -> h[g] + cmp[g] + gd1b2_hs[g]	0	20446.1	0	1000		Sphingolipid Metabolism			
ST6GALNAC25	Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	cmpacna[g] + gd1a_hs[g] -> h[g] + cmp[g] + gt1alpha_hs[g]	0	50935.1	0	1000		Sphingolipid Metabolism			
ST6GALNAC26	Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	cmpacna[g] + gt1alpha_hs[g] -> h[g] + cmp[g] + gq1balpha_hs[g]	0	20446.1	0	1000		Sphingolipid Metabolism			
ST6GALNAC27	Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	gt1c_hs[g] + cmpacna[g] -> h[g] + cmp[g] + gq1c_hs[g]	0	20446.1	0	1000		Sphingolipid Metabolism			
ST6GALNAC28	Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	cmpacna[g] + gq1c_hs[g] -> h[g] + cmp[g] + gp1c_hs[g]	0	20446.1	0	1000		Sphingolipid Metabolism			
ST6GALNAC31	Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 3	cmpacna[g] + gm1b_hs[g] -> h[g] + cmp[g] + gd1a_hs[g]	0	50935.1 or 26938.1 or 20447.1	0	1000	2	Sphingolipid Metabolism			
ST6GALNAC61	sialytransferase 7 ((alpha-N-acetylneuraminyl 2,3-betagalactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialytransferase) F	cmpacna[g] + gd1alpha_hs[g] -> h[g] + cmp[g] + gt1alpha_hs[g]	0	20446.1	0	1000		Sphingolipid Metabolism			
ST6GALNAC62	sialytransferase 7 ((alpha-N-acetylneuraminyl 2,3-betagalactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialytransferase) F	cmpacna[g] + gt1b_hs[g] -> h[g] + cmp[g] + gq1balpha_hs[g]	0	50935.1	0	1000		Sphingolipid Metabolism			

ST8SIA11	Beta-galactoside alpha-2,3-sialyltransferase	cmpacna[g] + acngalgbside_hs[g] -> h[g] + acnacngalgbside_hs[g] + cmp[g]	0	20449.1	0	1000		Sphingolipid Metabolism			
ST8SIA12	Beta-galactoside alpha-2,3-sialyltransferase	cmpacna[g] + gm3_hs[g] -> h[g] + cmp[g] + gd3_hs[g]	0	20449.1	0	1000		Sphingolipid Metabolism			
ST8SIA51g	Beta-galactoside alpha-2,3-sialyltransferase	cmpacna[g] + gd3_hs[g] -> h[g] + cmp[g] + gt3_hs[g]	0	225742.1	0	1000		Sphingolipid Metabolism			
ST8SIA52g	Beta-galactoside alpha-2,3-sialyltransferase	cmpacna[g] + gt1b_hs[g] -> h[g] + cmp[g] + gq1b_hs[g]	0	225742.1	0	1000		Sphingolipid Metabolism			
ST8SIA53g	Beta-galactoside alpha-2,3-sialyltransferase	cmpacna[g] + gd1a_hs[g] -> h[g] + cmp[g] + gt1a_hs[g]	0	225742.1	0	1000		Sphingolipid Metabolism			
ST8SIA54g	Beta-galactoside alpha-2,3-sialyltransferase	cmpacna[g] + gm1b_hs[g] -> h[g] + cmp[g] + gd1c_hs[g]	0	225742.1	0	1000		Sphingolipid Metabolism			
ST8SIA55g	Beta-galactoside alpha-2,3-sialyltransferase	cmpacna[g] + gq1c_hs[g] -> h[g] + cmp[g] + gp1calpha_hs[g]	0	225742.1	0	1000		Sphingolipid Metabolism			
ST8SIA56g	Alpha-2,8-sialyltransferase 8E	cmpacna[g] + acngal14acglcgalgluside_hs[g] -> h[g] + acnacngal14acglcgalgluside_hs[g] + cmp[g]	0	225742.1	0	1000		Blood Group Biosynthesis			
STCOAtx	fatty acid intracellular transport	stcoa[c] <=> stcoa[x]	1		-1000	1000		Transport, Peroxisomal			
STN_ANTIGENt	sTn_antigen (mucin O-glycan) export	sTn_antigen[g] -> sTn_antigen[e]	0		0	1000	2	Transport, Extracellular	PMID: 10430883, PMID: 848954	Reaction that provides mucin O-glycans to gut microbiota, e.g. B. thetaiotaomicron. BT is well known to degrade mucin. The subsystem "O-Glycan Biosynthesis" in Recon1 represents mucin biosynthesis.	
STRDNCCPT1	carnitine O-palmitoyltransferase	crn[c] + strdnccoa[c] -> coa[c] + strdnccrn[c]	0	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	0	1000		Carnitine shuttle			
STRDNCCPT2	carnitine transferase	coa[m] + strdnccrn[m] -> crn[m] + strdnccoa[m]	0	12896.1	0	1000		Carnitine shuttle			
STRDNCCRNt	transport into the mitochondria (carnitine)	strdnccrn[c] -> strdnccrn[m]	0	57279.1	0	1000		Carnitine shuttle			
STRDNCt	fatty acid transport via diffusion	strdnc[e] <=> strdnc[c]	1		-1000	1000		Transport, Extracellular			
SUCCt2m	succinate transport, mitochondrial	pi[m] + succ[c] <=> pi[c] + succ[m]	1	27376.1	-1000	1000		Transport, Mitochondrial			
SUCCt4_2	succinate transport via sodium symport	2 na1[e] + succ[e] <=> 2 na1[c] + succ[c]	1	20500.1	-1000	1000		Transport, Extracellular			
SUCCt4_3	succinate transport via sodium symport	3 na1[e] + succ[e] <=> 3 na1[c] + succ[c]	1	114644.1 or 114644.2	-1000	1000		Transport, Extracellular			
SUCCtp	succinate transporter, peroxisome	succ[c] <=> succ[x]	1		-1000	1000		Transport, Peroxisomal			
SUCD1m	succinate dehydrogenase	fad[m] + succ[m] <=> fadh2[m] + fum[m]	1	66945.1 and 66052.1 and 67680.1 and 66925.1	-1000	1000		Citric Acid Cycle			
SUCOAS1m	Succinate--CoA ligase (GDP-forming)	coa[m] + gtp[m] + succ[m] <=> pi[m] + gdp[m] + succoa[m]	1	20917.1 and 56451.1	-1000	1000		Citric Acid Cycle			
SUCOASm	Succinate--CoA ligase (ADP-forming)	coa[m] + atp[m] + succ[m] <=> adp[m] + pi[m] + succoa[m]	1	56451.1 and 20916.1	-1000	1000		Citric Acid Cycle			
SUCRe	sucrose hydrolyzing enxyme, extracellular	h2o[e] + sucr[e] -> glc-D[e] + fru[e]	0	232714.1 or 69983.1	0	1000		Galactose metabolism			
SULFOX	sulfite oxidase	h2o[c] + so3[c] + 2 ficytC[m] -> 2 h[c] + 2 focytC[m] + so4[c]	0	211389.1	0	1000		Cysteine Metabolism			
Ser_Thrtg	Ser/Thr intracellular transport	Ser_Thr[g] <=> Ser_Thr[l]	1		-1000	1000		Transport, Golgi Apparatus			
T2M26DCOAHLm	trans-2-Methyl-5-isopropylhexa-2,5-dienoyl-CoA hydro-lyase (m)	h2o[m] + t2m26dcoa[m] <=> 3h26dm5coa[m]	1	11992.1 or 231086.1 or 97212.1	-1000	1000		Limonene and pinene degradation			
T2M26DCOAHLx	trans-2-Methyl-5-isopropylhexa-2,5-dienoyl-CoA hydro-lyase (x)	h2o[x] + t2m26dcoa[x] <=> 3h26dm5coa[x]	1	74147.1 or 51798.1	-1000	1000		Limonene and pinene degradation			
T4HCINNMFM	4-hydroxycinnamate formation	34hpl[m] -> h2o[m] + T4hcinnm[m]	0		0	1000		Ubiquinone Biosynthesis			
T4HCINNOX	4-Coumarate:oxygen oxidoreductase	o2[c] + 2 T4hcinnm[c] -> 2 34dhcinm[c]	0	22173.1	0	1000		Stilbene, coumarine and lignin biosynthesis			
TAGAT_Dt	D-tagatose uptake via diffusion	tagat-D[e] -> tagat-D[c]	0		0	1000		Transport, Extracellular			
TAGHSTDe	Transport, extracellular	tag_hs[c] -> tag_hs[e]	0		0	1000	2	Transport, Extracellular	Sareen S. Gropper, jack L. Smith, James L. Groff (2009) Wadaworth cengage learning, Advanced nutrition and human metabolism, 5th edition, page 142-148.	transported in chylomicrons into lymph	
TAGt	triacylglycerol 2 (homo sapiens) transport	tag_hs[e] <=> tag_hs[c]	1		-1000	1000		Transport, Extracellular			
TALA	transaldolase	g3p[c] + s7p[c] <=> f6p[c] + e4p[c]	1	21351.1	-1000	1000	2	Pentose Phosphate Pathway			
TAUBETAtc	transport of taurine into the intestinal cells by beta transport system	2 na1[u] + cl[u] + taur[u] -> 2 na1[c] + cl[c] + taur[c]	0	21366.1	0	1000	3	Transport, Lumen	PMID: 19074966, PMID: 2206910, PMID: 1324004, PMID: 16956961, PMID: 15166008, PMID: 18195088	beta transporter system requires chloride ions for optimal uptake of amino acids into the cells. Expressed on both apical and basolateral membranes of renal cells. Transports taurine and beta alanine. (PMID: 18195088)	
TAUPAT1c	transport of taurine into the intestinal cells by PAT1	h[u] + taur[u] -> h[c] + taur[c]	0	215335.1	0	1000	3	Transport, Lumen	PMID: 19074966, PMID:18195088, PMID:18400692, PMID: 15345686, PMID: 17123464, PMCID: PMC34648	PAT2 is strongly expressed in heart and lung and more weakly in kidney and muscle (PMID:18400692). PAT2 doest not strongly discriminate between L and D isomers (PMID: 18400692). PAT1 proton-amino acid co-transporter with 1:1 stoichiometry, does not discriminate between L and D isomers, located on the apical membrane of kidney and intestine (PMID: 18400692, PMID: 18195088).	
TAURt4_2_r	taurine transport (sodium symport) (2:1)	2 na1[e] + taur[e] <=> 2 na1[c] + taur[c]	1	21366.1	-1000	1000		Transport, Extracellular			
TAURtcx	taurine transport (sodium symport) (cytosol to peroxisome)	na1[c] + taur[c] <=> taur[x] + na1[x]	1	21366.1	-1000	1000		Taurine and hypotaurine metabolism			
TAXOLte	xenobiotic transport	taxol[e] <=> taxol[c]	1		-1000	1000		Transport, Extracellular			
TCHOLAt2	taurocholate transport via sodium cotransport	2 na1[e] + tchola[e] -> 2 na1[c] + tchola[c]	0	20494.1 or 20493.1	0	1000		Transport, Extracellular			
TCHOLAt3	ABC bile acid transporter	h2o[c] + atp[c] + tchola[c] -> adp[c] + h[c] + pi[c] + tchola[e]	0	27413.1 or 76408.2 or 76408.3 or 76408.1	0	1000		Transport, Extracellular			
TCHOLAte	bile acid intracellular transport	tchola[e] <=> tchola[c]	1		-1000	1000		Transport, Extracellular			
TCHOLAtx	bile acid intracellular transport	tchola[x] <=> tchola[c]	1		-1000	1000		Transport, Peroxisomal			
TCYNTt	Thiocyanate transport via diffusion (cytosol to extracellular)	tcynt[c] -> tcynt[e]	0		0	1000		Transport, Extracellular			
TCYNTtm	Thiocyanate transport via diffusion (mitochondrial)	tcynt[m] -> tcynt[c]	0		0	1000		Transport, Mitochondrial			
TDCHOLAte	bile acid intracellular transport	tdchola[e] <=> tdchola[c]	1		-1000	1000		Transport, Extracellular			
TDCHOLAtx	bile acid intracellular transport	tdchola[x] <=> tdchola[c]	1		-1000	1000		Transport, Peroxisomal			
TDECHOLAt	Taurodeoxycholic acid transport	tdechola[e] <=> tdechola[c]	1		-1000	1000	1	Transport, Extracellular		Needed to provide this metabolite for reaction BGLUTDECHOe and PSYTDECHe in joint model.	
TDP	thiamin pyrophosphatase	h2o[c] + thmpp[c] -> h[c] + pi[c] + thmmp[c]	0		0	1000		Thiamine Metabolism			
TDPDRE	dTDP-4-dehydrorhamnose 3,5-epimerase	dtdp4d6dg[c] -> dtdp4d6dm[c]	0		0	1000		Nucleotide Sugar Metabolism			
TDPDRR	dTDP-4-dehydrorhamnose reductase	h[c] + nadph[c] + dtdp4d6dm[c] -> nadp[c] + dtdprmn[c]	0		0	1000		Nucleotide Sugar Metabolism			
TDPGDH	dTDPglucose 4,6-dehydratase	dtdpglu[c] -> h2o[c] + dtdp4d6dg[c]	0	76355.1	0	1000		Nucleotide Sugar Metabolism			
TDPm	thiamin pyrophosphatase, mitochondrial	h2o[m] + thmpp[m] -> h[m] + pi[m] + thmmp[m]	0		0	1000		Thiamine Metabolism			
TETHEX3COAtx	fatty acid intracellular transport	tethex3coa[c] <=> tethex3coa[x]	1		-1000	1000		Transport, Peroxisomal			
TETHEX3t	fatty acid transport via diffusion	tethex3[e] <=> tethex3[c]	1		-1000	1000		Transport, Extracellular			
TETPENT3COAtx	fatty acid intracellular transport	tetpent3coa[c] <=> tetpent3coa[x]	1		-1000	1000		Transport, Peroxisomal			
TETPENT3CPT1	carnitine O-palmitoyltransferase	crn[c] + tetpent3coa[c] -> coa[c] + tetpent3crn[c]	0	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	0	1000		Carnitine shuttle			
TETPENT3CPT2	carnitine transferase	coa[m] + tetpent3crn[m] -> crn[m] + tetpent3coa[m]	0	12896.1	0	1000		Carnitine shuttle			
TETPENT3CRNt	transport into the mitochondria (carnitine)	tetpent3crn[c] -> tetpent3crn[m]	0	57279.1	0	1000		Carnitine shuttle			
TETPENT3t	fatty acid transport via diffusion	tetpent3[e] <=> tetpent3[c]	1		-1000	1000		Transport, Extracellular			
TETPENT6COAtx	fatty acid intracellular transport	tetpent6coa[c] <=> tetpent6coa[x]	1		-1000	1000		Transport, Peroxisomal			
TETPENT6CPT1	carnitine O-palmitoyltransferase	crn[c] + tetpent6coa[c] -> coa[c] + tetpent6crn[c]	0	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	0	1000		Carnitine shuttle			
TETPENT6CPT2	carnitine transferase	coa[m] + tetpent6crn[m] -> crn[m] + tetpent6coa[m]	0	12896.1	0	1000		Carnitine shuttle			
TETPENT6CRNt	transport into the mitochondria (carnitine)	tetpent6crn[c] -> tetpent6crn[m]	0	57279.1	0	1000		Carnitine shuttle			
TETPENT6t	fatty acid transport via diffusion	tetpent6[e] <=> tetpent6[c]	1		-1000	1000		Transport, Extracellular			
TETTET6COAtx	fatty acid intracellular transport	tettet6coa[c] <=> tettet6coa[x]	1		-1000	1000		Transport, Peroxisomal			
TETTET6CPT1	carnitine O-palmitoyltransferase	crn[c] + tettet6coa[c] -> coa[c] + tettet6crn[c]	0	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	0	1000		Carnitine shuttle			
TETTET6CPT2	carnitine transferase	coa[m] + tettet6crn[m] -> crn[m] + tettet6coa[m]	0	12896.1	0	1000		Carnitine shuttle			
TETTET6CRNt	transport into the mitochondria (carnitine)	tettet6crn[c] -> tettet6crn[m]	0	57279.1	0	1000		Carnitine shuttle			
TETTET6t	fatty acid transport via diffusion	tettet6[e] <=> tettet6[c]	1		-1000	1000		Transport, Extracellular			
THBPT4ACAMDASE	Tetrahydrobiopterin-4a-carbinolamine dehydratase	thbpt4acam[c] -> h2o[c] + dhbpt[c]	0	13180.1 or 13180.2	0	1000		Tetrahydrobiopterin			
THCHOLSTOICtm	lipid, flip-flop intracellular transport	thcholstoic[m] <=> thcholstoic[x]	1		-1000	1000		Transport, Peroxisomal			
THD1m	NAD(P) transhydrogenase	h[c] + nadp[m] + nadh[m] <=> h[m] + nadph[m] + nad[m]	1	18115.1 or 18115.2	0	0		NAD Metabolism			
THFt2	tetrahydrofolate transport via anion exchange	oh1[c] + thf[e] <=> oh1[e] + thf[c]	1	20509.1 or 20509.2	-1000	1000		Transport, Extracellular			
THFtl	5,6,7,8-Tetrahydrofolate transport, diffusion, lysosomal	thf[c] <=> thf[l]	1		-1000	1000		Transport, Lysosomal			
THFtm	5,6,7,8-Tetrahydrofolate transport, diffusion, mitochondrial	thf[c] <=> thf[m]	1		-1000	1000		Transport, Mitochondrial			
THMATPe	thiamine exit from the neterocytes	h2o[c] + atp[c] + thm[c] -> adp[c] + h[c] + pi[c] + thm[e]	0		0	1000	3	Transport, Extracellular	PMID: 10964259, PMID: 8254515, G.F.M. Ball (2006) Vitamins their role in the human body, Blackwell publishing, chapter 11, page 275.	thiamine exit from the enterocytes, depends on sodium and energy mediated by Na/K ATPase. Thiamine exit is directly coupled to ATP hydrolysis (PMID: 12645798).	
THMDt4	thymidine transport in via sodium symport	na1[e] + thymd[e] -> na1[c] + thymd[c]	0	114304.1 or 434203.1 or 434203.2	0	1000		Transport, Extracellular			
THMDt5	thymidine transport (1:2 Na/Thymd cotransport)	2 na1[e] + thymd[e] -> 2 na1[c] + thymd[c]	0	114304.1	0	1000		Transport, Extracellular			
THMMPt4	Thiamine monophosphate transport in via anion antiport	oh1[c] + thmmp[e] <=> oh1[e] + thmmp[c]	1	20509.1 or 20509.2	-1000	1000		Transport, Extracellular			
THMMPtm	Thiamine monophosphate transport, mitochondrial	thmmp[c] + oh1[m] <=> oh1[c] + thmmp[m]	1		0	1000		Transport, Mitochondrial			
THMP	thiamin phosphatase	h2o[c] + thmmp[c] -> pi[c] + thm[c]	0		0	1000		Thiamine Metabolism			
THMPPtm	Thiamine diphosphate transport in via anion antiport, mitochondria	thmpp[c] + 2 oh1[m] -> 2 oh1[c] + thmpp[m]	0		0	1000		Transport, Mitochondrial			
THMTP	thiamine-triphosphatase	h2o[c] + thmtp[c] -> h[c] + pi[c] + thmpp[c]	0	105663.1	0	1000		Thiamine Metabolism			
THMTPt	Thiamine triphosphate transport in via anion antiport	3 oh1[e] + thmtp[c] -> 3 oh1[c] + thmtp[e]	0	20509.1 or 20509.2	0	1000		Transport, Extracellular			
THMt2m	Thiamine transport in via proton symport, mitochondrial	h[c] + thm[c] -> h[m] + thm[m]	0		-1000	1000		Transport, Mitochondrial			
THMt3	Thiamine transport in via proton antiport	h[c] + thm[e] <=> h[e] + thm[c]	1	116914.1 or 80721.1	-1000	1000		Transport, Extracellular			
THP2Ctp	2,3,4,5-Tetrahydropyridine-2-carboxylate transport, peroxisomal	thp2c[c] <=> thp2c[x]	1		-1000	1000		Transport, Peroxisomal			
THRALANaEx	L-alanine/L-threonine Na-dependent exchange (Thr-L in)	na1[e] + ala-L[c] + thr-L[e] -> na1[c] + ala-L[e] + thr-L[c]	0	20514.1 or 55963.1	0	1000		Transport, Extracellular			
THRASNNaEx	L-threonine/L-asparagine Na-dependent exchange (Thr-L in)	na1[e] + asn-L[c] + thr-L[e] -> na1[c] + asn-L[e] + thr-L[c]	0	20514.1	0	1000		Transport, Extracellular			
THRATB0tc	transport of L-Threonine into the intestinal cells by ATB0 transporter	2 na1[u] + cl[u] + thr-L[u] -> 2 na1[c] + cl[c] + thr-L[c]	0	56774.1	0	1000	3	Transport, Lumen	PMID:18195088	ATB0 is both sodium and chloride coupled, with reaction stoichiometry 2Na+:1cl:1amino acid. The transporter is localted in the intestine, has a broad substrate specificity (both neutral and cationic amino acids), but is not involved in the transport of aspartate, glutamate and proline (PMID:18195088).	

THRB0ATi1c	transport of L-Threonine by the apical neutral amino acid transporters in kidney and intestine	na1[u] + thr-L[u] -> na1[c] + thr-L[c]	0	(70008.1 or (74338.1 and 57394.1))	0	1000	3	Transport, Lumen	PMID: 19472175, PMID: 15804236, PMID: 18400692	transports all the neutral amino acids with preference for methionine, leucine and valine. Reaction stoichiometry is 1:1. Requires heterodimerization with collectrin protein for increased affinity. Found in kidney and intestine, however also reported to be expressed in skin. Requires association with ACE2 for expression in intestine but with collectrin for expression in kidney.	3.4.17.23
THRCYSNaEx	L-cysteine/L-threonine Na-dependent exchange (Thr-L in)	na1[e] + cys-L[c] + thr-L[e] -> na1[c] + cys-L[e] + thr-L[c]	0	20514.1 or 55963.1	0	1000		Transport, Extracellular			
THRD_L	L-threonine deaminase	thr-L[c] -> nh4[c] + 2obut[c]	0	231691.1	0	1000		Glycine, Serine, and Threonine Metabolism			
THRGLNNaEx	L-threonine/L-glutamine Na-dependent exchange (Thr-L in)	na1[e] + gln-L[c] + thr-L[e] -> na1[c] + gln-L[e] + thr-L[c]	0	20514.1	0	1000		Transport, Extracellular			
THRGLNtcR	L-threonine/glycine reversible exchange	gln-L[c] + thr-L[e] <=> gln-L[e] + thr-L[c]	1	53896.1 or 17254.1	-1000	1000		Transport, Extracellular			
THRGLYtcR	L-threonine/glycine reversible exchange	gly[c] + thr-L[e] <=> gly[e] + thr-L[c]	1	53896.1 or 17254.1	-1000	1000		Transport, Extracellular			
THRILELAT2tc	transport of L-Threonine into the cell and efflux of L-Isoleucine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	ile-L[c] + thr-L[e] -> ile-L[e] + thr-L[c]	0	(20539.1 and 17254.1)	0	1000	3	Transport, Extracellular	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID 10195088, Am J Physiol (2001) 281:C1077-C1093.	biger affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274).	
THRPHELAT2tc	transport of L-Threonine into the cell and efflux of L-Phenylalanine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	phe-L[c] + thr-L[e] -> phe-L[e] + thr-L[c]	0	(20539.1 and 17254.1)	0	1000	3	Transport, Extracellular	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID 10195088, Am J Physiol (2001) 281:C1077-C1093.	biger affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274).	
THRS	threonine synthase	h2o[c] + phom[c] -> pi[c] + thr-L[c]	0	208967.1	0	1000		Glycine, Serine, and Threonine Metabolism			
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]	0	20514.1 or 55963.1	0	1000		Transport, Extracellular			
THRt4	L-threonine via sodium symport	na1[e] + thr-L[e] -> na1[c] + thr-L[c]	0	105727.1 or 67760.1 or 56774.1	0	1000		Transport, Extracellular			
THYMDt1	thymid transport	thymd[e] -> thymd[c]	0	13340.1 or 63959.1	0	1000		Transport, Extracellular			
THYMDtl	thymidine facilated transport from lysosome	thymd[l] <=> thymd[c]	1	71279.1	-1000	1000		Transport, Lysosomal			
THYMDtm	thymid transport	thymd[c] <=> thymd[m]	1	63959.1	-1000	1000		Transport, Mitochondrial			
THYMt	thymine reversible transport via facilated diffusion	thym[e] <=> thym[c]	1	13340.1	-1000	1000		Transport, Extracellular			
THYOX2	T4 transport via facilitated diffusion	thyox-L[e] <=> thyox-L[c]	1	20502.1	-1000	1000		Transport, Extracellular			
THYPX	thyroid peroxidase	h2o2[c] + 2 h[c] + 2 I-[c] -> 2 h2o[c] + iodine[c]	0	22018.1 or 22018.2 or 22018.3 or 22018.4 or 220185	0	1000		Tyrosine metabolism			
TKT1	transketolase	r5p[c] + xu5p-D[c] <=> g3p[c] + s7p[c]	1	74419.1 or 11670.1 or 83553.1 or 21881.1	-1000	1000		Pentose Phosphate Pathway			
TKT2	transketolase	xu5p-D[c] + e4p[c] <=> g3p[c] + f6p[c]	1	74419.1 or 11670.1 or 83553.1	-1000	1000		Pentose Phosphate Pathway			
TMABADH	4-trimethylaminobutyraldehyde dehydrogenase	h2o[c] + nad[c] + 4tmeabutn[c] -> 2 h[c] + nadh[c] + 4tmeabutn[c]	0	56752.1	0	1000		Lysine Metabolism			
TMDK1	thymidine kinase (ATP:thymidine)	atp[c] + thymd[c] -> adp[c] + h[c] + dtmp[c]	0	57813.1 or 619653.1	0	1000		Nucleotides			
TMDK1m	thymidine kinase (ATP:thymidine)	atp[m] + thymd[m] -> h[m] + adp[m] + dtmp[m]	0	57813.1	0	1000		Nucleotides			
TMDPK	thiamine diphosphokinase	atp[c] + thm[c] -> h[c] + amp[c] + thmpp[c]	0	29807.1	0	1000		Thiamine Metabolism			
TMDPP	thymidine phosphorylase	pi[c] + thymd[c] <=> 2dr1p[c] + thym[c]	1	72962.1	-1000	1000		Pyrimidine Catabolism			
TMDPPK	thiamine-diphosphate kinase	atp[c] + thmpp[c] -> adp[c] + thmp[c]	0		0	1000		Thiamine Metabolism			
TMDS	thymidylate synthase	dump[c] + mlthf[c] -> dhf[c] + dtmp[c]	0	22171.1	0	1000		Nucleotides			
TMLYSOX	trimethyllysine dioxygenase	o2[c] + akg[c] + tmlys[c] -> co2[c] + succ[c] + 3hmelys[c]	0	192289.1	0	1000		Lysine Metabolism			
TMLYStex	trimethyl-L-lysine transport (ER to cytosol)	tmlys[r] -> tmlys[c]	0		0	1000		Transport, Endoplasmic Reticular			
TMNDNCCOAtx	fatty acid intracellular transport	tmndnccoa[c] <=> tmndnccoa[x]	1		-1000	1000		Transport, Peroxisomal			
TMNDNCCPT1	carnitine O-palmitoyltransferase	crn[c] + tmndnccoa[c] -> coa[c] + tmndnccrn[c]	0	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	0	1000		Carnitine shuttle			
TMNDNCCPT2	carnitine transferase	coa[m] + tmndnccrn[m] -> crn[m] + tmndnccoa[m]	0	12896.1	0	1000		Carnitine shuttle			
TMNDNCCRNt	transport into the mitochondria (carnitine)	tmndnccrn[c] -> tmndnccrn[m]	0	57279.1	0	1000		Carnitine shuttle			
TMNDNCt	fatty acid transport via diffusion	tmndnc[e] <=> tmndnc[c]	1		-1000	1000		Transport, Extracellular			
TOLRGTAMIDEte	xenobiotic transport	tolbutamide[e] <=> tolbutamide[c]	1		-1000	1000		Transport, Extracellular			
TPI	triose-phosphate isomerase	dhap[c] <=> g3p[c]	1	21991.1	-1000	1000		Glycolysis/Gluconeogenesis			
TRDR	thioredoxin reductase (NADPH)	h[c] + nadph[c] + trdox[c] -> nadp[c] + trdrd[c]	0	50493.1 or 50493.2 or 50493.3 or 50493.4	0	1000		Nucleotides			
TRDR2	Thioredoxin (ubiquinone 10) reductase (NADPH)	h[c] + nadph[c] + q10[c] -> nadp[c] + q10h2[c]	0	50493.1 or 50493.2 or 50493.3 or 50493.4	0	1000		Miscellaneous			
TRDR3	Thioredoxin (ubiquinone 10) reductase (NADH)	h[c] + nadh[c] + q10[c] -> nad[c] + q10h2[c]	0	50493.1 or 50493.2 or 50493.3 or 50493.4	0	1000		Miscellaneous			
TRDRm	thioredoxin reductase (NADPH)	h[m] + nadph[m] + trdox[m] -> nadp[m] + trdrd[m]	0	26462.1 or 232223.1 or 26462.2 or 26462.3	0	1000		Nucleotides			
TREH	alpha,alpha-trehalase	h2o[c] + tre[c] -> 2 glc-D[c]	0	212974.1	0	1000		Starch and Sucrose Metabolism			
TREHe	alpha,alpha-trehalase	h2o[e] + tre[e] -> 2 glc-D[e]	0	98866.1	0	1000		Starch and Sucrose Metabolism			
TRIODTHYSUFt	Triiodothyronine sulfate transport (diffusion)	triodthysulf[c] -> triodthysulf[e]	0		0	1000		Transport, Extracellular			
TRIODTHYSULT	Triiodothyronine Sulfotransferase	paps[c] + triodthy[c] -> h[c] + pap[c] + triodthysulf[c]	0	20887.1 or 20887.2 or 20887.3 or 20887.4 or 20887.5	0	1000		Tyrosine metabolism			
TRIODTHYt2	T3 transport via facilitated diffusion	triodthy[e] <=> triodthy[c]	1	20502.1	-1000	1000		Transport, Extracellular			
TRIOK	triokinase	atp[c] + glyald[c] -> adp[c] + h[c] + g3p[c]	0		0	1000		Fructose and Mannose Metabolism			
TRPATBItc	transport of L-Tryptophan into the intestinal cells by ATB0 transporter	2 na1[u] + cl[u] + trp-L[u] -> 2 na1[c] + cl[c] + trp-L[c]	0	56774.1	0	1000	3	Transport, Lumen	PMID:18195088	ATB0 is both sodium and chloride coupled, with reaction stoichiometry 2Na+:1cl:1amino acid. The transporter is located in the intestine, has a broad substrate specificity (both neutral and cationic amino acids), but is not involved in the transport of aspartate, glutamate and proline (PMID:18195088).	
TRPB0AT1tc	transport of L-Tryptophan by the apical neutral amino acid transporters in kidney and intestine	na1[u] + trp-L[u] -> na1[c] + trp-L[c]	0	(70008.1 or (74338.1 and 57394.1))	0	1000	3	Transport, Lumen	PMID: 19472175, PMID: 15804236, PMID: 18400692	transports all the neutral amino acids with preference for methionine, leucine and valine. Reaction stoichiometry is 1:1. Requires heterodimerization with collectrin protein for increased affinity. Found in kidney and intestine, however also reported to be expressed in skin. Requires association with ACE2 for expression in intestine but with collectrin for expression in kidney.	3.4.17.23
TRPHYDRO2	L-Tryptophan,tetrahydrobiopterin:oxygen oxidoreductase (5-hydroxylating)	o2[c] + thbpt[c] + trp-L[c] -> 5htrp[c] + thbpt4acam[c]	0	21990.1 or 216343.1	0	1000		Tryptophan metabolism			
TRPLELAT2tc	transport of L-Tryptophan into the cell and efflux of L-Isoleucine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	ile-L[c] + trp-L[e] -> ile-L[e] + trp-L[c]	0	(20539.1 and 17254.1)	0	1000	3	Transport, Extracellular	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID 10195088, Am J Physiol (2001) 281:C1077-C1093.	biger affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274).	
TRPLAT1tc	transport of L-Tryptophan by LAT1 in association with 4F2hc, across the apical surface of the membranes.	leu-L[c] + trp-L[u] -> leu-L[u] + trp-L[c]	0	(20539.1 and 17254.1)	0	1000	3	Transport, Lumen	Hans Gerhard Vogel, Franz J. Hock, Jochen Maas, Dieter Mayer (2006), Drug discovery and evaluation: Safety and pharmacokinetic assays, Springer publication, Chapter II D, page 456, table 3, PMID: 19035290, PMID: 12634921, European Journal of Pharmacology 441 (2002) 127–132. Am J Physiol Cell Physiol 281:C1077-C1093, 2001. Amino Acids (2005) 29: 229–233 DOI 10.1007/s00726-005-0221-x. PMID 11901210	leucine is the only amino acid tested for efflux. Expressed in ovary, placenta, brain, spleen, testis, activated lymphocytes and some tumor cells. Functions as a antiport transport system (DOI 10.1016/j.cell.2009.01.02), requires heterodimerization with glycoprotein CD98 (Pflugers Arch-Eur J Physiol (2000) 440:503-512, DOI 10.1007/s004200000274, PMID: 10958334).	
TRPO2	L-Tryptophan:oxygen 2,3-oxidoreductase (decyclizing)	o2[c] + trp-L[c] -> l-kynur[c]	0	56720.1	0	1000		Tryptophan metabolism			
TRPPHELAT1tc	transport of L-Tryptophan into the cell and efflux of L-Phenylalanine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	phe-L[c] + trp-L[e] -> phe-L[e] + trp-L[c]	0	(20539.1 and 17254.1)	0	1000	3	Transport, Extracellular	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID 10195088, Am J Physiol (2001) 281:C1077-C1093.	biger affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274).	
TRPt4	L-tryptophan transport in via sodium symport	na1[e] + trp-L[e] -> na1[c] + trp-L[c]	0	56774.1	0	1000		Transport, Extracellular			
TRYPTAO3t	Tryptamine:oxygen oxidoreductase(deaminating)(flavin-containing)	h2o[c] + o2[c] + trypta[c] -> h2o2[c] + nh4[c] + id3acald[c]	0	109731.1 or 237940.1 or 17161.1 or 237940.2 or 76507.1	0	1000		Tryptophan metabolism			
TS3	Tachysterol 3 formation	pre3[c] <=> tx3[c]	1		-1000	1000		Vitamin D			
TSTSTERONEGLCte	glucuronidated compound transport	h2o[c] + atp[c] + testosmegl[c] -> adp[c] + h[c] + pi[c] + testosmegl[e]	0	17250.1	0	1000		Transport, Extracellular			
TSTSTERONEGLCtr	glucuronidated compound transport	testosmegl[c] <=> testosmegl[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
TSTSTERONESULT	testosterone sulfotransferase	paps[c] + testosone[c] -> h[c] + pap[c] + testosmes[c]	0	20859.1	0	1000		Steroid Metabolism			
TSTSTERONEte	sulfonated testosterone transport	testosones[c] <=> testosones[e]	1		-1000	1000		Transport, Extracellular			
TSTSTERONEt	testosterone transmembrane (homo sapiens) transport	testosone[e] <=> testosone[c]	1		-1000	1000		Transport, Extracellular			
TSTSTERONEtr	testosterone intracellular transport	testosone[c] <=> testosone[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
TSULt4_3	thiosulfate transport via sodium symport	3 na1[e] + tsul[e] <=> 3 na1[c] + tsul[c]	1	55961.1	-1000	1000		Transport, Extracellular			
TTDCAt	Tetradecanoate (n-C14:0) transport in via uniport	ttdca[e] -> ttdca[c]	0		0	1000		Transport, Extracellular			
TTDCAte	fatty acid transport	ttdca[e] <=> ttdca[c]	1		-1000	1000		Transport, Extracellular			
TTDCPT1	carnitine O-palmitoyltransferase	crn[c] + ttdcoa[c] -> coa[c] + ttdcrn[c]	0	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	0	1000		Carnitine shuttle			
TTDCPT2	carnitine transferase	coa[m] + ttdcrn[m] -> crn[m] + ttdcoa[m]	0	12896.1	0	1000		Carnitine shuttle			
TTDCRNt	transport into the mitochondria (carnitine)	ttdcrn[c] -> ttdcrn[m]	0	57279.1	0	1000		Carnitine shuttle			

TXA2te	thromboxane A2 transport	txa2[e] <=> txa2[c]	1		-1000	1000		Transport, Extracellular			
TXA2tr	thromboxane A2 intracellular transport	txa2[c] <=> txa2[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
TXASr	Thromboxane-A synthase	prostgh2[r] -> txa2[r]	0	21391.1	0	1000		Eicosanoid Metabolism			
TYMSFt	Tyramine O-sulfate transport (diffusion)	tymsf[c] -> tymsf[e]	0		0	1000		Transport, Extracellular			
TYR3MO2	tyrosine 3-monooxygenase	o2[c] + thbpt[c] + tyr-L[c] -> 34dhphe[c] + thbpt4acam[c]	0	21823.1 or 21823.2 or 21823.3	0	1000		Tyrosine metabolism			
TYRASE	Tyrosinase	56dihindlcrbxlt[c] -> melanin[c]	0	22178.1	0	1000		Tyrosine metabolism			
TYRATB0tc	transport of L-Tyrosine into the intestinal cells by ATB0 transporter	2 na1[u] + cl[u] + tyr-L[u] -> 2 na1[c] + cl[c] + tyr-L[c]	0	56774.1	0	1000	3	Transport, Lumen	PMID:18195088	ATB0 is both sodium and chloride coupled, with reaction stoichiometry 2Na+:1cl:1amino acid. The transporter is localted in the intestine, has a broad substrate specificity (both neutral and cationic amino acids), but is not involved in the transport of aspartate, glutamate and proline (PMID:18195088).	
TYRB0AT1tc	transport of L-Tyrosine by the apical neutral amino acid transporter B(0)AT1 in kidney and intestine	na1[u] + tyr-L[u] -> na1[c] + tyr-L[c]	0	(70008.1 or (74338.1 and 57394.1))	0	1000	3	Transport, Lumen	PMID: 19472175, PMID: 15804236, PMID: 18400692	transports all the neutral amino acids with preference for methionine, leucine and valine. Reaction stoichiometry is 1:1. Requires heterodimerization with collectrin protein for increased affinity. Found in kidney and intestine, however also reported to be expressed in skin. Requires association with ACE2 for expression in intestine but with collectrin for expression in kidney.	3.4.17.23
TYRCBOX	L-Tyrosine carboxy-lyase	h[c] + tyr-L[c] -> co2[c] + tym[c]	0	13195.1	0	1000		Tyrosine metabolism			
TYRDOPO	Tyrosine:dopa oxidase	o2[c] + 2 tyr-L[c] -> 2 34dhphe[c]	0	22173.1	0	1000		Tyrosine metabolism			
TYRDOPO3	Tyrosine:dopa oxidase (dopaquinone producing 2)	o2[c] + 2 34dhphe[c] -> 2 h2o[c] + 2 dopaqn[c]	0	22173.1	0	1000		Tyrosine metabolism			
TYRILELAT2tc	transport of L-Tyrosine into the cell and efflux of L-Isoleucine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	ile-L[c] + tyr-L[e] -> ile-L[e] + tyr-L[c]	0	(20539.1 and 17254.1)	0	1000	3	Transport, Extracellular	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s00420000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	higer affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of memebranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for traficking of the complex to the mebrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s00420000274).	
TYRLAT1tc	transport of L-Tyrosine by LAT1 in association with 4F2hc, across the apical surface of the memebranes.	leu-L[c] + tyr-L[u] -> leu-L[u] + tyr-L[c]	0	(20539.1 and 17254.1)	0	1000	3	Transport, Lumen	Hans Gerhard Vogel, Franz J. Hock, Jochen Maas, Dieter Mayer (2006), Drug discovery and evaluation: Safety and pharmacokinetic assays, Springer publication, Chapter II D, page 456, table 3, PMID: 19035290, PMID: 12634921, European Journal of Pharmacology 441 (2002) 127-132. Am J Physiol Cell Physiol 281:C1077-C1093, 2001. Amino Acids (2005) 29: 229–233 DOI 10.1007/s00726-005-0221-x. PMID: 11901210	leucine is the only amino acid tested for efflux. Expressed in ovary, placenta, brain, spleen, testis, activated lymphocytes and some tumor cells. Functions as a antiport transport system (DOI 10.1016/j.cell.2009.01.02), requires heterodimerization with glycoprotein CD98 (Pflugers Arch-Eur J Physiol (2000) 440:503-512, DOI 10.1007/s004240000274, PMID: 10958334).	
TYROXDAc	Tyramine:oxygen oxidoreductase(deaminating)(flavin-containing) (cytosol)	h2o[c] + o2[c] + tym[c] -> h2o2[c] + nh4[c] + 4hoxpacd[c]	0	109731.1 or 17161.1	0	1000		Tyrosine metabolism			
TYRPHELAT2tc	transport of L-Tyrosine into the cell and efflux of L-Phenylalanine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	phe-L[c] + tyr-L[e] -> phe-L[e] + tyr-L[c]	0	(20539.1 and 17254.1)	0	1000	3	Transport, Extracellular	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s00420000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	higer affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of memebranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for traficking of the complex to the mebrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s00420000274).	
TYRTA	tyrosine transaminase	akg[c] + tyr-L[c] <=> 34hpp[c] + glu-L[c]	1	14718.1	-1000	1000		Tyrosine metabolism			
TYRTAm	tyrosine transaminase, mitochondrial	akg[m] + tyr-L[m] <=> 34hpp[m] + glu-L[m]	1	234724.1 or 14719.1	-1000	1000		Tyrosine metabolism			
TYRt4	L-tyrosine transport in via sodium symport	na1[e] + tyr-L[e] -> na1[c] + tyr-L[c]	0	56774.1	0	1000		Transport, Extracellular			
UAG2EMAi	UDP-N-acetyl-D-glucosamine 2-epimerase (Hydrolysis)	h2o[c] + uacgam[c] -> h[c] + udp[c] + acmana[c]	0	50798.1	0	1000		Aminosugar Metabolism			
UAG4E	UDP-N-acetylglucosamine 4-epimerase	uacgam[c] <=> udpacgal[c]	1	74246.1 or 74246.2	-1000	1000		Aminosugar Metabolism			
UAGALDP	UDP-N-acetylgalactosamine diphosphorylase	h[c] + acgal1p[c] + utp[c] -> ppi[c] + udpacgal[c]	0		0	1000		Aminosugar Metabolism			
UAGDP	UDP-N-acetylglucosamine diphosphorylase	h[c] + acgam1p[c] + utp[c] -> ppi[c] + uacgam[c]	0	227620.1 or 107652.1	0	1000		Aminosugar Metabolism			
UDPACGALtl	udpacgal intracellular transport	udpacgal[c] <=> udpacgal[l]	1		-1000	1000		Transport, Lysosomal			
UDPDOLPT_L	UDPglucose:dolichyl-phosphate beta-D-glucosyltransferase (liver)	0.1 dolp_L[c] + udpg[c] -> udp[c] + 0.1 dolglcp_L[c]	0	66248.1	0	1000		N-Glycan Biosynthesis			
UDPDOLPT_U	UDPglucose:dolichyl-phosphate beta-D-glucosyltransferase (uterus)	0.1 dolp_U[c] + udpg[c] -> udp[c] + 0.1 dolglcp_U[c]	0	66248.1	0	1000		N-Glycan Biosynthesis			
UDPG1P	UDPglucuronate uridine-monophosphohydrolase	h2o[c] + udpglcur[c] -> 2 h[c] + ump[c] + glcur1p[c]	0		0	1000		Pentose and Glucuronate Interconversions			
UDPG4E	UDPglucose 4-epimerase	udpg[c] <=> udpgal[c]	1	74246.1 or 74246.2	-1000	1000		Galactose metabolism			
UDPGALt2g	UDPgalactose transport (Golgi apparatus)	udpgal[c] -> udpgal[g]	0		0	1000		Transport, Golgi Apparatus			
UDPGALtg	UDP-Gal Golgi transport via CMP antiport	udpgal[c] + ump[g] <=> udpgal[g] + ump[c]	1	22232.1	-1000	1000		Transport, Golgi Apparatus			
UDPGD	UDPglucose 6-dehydrogenase	h2o[c] + 2 nad[c] + udpg[c] -> 3 h[c] + 2 nadh[c] + udpglcur[c]	0	22235.1	0	1000		Starch and Sucrose Metabolism			
UDPGLCAter	UDPGlcA endoplasmic reticulum transport via UMP antiport	ump[c] + udpglcur[r] <=> udpglcur[c] + ump[r]	1	242585.1	-1000	1000		Transport, Endoplasmic Reticular			
UDPGLCAtg	UDPGlcA Golgi transport via UMP antiport	udpglcur[g] + ump[c] <=> udpglcur[c] + ump[g]	1		-1000	1000		Transport, Golgi Apparatus			
UDPGLCter	UDP-Glc endoplasmic reticulum transport via CMP antiport	udpg[c] + ump[r] <=> ump[c] + udpg[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
UDPGLCtg	UDP-Glc Golgi transport via CMP antiport	udpg[c] + ump[g] <=> ump[c] + udpg[g]	1	58246.1 or 229782.1 or 70484.1	-1000	1000		Transport, Golgi Apparatus			
UDPGLDCg	UDP-D-glucuronate decarboxylase, Golgi apparatus	h[g] + udpglcur[g] -> co2[g] + udpxyl[g]	0	67883.1	0	1000		Nucleotide Sugar Metabolism			
UDPGNP	UDPglucuronate uridine-diphosphohydrolase	h2o[c] + udpglcur[c] -> h[c] + udp[c] + glcur[c]	0		0	1000		Pentose and Glucuronate Interconversions			
UDPGP	UDPglucose pyrophosphohydrolase	h2o[c] + udpg[c] -> 2 h[c] + g1p[c] + ump[c]	0	18605.1 or 18606.1 or 209558.1	0	1000		Starch and Sucrose Metabolism			
UDPXYLter	UDP-Xyl endoplasmic reticular transport via CMP antiport	ump[r] + udpxyl[c] <=> ump[c] + udpxyl[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
UDPXYLtg	UDP-Xyl Golgi transport via CMP antiport	ump[g] + udpxyl[c] <=> ump[c] + udpxyl[g]	1	58246.1	-1000	1000		Transport, Golgi Apparatus			
UDPtl	udp intracellular transport	udp[c] <=> udp[l]	1		-1000	1000		Transport, Lysosomal			
UGALGTg	UDPgalactose:D-glucose 4-beta-D-galactosyltransferase, Golgi apparatus	udpgal[g] + glc-D[g] -> h[g] + udp[g] + lcts[g]	0	16770.1 or 14595.1 or 53418.1 or 53418.2	0	1000		Galactose metabolism			
UGALNACter	UDP-GalNAc endoplasmic reticulum transport via CMP antiport	ump[r] + udpacgal[c] <=> ump[c] + udpacgal[r]	1	242585.1	-1000	1000		Transport, Endoplasmic Reticular			
UGALNACtg	UDP-GalNAc Golgi transport via CMP antiport	ump[g] + udpacgal[c] <=> udpacgal[g] + ump[c]	1	22232.1	-1000	1000		Transport, Golgi Apparatus			
UGCG	Ceramide glucosyltransferase	crm_hs[r] + udpg[r] -> h[r] + gluside_hs[r] + udp[r]	0	22234.1	0	1000		Sphingolipid Metabolism			
UGLCNACtg	UDP-GlcNAc Golgi transport via CMP antiport	uacgam[c] + ump[g] <=> uacgam[g] + ump[c]	1	70484.1	-1000	1000		Transport, Golgi Apparatus			
UGLT	UDPglucose--hexose-1-phosphate uridylyltransferase	gal1p[c] + udpg[c] <=> udpgal[c] + g1p[c]	1	14430.1 or 14430.2 or 14430.3	-1000	1000		Galactose metabolism			
UGT1A9r	UDP-glucuronosyltransferase 1-10 precursor, microsomal	5adtststerone[r] + udpglcur[r] -> 5adtststeroneglc[r] + udp[r]	0		0	1000		Steroid Metabolism			
UMPK	UMP kinase	atp[c] + ump[c] <=> adp[c] + udp[c]	1	66588.1	-1000	1000		Nucleotides			
UMPK2	UMP kinase (CTP)	ctp[c] + ump[c] <=> udp[c] + cdp[c]	1	66588.1	-1000	1000		Nucleotides			
UMPK2n	UMP kinase (CTP),nuclear	ctp[n] + ump[n] <=> cdp[n] + udp[n]	1	66588.1	-1000	1000		Nucleotides			
UMPK3	UMP kinase (UTP)	utp[c] + ump[c] <=> 2 udp[c]	1	66588.1	-1000	1000		Nucleotides			
UMPK3n	UMP kinase (UTP),nuclear	utp[n] + ump[n] <=> 2 udp[n]	1	66588.1	-1000	1000		Nucleotides			
UMPK4	UMP kinase (GTP)	gtp[c] + ump[c] <=> udp[c] + gdp[c]	1	66588.1	-1000	1000		Nucleotides			
UMPK4n	UMP kinase (GTP),nuclear	gtp[n] + ump[n] <=> udp[n] + gdp[n]	1	66588.1	-1000	1000		Nucleotides			
UMPK5	UMP kinase (dATP)	datp[c] + ump[c] <=> udp[c] + dadp[c]	1	66588.1	-1000	1000		Nucleotides			
UMPK5n	UMP kinase (dATP),nuclear	datp[n] + ump[n] <=> dadp[n] + udp[n]	1	66588.1	-1000	1000		Nucleotides			
UMPK6	UMP kinase (dCTP)	dctp[c] + ump[c] <=> udp[c] + dcdp[c]	1	66588.1	-1000	1000		Nucleotides			
UMPK6n	UMP kinase (dCTP),nuclear	dctp[n] + ump[n] <=> dcdp[n] + udp[n]	1	66588.1	-1000	1000		Nucleotides			
UMPK7	UMP kinase (dGTP)	dgtp[c] + ump[c] <=> udp[c] + dgdp[c]	1	66588.1	-1000	1000		Nucleotides			
UMPK7n	UMP kinase (dGTP),nuclear	dgtp[n] + ump[n] <=> dgdp[n] + udp[n]	1	66588.1	-1000	1000		Nucleotides			
UMPKm	UMP kinase (mitochondrial, ATP)	atp[m] + ump[m] <=> adp[m] + udp[m]	1		-1000	1000		Nucleotides			
UMPKn	UMP kinase, nuclear	atp[n] + ump[n] <=> udp[n] + adp[n]	1	66588.1	-1000	1000		Nucleotides			
UMPtr	UMP intracellular transport	ump[c] <=> ump[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
UNK2	2-keto-4-methylthiobutyrate transamination	h[c] + gln-L[c] + 2kmb[c] -> glu-L[c] + met-L[c]	0		0	1000		Arginine and Proline Metabolism			
UNK3	2-keto-4-methylthiobutyrate transamination	glu-L[c] + 2kmb[c] -> akg[c] + met-L[c]	0		0	1000		Arginine and Proline Metabolism			
UPP3S	uroporphyrinogen-III synthase	hmbil[c] -> h2o[c] + uppg3[c]	0	22276.1	0	1000		Heme Biosynthesis			
UPPDC1	uroporphyrinogen decarboxylase (uroporphyrinogen III)	4 h[c] + uppg3[c] -> 4 co2[c] + cpppg3[c]	0	22275.1	0	1000		Heme Biosynthesis			
UPPN	b-ureidopropionase	h2o[c] + 2 h[c] + cala[c] -> nh4[c] + co2[c] + ala-B[c]	0	103149.1	0	1000		Pyrimidine Catabolism			
URATEt	urate export from cytosol	urate[c] -> urate[e]	0		0	1000		Transport, Extracellular			
URATEtx	urate export from peroxisome	urate[x] -> urate[c]	0		0	1000		Transport, Peroxisomal			
URAt	uracil transport via facilated diffusion	ura[e] <=> ura[c]	1	13340.1	-1000	1000		Transport, Extracellular			
URCN	urocanase	h2o[c] + urcan[c] -> 4izp[c]	0	243537.1	0	1000		Histidine Metabolism			
UREAt	Urea transport via facilitate diffusion	urea[e] <=> urea[c]	1	108052.1 or 27411.1 or 20537.1 or 114479.1	-1000	1000		Transport, Extracellular			
UREAt5	urea, water cotransport	h2o[e] + urea[e] <=> h2o[c] + urea[c]	1	20537.1	-1000	1000		Transport, Extracellular			
UREAtm	Urea transport via diffusion	urea[c] <=> urea[m]	1	64008.1	-1000	1000		Urea cycle/amino group metabolism			
URIDK2m	uridylate kinase (dUMP), mitochondrial	atp[m] + dump[m] <=> adp[m] + dudp[m]	1		-1000	1000		Nucleotides			
URIK1	uridine kinase (ATP:Uridine)	atp[c] + uri[c] -> adp[c] + h[c] + ump[c]	0	22245.1 or 80914.1	0	1000		Pyrimidine Biosynthesis			
URIt	uridine facilated transport in cytosol	uri[e] <=> uri[c]	1	13340.1 or 63959.1	-1000	1000		Transport, Extracellular			
URIt4	uridine transport in via sodium symport	na1[e] + uri[e] -> na1[c] + uri[c]	0	114304.1 or 434203.1 or 434203.2 or 269346.1	0	1000		Transport, Extracellular			
URIt5	uridine transport in via sodium symport (1:2)	2 na1[e] + uri[e] -> 2 na1[c] + uri[c]	0	114304.1	0	1000		Transport, Extracellular			
UROLACer	uronolactonase, endoplasmic reticulum	h[r] + glcur[r] <=> h2o[r] + glac[r]	1		-1000	1000		Ascorbate and Aldarate Metabolism			
UTPtn	UTP diffusion in nucleus	utp[c] <=> utp[n]	1		-1000	1000		Transport, Nuclear			
Uritl	uridine facilated transport from lysosome	uri[l] <=> uri[c]	1	71279.1	-1000	1000		Transport, Lysosomal			
Uritm	uridine facilated transport in mitochondria	uri[c] <=> uri[m]	1	63959.1	-1000	1000		Transport, Mitochondrial			
Uritn	uridine transport in nucleus	uri[c] <=> uri[n]	1		-1000	1000		Transport, Nuclear			
VACCCPT1	carnitine O-palmitoyltransferase	crn[c] + vacccoa[c] -> coa[c] + vacccrn[c]	0	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	0	1000		Carnitine shuttle			
VACCCPT2	carnitine transferase	coa[m] + vacccrn[m] -> crn[m] + vacccoa[m]	0	12896.1	0	1000		Carnitine shuttle			

VACCCRNt	transport into the mitochondria (carnitine)	vaccrn[c] -> vaccrn[m]	0	57279.1	0	1000		Carnitine shuttle			
VACCt	fatty acid transport via diffusion	vacc[e] <=> vacc[c]	1		-1000	1000		Transport, Extracellular			
VALATB0tc	transport of L-Valine into the intestinal cells by ATB0 transporter	2 na1[u] + cl[u] + val-L[u] -> 2 na1[c] + cl[c] + val-L[c]	0	56774.1	0	1000	3	Transport, Lumen	PMID:18195088	ATB0 is both sodium and chloride coupled, with reaction stoichiometry 2Na+:1cl: 1amino acid. The transporter is localized in the intestine, has a broad substrate specificity (both neutral and cationic amino acids), but is not involved in the transport of aspartate, glutamate and proline (PMID:18195088).	
VALB0ATlc	transport of L-Valine by the apical neutral amino acid transporters B(0)AT1 or B(0)AT2 in kidney, intestine or brain	na1[u] + val-L[u] -> na1[c] + val-L[c]	0	(70008.1 or (74338.1 and 57394.1))	0	1000	3	Transport, Lumen	PMID: 19472175, PMID: 15804236, PMID: 18400692, PMID: 16185194, PMID: 18195088	B(0)AT1 transports all the neutral amino acids with preference for methionine, leucine and valine. Reaction stoichiometry is 1:1. Requires heterodimerization with collectrin protein for increased affinity. Found in kidney and intestine, however also reported to be expressed in skin. Requires association with ACE2 for expression in intestine but with collectrin for expression in kidney. The localization of the B(0)AT2 transporter has been studied in brain tissue but data from the kidney have not been reported (PMID: 18195088).	3.4.17.23
VALILELAT2tc	transport of L-Valine into the cell and efflux of L-Isoleucine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	ile-L[c] + val-L[e] -> ile-L[e] + val-L[c]	0	(20539.1 and 17254.1)	0	1000	3	Transport, Extracellular	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	Itger affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ovary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the mebrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274).	

VALLAT1tc	transport of L-Valine by LAT1 in association with 4F2hc, across the apical surface of the memebranes.	leu-L[c] + val-L[u] -> leu-L[u] + val-L[c]	0	(20539.1 and 17254.1)	0	1000	4	Transport, Lumen	Hans Gerhard Vogel, Franz J. Hock, Jochen Maas, Dieter Mayer (2006), Drug discovery and evaluation: Safety and pharmacokinetic assays, Springer publication, Chapter II D, page 456, table 3, PMID: 19035290, PMID: 12634921, European Journal of Pharmacology 441 (2002) 127-132. Am J Physiol Cell Physiol 281:C1077-C1093, 2001. Amino Acids (2005) 29: 229–233 DOI 10.1007/s00726-005-0221-x. PMID: 11901210	leucine is the only amino acid tested for efflux. Expressed in ovary, placenta, brain, spleen, testis, activated lymphocytes and some tumor cells. Functions as a antiport transport system (DOI 10.1016/j.cell.2009.01.02), requires heterodimerization with glycoprotein CD98 (Pflugers Arch-Eur J Physiol (2000) 440:503-512, DOI 10.1007/s004240000274, PMID: 10958334).	
VALPHELAT2tc	transport of L-Valine into the cell and efflux of L-Phenylalanine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	phe-L[c] + val-L[e] -> phe-L[e] + val-L[c]	0	(20539.1 and 17254.1)	0	1000	3	Transport, Extracellular	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s00420000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	higer affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of memebranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for traficking of the complex to the mebrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s00420000274).	
VALTA	valine transaminase	akg[c] + val-L[c] <=> glu-L[c] + 3mob[c]	1	12035.1	-1000	1000		Valine, Leucine, and Isoleucine Metabolism			
VALTAm	valine transaminase, mitochondiral	akg[m] + val-L[m] <=> glu-L[m] + 3mob[m]	1	12036.1	-1000	1000		Valine, Leucine, and Isoleucine Metabolism			
VALt4	L-valine transport in via sodium symport	na1[e] + val-L[e] -> na1[c] + val-L[c]	0	56774.1	0	1000		Transport, Extracellular			
VALt5m	Valine reversible mitochondrial transport	val-L[c] <=> val-L[m]	1		-1000	1000		Transport, Mitochondrial			
VALtec	L-valine transport via diffusion (extracellular to cytosol)	val-L[e] <=> val-L[c]	1	215113.1 or 72401.1	-1000	1000		Transport, Extracellular			
VD3	Vitamin D3 formation	pd3[c] <=> vitd3[c]	1		-1000	1000		Vitamin D			
VITD2Hm	Vitamin D-25-hydroxylase (D2)	h[m] + nadph[m] + o2[m] + vitd2[m] -> h2o[m] + nadp[m] + 25hvitd2[m]	0	104086.1	0	1000		Vitamin D			
VITD2t	Vitamin D2 release	vitd2[c] -> vitd2[e]	0		0	1000		Transport, Extracellular			
VITD2tm	Vitamin D2 transport from mitochondria	vitd2[m] <=> vitd2[c]	1		-1000	1000		Transport, Mitochondrial			
VITD3Hm	Vitamin D-25-hydroxylase (D3)	h[m] + nadph[m] + o2[m] + vitd3[m] -> h2o[m] + nadp[m] + 25hvitd3[m]	0	104086.1	0	1000		Vitamin D			
VITD3Te	release of vitamin D into lymph	vitd3[c] <=> vitd3[e]	1		-1000	1000	2	Transport, Extracellular	G.F.M. Ball (2006) Vitamins their role in the human body, Blackwell publishing, chapter 8, page 195-196.	incorporated into chylomicrons and transported into lymph.	
VITD3lu	uptake of vitamin D by enterocytes	vitd3[u] <=> vitd3[c]	1		-1000	1000	2	Transport, Lumen	G.F.M. Ball (2006) Vitamins their role in the human body, Blackwell publishing, chapter 8, page 195-196.	uptake of vitamin D by simple diffusion.	
VITD3t	Vitamin D3 release	vitd3[c] -> vitd3[e]	0		0	1000		Transport, Extracellular			
VITD3t2	Vitamin D3 uptake	vitd3[e] -> vitd3[c]	0		0	1000		Transport, Extracellular			
VITD3tm	Vitamin D3 transport from mitochondria	vitd3[m] -> vitd3[c]	0		0	1000		Transport, Mitochondrial			
VITD3tm3	Vitamin D3 transport in mitochondria	vitd3[c] -> vitd3[m]	0		0	1000		Transport, Mitochondrial			
VITEtc	uptake of alpha-Tocopherol into the enterocytes	avite1[u] -> avite1[c]	0	(20778.1 and 237636.1)	0	1000	3	Transport, Lumen	PMID: 15213020, PMID: 17320165, PMID: 18403720, PMID: 16380385, PMID: 15135148	vitamin E uptake is similar to cholesterol, although passive diffusion has been observed, receptor mediated transport is faster.	
VITEtl	efflux of alpha-Tocopherol into the lyphatics in chylomicrons	h2o[c] + atp[c] + avite1[c] -> adp[c] + h[c] + pi[c] + avite1[e]	0	11303.1	0	1000	3	Transport, Extracellular	PMID: 15213020, PMID: 17320165	ATP binding cassete required for efflux of the vitamin E into the lymph form the enterocytes.	
VITKtl	transport of vit K into lymph	phyQ[c] -> phyQ[e]	0		0	1000	2	Transport, Extracellular	PMID: 18841274	vit K release into lymph via chylomicrons	
VLCS2p	Very-long-chain-fatty-acid-CoA ligase	coa[x] + atp[x] + dhcholestanate[x] -> dhcholestancoa[x] + amp[x] + ppi[x]	0	26458.1	0	1000		Bile Acid Biosynthesis			
VLCS2r	Very-long-chain-fatty-acid-CoA ligase	atp[r] + coa[r] + dhcholestanate[r] -> dhcholestancoa[r] + amp[r] + ppi[r]	0	26458.1	0	1000		Bile Acid Biosynthesis			
VLCSp	Very-long-chain-fatty-acid-CoA ligase	coa[x] + atp[x] + thcholstoic[x] -> cholcoar[x] + amp[x] + ppi[x]	0	26458.1	0	1000		Bile Acid Biosynthesis			
VLCSr	Very-long-chain-fatty-acid-CoA ligase	atp[r] + coa[r] + thcholstoic[r] -> cholcoar[r] + amp[r] + ppi[r]	0	26458.1	0	1000		Bile Acid Biosynthesis			
WHDDCAte	xenobiotic transport	whddca[e] <=> whddca[c]	1		-1000	1000		Transport, Extracellular			
WHHDCAte	xenobiotic transport	whhdca[e] <=> whhdca[c]	1		-1000	1000		Transport, Extracellular			
WHTSTSTERONEte	omega hydroxy testosterone transport	whtststerone[c] <=> whtststerone[e]	1		-1000	1000		Transport, Extracellular			
WHTTDCAte	xenobiotic transport	whttdca[e] <=> whttdca[c]	1		-1000	1000		Transport, Extracellular			
XANDp	xanthine dehydrogenase, peroxisomal	nad[x] + h2o[x] + xan[x] -> h[x] + nadh[x] + urate[x]	0	22436.1	0	1000		Purine Catabolism			
XANtx	xanthine diffusion in peroxisome	xan[c] -> xan[x]	0		0	1000		Transport, Peroxisomal			
XAO2x	xanthine oxidase	o2[x] + h2o[x] + hxan[x] -> h2o2[x] + xan[x]	0	22436.1	0	1000		Purine Catabolism			
XAOx	xanthine oxidase,peroxisomal	o2[x] + h2o[x] + xan[x] -> h2o2[x] + urate[x]	0	22436.1	0	1000		Purine Catabolism			
XOL27OHtm	27 hydroxy cholesterol transport	xol27oh[r] <=> xol27oh[m]	1		-1000	1000		Transport, Mitochondrial			
XOL7AH2tm	lipid, flip-flop intracellular transport	xol7ah2[c] <=> xol7ah2[m]	1		-1000	1000		Transport, Mitochondrial			
XOL7AH2tr	lipid, flip-flop intracellular transport	xol7ah2[c] <=> xol7ah2[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
XOL7AONEtr	lipid, flip-flop intracellular transport	xol7aone[c] <=> xol7aone[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
XOLDIOLONEt	lipid, flip-flop intracellular transport	xoldiolone[c] <=> xoldiolone[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
XOLDIOLONEtm	lipid, flip-flop intracellular transport	xoldiolone[m] <=> xoldiolone[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
XOLEST2HSTDlu	Transport, extracellular	xolest2_hs[c] -> xolest2_hs[e]	0		0	1000	2	Transport, Extracellular	Sareen S. Gropper, jack L. Smith, James L. Groff (2009) Wadaworth cengage learning, Advanced nutrition and human metabolism, 5th edition, page 142-148.	transported in chylomicrons into lymph	
XOLEST2te	cholesterol ester transporter	xolest2_hs[e] <=> xolest2_hs[c]	1		-1000	1000		Transport, Extracellular			
XOLESTte	cholesterol ester transporter	xolest_hs[e] <=> xolest_hs[c]	1		-1000	1000		Transport, Extracellular			
XOLTRI24tc	24 trihydroxy cholesterol transport	xoltri24[r] <=> xoltri24[c]	1		-1000	1000		Transport, Endoplasmic Reticular			
XOLTRI24te	24 trihydroxy cholesterol transport	xoltri24[c] <=> xoltri24[e]	1		-1000	1000		Transport, Extracellular			
XOLTRI25tc	25 trihydroxy cholesterol transport	xoltri25[r] <=> xoltri25[c]	1		-1000	1000		Transport, Endoplasmic Reticular			
XOLTRI25te	25 trihydroxy cholesterol transport	xoltri25[c] <=> xoltri25[e]	1		-1000	1000		Transport, Extracellular			
XOLTRI27tc	27 trihydroxy cholesterol transport	xoltri27[r] <=> xoltri27[c]	1		-1000	1000		Transport, Endoplasmic Reticular			
XOLTRI27te	27 trihydroxy cholesterol transport	xoltri27[c] <=> xoltri27[e]	1		-1000	1000		Transport, Extracellular			
XOLTRIOLtm	lipid, flip-flop intracellular transport	xoltriol[c] <=> xoltriol[m]	1		-1000	1000		Transport, Mitochondrial			
XOLTRIOLtr	lipid, flip-flop intracellular transport	xoltriol[c] <=> xoltriol[r]	1		-1000	1000		Transport, Endoplasmic Reticular			
XSERtg	Xyl-L-Ser (protein) transport from endoplasmic reticulum to Golgi apparatus	xser[r] -> xser[g]	0		0	1000		Transport, Golgi Apparatus			
XYLK	xylulokinase	atp[c] + xylu-D[c] -> adp[c] + h[c] + xu5p-D[c]	0	102448.1	0	1000		Pentose and Glucuronate Interconversions			
XYLTD_Dr	xylitol dehydrogenase (D-xylose-forming)	nad[c] + xylt[c] <=> h[c] + nadh[c] + xylu-D[c]	1		-1000	1000		Pentose and Glucuronate Interconversions			
XYLTer	UDP-xylose:protein xylosyltransferase, endoplasmic reticulum	Ser_Gly_Ala_X_Gly[r] + udpxyl[r] -> h[r] + udp[r] + xser[r]	0	217119.1 or 233781.1	0	1000		Chondroitin / heparan sulfate biosynthesis			
XYLTt	Xylitol transport via passive diffusion	xylt[e] <=> xylt[c]	1		-1000	1000		Transport, Extracellular			
XYLUR	xylulose reductase	h[c] + nadph[c] + xylu-L[c] <=> nadp[c] + xylt[c]	1	67880.1	-1000	1000		Pentose and Glucuronate Interconversions			
XYLt	D-xylose reversible transport	xyl-D[e] <=> xyl-D[c]	1	20527.1	-1000	1000		Transport, Extracellular			
XYLtly	Xylose efflux from lysosome	xyl-D[l] -> xyl-D[c]	0		0	1000		Transport, Lysosomal			
YVITEt	gamma-Tocopherol (Vit. E) transport	yvite[e] -> yvite[c]	0		0	1000		Transport, Extracellular			
biomass_mm_1_no_glygln	Biomass_reaction_mm_1_no_glygln	43.153 h2o[c] + 43.153 atp[c] + 0.564 leu-L[c] + 0.386 glu L[c] + 0.359 asp-L[c] + 0.033 amp[c] + 0.0148 damp[c] + 0.0551 cmp[c] + 0.6 ala-L[c] + 0.2881 asn-L[c] + 0.145 cys-L[c] + 0.322 gln-L[c] + 0.538 gly[c] + 0.324 ile-L[c] + 0.219 phe-L[c] + 0.43 ser-L[c] + 0.386 thr-L[c] + 0.377 arg-L[c] + 0.57 lys-L[c] + 0.138 met-L[c] + 0.143 his-L[c] + 0.01 pail_hs[c] + 0.069 pchol_hs[c] + 0.026 pe_hs[c] + 0.018 chsterol[c] + 0.001 pglyc_hs[c] + 0.003 clpn_hs[c] + 0.0099 dcmp[c] + 0.0099 dgmp[c] + 0.0148 dtmp[c] + 0.0624 gmp[c] + 0.033 ump[c] + 0.313 pro-L[c] + 0.182 tyr-L[c] + 0.044 trp-L[c] + 0.003 ps_hs[c] + 0.008 sphmyln_hs[c] + 0.416 val-L[c] -> 43.153 adp[c] + 43.153 h[c] + 43.153 pi[c]	0		0	1000	0	Biomass			
sink_citr-L	sink_citr-L	citr-L[c] <=>	1		0	0		Exchange/ demand			
sink_pre_prot(er)	sink_pre_prot(er)	pre_prot[r] <=>	1		-1	1000		Exchange/ demand			
sink_citr-L	sink_citr-L	citr-L[c] <=>	1		0	0		Exchange/ demand			
sink_pre_prot(er)	sink_pre_prot(er)	pre_prot[r] <=>	1		-1	1000		Exchange/ demand			

Table S11b: Intestinal absorption and transport reactions module with supporting references.

Rev = Reversibility (1 = reversible, 0 = irreversible), CS = Confidence score

BIGG Rxn ID	Rxn Full Name	Rxn Formula	Mouse GeneID Association	Human GeneID Association	Protein	EC Number	Protein-Association	Catalyzing enzymes	Notes	References	Rev	CS
25HVITD3tc	transport of 25-Hydroxyvitamin D3 into the intestine for absorption and into the renal cells for hydroxylation into active form of vitamin D	25hvitd3[u] -> 25hvitd3[c]	(14473.1 and 14725.1 and 65969.1)	(2638.1 and 436.1 and 829.1)	Vitamin D-binding protein Low-density lipoprotein receptor-related protein 2 Cubilin		Vitamin D-binding protein and Low-density lipoprotein receptor-related protein 2 and Cubilin		DBP has higher affinity for 25(OH)D than for D3 (G.F.M. Ball (2006) Vitamins their role in the human body, Blackwell publishing, chapter 8, page 195-196). 25(OH) D binds DBP and is then recruited by megalin and cubilin for further hydroxylation in kidney and cellular uptake in intestine (PMID: 15951480).	PMID: 19646505, PMID: 15951480, PMID: 12401816	0	4
34DHPHELATtc	transport of 3,4-Dihydroxy-L-phenylalanine by LAT1 in association with 4F2hc, across the apical surface of the membranes.	34dhphe[u] + leu_L[c] -> 34dhphe[c] + leu_L[u]	(2539.1 and 17254.1)	(814.1 and 652.1)	Large neutral amino acids transporter small subunit 1 4F2 cell-surface antigen heavy chain		Large neutral amino acids transporter small subunit 1 and 4F2 cell-surface antigen heavy chain		leucine is the only amino acid tested for efflux. Expressed in ovary, placenta, brain, spleen, testis, activated lymphocytes and some tumor cells. Functions as a antiport transport system (DOI 10.1016/j.cell.2009.01.02), requires heterodimerization with glycoprotein CD98 (Pflugers Arch-Eur J Physiol (2000) 440:503-512, DOI 10.1007/s004240000274, PMID: 10958334).	Hans Gerhard Vogel, Franz J. Hock, Jochen Maas, Dieter Mayer (2006), Drug discovery and evaluation: Safety and pharmacokinetic assays, Springer publication, Chapter II D, page 458, table 3, PMID: 19035290, PMID: 12634921, European Journal of Pharmacology 441 (2002) 127-132. Am J Physiol Cell Physiol 281:C1077-C1093, 2001. Amino Acids (2005) 29: 229–233 DOI 10.1007/s00726-005-0221-x. PMID: 11903210	0	4
4OHPROIMINOtc	transport of L-OH-Proline by the apical IMINO amino acid transporters in kidney and intestine	4hpro_LT[u] + 2 na1[u] + cl[u] -> 4hpro_LT[c] + 2 na1[c] + cl[c]	(1268.1 and 57394.1)	(54716.1 and 57393.1)	Sodium- and chloride-dependent transporter XTRP3 Collectrin		Sodium- and chloride-dependent transporter XTRP3 and Collectrin		IMINO transporter is suggested to be a candidate for iminoglycinuria (PMID: 16052352). Associted with collectrin in kidney.	PMID: 19657969, PMID: 15632147, PMID: 18195088, PMID: 18400692, PMID:19184091	0	4
5MTHFtc	transport of 5-Methyltetrahydrofolate by folate receptor protein	5mthf[u] -> 5mthf[c]	(14275.1 or 14276.1)	(2348.1 or 235.1 or 2352.1)	Folate receptor alpha Folate receptor beta Folate receptor gamma		Folate receptor alpha or Folate receptor beta or Folate receptor gamma		the folate receptor is encoaled by atleast 3 genes, most tissues expressing the alpha form. The folate receptor like protein mediates unidirectional flux following internalization of the folate-receptor complex. (James Zempleni, Robert B. Rucker, Donald B. McCormick, John W. Suttie (2007) Handbook of vitamins, CRC press, chapter 12, page 390-391)	James Zempleni, Robert B. Rucker, Donald B. McCormick, John W. Suttie (2007) Handbook of vitamins, CRC press, chapter 12, page 390-391, Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Advanced nutrition and human metabolism, Wadsworth cengage learning, 5th edition, page 349-351, G.F.M. Ball (2006) Vitamins their role in the human body, Blackwell publishing, chapter 17, page 351-356	0	4
ALAALACNc	peptide absorption	alaala[c] + h2o[c] <=> ala_L[c] + ala_L[c]	(33843.1 or 6654.1)	(84735.1 or 55748.1)	Beta-Ala-His dipeptidase Cytosolic non-specific dipeptidase	3.4.13.2 or 3.4.13.18	Beta-Ala-His dipeptidase or Cytosolic non-specific dipeptidase		Dipeptides and tripeptides enter the brush border of the intestinal mucosal cells, where they are hydrolyzed to free amino acids, which are then transported into hepatic portal vein. Peptides entering by transcellular or paracellular mechanismm elicit allergic reactions to food (Robert K. Murray, David A. Bender, Kathleen M. Botham, Peter J. kennelly, Victor W. Rodwell, P. Anthony Weil (2009) 28th edition, Harpers illustrated biochemistry,Mc Graw Hill, page 462). formation and hydrolysis of diglycine is a reversible process (David L. Nelson, Michael M. Cox, Lehninger principles of biochemistry (2008), 3rd edition, worth publishers,page 69, figure 3a). CN1 is expressed in brain where as CN2 is more ubiquitously expressed (PMID: 12473676).	PMID: 6993048, PMCID: PMC1412501, PMID: 4919261, PMID: 20178671, PMID: 12473676	1	4
ALAALAPEPT1tc	transport of Alanylalanine by the apical PEPT1 amino acid transporters across the brush border cells of the enterocytes of the intestine and renal cells	alaala[u] + h[u] -> alaala[c] + h[c]	215335.1	(6564.1)	Solute carrier family 15 member 1		Solute carrier family 15 member 1		PEPT1 appears to transport all di- and tri- peptides across the brush border of the intestinal cells (Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Advanced nutrition and human metabolism, Wadsworth congage learning, 5th edition, page 193). PEPT1 is expressed highly in intestinal cells where as PEPT2 is localized to renal cells (PMID: 10330047).	PMID: 7858848, PMID: 14965252, PMID: 14977407, PMID: 10330047	0	4
ALAATB0tc	transport of L-Alanine into the intestinal cells by ATB0 transporter	ala_L[u] + 2 na1[u] + cl[u] -> ala_L[c] + 2 na1[c] + cl[c]	56774.1	(11254.1)	Sodium- and chloride-dependent neutral and basic amino acid transporter B(+)		Sodium- and chloride-dependent neutral and basic amino acid transporter B(+)		ATB0 is both sodium and chloride coupled, with reaction stoichiometry 2Na+: 1cl- lumino acid. The transporter is located in the intestine, has a broad substrate specificity (both neutral and cationic amino acids), but is not involved in the transport of aspartate, glutamate and proline (PMID:18195088).	PMID:18195088	0	4
ALADPATtc	transport of D-Alanine by the apical PAT2 or PAT1 amino acid transporters in kidney and intestine	ala_D[u] + h[u] -> ala_D[c] + h[c]	215335.1	(26358.1)	Proton-coupled amino acid transporter 1		Proton-coupled amino acid transporter 1		PAT2 is strongly expressed in heart and lung and more weakly in kidney and muscle (PMID:18400692). PAT2 doest not strongly discriminate between L and D isomers (PMID 18400692). PAT1 proton-amino acid co-transporter with 1:1 stoichiometry, does not discriminate between L and D isomers, located on the apical membrane of kidney and intestine (PMID: 18400692, PMID: 18195088).	PMID:18195088, PMID:18400692, PMID: 15345686, PMID: 17123464, PMCID: PMC34647, PMID: 10958334	0	4
ALAILELAT2tc	transport of L-Alanine into the cell and efflux of L-leucine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	ala_L[e] + ile_L[c] -> ala_L[c] + ile_L[e]	(2539.1 and 17254.1)	(23428.1 and 652.1)	Large neutral amino acids transporter small subunit 2 4F2 cell-surface antigen heavy chain		Large neutral amino acids transporter small subunit 2 and 4F2 cell-surface antigen heavy chain		higher affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274).	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-x, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	0	4
ALALPATtc	transport of L-Alanine by the apical PAT2 or PAT1 amino acid transporters in kidney and intestine	ala_L[u] + h[u] -> ala_L[c] + h[c]	215335.1	(26358.1)	Proton-coupled amino acid transporter 1		Proton-coupled amino acid transporter 1		PAT2 is strongly expressed in heart and lung and more weakly in kidney and muscle (PMID:18400692). PAT2 doest not strongly discriminate between L and D isomers (PMID 18400692). PAT1 proton-amino acid co-transporter with 1:1 stoichiometry, does not discriminate between L and D isomers, located on the apical membrane of kidney and intestine (PMID: 18400692, PMID: 18195088).	PMID:18195088, PMID:18400692, PMID: 17123464, PMCID: PMC34647, PMID: 15345686	0	4
ALAPHELAT2tc	transport of L-Alanine into the cell and efflux of L-Phenylalanine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	ala_L[e] + phe_L[c] -> ala_L[c] + phe_L[e]	(2539.1 and 17254.1)	(23428.1 and 652.1)	Large neutral amino acids transporter small subunit 2 4F2 cell-surface antigen heavy chain		Large neutral amino acids transporter small subunit 2 and 4F2 cell-surface antigen heavy chain		higher affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274).	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-x, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	0	4
ALAt4tc	transport of L-Alanine by the apical neutral amino acid transporters in kidney and intestine	ala_L[u] + na1[u] -> ala_L[c] + na1[c]	(78.1 or 74338.1 and 57394.1))	(3424.1) and (57393.1 or 58272.1)	Sodium-dependent neutral amino acid transporter B(0)AT1 Collectrin Angiotensin-converting enzyme 2	3.4.17.23	Sodium-dependent neutral amino acid transporter B(0)AT1 and Collectrin or Angiotensin-converting enzyme 2	Angiotensin-converting enzyme 2	transports all the neutral amino acids with preference for methionine, leucine and valine. Reaction stoichiometry is 1:1. Requires heterodimerization with collectrin protein for increased affinity. Found in kidney and intestine, however also reported to be expressed in skin. Requires association with ACE2 for expression in intestine but with collectrin for expression in kidney.	PMID: 19472175, PMID: 15804236, PMID: 18400692	0	4
ALAyLATtc	transport of L-Alanine by y+LAT1 or y+LAT2 transporters in small intestine and kidney	ala_L[e] + na1[e] + arg_L[c] -> ala_L[c] + na1[c] + arg_L[e]	(254.1 or (33836.1 and 17254.1))	(956.1 or 957.1) and (652.1)	Y+L amino acid transporter 1 Y+L amino acid transporter 2 4F2 cell-surface antigen heavy chain		Y+L amino acid transporter 1 or Y+L amino acid transporter 2 and 4F2 cell-surface antigen heavy chain		y+LAT1 and y+LAT2 transporters requires CD98 for sequestorization to the plasma membrane. Acts as an amino acid exchanger, with influx of neutral aminoa acids and efflux of cationic amino acid, requires Na+ for optimal activity. Can also operate with H+ in absence of Na+ (PMID: 11546643).	PMID: 11546643, PMID:18195088	0	4

ALAyLAT4tc	transport of Alanine by y+LAT1 or y+LAT2 with co-transporter of h in small intestine and kidney	ala_L[e] + h[e] + arg_L[c] -> ala_L[c] + h[c] + arg_L[e]	(254.1 or (33836.1 and 17254.1))	(956.1 or 957.1) and (652.1)	Y+L amino acid transporter 1 Y+L amino acid transporter 2 4F2 cell-surface antigen heavy chain		Y+L amino acid transporter 1 or Y+L amino acid transporter 2 and 4F2 cell-surface antigen heavy chain		y+LAT1 and y+LAT2 transporters requires CD98 for sequestrization to the plasma membrane. Acts as an amino acid exchanger, with influx of neutral aminoa acids and efflux of cationic amino acid, requires Na+ for optimal activity. Can also operate with H+ in absence of Na+ (PMID: 11546643).	PMID: 11546643, PMID:18195088	0	4
ALINOFABPpmtc	uptake of alpha-Linolenic acid by the enterocytes	lnlnca[u] -> lnlnca[c]	(14719.1 or 12491.1)	(286.1 or 948.1)	Aspartate aminotransferase, mitochondrial Platelet glycoprotein 4		Aspartate aminotransferase, mitochondrial or Platelet glycoprotein 4		GOT2 encodes FABPpm that may either act alone or in co-ordination with CD36, for the uptake of long chain fatty acids (exhibits a selective preference for long chain PUFA and essential fatty acids over non-essential fatty acids). The fatty acids alternatively can undergo passive diffusion. once inside the cell, they bind to the cytoplasmic fatty acid binding protein (FABPc) and thereby undergo activation or esterification. Additionally, a minority of fatty acids are thought to be transported by FATP1 and rapidly activated by plasma membrane acyl-CoA synthetase (ACS1) to form acyl-Co esters. (PMID: 20086080)	PMID: 20086080, PMID: 10617989, PMID: 8717462, Progress in Lipid Research Volume 48, Issue 2, March 2009, Pages 101-115	0	4
ARACHFABPpmtc	uptake of arachidonic acid by the enterocytes	arachd[u] -> arachd[c]	(14719.1 or 12491.1)	(286.1 or 948.1)	Aspartate aminotransferase, mitochondrial Platelet glycoprotein 4		Aspartate aminotransferase, mitochondrial or Platelet glycoprotein 4		GOT2 encodes FABPpm that may either act alone or in co-ordination with CD36, for the uptake of long chain fatty acids (exhibits a selective preference for long chain PUFA and essential fatty acids over non-essential fatty acids). The fatty acids alternatively can undergo passive diffusion. once inside the cell, they bind to the cytoplasmic fatty acid binding protein (FABPc) and thereby undergo activation or esterification. Additionally, a minority of fatty acids are thought to be transported by FATP1 and rapidly activated by plasma membrane acyl-CoA synthetase (ACS1) to form acyl-Co esters. (PMID: 20086080)	PMID: 20086080, PMID: 10617989, PMID: 8717462, Progress in Lipid Research Volume 48, Issue 2, March 2009, Pages 101-115	0	4
ARGALArBATtc	transport of L-Arginine into the cell in exchange for L-Alanine by b0,+AT transporter at the apical surfaces of the membranes of small intestine and renal cells.	arg_L[u] + ala_L[c] -> arg_L[c] + ala_L[u]	(3962.1 and 2532.1)	(11136.1 and 6519.1)	B(,+)-type amino acid transporter 1 Neutral and basic amino acid transport protein rBAT		B(,+)-type amino acid transporter 1 and Neutral and basic amino acid transport protein rBAT		sodium independant antiport transport system, exchanges di-basic amino acids into the cells and neutral amino acids out of the cell. Located on the apical surfaces of transporting epithelia. Cellular localization being small intestine, kidney (proximal tubule), lung, placenta, brain and thymus. Requires the heterodimerization with rBAT glycoprotein. (PMID: 10958334).	PMID: 10958334, PMID: 19184091, PMID: 18195088, PMID: 11546643	0	4
ARGATB0tc	transport of L-Arginine into the intestinal cells by ATB0 transporter	arg_L[u] + 2 na1[u] + cl[u] -> arg_L[c] + 2 na1[c] + cl[c]	56774.1	(11254.1)	Sodium- and chloride-dependent neutral and basic amino acid transporter B(+)		Sodium- and chloride-dependent neutral and basic amino acid transporter B(+)		ATB0 is both sodium and chloride coupled, with reaction stoichiometry 2Na+:1cl:1amino acid. The transporter is located in the intestine, has a broad substrate specificity (both neutral and cationic amino acids), but is not involved in the transport of aspartate, glutamate and proline (PMID:18195088).	PMID:18195088	0	4
ARGLEUrBATtc	transport of L-Arginine into the cell in exchange for L-Leucine by b0,+AT transporter at the apical surfaces of the membranes of small intestine and renal cells.	arg_L[u] + leu_L[c] -> arg_L[c] + leu_L[u]	(3962.1 and 2532.1)	(11136.1 and 6519.1)	B(,+)-type amino acid transporter 1 Neutral and basic amino acid transport protein rBAT		B(,+)-type amino acid transporter 1 and Neutral and basic amino acid transport protein rBAT		sodium independant antiport transport system, exchanges di-basic amino acids into the cells and neutral amino acids out of the cell. Located on the apical surfaces of transporting epithelia. Cellular localization being small intestine, kidney (proximal tubule), lung, placenta, brain and thymus. Requires the heterodimerization with rBAT glycoprotein. (PMID: 10958334).	PMID: 10958334, PMID: 19184091, PMID: 18195088, PMID: 11546643	0	4
ARGtSe	transport of L-Arginine by y+ transporter	arg_L[c] <=> arg_L[e]	11987.1	(6541.1)	High affinity cationic amino acid transporter 1		High affinity cationic amino acid transporter 1		ubiquitously expressed y+ transport system, mediates uniport transport of arginine, lysine, ornithine and histidine. (PMID: 18195088). Located on the basolateral surface, mediates a bidirectional uniport transport of acationic amino acid and is Na+ independant (PMID: 17494634). Recon 1 contains the reactions but with irreversible form.	PMID: 14770310, PMID: 12506130, PMID: 17494634,PMID:18195088.	1	4
ASCBSVCTtc	transport of L-Ascorbate by SVCT1 or SVCT2 transporter	asch_L[u] + 2 na1[u] + atp[c] + h2o[c] -> asch_L[c] + 2 na1[c] + adp[c] + pi[c] + h[c]	2522.1 or 54338.1	(9963.1 or 9962.1)	Solute carrier family 23 member 1 Solute carrier family 23 member 2		Solute carrier family 23 member 1 or Solute carrier family 23 member 2		SVCT1 and SVCT2 differ in their tissue distribution, SVCT1 is more ubiquitously expressed, where as SVCT1 is confined to intestine, liver and kidney. The Na+ symport transport is energised by Na+/K+ ATPase, therefore its a secondary active transport (G.F.M. Ball (2006) Vitamins their role in the human body, Blackwell publishing, chapter 19, page 395-398). Vitamin C is absorbed only in ascorbate form, can be oxidised into dehydroascorbate, and can then enter the blood stream (Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Advanced nutrition and human metabolism, Wadsworth cengage learning, 5th edition, page 312-313).	PMID: 18094143, PMID: 11396616, G.F.M. Ball (2006) Vitamins their role in the human body, Blackwell publishing, chapter 19, page 395-398, PMID: 17222174	0	4
ASNATB0tc	transport of L-Asparagine into the intestinal cells by ATB0 transporter	asn_L[u] + 2 na1[u] + cl[u] -> asn_L[c] + 2 na1[c] + cl[c]	56774.1	(11254.1)	Sodium- and chloride-dependent neutral and basic amino acid transporter B(+)		Sodium- and chloride-dependent neutral and basic amino acid transporter B(+)		ATB0 is both sodium and chloride coupled, with reaction stoichiometry 2Na+:1cl:1amino acid. The transporter is located in the intestine, has a broad substrate specificity (both neutral and cationic amino acids), but is not involved in the transport of aspartate, glutamate and proline (PMID:18195088).	PMID:18195088	0	4
ASNB0AT1tc	transport of L-Asparagine by the apical neutral amino acid transporters in kidney and intestine	asn_L[u] + na1[u] -> asn_L[c] + na1[c]	(78.1 or (74338.1 and 57394.1))	(3424.1) and (57393.1 or 59272.1)	Sodium-dependent neutral amino acid transporter B(0)AT1 Collectin Angiotensin-converting enzyme 2	3.4.17.23	Sodium-dependent neutral amino acid transporter B(0)AT1 and Collectin or Angiotensin-converting enzyme 2	Angiotensin-converting enzyme 2	transports all the neutral amino acids with preference for methionine, leucine and valine. Reaction stoichiometry is 1:1. Requires heterodimerization with collectrin protein for increased affinity. Found in kidney and intestine, however also reported to be expressed in skin. Requires association with ACE2 for expression in intestine but with collectrin for expression in kidney.	PMID: 19472175, PMID: 15804236, PMID: 18400892	0	4
ASNILELAT2tc	transport of L-Asparagine into the cell and efflux of L-Isoleucine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	asn_L[e] + ile_L[c] -> asn_L[c] + ile_L[e]	(2539.1 and 17254.1)	(23428.1 and 652.1)	Large neutral amino acids transporter small subunit 2 4F2 cell-surface antigen heavy chain		Large neutral amino acids transporter small subunit 2 and 4F2 cell-surface antigen heavy chain		higher affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s0042000000274).	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s0042000000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	0	4
ASNPHELAT2tc	transport of L-Asparagine into the cell and efflux of L-Phenylalanine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	asn_L[e] + phe_L[c] -> asn_L[c] + phe_L[e]	(2539.1 and 17254.1)	(23428.1 and 652.1)	Large neutral amino acids transporter small subunit 2 4F2 cell-surface antigen heavy chain		Large neutral amino acids transporter small subunit 2 and 4F2 cell-surface antigen heavy chain		higher affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s0042000000274).	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s0042000000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	0	4
BALABETAtc	transport of beta alanine into the intestinal cells by beta transport system	ala_B[u] + 2 na1[u] + cl[u] -> ala_B[c] + 2 na1[c] + cl[c]	56774.1	(6533.1)	Sodium- and chloride-dependent taurine transporter		Sodium- and chloride-dependent taurine transporter		beta transporter system requires chloride ions for optimal uptake of amino acids into the cells. Expressed on both apical and basolateral membranes of renal cells. Transports taurine and beta alanine. (PMID: 18195088)	PMID: 19074966, PMID: 2206910, PMID: 1324004, PMID: 16956961, PMID: 15166008, PMID: 18195088	0	4

BALAPAT1tc	transport of beta alanine by PAT1 in renal and intestinal cells	ala_B[s] + h[s] -> ala_B[c] + h[c]	215335.1	(26358.1)	Proton-coupled amino acid transporter 1		Proton-coupled amino acid transporter 1		PAT1 proton-amino acid co-transporter with 1:1 stoichiometry, does not discriminate between L and D isomers, located on the apical membrane of kidney and intestine (PMID: 18400692, PMID: 18195088).	PMID: 17123464, PMID: 18400692, PMCID: PMC34647, PMID: 15345686, PMID: 18195088	0	4
BGLUGCHe	binding of betaglucans with glycocholate in the intestinal lumen, reducing serum cholesterol levels.	bglc[u] + gchola[u] -> gbglchl[u]							oxidized beta glucan forms binds the bile acids more effectively. beta glucan binds bile acids and leads to enhanced excretion, there by the 7-alpha hydroxylase pathway is activated leading to increased cholesterol catabolism for synthesis of more bile acids (regulates cholesterol metabolism). however the decreased serum cholesterol levels are brought about by many other cumulative effects (water unstirred action of dietary fibres, glycemic role etc) (PMID: 18302966, Gunness P, Gidley MJ. (2010). Food & Function 1: 149-55).	Park SY, Bae IY, Lee S, Lee HG. (2009). Journal of Agricultural and Food Chemistry 57: 439-43, PMCID: PMC2663451, PMID: 17251929	0	3

BGLUTCHLe	binding of betaglucans with taurocholate in the intestinal lumen, reducing serum cholesterol levels.	bglc[u] + tchola[u] -> gltcha[u]							oxidized beta glucan forms binds the bile acids more effectively. beta glucan binds bile acids and leads to enhanced excretion, there by the 7-alpha hydroxylase pathway is activated leading to increased cholesterol catabolism for synthesis of more bile acids (regulates cholesterol metabolism). however the decreased serum cholesterol levels are brought about by many other cumulative effects (water unstirred action of dietatary fibres, glycemic role etc) (PMID: 18302966, Gunness P, Gidley MJ. (2010). Food & Function 1: 149-55).	Park SY, Bae IY, Lee S, Lee HG. (2009). Journal of Agricultural and Food Chemistry 57: 439-43, PMCID: PMC2663451, PMID: 17251929	0	3
BGLUTDECHOe	binding of betaglucans with taurodeoxycholate in the intestinal lumen, reducing serum cholesterol levels.	bglc[u] + tdechola[u] -> glutechol[u]							oxidized beta glucan forms binds the bile acids more effectively. beta glucan binds bile acids and leads to enhanced excretion, there by the 7-alpha hydroxylase pathway is activated leading to increased cholesterol catabolism for synthesis of more bile acids (regulates cholesterol metabolism). however the decreased serum cholesterol levels are brought about by many other cumulative effects (water unstirred action of dietatary fibres, glycemic role etc) (PMID: 18302966, Gunness P, Gidley MJ. (2010). Food & Function 1: 149-55).	Park SY, Bae IY, Lee S, Lee HG. (2009). Journal of Agricultural and Food Chemistry 57: 439-43, PMCID: PMC2663451, PMID: 17251929	0	3
BTNTe	release of biotin across the basolatral membrane	btn[c] -> btn[e]							biotin release from the enterocytes along the baso-lateral membrane is carrier protein mediated, Na+ independant and eletroneutral (exact protein involved needs to be further investigated). However pantothenic acid seems to compete with biotin for uptake. also in the presence of pantothenate, more amount of biotin exits enterocytes (PMID: 10064315).	PMID: 1953660, PMID: 21749121, G.F.M. Ball (2006) Vitamins their role in the human body, Blackwell publishing, chapter 16, page 339-340.	0	1
CARbPTtc	transport of L-Carnosine by hPT3 or hPT4 peptide transporter.	carn[i] + h[i] -> carn[c] + h[c]	27416.1 or 27416.2 or 239273.1	(51296.1 or 12126.1)	Solute carrier family 15 member 3 Solute carrier family 15 member 4		Solute carrier family 15 member 3 or Solute carrier family 15 member 4		hPT3 (human peptide transporter 3) transports histidine and di-peptides from the lysosomes into the cytosol. Co-transports proton, expressed in lung, thymus, spleen and faintly in brain, placenta, liver, adrenal gland and heart (PMID: 12905028). hPT4 expressed in brain, placenta and retina. Transports carnosine and histidine in a proton symport mechanism. (PMID: 12905028).	PMID: 16289537, PMID: 12905028, PMID: 17681807	1	4
CARNCNc	hydrolysis of L-Carnosine for uptake	carn[c] + h2o[c] <=> ala_B[c] + his_L[c]	(33843.1 or 6654.1)	(84735.1 or 55748.1)	Beta-Ala-His dipeptidase Cytosolic non-specific dipeptidase	3.4.13.2 or 3.4.13.18	Beta-Ala-His dipeptidase or Cytosolic non-specific dipeptidase		Dipeptides and tripeptides enter the brush border of the intestinal mucosal cells, where they are hydrolyzed to free amino acids, which are then transported into hepatic portal vein. Peptides entering by transcellular or paracellular mechanisms elicit allergic reactions to food (Robert K. Murray, David A. Bender, Kathleen M. Botham, Peter J. kennelly, Victor W. Rodwell, P. Anthony Weil (2009) 28th edition, Harpers illustrated biochemistry,Mc Graw Hill, page 462). formation and hydrolysis of diglycine is a reversible process (David L. Nelson, Michael M. Cox, Lehninger principles of biochemistry (2000), 3rd edition, worth publishers,page 69, figure 3a). CN1 is expressed in brain where as CN2 is more ubiquitously expressed (PMID: 12473670). Recon 1 mentions this reaction as NBAHH_ir which needs to be replaced.	PMID: 6993048, PMCID: PMC1412501, PMID: 4919261, PMID: 20178671, PMID: 12473676	1	4
CARPEPT1tc	transport of L-Carnosine by the apical PEPT1 amino acid transporters across the brush border cells of the enterocytes of the intestine and renal cells	carn[u] + h[u] -> carn[c] + h[c]	(65221.1 or 1561.1)	(6564.1)	Solute carrier family 15 member 1		Solute carrier family 15 member 1		PEPT1 appears to transport all di- and tri- peptides across the brush border of the intestinal cells (Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Advanced nutrition and human metabolism, Wadsworth cengage learning, 5th edition, page 193). PEPT1 is expressed highly in intestinal cells where as PEPT2 is localized to renal cells (PMID: 10330047).	PMID: 7858848, PMID: 14965252, PMID: 14977407, PMID: 10330047	0	4
CBLTDe_r	release of B12 by simple diffusion, reversible	adocbl[c] <=> adocbl[e]							binds to transcobalamin II within the enterocyte before release into the portal blood.	Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Advanced nutrition and human metabolism, Wadsworth cengage learning, 5th edition, page 359-360.	0	1
CBLtu	transport of Adenosylcobalamin into the intestine	adocbl[u] -> adocbl[c]	(1465.1 or 65969.1 or 93835.1)	(2694.1 and 829.1 and 81683.1)	Gastric intrinsic factor Cubilin Protein amnionless		Gastric intrinsic factor and Cubilin and Protein amnionless		Cobalamin binds intrinsic factor and then the complex binds cubilin and amnionless (that serve as anchors for the receptor). Even though megalin (MACI) and receptor-associated protein (RAP) can interact with CUB, the precise role if any, of these proteins in CUB-mediated absorption of IF-Cbl has not been determined (PMCID: PMC2809139). absorption of cobalamin can also occur by simple diffusion along the entire small intestine, this accounts for 1-3% of the dietary vitamin, however significant role under pharmacological doses (G.F.M. Ball (2006) Vitamins their role in the human body, Blackwell publishing, chapter 18, page 386).	PMCID: PMC2809139, Janos Zempleni, Robert B. Rucker, Donald B. McCormick, John W. Suttie (2007) Handbook of vitamins, CRC press, chapter 13, page 418-422	0	4
CHOLABCAet	efflux of Cholesterol into the lymph	chsterol[c] + atp[c] + h2o[c] -> chsterol[u] + adp[c] + p4[c] + h[c]	1133.1	(19.1)	ATP-binding cassette sub-family A member 1		ATP-binding cassette sub-family A member 1		ABCA1 is responsible for the efflux of cholesterol from the enterocytes into the lymph, for incorporation into nascent HDL, accounts for 30% of reverse cholesterol transfer (PMID: 21188557)	PMID: 21188557, PMID: 18692849, PMID: 20454462	0	4
CHOLABSetc	efflux of Cholesterol from the enterocytes into lumen	chsterol[c] + atp[c] + h2o[c] -> chsterol[u] + adp[c] + p4[c] + h[c]	(2749.1 and 6747.1)	(6424.1 and 64241.1)	ATP-binding cassette sub-family G member 5 ATP-binding cassette sub-family G member 8		ATP-binding cassette sub-family G member 5 and ATP-binding cassette sub-family G member 8		ABCG5 and ABCG8 are heterodimers, expressed in the enterocytes, involved in the efflux of the cholesterol from small intestine (i.e. Enterocytes) into the luminal cells of the small intestine, to reduce cholesterol uptake.	PMID: 18692849, PMID: 18850127, PMID: 15992510, PMID: 20454462	0	4
CHOLESTTDe	Transport, extracellular	chsterol[c] -> chsterol[e]							transported in chylomicrons into lymph	Sareen S. Gropper, jack L. Smith, James L. Groff (2009) Wadsworth cengage learning, Advanced nutrition and human metabolism, 5th edition, page 142-148.	0	2
CHOLETDIu	diffussion of cholesterol accross the brush border membrane	chsterol[u] <=> chsterol[c]								Sareen S. Gropper, jack L. Smith, James L. Groff (2009) Wadsworth cengage learning, Advanced nutrition and human metabolism, 5th edition, page 142-144.	1	2
CHOLNPtc	uptake of Cholesterol from the lumen	chsterol[u] -> chsterol[c]	237636.1	(29881.1)	Niemann-Pick C1-like protein 1		Niemann-Pick C1-like protein 1		Niemann-Pick C1-like protein 1 is indespensable for intestinal uptake of cholesterol from the mixed micelles. SR-BI has no apparent role in intestinal uptake of cholesterol and that NPC1L1 is mainly responsible (PMID: 18585981)	PMID: 21188557, PMID: 21602275, PMID: 20454462, PMID: 18692849, PMID: 14976318, PMID: 18585981	0	4
CYSATB0tc	transport of L-Cysteine into the intestinal cells by ATB0 transporter	cys_L[u] + 2 na1[u] + cl[u] -> cys_L[c] + 2 na1[c] + cl[c]	56774.1	(11254.1)	Sodium- and chloride-dependent neutral and basic amino acid transporter B(+)		Sodium- and chloride-dependent neutral and basic amino acid transporter B(+)		ATB0 is both sodium and chloride coupled, with reaction stoichiometry 2Na+:1cl:1amino acid. The transporter is localized in the intestine, has a broad substrate specificity (both neutral and cationic amino acids), but is not involved in the transport of aspartate, glutamate and proline (PMID:18195088).	PMID:18195088	0	4
CYSB0AT1Atc	transport of L-Cysteine by the apical neutral amino acid transporters in kidney and intestine	cys_L[u] + na1[u] -> cys_L[c] + na1[c]	(78.1 or (74338.1 and 57394.1))	(3424.1) and (57393.1 or 59272.1)	Sodium-dependent neutral amino acid transporter B(AT1 Collectrin Angiotensin-converting enzyme 2	3.4.17.23	Sodium-dependent neutral amino acid transporter B(AT1 and Collectrin or Angiotensin-converting enzyme 2	Angiotensin-converting enzyme 2	transports all the neutral amino acids with preference for methionine, leucine and valine. Reaction stoichiometry is 1:1. Requires heterodimerization with collectrin protein for increased affinity. Found in kidney and intestine, however also reported to be expressed in skin. Requires association with ACE2 for expression in intestine but with collectrin for expression in kidney.	PMID: 19472175, PMID: 15804236, PMID: 18400892	0	4

CYSGLYex	L-cysteine/glycine exchanger	cys_L[c] + gly[e] -> cys_L[e] + gly[c]	5934.1 or 17254.1 or 5934.2	(23428.1 and 652.1)	Large neutral amino acids transporter small subunit 2 4F2 cell-surface antigen heavy chain		Large neutral amino acids transporter small subunit 2 and 4F2 cell-surface antigen heavy chain		higher affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274).	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274, PMID: 10574935, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	0	4
CYSILELAT2tc	transport of L-Cysteine into the cell and efflux of L-Isoleucine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	cys_L[e] + ile_L[c] -> cys_L[c] + ile_L[e]	(2539.1 and 17254.1)	(23428.1 and 652.1)	Large neutral amino acids transporter small subunit 2 4F2 cell-surface antigen heavy chain		Large neutral amino acids transporter small subunit 2 and 4F2 cell-surface antigen heavy chain		higher affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274).	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274, PMID: 10574935, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	0	4
CYSPHELAT2tc	transport of L-Cysteine into the cell and efflux of L-Phenylalanine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	cys_L[e] + phe_L[c] -> cys_L[c] + phe_L[e]	(2539.1 and 17254.1)	(23428.1 and 652.1)	Large neutral amino acids transporter small subunit 2 4F2 cell-surface antigen heavy chain		Large neutral amino acids transporter small subunit 2 and 4F2 cell-surface antigen heavy chain		higher affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274).	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274, PMID: 10574935, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	0	4
CYSSNAT5tc	transport of L-Cysteine into the cell coupled with co-transport with Sodium and counter transport with proton by SNAT5 transporter.	cys_L[e] + na1[e] + h[c] <=> cys_L[c] + na1[c] + h[e]	29837.1	(92745.1)	Sodium-coupled neutral amino acid transporter 5		Sodium-coupled neutral amino acid transporter 5		SNAT5 performs both symport with sodium and antiport with proton, for the net transport of neutral amino acid into the cell. Cellular localization has been reported in stomach, brain, liver, lung, small intestine, spleen, colon and kidney. (PMID: 12845534)	PMID: 12845534, PMCID: PMC1665133, PMID:18195088	1	4
CYSTALArBATc	transport of L-Cystine into the cell in exchange for L-Alanine by b0,+AT transporter at the apical surfaces of the membranes of small intestine and renal cells.	Lcystin[e] + ala_L[c] -> Lcystin[c] + ala_L[e]	(3962.1 and 2532.1)	(11136.1 and 6519.1)	B(,+)-type amino acid transporter 1 Neutral and basic amino acid transport protein rBAT		B(,+)-type amino acid transporter 1 and Neutral and basic amino acid transport protein rBAT		sodium independant antiport transport system, exchanges di-basic amino acids into the cells and neutral amino acids out of the cell. Located on the apical surfaces of transporting epithelia. Cellular localization being small intestine, kidney (proximal tubule), lung, placenta, brain and thymus. Requires the heterodimerization with rBAT glycoprotein. (PMID: 10958334).	PMID: 10958334, PMID: 19184091, PMID: 18195088, PMID: 11546643	0	4
CYSTLEUrBATc	transport of L-Cystine into the cell in exchange for L-Leucine by b0,+AT transporter at the apical surfaces of the membranes of small intestine and renal cells.	Lcystin[e] + leu_L[c] -> Lcystin[c] + leu_L[e]	(3962.1 and 2532.1)	(11136.1 and 6519.1)	B(,+)-type amino acid transporter 1 Neutral and basic amino acid transport protein rBAT		B(,+)-type amino acid transporter 1 and Neutral and basic amino acid transport protein rBAT		sodium independant antiport transport system, exchanges di-basic amino acids into the cells and neutral amino acids out of the cell. Located on the apical surfaces of transporting epithelia. Cellular localization being small intestine, kidney (proximal tubule), lung, placenta, brain and thymus. Requires the heterodimerization with rBAT glycoprotein. (PMID: 10958334).	PMID: 10958334, PMID: 19184091, PMID: 18195088, PMID: 11546643	0	4
DAGHSTDIu	diffussion of di-acyl glycerol accross the brush border membrane	dag_hs[u] <=> dag_hs[c]							0	Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Wadsworth cengage learning, Advanced nutrition and human metabolism, 5th edition, page 142-144.	1	2
EPAFABPpmtc	uptake of Eicosapentaenoic acid by the enterocytes	tmndnc[u] -> tmndnc[c]	(14719.1 or 12491.1)	(286.1 or 948.1)	Aspartate aminotransferase, mitochondrial Platelet glycoprotein 4		Aspartate aminotransferase, mitochondrial or Platelet glycoprotein 4		GOT2 encodes FABPpm that may either act alone or in co-ordination with CD36, for the uptake of long chain fatty acids (exhibits a selective preference for long chain PUFA and essential fatty acids over non-essential fatty acids). The fatty acids alternatively can undergo passive diffusion. once inside the cell, they bind to the cytoplasmic fatty acid binding protein (FABPc) and thereby undergo activation or esterification. Additionally, a minority of fatty acids are thought to be transported by FATP1 and rapidly activated by plasma membrane acyl-CoA synthetase (ACS1) to form acyl-Co esters. (PMID: 20086080)	PMID: 20086080, PMID: 10617989, PMID: 8717462, Progress in Lipid Research Volume 48, Issue 2, March 2009, Pages 101-115	0	4
FOLTDIu	folate uptake into the enterocytes	fol[u] -> fol[c]							upake by diffusion.	G.F.M. Ball (2006) Vitamins their role in the human body, Blackwell publishing, chapter 17, page 353.	0	3
FOLTIu	folate uptake into the enterocytes	fol[u] + h[u] -> fol[c] + h[c]	259.1 or 259.2	(113235.1)	Proton-coupled folate transporter		Proton-coupled folate transporter		carrier protein mediated. H+ symport. Mutations in this gene is associated with hereditary folate mal-absorption syndrome (HM) (PMID: 19762432) .	G.F.M. Ball (2006) Vitamins their role in the human body, Blackwell publishing, chapter 17, page 353, PMID: 19762432.	0	3
GABAPATtc	transport of GABA by PAT1 in renal and intestinal cells	4abut[u] + h[u] -> 4abut[c] + h[c]	215335.1	(26358.1)	Proton-coupled amino acid transporter 1		Proton-coupled amino acid transporter 1		PAT1 proton-amino acid co-transporter with 1:1 stoichiometry, does not discriminate between L and D isomers, located on the apical membrane of kidney and intestine (PMID: 18400692, PMID: 18195088).	PMID: 17123464, PMID: 18400692, PMCID: PMC34647, PMID: 15345886, PMID: 18195088	0	4
GALSGLT1tu	transport of D-Galactose from extracellular space to cytosol of mucosal cells in small intestine	gal[u] + 2 na1[u] + atp[c] + h2o[c] -> gal[c] + 2 na1[c] + adp[c] + pi[c] + h[c]	2537.1	(6523.1)	Sodium/glucose cotransporter 1		Sodium/glucose cotransporter 1		SGLT-1 can also transport sugars coupled with H+ instead of Na+, under conditions of decreased extra-cellular ph. However, the affinity for glucose decreases with H+ coupled transport. (PMID: 17468205). The transport system is energized by Na/K ATPase activity (PMID: 7710974, Journal of animal science (2001) volume 79, (E suppl) E339-E72). Reversible transport for SGLT-1 has been suggested in a 6-state model in PMCID: PMC3000923.	PMID: 20522896, PMID: 14642859, Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Advanced nutrition and human metabolism, Wadsworth cengage learning, 5th edition, page 71-72	0	4
GLCSGLT1tu	transport of D-glucose from lumen to cytosol of mucosal cells in small intestine	glc_D[u] + 2 na1[u] + atp[c] + h2o[c] -> glc_D[c] + 2 na1[c] + adp[c] + pi[c] + h[c]	2537.1	(6523.1)	Sodium/glucose cotransporter 1		Sodium/glucose cotransporter 1		SGLT-1 can also transport sugars coupled with H+ instead of Na+, under conditions of decreased extra-cellular ph. However, the affinity for glucose decreases with H+ coupled transport. (PMID: 17468205). The transport system is energized by Na/K ATPase activity (PMID: 7710974, Journal of animal science (2001) volume 79, (E suppl) E339-E72). Reversible transport for SGLT-1 has been suggested in a 6-state model in PMCID: PMC3000923.	PMID: 20522896, PMID: 14642859, Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Advanced nutrition and human metabolism, Wadsworth cengage learning, 5th edition, page 71-72	0	4
GLNOFABPpmtc	uptake of gamma-linolenic acid by the enterocytes	lnlncg[u] -> lnlncg[c]	(14719.1 or 12491.1)	(286.1 or 948.1)	Aspartate aminotransferase, mitochondrial Platelet glycoprotein 4		Aspartate aminotransferase, mitochondrial or Platelet glycoprotein 4		GOT2 encodes FABPpm that may either act alone or in co-ordination with CD36, for the uptake of long chain fatty acids (exhibits a selective preference for long chain PUFA and essential fatty acids over non-essential fatty acids). The fatty acids alternatively can undergo passive diffusion. once inside the cell, they bind to the cytoplasmic fatty acid binding protein (FABPc) and thereby undergo activation or esterification. Additionally, a minority of fatty acids are thought to be transported by FATP1 and rapidly activated by plasma membrane acyl-CoA synthetase (ACS1) to form acyl-Co esters. (PMID: 20086080)	PMID: 20086080, PMID: 10617989, PMID: 8717462, Progress in Lipid Research Volume 48, Issue 2, March 2009, Pages 101-115	0	4
GLNATB0tc	transport of L-Glutamine into the intestinal cells by ATB0 transporter	gln_L[u] + 2 na1[u] + cl[u] -> gln_L[c] + 2 na1[c] + cl[c]	56774.1	(11254.1)	Sodium- and chloride-dependent neutral and basic amino acid transporter B(+)		Sodium- and chloride-dependent neutral and basic amino acid transporter B(+)		ATB0 is both sodium and chloride coupled, with reaction stoichiometry 2Na+:1cl:1amino acid. The transporter is localized in the intestine, has a broad substrate specificity (both neutral and cationic amino acids), but is not involved in the transport of aspartate, glutamate and proline (PMID: 18195088).	PMID:18195088	0	4

GLNB0AT1tc	transport of L-Glutamine by the apical neutral amino acid transporters in kidney and intestine	gln_L[sn] + na1[sn] -> gln_L[c] + na1[c]	(78.1 or (74338.1 and 57394.1))	(34244.1) and (57393.1 or 59272)	Sodium-dependent neutral amino acid transporter B(0)AT1 Collectrin Angiotensin-converting enzyme 2	3.4.17.23	Sodium-dependent neutral amino acid transporter B(0)AT1 and Collectrin or Angiotensin-converting enzyme 2	Angiotensin-converting enzyme 2	transports all the neutral amino acids with preference for methionine, leucine and valine. Reaction stoichiometry is 1:1. Requires heterodimerization with collectrin protein for increased affinity. Found in kidney and intestine, however also reported to be expressed in skin. Requires association with ACE2 for expression in intestine but with collectrin for expression in kidney.	PMID: 19472175, PMID: 15804236, PMID: 18400692	0	4
GLNLELAT2tc	transport of L-Glutamine into the cell and efflux of L-Isoleucine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	gln_L[e] + ile_L[c] -> gln_L[c] + ile_L[e]	(2539.1 and 17254.1)	(23428.1 and 652.1)	Large neutral amino acids transporter small subunit 2 4F2 cell-surface antigen heavy chain		Large neutral amino acids transporter small subunit 2 and 4F2 cell-surface antigen heavy chain		higher affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s0042000002741).	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s0042000002741, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-x, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	0	4
GLNLAT1tc	transport of L-Glutamine by LAT1 in association with 4F2hc, across the apical surface of the membranes.	gln_L[sn] + leu_L[c] -> gln_L[c] + leu_L[sn]	(2539.1 and 17254.1)	(814.1 and 652.1)	Large neutral amino acids transporter small subunit 1 4F2 cell-surface antigen heavy chain		Large neutral amino acids transporter small subunit 1 and 4F2 cell-surface antigen heavy chain		leucine is the only amino acid tested for efflux. Expressed in ovary, placenta, brain, spleen, testis, activated lymphocytes and some tumor cells. Functions as a antiport transport system (DOI 10.1016/j.ceil.2009.01.02), requires heterodimerization wih glycoprotein CD98 (Pflugers Arch-Eur J Physiol (2000) 440:503-512, DOI 10.1007/s0042400002741, PMID: 10958334).	Hans Gerhard Vogel, Franz J. Hock, Jochen Maas, Dieter Mayer (2006), Drug discovery and evaluation: Safety and pharmacokinetic assays, Springer publication, Chapter II D, page 456, table 3, PMID: 19035290, PMID: 12634921, European Journal of Pharmacology 441 (2002) 127-132, Am J Physiol Cell Physiol 281:C1077-C1093, 2001. Amino Acids (2005) 29: 229–233 DOI 10.1007/s00726-005-0221-x, PMID: 11901210	0	4
GLNPHELAT2tc	transport of L-Glutamine into the cell and efflux of L-Phenylalanine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	gln_L[e] + phe_L[c] -> gln_L[c] + phe_L[e]	(2539.1 and 17254.1)	(23428.1 and 652.1)	Large neutral amino acids transporter small subunit 2 4F2 cell-surface antigen heavy chain		Large neutral amino acids transporter small subunit 2 and 4F2 cell-surface antigen heavy chain		higher affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s0042000002741).	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s0042000002741, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-x, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	0	4
GLNyLAT1c	transport of L-Glutamine by y+LAT1 or y+LAT2 transporters in small intestine and kidney	gln_L[e] + na1[e] + arg_L[c] -> gln_L[c] + na1[c] + arg_L[e]	(254.1 or (33836.1 and 17254.1))	(956.1 or 957.1) and (652.1)	Y+L amino acid transporter 1 Y+L amino acid transporter 2 4F2 cell-surface antigen heavy chain		Y+L amino acid transporter 1 or Y+L amino acid transporter 2 and 4F2 cell-surface antigen heavy chain		y+LAT1 and y+LAT2 transporters requires CD98 for sequentrization to the plasma membrane. Acts as an amino acid exchanger, with influx of neutral aminos acids and efflux of cationic amino acid, requires Na+ for optimal activity. Can also operate with H+ in absence of Na+ (PMID: 11546643).	PMID: 11546643, PMID:18195088	0	4
GLNyLAT4tc	transport of Glutamine by y+LAT1 or y+LAT2 with co-transporter of h in small intestine and kidney	gln_L[e] + h[e] + arg_L[c] -> gln_L[c] + h[c] + arg_L[e]	(254.1 or (33836.1 and 17254.1))	(956.1 or 957.1) and (652.1)	Y+L amino acid transporter 1 Y+L amino acid transporter 2 4F2 cell-surface antigen heavy chain		Y+L amino acid transporter 1 or Y+L amino acid transporter 2 and 4F2 cell-surface antigen heavy chain		y+LAT1 and y+LAT2 transporters requires CD98 for sequentrization to the plasma membrane. Acts as an amino acid exchanger, with influx of neutral aminoa acids and efflux of cationic amino acid, requires Na+ for optimal activity. Can also operate with H+ in absence of Na+ (PMID: 11546643).	PMID: 11546643, PMID:18195088	0	4
GLYATB0tc	transport of Glycine into the intestinal cells by ATB0 transporter	gly[u] + 2 na1[u] + cl[u] -> gly[c] + 2 na1[c] + cl[c]	56774.1	(11254.1)	Sodium- and chloride-dependent neutral and basic amino acid transporter B(+)		Sodium- and chloride-dependent neutral and basic amino acid transporter B(+)		ATB0 is both sodium and chloride coupled, with reaction stoichiometry 2Na+:1cl:1amino acid. The transporter is located in the intestine, has a broad substrate specificity (both neutral and cationic amino acids), but is not involved in the transport of aspartate, glutamate and proline (PMID:18195088).	PMID:18195088	0	4

GLYB0AT1tc	transport of Glycine by the apical neutral amino acid transporters in kidney and intestine	gly[su] + na1[su] -> gly[c] + na1[c]	(78.1 or (74338.1 and 57394.1))	(34244.1) and (57393.1 or 59272.1)	Sodium-dependent neutral amino acid transporter B(0)AT1 Collectrin Angiotensin-converting enzyme 2	3.4.17.23	Sodium-dependent neutral amino acid transporter B(0)AT1 and Collectrin or Angiotensin-converting enzyme 2	Angiotensin-converting enzyme 2	transports all the neutral amino acids with preference for methionine, leucine and valine. Reaction stoichiometry is 1:1. Requires heterodimerization with collectrin protein for increased affinity. Found in kidney and intestine, however also reported to be expressed in skin. Requires association with ACE2 for expression in intestine but with collectrin for expression in kidney.	PMID: 19472175, PMID: 15804236, PMID: 18400692	0	4
GLYGLYCNc	hydrolysis of glycylglycine for uptake	glygly[c] + h2o[c] <=> gly[c] + gly[c]	(33843.1 or 6654.1)	(84735.1 or 55748.1)	Beta-Ala-His dipeptidase Cytosolic non-specific dipeptidase	3.4.13.2 or 3.4.13.18	Beta-Ala-His dipeptidase or Cytosolic non-specific dipeptidase		Dipeptides and tripeptides enter the brush border of the intestinal mucosal cells, where they are hydrolyzed to free amino acids, which are then transported into hepatic portal vein. Peptides entering by transcellular or paracellular mechanisms elicit allergic reactions to food (Robert K. Murray, David A. Bender, Kathleen M. Botham, Peter J. kennelly, Victor W. Rodwell, P. Anthony Weil (2009) 28th edition, Harpers illustrated biochemistry,Mc Graw Hill, page 462). formation and hydrolysis of diglycine is a reversible process (David L. Nelson, Michael M. Cox, Lehninger principles of biochemistry (2008), 3rd edition, worth publishers,page 69, figure 3a). CN1 is expressed in brain where as CN2 is more ubiquitously expressed (PMID: 12473676).	PMID: 6993048, PMCID: PMC1412503, PMID: 4919261, PMID: 20178671, PMID: 12473676	1	4
GLYGLYPEPT1tc	transport of Glycyl-glycine by the apical PEPT1 amino acid transporters across the brush border cells of the enterocytes of the intestine and renal cells	glygly[su] + h[su] -> glygly[c] + h[su]	215335.1	(6564.1)	Solute carrier family 15 member 1		Solute carrier family 15 member 1		PEPT1 appears to transport all di- and tri- peptides across the brush border of the intestinal cells (Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Advanced nutrition and human metabolism, Wadsworth cengage learning, 5th edition, page 193). PEPT1 is expressed highly in intestinal cells where as PEPT2 is localized to renal cells (PMID: 10330047).	PMID: 7858848, PMID: 14965252, PMID: 14977407, PMID: 10330047	0	4
GLYLEUHYDROc	hydrolysis of Glycylleucine in the small intestine for cellular uptake	glyleu[c] + h2o[c] <=> gly[c] + leu_L[c]	(13479.1 or 6654.1)	(18.1 or 55748.1)	membrane dipeptidase cytosol nonspecific dipeptidase	3.4.13.19 or 3.4.13.18	membrane dipeptidase or cytosol nonspecific dipeptidase		BRENDA also lists beta-Ala-His dipeptidase (E.C. 3.4.13.20) as another enzyme catalyzing this reaction, but no literature evidence found.	PMID: 4074331, PMID: 964683	1	4
GLYLEUPEPT1tc	transport of Glycylleucine by the apical PEPT1 amino acid transporters across the brush border cells of the enterocytes of the intestine and renal cells	glyleu[su] + h[su] -> glyleu[c] + h[c]	215335.1	(6564.1)	Solute carrier family 15 member 1		Solute carrier family 15 member 1		PEPT1 appears to transport all di- and tri- peptides across the brush border of the intestinal cells (Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Advanced nutrition and human metabolism, Wadsworth cengage learning, 5th edition, page 193). PEPT1 is expressed highly in intestinal cells where as PEPT2 is localized to renal cells (PMID: 10330047).	PMID: 7858848, PMID: 14965252, PMID: 14977407, PMID: 10330047	0	4
GLYPATtc	transport of Glycine by the apical PAT2 or PAT1 amino acid transporters in kidney and intestine	gly[su] + h[su] -> gly[c] + h[c]	215335.1	(26358.1)	Proton-coupled amino acid transporter 1		Proton-coupled amino acid transporter 1		PAT2 is strongly expressed in heart and lung and more weakly in kidney and muscle (PMID:18400692). PAT2 can also transport glycine bidirectionally, depending on the membrane potential and substrate/proton gradient (PMID: 14680153). PAT1 proton-amino acid co-transporter with 1:1 stoichiometry, does not discriminate between L and D isomers, located on the apical membrane of kidney and intestine (PMID: 18400692, PMID: 18195088).	PMID:18195088, PMID:18400692, PMID: 17123464, PMCID: PMC34647, PMID: 15345686	0	4
GLYPHEPEPT1tc	transport of Glycylphenylalanine by the apical PEPT1 amino acid transporters across the brush border cells of the enterocytes of the intestine and renal cells	glyphe[su] + h[su] -> glyphe[c] + h[c]	215335.1	(6564.1)	Solute carrier family 15 member 1		Solute carrier family 15 member 1		PEPT1 appears to transport all di- and tri- peptides across the brush border of the intestinal cells (Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Advanced nutrition and human metabolism, Wadsworth cengage learning, 5th edition, page 193). PEPT1 is expressed highly in intestinal cells where as PEPT2 is localized to renal cells (PMID: 10330047).	PMID: 7858848, PMID: 14965252, PMID: 14977407, PMID: 10330047	0	4
GLYPROPEPT1tc	transport of Glycylproline by the apical PEPT1 amino acid transporters across the brush border cells of the enterocytes of the intestine and renal cells	glypro[su] + h[su] -> glypro[c] + h[c]	215335.1	(6564.1)	Solute carrier family 15 member 1		Solute carrier family 15 member 1		PEPT1 appears to transport all di- and tri- peptides across the brush border of the intestinal cells (Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Advanced nutrition and human metabolism, Wadsworth cengage learning, 5th edition, page 193). PEPT1 is expressed highly in intestinal cells where as PEPT2 is localized to renal cells (PMID: 10330047).	PMID: 7858848, PMID: 14965252, PMID: 14977407, PMID: 10330047	0	4
GLYPROPRO1c	hydrolysis of Prolylglycine in the small intestine for cellular uptake	glypro[c] + h2o[c] <=> gly[c] + pro_L[c]	18624.1	(5184.1)	Xaa-Pro dipeptidase	3.4.13.9	Xaa-Pro dipeptidase		prolidase 1 and 2 both have same E.C. Numbers, prolidase 1 has a substrate preference for glycylproline where as prolidase 2 catalyzes very slowly this reaction (PMID: 14580160).	PMID: 14580160, PMID: 2317925, PMID: 18340504, Rubino A, Pierro M, Torretta GL, Vetrella M, Martino DD, Auricch S. (1969). Pediatric Research 3: 313-9	1	4
GLYSARCNc	hydrolysis of glycylsarcosine for uptake	glysar[c] + h2o[c] <=> gly[c] + sarcs[c]	12751.1	(12.1)	Tripeptidyl-peptidase I	3.4.14.9	Tripeptidyl-peptidase I		glycine-sarcosine is resistant to hydrolysis and the only enzyme to catalyze hydrolysis is prolidase in rabbit intestine (PMID:6746633). Further glycine-sarcosine and glycylalanine have been assumed to have a common transport system. It may also remain intact (PMID: 3293467).	PMID:6746633, PMID: 4778846, PMID: 7171621, PMID: 3293467	1	3
GLYSARPEPT1tc	transport of Glycylsarcosine by the apical PEPT1 amino acid transporters across the brush border cells of the enterocytes of the intestine, renal cells and brain.	glysar[su] + h[su] -> glysar[c] + h[c]	215335.1	(6564.1)	Solute carrier family 15 member 1		Solute carrier family 15 member 1		PEPT1 appears to transport all di- and tri- peptides across the brush border of the intestinal cells (Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Advanced nutrition and human metabolism, Wadsworth cengage learning, 5th edition, page 193). PEPT1 is expressed highly in intestinal cells where as PEPT2 is localized to renal cells (PMID: 10330047). glycine-sarcosine is also transported across the brain specifically by PEPT2 (PMID: 20571525).	PMID: 7858848, PMID: 14965252, PMID: 14977407, PMID: 10330047	0	4
GLYSNAT5tc	transport of Glycine into the cell coupled with co-transport with Sodium and counter transport with proton by SNAT5 transporter.	gly[su] + na1[su] + h[c] <=> gly[c] + na1[c] + h[su]	29837.1	(92745.1)	Sodium-coupled neutral amino acid transporter 5		Sodium-coupled neutral amino acid transporter 5		SNAT5 performs both symport with sodium and antiport with proton, for the net transport of neutral amino acid into the cell. Cellular localization has been reported in stomach, brain, liver, lung, small intestine, spleen, colon and kidney. (PMID: 12845534)	PMID: 12845534, PMCID: PMC1665133, PMID:18195088	1	4
GUMDCHAe	binding of guar gums with deoxycholic acid in the intestinal lumen, reducing serum cholesterol levels.	gum[su] + dchac[su] -> gumdchac[su]							guar gum binds bile acids and leads to enhanced excretion, there by the 7-alpha hydroxylase pathway is activated leading to increased cholesterol catabolism for synthesis of more bile acids (regulates cholesterol metabolism). however the decreased serum cholesterol levels are brought about by many other cumulative effects (water unstirred action of dieatary fibres, glycemic rsle etc) (PMID: 18302966, Gunness P, Gidley MJ. (2010). Food & Function 1: 149-55).	PMID: 21611850, PMID: 7825524, McFadzean B, Dicks P, Groenmeyer G, Harris P, OConnor C. (2011). Minerals Engineering 24: 463-9, T.Pandolf and F.M. Clydesdale (1992) Journal of food science, vol.57, no.5, 1242-1245.	0	3
GUMGCHLe	binding of guar gums with glycocholate in the intestinal lumen, reducing serum cholesrol levels.	gum[su] + gchola[su] -> gumgchol[su]							guar gum binds bile acids and leads to enhanced excretion, there by the 7-alpha hydroxylase pathway is activated laeding to increased cholesterol catabolism for synthesis of more bile acids (regulates cholesterol metabolism). however the decreased serum cholesterol levels are brought about by many other cumulative effects (water unstirred action of dieatary fibres, glycemic rsle etc) (PMID: 18302966, Gunness P, Gidley MJ. (2010). Food & Function 1: 149-55).	PMID: 21611850, PMID: 7825524, McFadzean B, Dicks P, Groenmeyer G, Harris P, OConnor C. (2011). Minerals Engineering 24: 463-9, T.Pandolf and F.M. Clydesdale (1992) journal of food science, vol.57, no.5, 1242-1245.	0	3

GLMTCHOLe	binding of guar gums with taurocholate in the intestinal lumen, reducing serum cholesterol levels.	gum[u] + tchola[u] -> gumtchol[u]							guar gum binds bile acids and leads to enhanced excretion, there by the 7-alpha hydroxylase pathway is activated leading to increased cholesterol catabolism for synthesis of more bile acids (regulates cholesterol metabolism). however the decreased serum cholesterol levels are brought about by many other cumulative effects (water unstirred action of dietatry fibres, glycemic role etc) (PMID: 18302966, Gunness P, Gidley MJ. (2010). Food & Function 1: 149-55).	PMID: 21611850, PMID: 7825524, McFadzean B, Dicks P, Groenmeyer G, Harris P, OConnor C. (2011). Minerals Engineering 24: 463-9, 7.Pandolf and F.M. Clydesdale (1992) journal of food science, vol.57, no.5, 1242-1245.	0	3
HISCAT1	transport of L-Histidine by y+ transporter	his_L[c] <=> his_L[e]	11987.1	(6541.1)	High affinity cationic amino acid transporter 1		High affinity cationic amino acid transporter 1		ubiquitously expressed y+ transport system, mediates uniport transport of arginine, lysine, ornithine and histidine. (PMID: 18195088). Located on the basolateral surface, mediates a bidirectional uniport transport of actionic amino acid and is Na+ independent (PMID: 17494634). Recon 1 contains the reactions but with irreversible form.	PMID: 14770310, PMID: 12506130, PMID: 17494634,PMID:18195088.	1	4
HIShPTtc	transport of L-Histidine by hPT3 or hPT4 peptide transporters.	his_L[l] + h[l] -> his_L[c] + h[c]	15186.1 or 13195.1	(51296.1 or 12126.1)	Solute carrier family 15 member 3 Solute carrier family 15 member 4		Solute carrier family 15 member 3 or Solute carrier family 15 member 4		hPT3 (human peptide transporter 3) transports histidine and di-peptides from the lysosomes into the cytosol. Co-transports proton, expressed in lung, thymus, spleen and faintly in brain, placenta, liver, adrenal gland and heart (PMID: 12905028). hPT4 expressed in brain, placenta and retina. Transports carnosine and histidine in a proton symport mechanism. (PMID: 12905028)	PMID: 16289537, PMID: 12905028, PMID: 17681807	0	4
HISILELAT2tc	transport of L-Histidine into the cell and efflux of L-Isoleucine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	his_L[e] + ile_L[c] -> his_L[c] + ile_L[e]	(2539.1 and 17254.1)	(23428.1 and 652.1)	Large neutral amino acids transporter small subunit 2 4F2 cell-surface antigen heavy chain		Large neutral amino acids transporter small subunit 2 and 4F2 cell-surface antigen heavy chain		higher affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274).	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-x, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	0	4
HISLAT1tc	transport of L-Histidine by LAT1 in association with 4F2hc, across the apical surface of the membranes.	his_L[u] + leu_L[c] -> his_L[c] + leu_L[u]	(2539.1 and 17254.1)	(814.1 and 652.1)	Large neutral amino acids transporter small subunit 1 4F2 cell-surface antigen heavy chain		Large neutral amino acids transporter small subunit 1 and 4F2 cell-surface antigen heavy chain		leucine is the only amino acid tested for efflux. Expressed in ovary, placenta, brain, spleen, testis, activated lymphocytes and some tumor cells. Functions as a antiport transport system (DOI 10.1016/j.ceil.2009.01.02), requires heterodimerization with glycoprotein CD98 (Pflugers Arch-Eur J Physiol (2000) 440:503-512, DOI 10.1007/s004240000274, PMID: 10958334).	Hans Gerhard Vogel, Franz J. Hock, Jochen Maas, Dieter Mayer (2006), Drug discovery and evaluation: Safety and pharmacokinetic assays, Springer publication, Chapter II G, page 456, table 3, PMID: 19035290, PMID: 12634921, European Journal of Pharmacology 441 (2002) 127-132. Am J Physiol Cell Physiol 281:C1077-C1093, 2001. Amino Acids (2005) 29: 229–233 DOI 10.1007/s00726-005-0221-x. PMID: 11901210	0	4
HISPHELAT2tc	transport of L-Histidine into the cell and efflux of L-Phenylalanine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	his_L[e] + phe_L[c] -> his_L[c] + phe_L[e]	(2539.1 and 17254.1)	(23428.1 and 652.1)	Large neutral amino acids transporter small subunit 2 4F2 cell-surface antigen heavy chain		Large neutral amino acids transporter small subunit 2 and 4F2 cell-surface antigen heavy chain		higher affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274).	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-x, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	0	4
HISSNAT5tc	transport of L-Histidine into the cell coupled with co-transport with Sodium and counter transport with proton by SNAT5 transporter.	his_L[u] + na1[u] + h[c] <=> his_L[c] + na1[c] + h[u]	29837.1	(92745.1)	Sodium-coupled neutral amino acid transporter 5		Sodium-coupled neutral amino acid transporter 5		SNAT5 performs both symport with sodium and antiport with proton, for the net transport of neutral amino acid into the cell. Cellular localization has been reported in stomach, brain, liver, lung, small intestine, spleen, colon and kidney. (PMID: 12845534)	PMID: 12845534, PMCID: PMC1665133, PMID:18195088	1	4
HISyLATtc	transport of L-Histidine by y+LAT1 or y+LAT2 transporters in small intestine and kidney	his_L[e] + na1[e] + arg_L[c] -> his_L[c] + na1[c] + arg_L[e]	(254.1 or (33836.1 and 17254.1))	(956.1 or 957.1) and (652.1)	Y+L amino acid transporter 1 Y+L amino acid transporter 2 4F2 cell-surface antigen heavy chain		Y+L amino acid transporter 1 or Y+L amino acid transporter 2 and 4F2 cell-surface antigen heavy chain		y+LAT1 and y+LAT2 transporters requires CD98 for sequestration to the plasma membrane. Acts as an amino acid exchanger, with influx of neutral amino acids and efflux of cationic amino acid, requires Na+ for optimal activity. Can also operate with H+ in absence of Na+ (PMID: 11546643).	PMID: 11546643, PMID:18195088	0	4
HISyLATtbc	transport of Histidine by y+LAT1 or y+LAT2 with co-transporter of h in small intestine and kidney	his_L[e] + h[e] + arg_L[c] -> his_L[c] + h[c] + arg_L[e]	(254.1 or (33836.1 and 17254.1))	(956.1 or 957.1) and (652.1)	Y+L amino acid transporter 1 Y+L amino acid transporter 2 4F2 cell-surface antigen heavy chain		Y+L amino acid transporter 1 or Y+L amino acid transporter 2 and 4F2 cell-surface antigen heavy chain		y+LAT1 and y+LAT2 transporters requires CD98 for sequestration to the plasma membrane. Acts as an amino acid exchanger, with influx of neutral amino acids and efflux of cationic amino acid, requires Na+ for optimal activity. Can also operate with H+ in absence of Na+ (PMID: 11546643).	PMID: 11546643, PMID:18195088	0	4
HPETFABP1tc	transport of 5-HPETE into the enterocytes	2 5HPET[c] <=> 2 5HPET[r]	148.1	(2168.1)	Fatty acid-binding protein, liver		Fatty acid-binding protein, liver		crystal structure of LFAB revealed 2 binding sites (in contrast to IFAB which has 1:1 stoichiometry) for oleate (PMID: 9054409). LFAB is expressed in liver, kidney, intestine, pancreas, stomach and lung (PMCID: PMC2670638). Once the long chain fatty acids enter the enterocytes, bind to the FABP reversibly, for transport into the E.R. to reconstitute triacylglycerols (PMID: 20522896, PMID: 19280710).	PMID: 9555061, PMCID: PMC2821027, PMID: 9054409, PMID: 9082452, PMCID: PMC2670638, http://msu3.libraries.rutgers.edu/dtr7/MP/rutgers-lib_20138-PDF-1.pdf	1	4
ILEATB0tc	transport of L-Isoleucine into the intestinal cells by ATB0 transporter	ile_L[e] + 2 na1[u] + cl[u] -> ile_L[c] + 2 na1[c] + cl[c]	56774.1	(11254.1)	Sodium- and chloride-dependent neutral and basic amino acid transporter B(0+)		Sodium- and chloride-dependent neutral and basic amino acid transporter B(+)		ATB0 is both sodium and chloride coupled, with reaction stoichiometry 2Na+:1cl:1amino acid. The transporter is localized in the intestine, has a broad substrate specificity (both neutral and cationic amino acids), but is not involved in the transport of aspartate, glutamate and proline (PMID:18195088).	PMID:18195088	0	4
ILEB0ATtc	transport of L-Isoleucine by the apical neutral amino acid transporters B(0)AT1 or B(0)AT2 in kidney, intestine or brain	ile_L[u] + na1[u] -> ile_L[c] + na1[c]	(78.1 or (74338.1 and 57394.1))	(3424.1) and (57393.1 or 59272.1)	Sodium-dependent neutral amino acid transporter B(0)AT1 Collectrin Angiotensin-converting enzyme 2	3.4.17.23	Sodium-dependent neutral amino acid transporter B(0)AT1 and Collectrin or Angiotensin-converting enzyme 2	Angiotensin-converting enzyme 2	B(0)AT1 transports all the neutral amino acids with preference for methionine, leucine and valine. Reaction stoichiometry is 1:1. Requires heterodimerization with collectrin protein for increased affinity. Found in kidney and intestine, however also reported to be expressed in skin. Requires association with ACE2 for expression in intestine but with collectrin for expression in kidney. The localization of the B(0)AT2 transporter has been studied in brain tissue but data from the kidney have not been reported (PMID: 18195088)	PMID: 19472175, PMID: 15804236, PMID: 18400692, PMID: 16185194, PMID: 18195088	0	4
ILELAT1tc	transport of L-Isoleucine by LAT1 in association with 4F2hc, across the apical surface of the membranes.	ile_L[u] + leu_L[c] -> ile_L[c] + leu_L[u]	(2539.1 and 17254.1)	(814.1 and 652.1)	Large neutral amino acids transporter small subunit 1 4F2 cell-surface antigen heavy chain		Large neutral amino acids transporter small subunit 1 and 4F2 cell-surface antigen heavy chain		leucine is the only amino acid tested for efflux. Expressed in ovary, placenta, brain, spleen, testis, activated lymphocytes and some tumor cells. Functions as a antiport transport system (DOI 10.1016/j.ceil.2009.01.02), requires heterodimerization with glycoprotein CD98 (Pflugers Arch-Eur J Physiol (2000) 440:503-512, DOI 10.1007/s004240000274, PMID: 10958334).	Hans Gerhard Vogel, Franz J. Hock, Jochen Maas, Dieter Mayer (2006), Drug discovery and evaluation: Safety and pharmacokinetic assays, Springer publication, Chapter II G, page 456, table 3, PMID: 19035290, PMID: 12634921, European Journal of Pharmacology 441 (2002) 127-132. Am J Physiol Cell Physiol 281:C1077-C1093, 2001. Amino Acids (2005) 29: 229–233 DOI 10.1007/s00726-005-0221-x. PMID: 11901210	0	4

ILEPHELAT2tc	transport of L-Isoleucine into the cell and efflux of L-Phenylalanine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	ile_L[e] + phe_L[c] -> ile_L[c] + phe_L[e]	(2539.1 and 17254.1)	(23428.1 and 652.1)	Large neutral amino acids transporter small subunit 2 4F2 cell-surface antigen heavy chain		Large neutral amino acids transporter small subunit 2 and 4F2 cell-surface antigen heavy chain		higher affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274).	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	0	4
LEUATB0tc	transport of L-Leucine into the intestinal cells by ATB0 transporter	leu_L[e] + 2 na1[e] + cl[e] -> leu_L[c] + 2 na1[c] + cl[c]	56774.1	(11254.1)	Sodium- and chloride-dependent neutral and basic amino acid transporter B(+)		Sodium- and chloride-dependent neutral and basic amino acid transporter B(+)		ATB0 is both sodium and chloride coupled, with reaction stoichiometry 2Na+:1cl:1amino acid. The transporter is localized in the intestine, has a broad substrate specificity (both neutral and cationic amino acids), but is not involved in the transport of aspartate, glutamate and proline (PMID:18195088).	PMID:18195088	0	4
LEUB0ATtc	transport of L-Leucine by the apical neutral amino acid transporters B(0)AT1 or B(0)AT2 in kidney, intestine or brain	leu_L[e] + na1[e] -> leu_L[c] + na1[c]	(78.1 or (74338.1 and 57394.1))	(34424.1) and (57393.1 or 59272.1)	Sodium-dependent neutral amino acid transporter B(AT1 Collectrin Angiotensin-converting enzyme 2	3.4.17.23	Sodium-dependent neutral amino acid transporter B(AT1 and Collectrin or Angiotensin-converting enzyme 2	Angiotensin-converting enzyme 2	transports all the neutral amino acids with preference for methionine, leucine and valine. Reaction stoichiometry is 1:1. Requires heterodimerization with collectrin protein for increased affinity. Found in kidney and intestine, however also reported to be expressed in skin. Requires association with ACE2 for expression in intestine but with collectrin for expression in kidney. The localization of the B(0)AT2 transporter has been studied in brain tissue but data from the kidney have not been reported (PMID: 18195088).	PMID: 19472175, PMID: 15804236, PMID: 18400692, PMID: 16185194, PMID: 18195088	0	4
LEUGLYHYc	hydrolysis of leucylglycine	h2o[c] + leuglyc[c] <=> leu-L[c] + gly[c]							most probable reaction.	[]	1	1
LEUGLYPEPT1tc	transport of Leucylglycine by the apical PEPT1 amino acid transporters across the brush border cells of the enterocytes of the intestine and renal cells	leuglyc[a] + h[a] -> leuglyc[c] + h[c]	215335.1	(6564.1)	Solute carrier family 15 member 1		Solute carrier family 15 member 1		PEPT1 appears to transport all di- and tri- peptides across the brush border of the intestinal cells (Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Advanced nutrition and human metabolism, Wadsworth cengage learning, 5th edition, page 193). PEPT1 is expressed highly in intestinal cells where as PEPT2 is localized to renal cells (PMID: 10330047).	PMID: 7858848, PMID: 14965252, PMID: 14977407, PMID: 10330047	0	4
LEULELAT2tc	transport of L-Leucine into the cell and efflux of L-Isoleucine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	leu_L[e] + ile_L[c] <=> leu_L[c] + ile_L[e]	(2539.1 and 17254.1)	(23428.1 and 652.1)	Large neutral amino acids transporter small subunit 2 4F2 cell-surface antigen heavy chain		Large neutral amino acids transporter small subunit 2 and 4F2 cell-surface antigen heavy chain		higher affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274). LAT2 carries both influx and efflux of phenylalanine, leucine and isoleucine, hence such reactions are reversible.	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	1	4
LEULELAPc	hydrolysis of Leucylleucine in the small intestine for cellular uptake	leuleu[c] + h2o[c] <=> leu_L[c] + leu_L[c]	66988.1	(5156.1)	leucyl aminopeptidase	3.4.11.1	leucyl aminopeptidase		both pig(E.C. 3.4.11.5) and human (3.4.11.1) amino peptidase have similar amino acid sequence and catalytic properties (PMID: 1908238)	PMID: 1908238, PMID: 1931152	1	4
LEULELUPEPT1tc	transport of Leucylleucine by the apical PEPT1 amino acid transporters across the brush border cells of the enterocytes of the intestine and renal cells	leuleu[a] + h[a] -> leuleu[c] + h[c]	215335.1	(6564.1)	Solute carrier family 15 member 1		Solute carrier family 15 member 1		PEPT1 appears to transport all di- and tri- peptides across the brush border of the intestinal cells (Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Advanced nutrition and human metabolism, Wadsworth cengage learning, 5th edition, page 193). PEPT1 is expressed highly in intestinal cells where as PEPT2 is localized to renal cells (PMID: 10330047).	PMID: 7858848, PMID: 14965252, PMID: 14977407, PMID: 10330047	0	4
LEUPHELAT2tc	transport of L-Leucine into the cell and efflux of L-Phenylalanine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	leu_L[e] + phe_L[c] -> leu_L[c] + phe_L[e]	(2539.1 and 17254.1)	(23428.1 and 652.1)	Large neutral amino acids transporter small subunit 2 4F2 cell-surface antigen heavy chain		Large neutral amino acids transporter small subunit 2 and 4F2 cell-surface antigen heavy chain		higher affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274). LAT2 carries both influx and efflux of phenylalanine, leucine and isoleucine, hence such reactions are reversible.	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	1	4
LEUyLATtc	transport of Leucine by y+LAT1 or y+LAT2 with co-transporter of h in small intestine and kidney	leu_L[e] + h[e] + arg_L[c] -> leu_L[c] + h[c] + arg_L[e]	(254.1 or (33836.1 and 17254.1))	(956.1 or 957.1) and (652.1)	Y+L amino acid transporter 1 Y+L amino acid transporter 2 4F2 cell-surface antigen heavy chain		Y+L amino acid transporter 1 or Y+L amino acid transporter 2 and 4F2 cell-surface antigen heavy chain		y+LAT1 and y+LAT2 transporters requires CD98 for sequesterization to the plasma membrane. Acts as an amino acid exchanger, with influx of neutral aminoa acids and efflux of cationic amino acid, requires Na+ for optimal activity. Can also operate with H+ in absence of Na+ (PMID: 11566643).	PMID: 11566643, PMID:18195088	0	4

LEUyLATtc	transport of Leucine by y+LAT1 or y+LAT2 transporters in small intestine and kidney	leu_L[e] + na1[e] + arg_L[c] -> leu_L[c] + na1[c] + arg_L[e]	(254.1 or (33836.1 and 17254.1))	(956.1 or 957.1) and (652.1)	Y+L amino acid transporter 1 Y+L amino acid transporter 2 4F2 cell-surface antigen heavy chain		Y+L amino acid transporter 1 or Y+L amino acid transporter 2 and 4F2 cell-surface antigen heavy chain		y+LAT1 and y+LAT2 transporters requires CD98 for sequestrization to the plasma membrane. Acts as an amino acid exchanger, with influx of neutral aminoa acids and efflux of cationic amino acid, requires Na+ for optimal activity. Can also operate with H+ in absence of Na+ (PMID: 11546643).	PMID: 11546643, PMID:18195088	0	4
LINOFABPpmtc	uptake of linoleic acid by the enterocytes	lnlc[sa] -> lnlc[c]	(14719.1 or 12491.1)	(286.1 or 948.1)	Aspartate aminotransferase, mitochondrial Platelet glycoprotein 4		Aspartate aminotransferase, mitochondrial or Platelet glycoprotein 4		GOT2 encodes FABPpm that may either act alone or in co-ordination with CD36, for the uptake of long chain fatty acids (exhibits a selective preference for long chain PUFA and essential fatty acids over non-essential fatty acids). The fatty acids alternatively can undergo passive diffusion. once inside the cell, they bind to the cytoplasmic fatty acid binding protein (FABPc) and thereby undergo activation or esterification. Additionally, a minority of fatty acids are thought to be transported by FATP1 and rapidly activated by plasma membrane acyl-CoA synthetase (ACS1) to form acyl-Co esters. (PMID: 20086080)	PMID: 20086080, PMID: 10617989, PMID: 8717462, Progress in Lipid Research Volume 48, Issue 2, March 2009, Pages 101-115	0	4
LINOFATPtc	uptake of linoleic acid by the enterocytes	lnlc[sa] + atp[c] + coa[c] -> lnlccoa[c] + amp[c] + ppi[c]	26569.1	(1999.1)	Long-chain fatty acid transport protein 4	6.2.1.-	Long-chain fatty acid transport protein 4		major intestinal fatty acid transport protein, may also act in co-ordination with acyl co-A synthetase. The transport is ATP driven, further the transporter itself has fatty acid activating enzymtic properties (PMID: 12856180).	PMID: 10518211, PMID: 20086080, PMID: 12856180, Immun., Endoc. & Metab. Agents in Med. Chem., 2009, 9, 11-17,	0	4
LPCHOLTDtu	diffusion of lysophosphatidylcholine accross the brush border membrane	lpchol_hs[u] <=> lpchol_hs[c]							0	Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Wadsworth cengage learning, Advanced nutrition and human metabolism, 5th edition, page 142-144.	1	2
LYSALArBATtc	transport of L-Lysine into the cell in exchange for L-Alanine by b0,+AT transporter at the apical surfaces of the membranes of small intestine and renal cells.	lys_L[u] + ala_L[c] -> lys_L[c] + ala_L[u]	(3962.1 and 2532.1)	(11136.1 and 6519.1)	B(,+)-type amino acid transporter 1 Neutral and basic amino acid transport protein rBAT		B(,+)-type amino acid transporter 1 and Neutral and basic amino acid transport protein rBAT		sodium independant antiport transport system, exchanges di-basic amino acids into the cells and neutral amino acids out of the cell. Located on the apical surfaces of transporting epithelia. Cellular localization being small intestine, kidney (proximal tubule), lung, placenta, brain and thymus. Requires the heterodimerization with rBAT glycoprotein. (PMID: 10958334).	PMID: 10958334, PMID: 19184091, PMID: 18195088, PMID: 11546643	0	4
LYSATBtc	transport of L-Lysine into the intestinal cells by ATB0 transporter	lys_L[u] + 2 na1[u] + cl[u] -> lys_L[c] + 2 na1[c] + cl[c]	56774.1	(11254.1)	Sodium- and chloride-dependent neutral and basic amino acid transporter B(+)		Sodium- and chloride-dependent neutral and basic amino acid transporter B(+)		ATB0 is both sodium and chloride coupled, with reaction stoichiometry 2Na+:1cl:1amino acid. The transporter is located in the intestine, has a broad substrate specificity (both neutral and cationic amino acids), but is not involved in the transport of aspartate, glutamate and proline (PMID:18195088).	PMID:18195088	0	4
LYSLEUtrBATtc	transport of L-Lysine into the cell in exchange for L-Leucine by b0,+AT transporter at the apical surfaces of the membranes of small intestine and renal cells.	lys_L[u] + leu_L[c] -> lys_L[c] + leu_L[u]	(3962.1 and 2532.1)	(11136.1 and 6519.1)	B(,+)-type amino acid transporter 1 Neutral and basic amino acid transport protein rBAT		B(,+)-type amino acid transporter 1 and Neutral and basic amino acid transport protein rBAT		sodium independant antiport transport system, exchanges di-basic amino acids into the cells and neutral amino acids out of the cell. Located on the apical surfaces of transporting epithelia. Cellular localization being small intestine, kidney (proximal tubule), lung, placenta, brain and thymus. Requires the heterodimerization with rBAT glycoprotein. (PMID: 10958334).	PMID: 10958334, PMID: 19184091, PMID: 18195088, PMID: 11546643	0	4
LYSCtr	transport of L-Lysine by y+ transporter	lys_L[c] <=> lys_L[e]	11987.1	(6541.1)	High affinity cationic amino acid transporter 1		High affinity cationic amino acid transporter 1		ubiquitously expressed y+ transport system, mediates unport transport of arginine, lysine, ornithine and histidine. (PMID: 18195088). Located on the basolateral surface, mediates a bidirectional unport transport of acrtionic amino acid and is Na+ independent (PMID: 17494634). Recon 1 contains the reactions but with irreversible form.	PMID: 14770310, PMID: 12506130, PMID: 17494634,PMID:18195088.	1	4
MAGHSTDtu	diffusion of mono-acyl glycerol accross the brush border membrane	mag_hs[u] <=> mag_hs[c]							0	Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Wadsworth cengage learning, Advanced nutrition and human metabolism, 5th edition, page 142-144.	1	2
METATBtc	transport of L-Methionine into the intestinal cells by ATB0 transporter	met_L[u] + 2 na1[u] + cl[u] -> met_L[c] + 2 na1[c] + cl[c]	56774.1	(11254.1)	Sodium- and chloride-dependent neutral and basic amino acid transporter B(+)		Sodium- and chloride-dependent neutral and basic amino acid transporter B(+)		ATB0 is both sodium and chloride coupled, with reaction stoichiometry 2Na+:1cl:1amino acid. The transporter is located in the intestine, has a broad substrate specificity (both neutral and cationic amino acids), but is not involved in the transport of aspartate, glutamate and proline (PMID:18195088).	PMID:18195088	0	4
METB0ATAtc	transport of L-Methionine by the apical neutral amino acid transporter B(0)ATI or B(0)AT2 in kidney, intestine or brain	met_L[u] + na1[u] -> met_L[c] + na1[c]	(78.1 or (74338.1 and 57394.1))	(3424.1) and (57393.1 or 59272.1)	Sodium-dependent neutral amino acid transporter B(0)AT1 Collectrin Angiotensin-converting enzyme 2	3.4.17.23	Sodium-dependent neutral amino acid transporter B(0)AT1 and Collectrin or Angiotensin-converting enzyme 2	Angiotensin-converting enzyme 2	B(0)AT1 transports all the neutral amino acids with preference for methionine, leucine and valine. Reaction stoichiometry is 1:1. Requires heterodimerization with collectrin protein for increased affinity. Found in kidney and intestine, however also reported to be expressed in skin. Requires association with ACE2 for expression in intestine but with collectrin for expression in kidney. The localization of the B(0)AT2 transporter has been studied in brain tissue but data from the kidney have not been reported (PMID: 18195088). also catalyzed by system A transporter (SLC38A4).	PMID: 19472175, PMID: 15804236, PMID: 18400692, PMID: 16185194, PMID: 18195088	0	4
METILELATt2tc	transport of L-Methionine into the cell and efflux of L-Isoleucine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	met_L[e] + ile_L[c] -> met_L[c] + ile_L[e]	(2539.1 and 17254.1)	(23428.1 and 652.1)	Large neutral amino acids transporter small subunit 2 4F2 cell-surface antigen heavy chain		Large neutral amino acids transporter small subunit 2 and 4F2 cell-surface antigen heavy chain		higher affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s0042000002741).	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s0042000002741, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	0	4
METLAT1tc	transport of L-Methionine by LAT1 in association with 4F2hc, across the apical surface of the membranes.	met_L[u] + leu_L[c] -> met_L[c] + leu_L[u]	(2539.1 and 17254.1)	(814.1 and 652.1)	Large neutral amino acids transporter small subunit 1 4F2 cell-surface antigen heavy chain		Large neutral amino acids transporter small subunit 1 and 4F2 cell-surface antigen heavy chain		leucine is the only amino acid tested for efflux. Expressed in ovary, placenta, brain, spleen, testis, activated lymphocytes and some tumor cells. Functions as a antiport transport system (DOI 10.1016/j.ceil.2009.01.02), requires heterodimerization with glycoprotein CD98 (Pflugers Arch-Eur J Physiol (2000) 440:503-512, DOI 10.1007/s0042400002741, PMID: 10958334).	Hans Gerhard Vogel, Franz J. Hock, Jochen Maas, Dieter Mayer (2006), Drug discovery and evaluation: Safety and pharmacokinetic assays, Springer publication, Chapter II D, page 456, table 3, PMID: 19035200, PMID: 12634921, European Journal of Pharmacology 441 (2002) 127-132. Am J Physiol Cell Physiol 281:C1077-C1093, 2001. Amino Acids (2005) 29: 229–233 DOI 10.1007/s00726-005-0221-x. PMID: 11901210	0	4
METPHELAT2tc	transport of L-Methionine into the cell and efflux of L-Phenylalanine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	met_L[e] + phe_L[c] -> met_L[c] + phe_L[e]	(2539.1 and 17254.1)	(23428.1 and 652.1)	Large neutral amino acids transporter small subunit 2 4F2 cell-surface antigen heavy chain		Large neutral amino acids transporter small subunit 2 and 4F2 cell-surface antigen heavy chain		higher affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s0042000002741).	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s0042000002741, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	0	4
METyLATtc	transport of L-Methionine by y+LAT1 or y+LAT2 transporters in small intestine and kidney	met_L[e] + na1[e] + arg_L[c] -> met_L[c] + na1[c] + arg_L[e]	(254.1 or (33836.1 and 17254.1))	(956.1 or 957.1) and (652.1)	Y+L amino acid transporter 1 Y+L amino acid transporter 2 4F2 cell-surface antigen heavy chain		Y+L amino acid transporter 1 or Y+L amino acid transporter 2 and 4F2 cell-surface antigen heavy chain		y+LAT1 and y+LAT2 transporters requires CD98 for sequestrization to the plasma membrane. Acts as an amino acid exchanger, with influx of neutral aminoa acids and efflux of cationic amino acid, requires Na+ for optimal activity. Can also operate with H+ in absence of Na+ (PMID: 11546643).	PMID: 11546643, PMID:18195088	0	4

METyLATthc	transport of Methionine by y+LAT1 or y+LAT2 with co-transporter of h in small intestine and kidney	met_L[e] + h[e] + arg_L[c] -> met_L[c] + h[c] + arg_L[e]	(254.1 or (33836.1 and 17254.1))	(956.1 or 957.1) and (652.1)	Y+L amino acid transporter 1 Y+L amino acid transporter 2 4F2 cell-surface antigen heavy chain		Y+L amino acid transporter 1 or Y+L amino acid transporter 2 and 4F2 cell-surface antigen heavy chain		y+LAT1 and y+LAT2 transporters requires CD98 for sequesterization to the plasma membrane. Acts as an amino acid exchanger, with influx of neutral aminoa acids and efflux of cationic amino acid, requires Na+ for optimal activity. Can also operate with H+ in absence of Na+ (PMID: 11546643).	PMID: 11546643, PMID:18195088	0	4
MTHFTe	transport of THF into the protal blood	5mthf[c] -> 5mthf[e]							5-methylfolate is found in the portal circulation, so this reaction was added as folate exit from the enterocytes. The transport is carrier proteen mediated, Na+ independant and electro-neutral.	Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Advanced nutrition and human metabolism, Wadsworth cengage learning, 5th edition, page 350, G.F.M. Ball (2006) Vitamins their role in the human body, Blackwell publishing, chapter 17, page 351-354.	0	2
NACDe	release of nicotinate at the basolateral surface	nac[c] -> nac[e]							diffusion process. Hypothetically created. Nothing much is known about nicain exit from the enterocytes.	PMID: 21749321.	0	1
NACHORCTL3lu	absoprtion of nicotinate at the brush border of enterocytes	nac[u] + h[u] -> nac[c] + h[c]	1257.1	(939.1)	Solute carrier family 22 member 13				nicotinate is essential for life expansion, needs to be re-absorbed. Can be either obtainedfrom diet, from tryptophan or breakdown of proteins. Low pH is required for an efficient uptake. The orphan transporter is highly operative in PCT og kidneys. Some authors have also suggested involvement of SLC5A8 in niacin uptake when niacin is administered at high pharmacological doses (PMID: 21749321).	PMID: 18411268, PMID: 15728713	0	2
NCAMDe	release of nicotinamide at the basolateral surface	ncam[c] -> ncam[e]							diffusion process. Hypothetically created. Nothing much is known about nicain exit from the enterocytes.	PMID: 21749321.	0	1
OCDEAFABP1tc	transport of octadecenoyl coA into the enterocytes	2 ocdcea[c] <=> 2 ocdcea[r]	148.1	(2168.1)	Fatty acid-binding protein, liver		Fatty acid-binding protein, liver		crystal structure of LFAB revealed 2 binding sites (in contrast to IFAB which has 1:1 stoichiometry) for oleate (PMID: 9054409). LFAB is expressed in liver, kidney, intestine, pancreas, stomach and lung (PMCID: PMC2670638). Once the long chain fatty acids enter the enterocytes, bind to the FABP reversibly, for transport into the E.R. to reconstitute triacylglycerols (PMID: 20522896, PMID: 19280719).	PMID: 9555061, PMCID: PMC2821027, PMID: 9054409, PMID: 9082452, PMCID: PMC2670638, http://mss3.libraries.rutgers.edu/dlr/TMP/rutgers-lib_26338-PDF-1.pdf	1	4
OLEICFATPtc	uptake of octadecenoate by the enterocytes	ocdcea[u] + atp[c] + coa[c] -> odecoa[c] + amp[c] + ppi[c]	26569.1	(1999.1)	Long-chain fatty acid transport protein 4	6.2.1.-	Long-chain fatty acid transport protein 4		major intestinal fatty acid transport protein, may also act in co-ordination with acyl co-A synthetase. The transport is ATP driven, further the transporter itself has fatty acid activating enzymic properties (PMID: 12856180).	PMID: 10518211, PMID: 20086080, PMID: 12856180, Immun., Endoc. & Metab. Agents in Med. Chem., 2009, 9, 11-17,	0	4
ORNALArBATtc	transport of L-Ornithine into the cell in exchange for L-Alanine by b0,+AT transporter at the apical surfaces of the membranes of small intestine and renal cells.	orn[u] + ala_L[c] -> orn[c] + ala_L[u]	(3962.1 and 2532.1)	(11136.1 and 6519.1)	B(,+)-type amino acid transporter 1 Neutral and basic amino acid transport protein rBAT		B(,+)-type amino acid transporter 1 and Neutral and basic amino acid transport protein rBAT		sodium independant antiport transport system, exchanges di-basic amino acids into the cells and neutral amino acids out of the cell. Located on the apical surfaces of transporting epithelia. Cellular localization being small intestine, kidney (proximal tubule), lung, placenta, brain and thymus. Requires the heterodimerization with rBAT glycoprotein. (PMID: 10958334).	PMID: 10958334, PMID: 19184091, PMID: 18195088, PMID: 11546643	0	4
ORNLEUrBATtc	transport of L-Ornithine into the cell in exchange for L-Leucine by b0,+AT transporter at the apical surfaces of the membranes of small intestine and renal cells.	orn[u] + leu_L[c] -> orn[c] + leu_L[u]	(3962.1 and 2532.1)	(11136.1 and 6519.1)	B(,+)-type amino acid transporter 1 Neutral and basic amino acid transport protein rBAT		B(,+)-type amino acid transporter 1 and Neutral and basic amino acid transport protein rBAT		sodium independant antiport transport system, exchanges di-basic amino acids into the cells and neutral amino acids out of the cell. Located on the apical surfaces of transporting epithelia. Cellular localization being small intestine, kidney (proximal tubule), lung, placenta, brain and thymus. Requires the heterodimerization with rBAT glycoprotein. (PMID: 10958334).	PMID: 10958334, PMID: 19184091, PMID: 18195088, PMID: 11546643	0	4
ORNt	transport of ornithine by y+ transporter	orn[c] <=> orn[e]	11987.1	(6541.1)	High affinity cationic amino acid transporter 1		High affinity cationic amino acid transporter 1		ubiquitously expressed y+ transport system, mediates uniport transport of arginine, lysine, ornithine and histidine. (PMID:18195088). Located on the basolateral surface, mediates a bidirectional uniport transport of actionic amino acid and is Na+ independent (PMID: 17494634). Recon 1 contains the reactions but with irrversible form.	PMID: 14770310, PMID: 12506130, PMID: 17494634,PMID:18195088.	1	4
PALFATPtc	uptake of Hexadecanoate by the enterocytes	hdca[u] + atp[c] + coa[c] -> pmtcoa[c] + amp[c] + ppi[c]	26569.1	(1999.1)	Long-chain fatty acid transport protein 4	6.2.1.-	Long-chain fatty acid transport protein 4		major intestinal fatty acid transport protein, may also act in co-ordination with acyl co-A synthetase. The transport is ATP driven, further the transporter itself has fatty acid activating enzymic properties (PMID: 12856180).	PMID: 10518211, PMID: 20086080, PMID: 12856180, Immun., Endoc. & Metab. Agents in Med. Chem., 2009, 9, 11-17,	0	4
PCHOLHSTDe	Transport, extracellular	pchol_hs[c] -> pchol_hs[e]							transported in chylomicrons into lymph	Sareen S. Gropper, jack L. Smith, James L. Groff (2009) Wadaworth cengage learning, Advanced nutrition and human metabolism, 5th edition, page 142-148.	0	2
PECDCHe	binding of pectins with deoxycholic acid in the intestinal lumen, reducing serum cholsterol levels.	pect[u] + dchac[u] + h[u] -> pectindchac[u]							pectin binds bile acids and leads to enhanced excretion, there by the 7-alpha hydroxylase pathway is activated laeding to increased cholesterol catabolism for synthesis of more bile acids (regulates cholesterol metabolism). however the decreased serum cholesterol levels are brought about by many other cumulative effects (water unstirred action of dieatary fibres, glycemic role etc) (PMID: 18302966, Gunness P, Gidley MJ. (2010). Food & Function 1: 149-55). pectin also binds more effeciently cholic acid.	PMID: 16925468, PMID: 12537466, PMID: 9808647, T.Pandolf and F.M. Clydesdale (1992) Journal of food science, vol.57, no.5, 1242-1245.	0	3
PECGCHLe	binding of pectins with glycocholate in the intestinal lumen, reducing serum cholsterol levels.	pect[u] + gchola[u] + h[u] -> pectingchol[u]							pectin binds bile acids and leads to enhanced excretion, there by the 7-alpha hydroxylase pathway is activated laeding to increased cholesterol catabolism for synthesis of more bile acids (regulates cholesterol metabolism). however the decreased serum cholesterol levels are brought about by many other cumulative effects (water unstirred action of dieatary fibres, glycemic role etc) (PMID: 18302966, Gunness P, Gidley MJ. (2010). Food & Function 1: 149-55). pectin also binds more effeciently cholic acid.	PMID: 16925468, PMID: 12537466, PMID: 9808647, T.Pandolf and F.M. Clydesdale (1992) Journal of food science, vol.57, no.5, 1242-1245.	0	3
PECTCHLe	binding of pectins with taurocholate in the intestinal lumen, reducing serum cholsterol levels.	pect[u] + tchola[u] + h[u] -> pectintchol[u]							pectin binds bile acids and leads to enhanced excretion, there by the 7-alpha hydroxylase pathway is activated laeding to increased cholesterol catabolism for synthesis of more bile acids (regulates cholesterol metabolism). however the decreased serum cholesterol levels are brought about by many other cumulative effects (water unstirred action of dieatary fibres, glycemic role etc) (PMID: 18302966, Gunness P, Gidley MJ. (2010). Food & Function 1: 149-55). pectin also binds more effeciently cholic acid.	PMID: 16925468, PMID: 12537466, PMID: 9808647, T.Pandolf and F.M. Clydesdale (1992) Journal of food science, vol.57, no.5, 1242-1245.	0	3
PEHSFABPe	transport of lysophosphatidylethanolamine into the enterocytes	2 pe_hs[c] <=> 2 pe_hs[r]	148.1	(2168.1)	Fatty acid-binding protein, liver		Fatty acid-binding protein, liver		crystal structure of LFAB revealed 2 binding sites (in contrast to IFAB which has 1:1 stoichiometry) for oleate (PMID: 9054409). LFAB is expressed in liver, kidney, intestine, pancreas, stomach and lung (PMCID: PMC2670638). Once the long chain fatty acids enter the enterocytes, bind to the FABP reversibly, for transport into the E.R. to reconstitute triacylglycerols (PMID: 20522896, PMID: 19280719).	PMID: 9555061, PMCID: PMC2821027, PMID: 9054409, PMID: 9082452, PMCID: PMC2670638, http://mss3.libraries.rutgers.edu/dlr/TMP/rutgers-lib_26338-PDF-1.pdf	1	4

PHEATB0tc	transport of L-Phenylalanine into the intestinal cells by ATB0 transporter	phe_L[e] + 2 na1[e] + cl[e] -> phe_L[c] + 2 na1[c] + cl[c]	56774.1	(11254.1)	Sodium- and chloride-dependent neutral and basic amino acid transporter B(+)		Sodium- and chloride-dependent neutral and basic amino acid transporter B(+)		ATB0 is both sodium and chloride coupled, with reaction stoichiometry 2Na+:1cl:1amino acid. The transporter is located in the intestine, has a broad substrate specificity (both neutral and cationic amino acids), but is not involved in the transport of aspartate, glutamate and proline (PMID:18195088).	PMID:18195088	0	4
PHEB0AT1tc	transport of L-Phenylalanine by the apical neutral amino acid transporters in kidney and intestine	phe_L[e] + na1[e] -> phe_L[c] + na1[c]	(78.1 or (74338.1 and 57394.1))	(3424.1) and (57393.1 or 59272.1)	3.4.17.23	Sodium-dependent neutral amino acid transporter B(0)AT1 Collectrin Angiotensin-converting enzyme 2	Sodium-dependent neutral amino acid transporter B(AT1 and Collectrin or Angiotensin-converting enzyme 2	Angiotensin-converting enzyme 2	transports all the neutral amino acids with preference for methionine, leucine and valine. Reaction stoichiometry is 1:1. Requires heterodimerization with collectrin protein for increased affinity. Found in kidney and intestine, however also reported to be expressed in skin. Requires association with ACE2 for expression in intestine but with collectrin for expression in kidney.	PMID: 19472175, PMID: 15804236, PMID: 18400692	0	4
PHEILELAT2tc	transport of L-Phenylalanine into the cell and efflux of L-Isoleucine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	phe_L[e] + ile_L[c] <=> phe_L[c] + ile_L[e]	(2539.1 and 17254.1)	(23428.1 and 652.1)	Large neutral amino acids transporter small subunit 2 4F2 cell-surface antigen heavy chain	Large neutral amino acids transporter small subunit 2 and 4F2 cell-surface antigen heavy chain		higher affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274). LAT2 carries both influx and efflux of phenylalanine, leucine and isolecuine, hence such reactions are reversible.	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	1	4
PHELAT1tc	transport of L-Phenylalanine by LAT1 in association with 4F2hc, across the apical surface of the membranes.	phe_L[e] + leu_L[c] -> phe_L[c] + leu_L[e]	(2539.1 and 17254.1)	(814.1 and 652.1)	Large neutral amino acids transporter small subunit 1 4F2 cell-surface antigen heavy chain	Large neutral amino acids transporter small subunit 1 and 4F2 cell-surface antigen heavy chain		leucine is the only amino acid tested for efflux. Expressed in ovary, placenta, brain, spleen, testis, activated lymphocytes and some tumor cells. Functions as a antiport transport system (DOI 10.1016/j.cell.2009.01.02), requires heterodimerization with glycoprotein CD98 (Pflugers Arch-Eur J Physiol (2000) 440:503-512, DOI 10.1007/s004240000274, PMID: 10958316).	Hans Gerhard Vogel, Franz J. Hock, Jochen Maas, Dieter Mayer (2006), Drug discovery and evaluation: Safety and pharmacokinetic assays, Springer publication, Chapter II D, page 456, table 3, PMID: 19035290, PMID: 12634921, European Journal of Pharmacology 441 (2002) 127-132. Am J Physiol Cell Physiol 281:C1077-C1093, 2001. Amino Acids (2005) 29: 229–233 DOI 10.1007/s00726-005-0221-x. PMID: 11902210	0	4
PHELAT3tc	transport of phenylalanine by LAT3 isintestinal cells	phe_L[e] <=> phe_L[c]	7241.1	(851.1)	Large neutral amino acids transporter small subunit 3	Large neutral amino acids transporter small subunit 3		LAT3 transports neutral amino acids and is Na+ independant. The transport mechanism is facilitated diffusion (PMID: 12930836). The substrate specificity is for leucine, isoleucine, methionine and phenylalanine (PMID: 18195088).	PMCID: PMC1864869, PMID: 12930836, PMID: 18195088	1	4
PHEyLATtc	transport of L-Phenylalanine by y+LAT1 or y+LAT2 transporters in small intestine and kidney	phe_L[e] + na1[e] + arg_L[c] -> phe_L[c] + na1[c] + arg_L[e]	(254.1 or (33836.1 and 17254.1))	(956.1 or 957.1) and (652.1)	Y+L amino acid transporter 1 Y+L amino acid transporter 2 4F2 cell-surface antigen heavy chain	Y+L amino acid transporter 1 or Y+L amino acid transporter 2 and 4F2 cell-surface antigen heavy chain		y+LAT1 and y+LAT2 transporters requires CD98 for sequestrization to the plasma membrane. Acts as an amino acid exchanger, with influx of neutral aminoa acids and efflux of cationic amino acid, requires Na+ for optimal activity. Can also operate with H+ in absence of Na+ (PMID: 11546643).	PMID: 11546643, PMID:18195088	0	4
PHEyLATtc	transport of Phenylalanine by y+LAT1 or y+LAT2 with co-transporter of h in small intestine and kidney	phe_L[e] + h[e] + arg_L[c] -> phe_L[c] + h[c] + arg_L[e]	(254.1 or (33836.1 and 17254.1))	(956.1 or 957.1) and (652.1)	Y+L amino acid transporter 1 Y+L amino acid transporter 2 4F2 cell-surface antigen heavy chain	Y+L amino acid transporter 1 or Y+L amino acid transporter 2 and 4F2 cell-surface antigen heavy chain		y+LAT1 and y+LAT2 transporters requires CD98 for sequestrization to the plasma membrane. Acts as an amino acid exchanger, with influx of neutral aminoa acids and efflux of cationic amino acid, requires Na+ for optimal activity. Can also operate with H+ in absence of Na+ (PMID: 11546643).	PMID: 11546643, PMID:18195088	0	4
PMTCOAFABP1tc	transport of palmitoyl coA into the enterocytes	2 pmtcoa[c] <=> 2 pmtcoa[r]	148.1	(2168.1)	Fatty acid-binding protein, liver	Fatty acid-binding protein, liver		crystal structure of LFAB revealed 2 binding sites (in contrast to IFAB which has 1:1 stoichiometry) for oleate (PMID: 9054409). LFAB is expressed in liver, kidney, intestine, pancreas, stomach and lung (PMCID: PMC2670638). Once the long chain fatty acids enter the enterocytes, bind to the FABP reversibly, for transport into the E.R. to reconstitute triacylglycerols (PMID: 20522896, PMID: 19280719).	PMID: 9555061, PMCID: PMC2821027, PMID: 9054409, PMID: 9082452, PMCID: PMC2670638, http://mss3.libraries.rutgers.edu/dlr/TMP/rutgers-lib_26338-PDF-1.pdf	1	4
PNTORDtc	release of pantothenate across the basolatral membrane	pnto_R[c] -> pnto_R[e]						not much is known about the pantothenic acid exit across the basolateral membrane. Diffusion reaction is hypothetical. However, uptake of pantothenate by RBCs takes place by simple diffusion (G.F.M. Ball (2006) Vitamins their role in the human body, Blackwell publishing, chapter 15, page 329.).	PMID: 21749321	0	1
PROB0ATtc	transport of L-Proline by the apical neutral amino acid transporters B(0)AT1 or B(0)AT2 in kidney, intestine or brain	pro_L[e] + na1[e] -> pro_L[c] + na1[c]	(78.1 or (74338.1 and 57394.1))	(3424.1) and (57393.1 or 59272.1)	3.4.17.23	Sodium-dependent neutral amino acid transporter B(0)AT1 and Collectrin or Angiotensin-converting enzyme 2	Sodium-dependent neutral amino acid transporter B(AT1 and Collectrin or Angiotensin-converting enzyme 2	Angiotensin-converting enzyme 2	B(0)AT1 transports all the neutral amino acids with preference for methionine, leucine and valine. Reaction stoichiometry is 1:1. Requires heterodimerization with collectrin protein for increased affinity. Found in kidney and intestine, however also reported to be expressed in skin. Requires association with ACE2 for expression in intestine but with collectrin for expression in kidney. The the localization of the B(0)AT2 transporter has been studied in brain tissue but data from the kidney have not been reported (PMID: 18195088).	PMID: 19472175, PMID: 15804236, PMID: 18400692, PMID: 16185194, PMID: 18195088	0	4
PRODPATtc	transport of D-Proline by the apical PAT2 or PAT1 amino acid transporters in kidney and intestine	pro_D[e] + h[e] -> pro_D[c] + h[c]	215335.1	(26358.1)	Proton-coupled amino acid transporter 1	Proton-coupled amino acid transporter 1		PAT2 is strongly expressed in heart and lung and more weakly in kidney and muscle (PMID:18400692). PAT2 doest not strongly discriminate between L and D isomers (PMID 18400692). PAT1 proton-amino acid co-transporter with 1:1 stoichiometry, does not discriminate between L and D isomers, located on the apical membrane of kidney and intestine (PMID: 18400692, PMID: 18195088).	PMID:18195088, PMID:18400692, PMID: 15345686, PMID: 17123464, PMCID: PMC34647	0	4
PROGLYPEPT1tc	transport of Prolylglycine by the apical PEPT1 amino acid transporters across the brush border cells of the enterocytes of the intestine and renal cells	progly[e] + h[e] -> progly[c] + h[c]	215335.1	(6564.1)	Solute carrier family 15 member 1	Solute carrier family 15 member 1		PEPT1 appears to transport all di- and tri- peptides across the brush border of the intestinal cells (Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Advanced nutrition and human metabolism, Wadsworth cengage learning, 5th edition, page 193). PEPT1 is expressed highly in intestinal cells where as PEPT2 is localized to renal cells (PMID: 10330047).	PMID: 7858448, PMID: 14995252, PMID: 14977407, PMID: 10330047	0	4
PROGLYPROtc	hydrolysis of glycylproline in the small intestine for cellular uptake	progly[c] + h2o[c] <=> pro_L[c] + gly[c]	18624.1	(5184.1)	Xaa-Pro dipeptidase	3.4.13.9	Xaa-Pro dipeptidase		0	PMID: 15552267	1	4
PROMINOtc	transport of L-Proline by the apical IMINO amino acid transporters in kidney and intestine	pro_L[e] + 2 na1[e] + cl[e] -> pro_L[c] + 2 na1[c] + cl[c]	(1268.1 and 57394.1)	(54716.1 and 57393.1)	Sodium- and chloride-dependent transporter XTRP3 Collectrin		Sodium- and chloride-dependent transporter XTRP3 and Collectrin		IMINO transporter is suggested to be a candidate for iminoglycinuria (PMID: 16052252). Associted with collectrin in kidney.	PMID: 19657989, PMID: 15632147, PMID: 18195088, PMID: 18400692	0	4
PROLPATtc	transport of L-Proline by the apical PAT2 or PAT1 amino acid transporters in kidney and intestine	pro_L[e] + h[e] -> pro_L[c] + h[c]	215335.1	(26358.1)	Proton-coupled amino acid transporter 1	Proton-coupled amino acid transporter 1		PAT2 is strongly expressed in heart and lung and more weakly in kidney and muscle (PMID:18400692). PAT2 doest not strongly discriminate between L and D isomers (PMID 18400692). PAT1 proton-amino acid co-transporter with 1:1 stoichiometry, does not discriminate between L and D isomers, located on the apical membrane of kidney and intestine (PMID: 18400692, PMID: 18195088).	PMID:18195088, PMID:18400692, PMID: 15345686, PMID: 17123464, PMCID: PMC34647	0	4

PSYGCHe	binding of psyllium with glycocholate in the intestinal lumen, reducing serum cholsterol levels.	psyl[u] + gchola[u] -> psylchol[u]							psyllium consists of two parts- arabinoxylan, which is a hemi-cellulose and beta-sitosterol. Psyllium binds bile acids and leads to enhanced excretion, there by the 7-alpha hydroxylase pathway is activated laeding to increased cholesterol catabolism for synthesis of more bile acids (regulates cholesterol metabolism). however the decreased serum cholesterol levels are brought about by many other cumulative effects (water unstirred action of dieatary fibres, glycemic role etc) (PMID: 18302966, Gunness P, Gidley MJ. (2010). Food & Function 1: 149-55).	Zacherl C, Eisner P, Engel K-H. (2011). Food Chemistry 126: 423-8, Dongowski G. (2007). Food Chemistry 104: 390-7	0	3
PSYTCHe	binding of psyllium with taurocholate in the intestinal lumen, reducing serum cholsterol levels.	psyl[u] + tchola[u] -> psyltchol[u]							psyllium consists of two parts- arabinoxylan, which is a hemi-cellulose and beta-sitosterol. Psyllium binds bile acids and leads to enhanced excretion, there by the 7-alpha hydroxylase pathway is activated laeding to increased cholesterol catabolism for synthesis of more bile acids (regulates cholesterol metabolism). however the decreased serum cholesterol levels are brought about by many other cumulative effects (water unstirred action of dieatary fibres, glycemic role etc) (PMID: 18302966, Gunness P, Gidley MJ. (2010). Food & Function 1: 149-55).	Zacherl C, Eisner P, Engel K-H. (2011). Food Chemistry 126: 423-8, Dongowski G. (2007). Food Chemistry 104: 390-7	0	3
PSYTDECHe	binding of psyllium with taurodeoxycholate in the intestinal lumen, reducing serum cholsterol levels.	psyl[u] + tdechola[u] -> psyltdechol[u]							psyllium consists of two parts- arabinoxylan, which is a hemi-cellulose and beta-sitosterol. Psyllium binds bile acids and leads to enhanced excretion, there by the 7-alpha hydroxylase pathway is activated laeding to increased cholesterol catabolism for synthesis of more bile acids (regulates cholesterol metabolism). however the decreased serum cholesterol levels are brought about by many other cumulative effects (water unstirred action of dieatary fibres, glycemic role etc) (PMID: 18302966, Gunness P, Gidley MJ. (2010). Food & Function 1: 149-55). Deoxycholic acid is a secondary bile salt formed by deconjugation and further 7-alpha-dehydroxylation by the bacterial action in the gut (Harpers illustrated biochemistry, 28th edition, page 228-231.). Taurodeoxy-cholic acid may be formed by the conjugation of taurine with deoxycholic acid (no evidence found for suc hreaction but the metabolite Taurodeoxycholic acid has been estimated in human blood and bile in trave amounts (HMDB00896)).	Zacherl C, Eisner P, Engel K-H. (2011). Food Chemistry 126: 423-8, Dongowski G. (2007). Food Chemistry 104: 390-7	0	3
RETINOLtc	transport of retinol into the intestine and liver cells	retinol[u] -> retinol[c]	(1966.1 or (19662.1 and 2897.1 and 19659.1))	(595.1 and 6422.1) and (5947.1 or 5948.1)	Retinol-binding protein 4 Stimulated by retinoic acid gene 6 protein homolog Retinol-binding protein 1 Retinol-binding protein 2		Retinol-binding protein 4 and Stimulated by retinoic acid gene 6 protein homolog and Retinol-binding protein 1 or Retinol-binding protein 2		circulating retinol is bound to the retinol binding protein-4 with high affinity forming retinol-RBP complex, STRA6 acts as a transporter of this complex and further actuvates signalling cascades (PMID: 21368206). after entry into the enterocytes, the CRBP 1 and 2 play role in uptake of retinol into the liver cells and also enhance retinol absorption (PMID:16011460).	PMID: 21482409, PMID: 21368206, PMID:16011460, Sareen S. Gropper, Jack L. Smith, James L. Groff (2009) Advanced nutrition and human metabolism, Wadsworth cengage learning, 5th edition, page 375-379	0	4
RIBFLVlu	absoprtion of riboflavin by diffusion	ribflv[u] -> ribflv[c]							absorption of riboflavin by simple diffusion at high concentration.	G.F.M. Ball (2006) Vitamins their role in the human body, Blackwell publishing, chapter 12, page 291.	0	2
RIBFLVte	release of riboflavin into the portal blood.	atp[c] + h2o[c] + ribflv[c] -> adp[c] + h[c] + pi[c] + ribflv[e]	5271.1	(5565.1)	Riboflavin transporter 1				both entry and exit of riboflavin from the enterocytes in energy dependant and Na+ independant. Carrier protein mediated.	G.F.M. Ball (2006) Vitamins their role in the human body, Blackwell publishing, chapter 12, page 291-292, PMID: 21854757, PMID: 20463145, Said HM, Hollander D, Mohammadkhani R. (1993). Biochimica et Biophysica Acta (BBA) - Biomembranes 1148: 263-8.	0	4
RTOTAL2TDlu	difussion of fatty acid accross the brush border membrane	Rtotal2[u] <=> Rtotal2[c]								Sareen S. Gropper, jack L. Smith, James L. Groff (2009) Wadaworth cengage learning, Advanced nutrition and human metabolism, 5th edition, page 142-144.	1	2
RTOTAL3TDlu	difussion of fatty acid accross the brush border membrane	Rtotal3[u] <=> Rtotal3[c]								Sareen S. Gropper, jack L. Smith, James L. Groff (2009) Wadaworth cengage learning, Advanced nutrition and human metabolism, 5th edition, page 142-144.	1	2
RTOTALDlu	difussion of fatty acid accross the brush border membrane	Rtotal[u] <=> Rtotal[c]								Sareen S. Gropper, jack L. Smith, James L. Groff (2009) Wadaworth cengage learning, Advanced nutrition and human metabolism, 5th edition, page 142-144.	1	2
SBTlu	diffusion of sorbitol into the enterocytes	sbt_D[u] <=> sbt_D[c]								Sareen S. Gropper, jack L. Smith, James L. Groff (2009) Wadaworth cengage learning, Advanced nutrition and human metabolism, 5th edition, page 68-74. PMID: 20522896, William F. Ganong Review of medical physiology 12th edition Lange publication pages 384-393	0	3
SBTt	D-sorbitol transport via diffusion (extracellular to cytosol)	sbt-D[e] <=> sbt-D[c]							Sorbitol is uptaken via diffusion in lumen	Sareen S. Gropper, jack L. Smith, James L. Groff (2009) Wadaworth cengage learning, Advanced nutrition and human metabolism, 5th edition, page 68-74. PMID: 20522896, William F. Ganong Review of medical physiology 12th edition Lange publication pages 384-393		
SERATB0tc	transport of L-Serine into the intestinal cells by ATB0 transporter	ser_L[u] + 2 na1[u] + cl[u] -> ser_L[c] + 2 na1[c] + cl[c]	56774.1	(11254.1)	Sodium- and chloride-dependent neutral and basic amino acid transporter B(+)		Sodium- and chloride-dependent neutral and basic amino acid transporter B(+)		ATB0 is both sodium and chloride coupled, with reaction stoichiometry 2Na+:1cl:1amino acid. The transporter is localted in the intestine, has a broad substrate specificity (both neutral and cationic amino acids), but is not involved in the transport of aspartate, glutamate and proline (PMID:18195088).	PMID:18195088	0	4
SERB0AT1tc	transport of L-Serine by the apical neutral amino acid transporters in kidney and intestine	ser_L[u] + na1[u] -> ser_L[c] + na1[c]	(78.1 or (74338.1 and 57394.1))	(3424.1) and (57393.1 or 59272.1)	Sodium-dependent neutral amino acid transporter B()AT1 Collectrin Angiotensin-converting enzyme 2	3.4.17.23	Sodium-dependent neutral amino acid transporter B()AT1 and Collectrin or Angiotensin-converting enzyme 2	Angiotensin-converting enzyme 2	transports all the neutral amino acids with preference for methionine, leucine and valine. Reaction stoichiometry is 1:1. Requires heterodimerization with collectrin protein for increased affinity. Found in kidney and intestine, however also reported to be expressed in skin. Requires association with ACE2 for expression in intestine but with collectrin for expression in kidney.	PMID: 19472175, PMID: 15804236, PMID: 18400692	0	4
SERILELAT2tc	transport of L-Serine into the cell and efflux of L-Isoleucine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	ser_L[e] + ile_L[c] -> ser_L[c] + ile_L[e]	(2539.1 and 17254.1)	(23428.1 and 652.1)	Large neutral amino acids transporter small subunit 2 4F2 cell-surface antigen heavy chain		Large neutral amino acids transporter small subunit 2 and 4F2 cell-surface antigen heavy chain		higher affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for traficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s00420000274).	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s00420000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	0	4
SERPHELAT2tc	transport of L-Serine into the cell and efflux of L-Phenylalanine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	ser_L[e] + phe_L[c] -> ser_L[c] + phe_L[e]	(2539.1 and 17254.1)	(23428.1 and 652.1)	Large neutral amino acids transporter small subunit 2 4F2 cell-surface antigen heavy chain		Large neutral amino acids transporter small subunit 2 and 4F2 cell-surface antigen heavy chain		higher affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for traficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s00420000274).	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s00420000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	0	4
TAGHSTDe	Transport, extracellular	tag_hs[c] -> tag_hs[e]							transported in chylomicrons into lymph	Sareen S. Gropper, jack L. Smith, James L. Groff (2009) Wadaworth cengage learning, Advanced nutrition and human metabolism, 5th edition, page 142-148.	0	2
TAUBETAtc	transport of taurine into the intestinal cells by beta transport system	taur[u] + 2 na1[u] + cl[u] -> taur[c] + 2 na1[c] + cl[c]	21366.1	(6533.1)	Sodium- and chloride-dependent taurine transporter		Sodium- and chloride-dependent taurine transporter		beta transporter system requires chloride ions for optimal uptake of amino acids into the cells. Expressed on both apical and basolateral membranes of renal cells. Transports taurine and beta alanine. (PMID: 18195088)	PMID: 19074966, PMID: 2206910, PMID: 1324004, PMID: 16956961, PMID: 15166008, PMID: 18195088	0	4

TAUPAT1c	transport of taurine into the intestinal cells by PAT1	taur[u] + h[u] -> taur[c] + h[c]	215335.1	(26358.1)	Proton-coupled amino acid transporter 2		Proton-coupled amino acid transporter 2		PAT2 is strongly expressed in heart and lung and more weakly in kidney and muscle (PMID:18400692). PAT2 doest not strongly discriminate between L and D isomers (PMID 18400692). PAT1 proton-amino acid co-transporter with 1:1 stoichiometry, does not discriminate between L and D isomers, located on the apical membrane of kidney and intestine (PMID: 18400692, PMID: 18195088).	PMID: 19074966, PMID:18195088, PMID:18400692, PMID: 15345686, PMID: 17123464, PMCID: PMC34648	0	4
THMATPe	thiamine exit from the enterocytes	thm[c] + atp[c] + h2o[c] -> thm[e] + adp[c] + pi[c] + h[c]							thiamine exit from the enterocytes, depends on sodium and energy mediated by Na/K ATPase. Thiamine exit is directly coupled to ATP hydrolysis (PMID: 12645798).	PMID: 10964259, PMID: 8254515, G.F.M. Ball (2006) Vitamins their role in the human body, Blackwell publishing, chapter 11, page 275.	0	3
THRATB0tc	transport of L-Threonine into the intestinal cells by ATB0 transporter	thr_L[u] + 2 na1[u] + cl[u] -> thr_L[c] + 2 na1[c] + cl[c]	56774.1	(11254.1)	Sodium- and chloride-dependent neutral and basic amino acid transporter B(0+)		Sodium- and chloride-dependent neutral and basic amino acid transporter B(0+)		ATB0 is both sodium and chloride coupled, with reaction stoichiometry 2Na+:1cl:1amino acid. The transporter is located in the intestine, has a broad substrate specificity (both neutral and cationic amino acids), but is not involved in the transport of aspartate, glutamate and proline (PMID:18195088).	PMID:18195088	0	4
THRB0AT1tc	transport of L-Threonine by the apical neutral amino acid transporters in kidney and intestine	thr_L[u] + na1[u] -> thr_L[c] + na1[c]	(78.1 or (74338.1 and 57394.1))	(3424.1) and (57393.1 or 59272.1)	Sodium-dependent neutral amino acid transporter B(0)AT1 Collectrin Angiotensin-converting enzyme 2	3.4.17.23	Sodium-dependent neutral amino acid transporter B(0)AT1 and Collectrin or Angiotensin-converting enzyme 2	Angiotensin-converting enzyme 2	transports all the neutral amino acids with preference for methionine, leucine and valine. Reaction stoichiometry is 1:1. Requires heterodimerization with collectrin protein for increased affinity. Found in kidney and intestine, however also reported to be expressed in skin. Requires association with ACE2 for expression in intestine but with collectrin for expression in kidney.	PMID: 19472175, PMID: 15804236, PMID: 18400692	0	4
THRBELAT2tc	transport of L-Threonine into the cell and efflux of L-holoucine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	thr_L[e] + ile_L[c] -> thr_L[c] + ile_L[e]	(2539.1 and 17254.1)	(23428.1 and 652.1)	Large neutral amino acids transporter small subunit 2 4F2 cell-surface antigen heavy chain		Large neutral amino acids transporter small subunit 2 and 4F2 cell-surface antigen heavy chain		higher affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s0042000000274).	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s0042000000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	0	4
THRPHELAT2tc	transport of L-Threonine into the cell and efflux of L-Phenylalanine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	thr_L[e] + phe_L[c] -> thr_L[c] + phe_L[e]	(2539.1 and 17254.1)	(23428.1 and 652.1)	Large neutral amino acids transporter small subunit 2 4F2 cell-surface antigen heavy chain		Large neutral amino acids transporter small subunit 2 and 4F2 cell-surface antigen heavy chain		higher affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s0042000000274).	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s0042000000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	0	4
TRPATB0tc	transport of L-Tryptophan into the intestinal cells by ATB0 transporter	trp_L[u] + 2 na1[u] + cl[u] -> trp_L[c] + 2 na1[c] + cl[c]	56774.1	(11254.1)	Sodium- and chloride-dependent neutral and basic amino acid transporter B(0+)		Sodium- and chloride-dependent neutral and basic amino acid transporter B(0+)		ATB0 is both sodium and chloride coupled, with reaction stoichiometry 2Na+:1cl:1amino acid. The transporter is located in the intestine, has a broad substrate specificity (both neutral and cationic amino acids), but is not involved in the transport of aspartate, glutamate and proline (PMID:18195088).	PMID:18195088	0	4
TRPB0AT1tc	transport of L-Tryptophan by the apical neutral amino acid transporters in kidney and intestine	trp_L[u] + na1[u] -> trp_L[c] + na1[c]	(78.1 or (74338.1 and 57394.1))	(3424.1) and (57393.1 or 59272.1)	Sodium-dependent neutral amino acid transporter B(0)AT1 Collectrin Angiotensin-converting enzyme 2	3.4.17.23	Sodium-dependent neutral amino acid transporter B(0)AT1 and Collectrin or Angiotensin-converting enzyme 2	Angiotensin-converting enzyme 2	transports all the neutral amino acids with preference for methionine, leucine and valine. Reaction stoichiometry is 1:1. Requires heterodimerization with collectrin protein for increased affinity. Found in kidney and intestine, however also reported to be expressed in skin. Requires association with ACE2 for expression in intestine but with collectrin for expression in kidney.	PMID: 19472175, PMID: 15804236, PMID: 18400692	0	4
TRPBELAT2tc	transport of L-Tryptophan into the cell and efflux of L-holoucine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	trp_L[e] + ile_L[c] -> trp_L[c] + ile_L[e]	(2539.1 and 17254.1)	(23428.1 and 652.1)	Large neutral amino acids transporter small subunit 2 4F2 cell-surface antigen heavy chain		Large neutral amino acids transporter small subunit 2 and 4F2 cell-surface antigen heavy chain		higher affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s0042000000274).	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s0042000000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	0	4
TRPLAT1tc	transport of L-Tryptophan by LAT1 in associations wih 4F2hc, across the apical surface of the membranes.	trp_L[u] + leu_L[c] -> trp_L[c] + leu_L[u]	(2539.1 and 17254.1)	(814 and 652.1)	Large neutral amino acids transporter small subunit 1 4F2 cell-surface antigen heavy chain		Large neutral amino acids transporter small subunit 1 and 4F2 cell-surface antigen heavy chain		leucine is the only amino acid tested for efflux. Expressed in ovary, placenta, brain, spleen, testis, activated lymphocytes and some tumor cells. Functions as a antiport transport system (DOI 10.1016/j.cell.2009.01.022), requires heterodimerization with glycoprotein CD98 (Pflugers Arch-Eur J Physiol (2000) 440:503-512, DOI 10.1007/s0042400000274, PMID: 10958134).	Hans Gerhard Vogel, Franz J. Hock, Jochen Maas, Dieter Mayer (2006), Drug discovery and evaluation: Safety and pharmacokinetic assays, Springer publication, Chapter II D, page 456, table 3, PMID: 19035290, PMID: 12634921, European Journal of Pharmacology 441 (2002) 127-132. Am J Physiol Cell Physiol 281:C1077-C1093, 2001. Amino Acids (2005) 29: 229–233 DOI 10.1007/s00726-005-0221-x. PMID: 11902210	0	4
TRPPHELAT1tc	transport of L-Tryptophan into the cell and efflux of L-Phenylalanine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	trp_L[e] + phe_L[c] -> trp_L[c] + phe_L[e]	(2539.1 and 17254.1)	(23428.1 and 652.1)	Large neutral amino acids transporter small subunit 2 4F2 cell-surface antigen heavy chain		Large neutral amino acids transporter small subunit 2 and 4F2 cell-surface antigen heavy chain		higher affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s0042000000274).	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s0042000000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	0	4
TYRATB0tc	transport of L-Tyrosine into the intestinal cells by ATB0 transporter	tyr_L[u] + 2 na1[u] + cl[u] -> tyr_L[c] + 2 na1[c] + cl[c]	56774.1	(11254.1)	Sodium- and chloride-dependent neutral and basic amino acid transporter B(0+)		Sodium- and chloride-dependent neutral and basic amino acid transporter B(0+)		ATB0 is both sodium and chloride coupled, with reaction stoichiometry 2Na+:1cl:1amino acid. The transporter is located in the intestine, has a broad substrate specificity (both neutral and cationic amino acids), but is not involved in the transport of aspartate, glutamate and proline (PMID:18195088).	PMID:18195088	0	4
TYRB0AT1tc	transport of L-Tyrosine by the apical neutral amino acid transporter B(0)AT1 in kidney and intestine	tyr_L[u] + na1[u] -> tyr_L[c] + na1[c]	(78.1 or (74338.1 and 57394.1))	(3424.1) and (57393.1 or 59272.1)	Sodium-dependent neutral amino acid transporter B(0)AT1 Collectrin Angiotensin-converting enzyme 2	3.4.17.23	Sodium-dependent neutral amino acid transporter B(0)AT1 and Collectrin or Angiotensin-converting enzyme 2	Angiotensin-converting enzyme 2	transports all the neutral amino acids with preference for methionine, leucine and valine. Reaction stoichiometry is 1:1. Requires heterodimerization with collectrin protein for increased affinity. Found in kidney and intestine, however also reported to be expressed in skin. Requires association with ACE2 for expression in intestine but with collectrin for expression in kidney.	PMID: 19472175, PMID: 15804236, PMID: 18400692	0	4
TYRBELAT2tc	transport of L-Tyrosine into the cell and efflux of L-holoucine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	tyr_L[e] + ile_L[c] -> tyr_L[c] + ile_L[e]	(2539.1 and 17254.1)	(23428.1 and 652.1)	Large neutral amino acids transporter small subunit 2 4F2 cell-surface antigen heavy chain		Large neutral amino acids transporter small subunit 2 and 4F2 cell-surface antigen heavy chain		higher affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s0042000000274).	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s0042000000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-z, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	0	4

TYRLAT1tc	transport of L-Tyrosine by LAT1 in association with 4F2hc, across the apical surface of the membranes.	tyr_L[us] + leu_L[c] -> tyr_L[c] + leu_L[us]	(2539.1 and 17254.1)	(814.4 and 652.1)	Large neutral amino acids transporter small subunit 1 4F2 cell-surface antigen heavy chain		Large neutral amino acids transporter small subunit 1 and 4F2 cell-surface antigen heavy chain		leucine is the only amino acid tested for efflux. Expressed in ovary, placenta, brain, spleen, testis, activated lymphocytes and some tumor cells. Functions as a antiport transport system (DOI 10.1016/j.ceil.2009.01.02), requires heterodimerization with glycoprotein CD98 (Pflugers Arch-Eur J Physiol (2000) 440:503-512, DOI 10.1007/s004240000274, PMID: 10958334).	Hans Gerhard Vogel, Franz J. Hock, Jochen Maas, Dieter Mayer (2006), Drug discovery and evaluation: Safety and pharmacokinetic assays, Springer publication, Chapter II D, page 456, table 3, PMID: 19035290, PMID: 12634921, European Journal of Pharmacology 441 (2002) 127-132. Am J Physiol Cell Physiol 281:C1077-C1093, 2001. Amino Acids (2005) 29: 229–233 DOI 10.1007/s00726-005-0221-x. PMID: 11902110	0	4
TYRPHELAT2tc	transport of L-Tyrosine into the cell and efflux of L-Phenylalanine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	tyr_L[e] + phe_L[c] -> tyr_L[c] + phe_L[e]	(2539.1 and 17254.1)	(23428.1 and 652.1)	Large neutral amino acids transporter small subunit 2 4F2 cell-surface antigen heavy chain		Large neutral amino acids transporter small subunit 2 and 4F2 cell-surface antigen heavy chain		higher affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274).	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-x, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	0	4
VALATB0tc	transport of L-Valine into the intestinal cells by ATB0 transporter	val_L[us] + 2 na1[us] + cl[us] -> val_L[c] + 2 na1[c] + cl[c]	56774.1	(11254.1)	Sodium- and chloride-dependent neutral and basic amino acid transporter B(^+)		Sodium- and chloride-dependent neutral and basic amino acid transporter B(^+)		ATB0 is both sodium and chloride coupled, with reaction stoichiometry 2Na+:1cl:1amino acid. The transporter is localized in the intestine, has a broad substrate specificity (both neutral and cationic amino acids), but is not involved in the transport of aspartate, glutamate and proline (PMID:18195088).	PMID:18195088	0	4
VALB0ATe	transport of L-Valine by the apical neutral amino acid transporters B(0)AT1 or B(0)AT2 in kidney, intestine or brain	val_L[us] + na1[us] -> val_L[c] + na1[c]	(78.1 or (74338.1 and 57394.1))	((3424.1) and (57393.1 or 59272)	3.4.17.23	Sodium-dependent neutral amino acid transporter B(0)AT1 Collectrin Angiotensin-converting enzyme 2	Angiotensin-converting enzyme 2		B(0)AT1 transports all the neutral amino acids with preference for methionine, leucine and valine. Reaction stoichiometry is 1:1. Requires heterodimerization with collectrin protein for increased affinity. Found in kidney and intestine, however also reported to be expressed in skin. Requires association with ACE2 for expression in intestine but with collectrin for expression in kidney. The localization of the B(0)AT2 transporter has been studied in brain tissue but data from the kidney have not been reported (PMID: 18195088).	PMID: 19472175, PMID: 15804236, PMID: 18400692, PMID: 16185194, PMID: 18195088	0	4
VALILELAT2tc	transport of L-Valine into the cell and efflux of L-Isoleucine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	val_L[e] + ile_L[c] -> val_L[c] + ile_L[e]	(2539.1 and 17254.1)	(23428.1 and 652.1)	Large neutral amino acids transporter small subunit 2 4F2 cell-surface antigen heavy chain		Large neutral amino acids transporter small subunit 2 and 4F2 cell-surface antigen heavy chain		higher affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274).	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-x, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	0	4
VALLAT1tc	transport of L-Valine by LAT1 in association with 4F2hc, across the apical surface of the membranes.	val_L[us] + leu_L[c] -> val_L[c] + leu_L[us]	(2539.1 and 17254.1)	(814.4 and 652.1)	Large neutral amino acids transporter small subunit 1 4F2 cell-surface antigen heavy chain		Large neutral amino acids transporter small subunit 1 and 4F2 cell-surface antigen heavy chain		leucine is the only amino acid tested for efflux. Expressed in ovary, placenta, brain, spleen, testis, activated lymphocytes and some tumor cells. Functions as a antiport transport system (DOI 10.1016/j.ceil.2009.01.02), requires heterodimerization with glycoprotein CD98 (Pflugers Arch-Eur J Physiol (2000) 440:503-512, DOI 10.1007/s004240000274, PMID: 10958334).	Hans Gerhard Vogel, Franz J. Hock, Jochen Maas, Dieter Mayer (2006), Drug discovery and evaluation: Safety and pharmacokinetic assays, Springer publication, Chapter II D, page 456, table 3, PMID: 19035290, PMID: 12634921, European Journal of Pharmacology 441 (2002) 127-132. Am J Physiol Cell Physiol 281:C1077-C1093, 2001. Amino Acids (2005) 29: 229–233 DOI 10.1007/s00726-005-0221-x. PMID: 11902110	0	4
VALPHELAT2tc	transport of L-Valine into the cell and efflux of L-Phenylalanine out of the cell by LAT2 on the basolateral surfaces of kidney and intestine.	val_L[e] + phe_L[c] -> val_L[c] + phe_L[e]	(2539.1 and 17254.1)	(23428.1 and 652.1)	Large neutral amino acids transporter small subunit 2 4F2 cell-surface antigen heavy chain		Large neutral amino acids transporter small subunit 2 and 4F2 cell-surface antigen heavy chain		higher affinity for small neutral amino acids that LAT1, functions as exchanger (antiport system), at the basolateral surface of membranes in transporting epithelia. Localized in the proximal tubule of kidney, small intestine. Lesser expression in ivary, placenta and brain. Heterodimerization with CD-98 for trafficking of the complex to the membrane. (Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274).	Pflugers Arch-Eur J Physiol (2000) 440:503-512 DOI 10.1007/s004200000274, PMID: 10574970, J Am Soc Nephrol 14: 837–847, 200, Pflugers Arch-Eur J Physiol (2003) 445:529-533 DOI 10.1007/s00424-002-0973-x, PMID: 18195088, Am J Physiol (2001) 281:C1077-C1093.	0	4
VITD3Ite	uptake of vitamin D by enterocytes	vitd3[us] <=> vitd3[c]							uptake of vitamin D by simple diffusion.	G.F.M. Ball (2006) Vitamins their role in the human body, Blackwell publishing, chapter 8. page 195-196.	1	2
VITD3Te	release of vitamin D into lymph	vitd3[c] <=> vitd3[e]							incorporated into chylomicrons and transported into lymph.	G.F.M. Ball (2006) Vitamins their role in the human body, Blackwell publishing, chapter 8. page 195-196.	1	2
VITEte	uptake of alpha-Tocopherol into the enterocytes	avite1[us] -> avite1[c]	(2778.1 and 237636.1)	(949.1 and 29881.1)	Scavenger receptor class B member 1 Niemann-Pick C1-like protein 1		Scavenger receptor class B member 1 and Niemann-Pick C1-like protein 1		vitamin E uptake is similar to cholesterol, although passive diffusion has been observed, receptor mediated transport is faster.	PMID: 15213020, PMID: 17320165, PMID: 18403720, PMID: 16380385, PMID: 15135148	0	4
VITEtd	efflux of alpha-Tocopherol into the lyphatics in chylomicrons	avite1[c] + atp[c] + h2o[c] -> avite1[e] + adp[c] + pi[c] + h[c]	1133.1	(19.1)	ATP-binding cassette sub-family A member 1		ATP-binding cassette sub-family A member 1		ATP binding cassette required for efflux of the vitamin E into the lymph form the enterocytes.	PMID: 15213020, PMID: 17320165	0	4
VITKtd	transport of vit K into lymph	phyQ[c] -> phyQ[e]							vit K release into lymph via chylomicrons	PMID: 18841274	0	2
XOLEST2HSTDHe	Transport, extracellular	xolest2_hs[c] -> xolest2_hs[e]							transported in chylomicrons into lymph	Sareen S. Gropper, jack L. Smith, James L. Groff (2009) Wadsworth cengage learning, Advanced nutrition and human metabolism, 5th edition, page 142-148.	0	2
4HPRO_LTi	trans-4-hydroxy-L-proline transport	4hpro-LT[e] + h[e] <=> 4hpro-LT[c] + h[c]							Needed to provide this metabolite for reaction 4OHPROMMNOr in joint model.		1	1
BGLCt	beta-glucan transport	bglc[e] + h[e] <=> bglc[c] + h[c]							Needed to provide this metabolite for reaction BGLUGCHe, BGLUTCHLe and BGLUTDECHOe in joint model.		1	1
BGLUGCHt	binding of betaglucans with glycocholate transport	glgchlo[e] + h[e] <=> glgchlo[c] + h[c]							Needed to provide this metabolite for reaction BGLUGCHe in joint model.		1	1
BGLUTCHLt	binding of betaglucans with taurocholate transport	gltchu[e] + h[e] <=> gltchu[c] + h[c]							Needed to provide this metabolite for reaction BGLUTCHLe in joint model.		1	1
BGLUTDECHOt	binding of betaglucans with taurodeoxycholate transport	gldechol[e] + h[e] <=> gldechol[c] + h[c]							Needed to provide this metabolite for reaction BGLUTDECHOe in joint model.		1	1
GLYGLYt	Glycylglycine transport	glygly[e] + h[e] <=> glygly[c] + h[c]							Needed to provide this metabolite for reaction GLYGLYPEPT1tc in joint model.		1	1
GLYPHEt	Glycylphenylalanine transport	glyphe[e] + h[e] <=> glyphe[c] + h[c]							Needed to provide this metabolite for reaction GLYPHEPEPT1tc in joint model.		1	1
GLYSARt	Glycylsarcosine transport	glysar[e] + h[e] <=> glysar[c] + h[c]							Needed to provide this metabolite for reaction GLYSARPEPT1tc in joint model.		1	1
GUMDCHAt	binding of guar gums with deoxycholic acid transport	guandchac[e] + h[e] <=> guandchac[c] + h[c]							Needed to provide this metabolite for reaction GUMDCHAe in joint model.		1	1
GUMGCHLt	binding of guar gums with glycocholate transport	guamgchol[e] + h[e] <=> guamgchol[c] + h[c]							Needed to provide this metabolite for reaction GUMGCHLe in joint model.		1	1
GUMt	Guar gum transport	gum[e] + h[e] <=> gum[c] + h[c]							Needed to provide this metabolite for reaction GUMDCHAe, GUMGCHLe and GUMTCHOLe in joint model.		1	1
GUMTCHOLt	binding of guar gums with taurocholate transport	guamchol[e] + h[e] <=> guamchol[c] + h[c]							Needed to provide this metabolite for reaction GUMTCHOLe in joint model.		1	1
LEUGLYt	L-Leucylglycine transport via proton symport	h[e] + leugly[e] -> h[c] + leugly[c]							Needed to provide this metabolite for reaction LEUGLYHYc in joint model.		0	1
LEULELt	L-leucyl-L-leucine transport via proton symport	h[e] + leuleu[e] -> h[c] + leuleu[c]							Needed to provide this metabolite for reaction LEULEULAPt in joint model.		0	1
PECDCHt	binding of pectins with deoxycholic acid transport	pectindchac[e] + h[e] <=> pectindchac[c] + h[c]							Needed to provide this metabolite for reaction PECDCHe in joint model.		1	1
PECGCHLt	binding of pectins with glycocholate transport	pectingchol[e] + h[e] <=> pectingchol[c] + h[c]							Needed to provide this metabolite for reaction PECGCHLe in joint model.		1	1
PECTCHLt	binding of pectins with taurocholate transport	pectintchol[e] + h[e] <=> pectintchol[c] + h[c]							Needed to provide this metabolite for reaction PECTCHLe in joint model.		1	1
PECTt	Pectins transport	pect[e] + h[e] <=> pect[c] + h[c]							Needed to provide this metabolite for reaction PECDCHe, PECGCHLe and PECTCHLe in joint model.		1	1

PROGLYt	L-prolylglycine transport via proton symport	h[e] + progly[e] -> h[c] + progly[c]										0	1
PSYGCHt	binding of psyllium with glycocholate transport	psylchol[e] + h[e] <=> psylchol[c] + h[c]							Needed to provide this metabolite for reaction PROGLYPEPT1tc in joint model.			1	1
PSYLt	Psyllium transport	psyll[e] + h[e] <=> psyll[c] + h[c]							Needed to provide this metabolite for reaction PSYTDECHe, PSYGCHe and PSYTCHe in joint model.			1	1
PSYTCHt	binding of psyllium with taurocholate transport	psylchol[e] + h[e] <=> psylchol[c] + h[c]							Needed to provide this metabolite for reaction PSYTCHe in joint model.			1	1
PSYTDECHt	binding of psyllium with taurodeoxycholate transport	psyldechol[e] + h[e] <=> psyldechol[c] + h[c]							Needed to provide this metabolite for reaction PSYTDECHe in joint model.			1	1
TDECHOLAt	Taurodeoxycholic acid transport	tdechola[e] <=> tdechola[c]							Needed to provide this metabolite for reaction BGLUTDECHOe and PSYTDECHe in joint model.			1	1
EX_25HVITD3(u)	EX_25HVITD3(u)	25hvitd3[u] <=>										1	1
EX_34DHPHE(u)	exchange reaction for 3,4-Dihydroxy-L-phenylalanine	34dhphe[u] <=>										1	1
EX_4ABUT(u)	exchange reaction for GABA	4abut[u] <=>										1	1
EX_4HPRO(e)	exchange reaction for 4-hydroxy proline	4hpro_LT[e] <=>										1	1
EX_5mthf(u)	exchange reaction for 5-Methyltetrahydrofolate	5mthf[u] <=>										1	1
EX_adocbl(e)	EX_adocbl(e)	adocbl[e] <=>										1	1
EX_ADPCBL(u)	exchange reaction for Adenosylcobalamin	adocbl[u] <=>										1	1
EX_ala_L(u)	exchange reaction for L-alanine	ala-L[u] <=>										1	1
EX_alaala(e)	EX_alaala(e)	alaala[e] <=>										1	1
EX_ALAALA(u)	exchange reaction for alanylalanine	alaala[u] <=>										1	1
EX_ala-B(u)	exchange reaction for beta alanine	ala-B[u] <=>										1	1
EX_ARACHD(u)	exchange reaction for arachidonic acid	arachd[u] <=>										1	1
EX_ARG-L(u)	exchange reaction for L-arginine	arg-L[u] <=>										1	1
EX_ASCB-L(u)	exchange reaction for L-ascorbate	ascb-L[u] <=>										1	1
EX_asn_L(u)	exchange reaction for L-asparagine	asn-L[u] <=>										1	1
EX_AVITE1(u)	exchange reaction for alpha-Tocopherol	avite1[u] <=>										1	1
EX_bglc(e)	exchange reaction for beta glucan	bglc[e] <=>										1	1
EX_BGLC(u)	exchange reaction for beta glucan	bglc[u] <=>										1	1
EX_carn(e)	EX_carn(e)	carn[e] <=>										1	1
EX_CARN(u)	exchange reaction for carnosine	carn[u] <=>										1	1
EX_chsterol(u)	exchange reaction for cholesterol	chsterol[u] <=>										1	1
EX_cl(u)	exchange reaction for Chloride	cl[u] <=>										1	1
EX_cys_L(u)	exchange reaction for L-cysteine	cys-L[u] <=>										1	1
EX_dag_hs(u)	exchange reaction for diglyceride	dag_hs[u] <=>										1	1
EX_fol(u)	exchange reaction for Folate	fol[u] <=>										1	1
EX_gal(u)	exchange reaction for D-Galactose	gal[u] <=>										1	1
EX_GCHOLA(u)	exchange reaction for glycocholate	gchola[u] <=>										1	1
EX_glc_D(u)	exchange reaction for D-glucose	glc-D[u] <=>										1	1
EX_glygrblo(e)	exchange reaction for beta glucan-glycocholate complex	glygrblo[e] <=>										1	1
EX_GLGCHLO(u)	exchange reaction for beta glucan-glycocholate complex	glgchlo[u] <=>										1	1
EX_gln_L(u)	exchange reaction for L-glutamine	gln-L[u] <=>										1	1
EX_glyche(e)	exchange reaction for beta glucan-taurocholic acid complex	glyche[e] <=>										1	1
EX_GLTCHO(u)	exchange reaction for beta glucan-taurocholic acid complex	glthcho[u] <=>										1	1
EX_glydechol(e)	exchange reaction for beta glucan-taurodeoxycholic acid complex	glydechol[e] <=>										1	1
EX_GLTDECHOL(u)	exchange reaction for beta glucan-taurodeoxycholic acid complex	gldechol[u] <=>										1	1
EX_gly(u)	exchange reaction for Glycine	gly[u] <=>										1	1
EX_glyglyt(e)	exchange reaction for glycylglycine	glyglyt[e] <=>										1	1
EX_GLYGLY(u)	exchange reaction for glycylglycine	glygly[u] <=>										1	1
EX_glyleu(e)	EX_glyleu(e)	glyleu[e] <=>										1	1
EX_GLYLEU(u)	exchange reaction for glycylleucine	glyleu[u] <=>										1	1
EX_glyphe(e)	exchange reaction for glycylphenylalaine	glyphe[e] <=>										1	1
EX_GLYPHE(u)	exchange reaction for glycylphenylalaine	glyphe[u] <=>										1	1
EX_glypro(e)	EX_glypro(e)	glypro[e] <=>										1	1
EX_GLYPRO(u)	exchange reaction for glycylproline	glypro[u] <=>										1	1
EX_glysar(e)	exchange reaction for glycylsarcosine	glysar[e] <=>										1	1
EX_GLYSAR(u)	exchange reaction for glycylsarcosine	glysar[u] <=>										1	1
EX_gsm(e)	exchange reaction for guar gums	gsm[e] <=>										1	1
EX_GUM(u)	exchange reaction for guar gums	gsm[u] <=>										1	1
EX_gumdchac(e)	exchange reaction for guar gum-deoxycholic acid complex	gumdchac[e] <=>										1	1
EX_GUMDCHAC(u)	exchange reaction for guar gum-deoxycholic acid complex	gumdchac[u] <=>										1	1
EX_gumgchol(e)	exchange reaction for guar gum-glycocholate complex	gumgchol[e] <=>										1	1
EX_GUMGCHOL(u)	exchange reaction for guar gum-glycocholate complex	gumgchol[u] <=>										1	1
EX_gumtchol(e)	exchange reaction for guar gum-taurocholic acid complex	gumtchol[e] <=>										1	1
EX_GUMTCHOL(u)	exchange reaction for guar gum-taurocholic acid complex	gumtchol[u] <=>										1	1
EX_h(u)	exchange reaction for proton	h[u] <=>										1	1
EX_HDCA(u)	exchange reaction for Hexadecanoate (n-C16:0)	hdca[u] <=>										1	1
EX_his_L(u)	exchange reaction for L-histidine	his-L[u] <=>										1	1
EX_ILE-L(u)	exchange reaction for L-isoleucine	ile-L[u] <=>										1	1
EX_LCYSTIN(u)	exchange reaction for cystine	L-cystin[u] <=>										1	1
EX_leu_L(u)	exchange reaction for L-leucine	leu-L[u] <=>										1	1
EX_leugly(e)	exchange reaction for leucylglycine	leugly[e] <=>										1	1
EX_LEUGLY(u)	exchange reaction for leucylglycine	leugly[u] <=>										1	1
EX_leuleu(e)	EX_leuleu(e)	leuleu[e] <=>										1	1
EX_LEULEU(u)	exchange reaction for leucylleucine	leuleu[u] <=>										1	1
EX_LNLC(u)	exchange reaction for linoleic acid (all cis C18:2) n-6	lnlc[u] <=>										1	1
EX_LNLNCA(u)	exchange reaction for alpha-Linolenic acid, C18:3, n-3	lnlnca[u] <=>										1	1
EX_LNLNCG(u)	exchange reaction for gamma-linolenic acid	lnlncg[u] <=>										1	1
EX_lpchol_hs(u)	exchange reaction for lysophosphatidylcholine	lpchol_hs[u] <=>										1	1
EX_LYS(u)	exchange reaction for lysine	lys-L[u] <=>										1	1
EX_mag_hs(u)	exchange reaction for monoacylglycerol 2	mag_hs[u] <=>										1	1
EX_MET-L(u)	exchange reaction for methionine	met-L[u] <=>										1	1
EX_na1(u)	exchange reaction for Sodium	na1[u] <=>										1	1
EX_NAC(u)	exchange reaction for nicotinate	nac[u] <=>										1	1
EX_OCDCEA(u)	exchange reaction for octadecenoate (n-C18:1)	ocdcea[u] <=>										1	1
EX_ORN(U)	exchange reaction for ornithine	orn[u] <=>										1	1
EX_pect(e)	exchange reaction for pectins	pect[e] <=>										1	1
EX_PECT(u)	exchange reaction for pectins	pect[u] <=>										1	1
EX_pectindchac(e)	exchange reaction for pectin-deoxycholic acid complex	pectindchac[e] <=>										1	1
EX_PECTINDCHAC(u)	exchange reaction for pectin-deoxycholic acid complex	pectindchac[u] <=>										1	1
EX_pectingchol(e)	exchange reaction for pectin-glycocholate complex	pectingchol[e] <=>										1	1
EX_PECTINGCHOL(u)	exchange reaction for pectin-glycocholate complex	pectingchol[u] <=>										1	1
EX_pectintchol(e)	exchange reaction for pectin-taurocholic acid complex	pectintchol[e] <=>										1	1
EX_PECTINTCHOL(u)	exchange reaction for pectin-taurocholic acid complex	pectintchol[u] <=>										1	1
EX_phe_L(u)	exchange reaction for L-phenylalanine	phe-L[u] <=>										1	1
EX_PRO-D(u)	exchange reaction for D-proline	pro-D[u] <=>										1	1
EX_progly(e)	EX_progly(e)	progly[e] <=>										1	1
EX_PROGLY(u)	exchange reaction for prolyl-glycine	progly[u] <=>										1	1
EX_PRO-L(u)	exchange reaction for L-Proline	pro-L[u] <=>										1	1
EX_psyl(e)	exchange reaction for psyllium	psyl[e] <=>										1	1
EX_PSYL(u)	exchange reaction for psyllium	psyl[u] <=>										1	1
EX_psylchol(e)	exchange reaction for psyllium-glycocholic acid complex	psylchol[e] <=>										1	1
EX_PSYLCHOL(u)	exchange reaction for psyllium-glycocholic acid complex	psylchol[u] <=>										1	1
EX_psyltchol(e)	exchange reaction for psyllium-taurocholic acid complex	psyltchol[e] <=>										1	1
EX_PSYLTCHOL(u)	exchange reaction for psyllium-taurocholic acid complex	psyltchol[u] <=>										1	1
EX_psyldechol(e)	exchange reaction for psyllium-taurodeoxycholic acid complex	psyldechol[e] <=>										1	1
EX_PSYLTDECHOL(u)	exchange reaction for psyllium-taurodeoxycholic acid complex	psyldechol[u] <=>										1	1
EX_RETINOL(u)	exchange reaction for retinol	retinol[u] <=>										1	1
EX_ribflv(u)	exchange reaction for Riboflavin	ribflv[u] <=>										1	1
EX_RTOTAL(u)	exchange reaction for Rutal	Rtotal[u] <=>										1	1
EX_RTOTAL2(u)	exchange reaction for Rutal2	Rtotal2[u] <=>										1	1
EX_RTOTAL3(u)	exchange reaction for Rutal3	Rtotal3[u] <=>										1	1
EX_sbt_D(e)	EX_sbt_D(e)	sbt-D[e] <=>										1	1
EX_SBT-D(u)	exchange reaction for D-Sorbitol	sbt-D[u] <=>										1	1
EX_ser_L(u)	exchange reaction for L-serine	ser-L[u] <=>										1	1
EX_TAUR(u)	exchange reaction for Taurine	taur[u] <=>										1	1
EX_TCHOLA(u)	exchange reaction for taurocholic acid	tchola[u] <=>										1	1
EX_tdechola(e)	exchange reaction for Taurodeoxycholic acid	tdechola[e] <=>										1	1
EX_TDECHOLA(u)	exchange reaction for Taurodeoxycholic acid	tdechola[u] <=>										1	1
EX_thr_L(u)	exchange reaction for L-threonine	thr-L[u] <=>										1	1
EX_TMNDNC(u)	exchange reaction for tetradotatic acid C20:5, n-3	tmndnc[u] <=>										1	1

EX_TRP-L(u)	exchange reaction for L-tryptophan	trp-L[u] <=>									1	1
EX_TYR-L(u)	exchange reaction for L-tyrosine	tyr-L[u] <=>									1	1
EX_VAL-L(u)	exchange reaction for L-valine	val-L[u] <=>									1	1
EX_vitd3(u)	exchange reaction for calcitriol	vitd3[u] <=>									1	1

Table S12: All reactions included in joint *B. thetaiotaomicron*/ mouse reconstruction iexGFMM_*BΘ*.

LB = lower bound, UB = upper bound

Reaction ID	Reaction Formula	LB	UB	GPR	Type
BT12ETHDt	BT12ethd[e] <=> BT12ethd[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT12PPDRt	BT12ppd-R[e] <=> BT12ppd-R[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT12PPDt	BT12ppd-S[e] <=> BT12ppd-S[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT23PDE2	BTh2o[c] + BT23cump[c] -> BTh[c] + BT3ump[c]	0	1000	BT_1236	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT23PDE4	BTh2o[c] + BT23ccmp[c] -> BTh[c] + BT3cmp[c]	0	1000	BT_1236	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT23PDE7	BTh2o[c] + BT23camp[c] -> BTh[c] + BT3amp[c]	0	1000	BT_1236	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT23PDE9	BTh2o[c] + BT23cgmp[c] -> BTh[c] + BT3gmp[c]	0	1000	BT_1236	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT26DAPLLATi	BTh2o[c] + BTh[c] + BThdp[c] + BTglu-L[c] -> BT26dap-LL[c] + BTakg[c]	0	1000	BT_0547	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT2AMEPHPAT	BT2ameph[c] + BTpyr[c] <=> BTala-L[c] + BTpalt[c]	-1000	1000	BT_1718	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT2FUCLAC_FUCASEe	BT2fuclac[e] + BTh2o[e] -> BTfuc-L[e] + BTfcts[e]	0	1000	((BT_1625 or BT_4136) and ((BT_4134 and BT_4135) or (BT_1630 and BT_1631)))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT2MBCOATA	BT2mbcoa[c] + BTACP[c] <=> BTcoa[c] + BT2mbutACP[c]	-1000	1000	BT_0789	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT2MMALD	BT2mmal[c] <=> BTh2o[c] + BT2mmale[c]	-1000	1000	(BT_1859 and BT_1860)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT2MMALD2	BTh2o[c] + BT2mmale[c] <=> BTe3mmal[c]	-1000	1000	(BT_1859 and BT_1860)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3DSPHR	BTh[c] + BTnadph[c] + BT3dsphgn[c] -> BTnadp[c] + BTsphgn[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3FUCLAC_FUCASEe	BTh2o[e] + BT3fuclac[e] -> BTfuc-L[e] + BTfcts[e]	0	1000	((BT_1625 or BT_4136) and ((BT_4134 and BT_4135) or (BT_1630 and BT_1631)))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3HACPR1	BT3hgACPm[c] -> BTh2o[c] + BTegACPm[c]	0	1000	BT_4206	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3HACPR2	BT3hpACPm[c] -> BTh2o[c] + BTepACPm[c]	0	1000	BT_4206	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3HAD100	BT3hdecACP[c] -> BTh2o[c] + BThdec2eACP[c]	0	1000	BT_4206	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3HAD10M11	BT10m3hundecACP[c] -> BTh2o[c] + BT10mtundec2eACP[c]	0	1000	BT_4206	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3HAD10M12	BT10m3hddcaACP[c] -> BTh2o[c] + BT10mtddec2eACP[c]	0	1000	BT_4206	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3HAD11M12	BT11m3hddcaACP[c] -> BTh2o[c] + BT11mtddec2eACP[c]	0	1000	BT_4206	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3HAD120	BT3hddecACP[c] -> BTh2o[c] + BThddec2eACP[c]	0	1000	BT_4206	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3HAD121	BT3hcddec5eACP[c] -> BTh2o[c] + BTi3c5ddeceACP[c]	0	1000	BT_4206	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3HAD12M13	BT12m3htridecACP[c] -> BTh2o[c] + BT12mtritec2eACP[c]	0	1000	BT_4206	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3HAD12M14	BT12m3hmyrsACP[c] -> BTh2o[c] + BT12mtmrs2eACP[c]	0	1000	BT_4206	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3HAD13M14	BT13m3hmyrsACP[c] -> BTh2o[c] + BT13mtmrs2eACP[c]	0	1000	BT_4206	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3HAD140	BT3hmrsACP[c] -> BTh2o[c] + BThmrs2eACP[c]	0	1000	BT_4206	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3HAD141	BT3hcmrs7eACP[c] -> BTh2o[c] + BTi3c7mrseACP[c]	0	1000	BT_4206	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3HAD14M15	BT14m3hpentdecACP[c] -> BTh2o[c] + BT14mtpentdec2eACP[c]	0	1000	BT_4206	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3HAD14M16	BT14m3hpalmACP[c] -> BTh2o[c] + BT14mtpalm2eACP[c]	0	1000	BT_4206	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3HAD15M16	BT15m3hpalmACP[c] -> BTh2o[c] + BT15mtpalm2eACP[c]	0	1000	BT_4206	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3HAD160	BT3hpalmACP[c] -> BTh2o[c] + BThpalm2eACP[c]	0	1000	BT_4206	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3HAD161	BT3hcpalm9eACP[c] -> BTh2o[c] + BTi3c9palmeACP[c]	0	1000	BT_4206	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3HAD180	BT3hoctaACP[c] -> BTh2o[c] + BThoctd2eACP[c]	0	1000	BT_4206	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3HAD181	BT3hcvac11eACP[c] -> BTh2o[c] + BTi3c11vaceACP[c]	0	1000	BT_4206	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3HAD40	BT3huACP[c] -> BTh2o[c] + BThut2eACP[c]	0	1000	BT_4206	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3HAD4M5	BT4m3hpentACP[c] -> BTh2o[c] + BT4mtpent2eACP[c]	0	1000	BT_4206	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3HAD4M6	BT4m3hhexACP[c] -> BTh2o[c] + BT4mthex2eACP[c]	0	1000	BT_4206	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3HAD5M6	BT5m3hhexACP[c] -> BTh2o[c] + BT5mthex2eACP[c]	0	1000	BT_4206	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3HAD60	BT3hhexACP[c] -> BTh2o[c] + BThhex2eACP[c]	0	1000	BT_4206	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3HAD6M7	BT6m3hheptACP[c] -> BTh2o[c] + BT6mthep2eACP[c]	0	1000	BT_4206	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3HAD6M8	BT6m3hoctACP[c] -> BTh2o[c] + BT6mtoct2eACP[c]	0	1000	BT_4206	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3HAD7M8	BT7m3hoctACP[c] -> BTh2o[c] + BT7mtoct2eACP[c]	0	1000	BT_4206	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3HAD80	BT3hoctACP[c] -> BTh2o[c] + BThoct2eACP[c]	0	1000	BT_4206	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3HAD8M10	BT8m3hddcaACP[c] -> BTh2o[c] + BT8mtdec2eACP[c]	0	1000	BT_4206	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3HAD8M9	BT8m3hnonACP[c] -> BTh2o[c] + BT8mtnon2eACP[c]	0	1000	BT_4206	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3HAD9M10	BT9m3hddcaACP[c] -> BTh2o[c] + BT9mtdec2eACP[c]	0	1000	BT_4206	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAACPR1	BTh[c] + BTnadph[c] + BT3ogACPm[c] -> BTnadp[c] + BT3hgACPm[c]	0	1000	BT_0409	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAACPR2	BTh[c] + BTnadph[c] + BT3opACPm[c] -> BTnadp[c] + BT3hpACPm[c]	0	1000	BT_0409	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAR100	BTh[c] + BTnadph[c] + BT3odecACP[c] <=> BTnadp[c] + BT3hdecACP[c]	-1000	1000	(BT_0972 or BT_2380)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAR10M11	BTh[c] + BTnadph[c] + BT10m3hundecACP[c] <=> BTnadp[c] + BT10m3hundecACP[c]	-1000	1000	(BT_0972 or BT_2380)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAR10M12	BTh[c] + BTnadph[c] + BT10m3oddcaACP[c] <=> BTnadp[c] + BT10m3hddcaACP[c]	-1000	1000	(BT_0972 or BT_2380)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAR11M12	BTh[c] + BTnadph[c] + BT11m3oddcaACP[c] <=> BTnadp[c] + BT11m3hddcaACP[c]	-1000	1000	(BT_0972 or BT_2380)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAR120	BTh[c] + BTnadph[c] + BT3oddecACP[c] <=> BTnadp[c] + BT3hddecACP[c]	-1000	1000	(BT_0972 or BT_2380)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAR121	BTh[c] + BTnadph[c] + BT3ocddec5eACP[c] -> BTnadp[c] + BT3hcddec5eACP[c]	0	1000	(BT_0972 or BT_2380)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAR12M13	BTh[c] + BTnadph[c] + BT12m3otridecACP[c] <=> BTnadp[c] + BT12m3htridecACP[c]	-1000	1000	(BT_0972 or BT_2380)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAR12M14	BTh[c] + BTnadph[c] + BT12m3omyrsACP[c] <=> BTnadp[c] + BT12m3hmyrsACP[c]	-1000	1000	(BT_0972 or BT_2380)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAR13M14	BTh[c] + BTnadph[c] + BT13m3omyrsACP[c] <=> BTnadp[c] + BT13m3hmyrsACP[c]	-1000	1000	(BT_0972 or BT_2380)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAR140	BTh[c] + BTnadph[c] + BT3omsACP[c] <=> BTnadp[c] + BT3hmrsACP[c]	-1000	1000	(BT_0972 or BT_2380)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAR141	BTh[c] + BTnadph[c] + BT3ocmrs7eACP[c] -> BTnadp[c] + BT3hcmrs7eACP[c]	0	1000	(BT_0972 or BT_2380)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAR14M15	BTh[c] + BTnadph[c] + BT14m3opentdecACP[c] <=> BTnadp[c] + BT14m3hpentdecACP[c]	-1000	1000	(BT_0972 or BT_2380)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAR14M16	BTh[c] + BTnadph[c] + BT14m3opalmACP[c] <=> BTnadp[c] + BT14m3hpalmACP[c]	-1000	1000	(BT_0972 or BT_2380)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAR15M16	BTh[c] + BTnadph[c] + BT15m3opalmACP[c] <=> BTnadp[c] + BT15m3hpalmACP[c]	-1000	1000	(BT_0972 or BT_2380)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAR160	BTh[c] + BTnadph[c] + BT3opalmACP[c] <=> BTnadp[c] + BT3hpalmACP[c]	-1000	1000	(BT_0972 or BT_2380)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAR161	BTh[c] + BTnadph[c] + BT3ocpalm9eACP[c] -> BTnadp[c] + BT3hcpalm9eACP[c]	0	1000	(BT_0972 or BT_2380)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAR180	BTh[c] + BTnadph[c] + BT3ooctdACP[c] <=> BTnadp[c] + BT3hoctaACP[c]	-1000	1000	(BT_0972 or BT_2380)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAR181	BTh[c] + BTnadph[c] + BT3ocvac11eACP[c] -> BTnadp[c] + BT3hcvac11eACP[c]	0	1000	(BT_0972 or BT_2380)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAR40	BTh[c] + BTnadph[c] + BTacsACP[c] <=> BTnadp[c] + BT3huACP[c]	-1000	1000	(BT_0972 or BT_2380)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAR4M5	BTh[c] + BTnadph[c] + BT4m3opentACP[c] <=> BTnadp[c] + BT4m3hpentACP[c]	-1000	1000	(BT_0972 or BT_2380)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAR4M6	BTh[c] + BTnadph[c] + BT4m3ohexACP[c] <=> BTnadp[c] + BT4m3hhexACP[c]	-1000	1000	(BT_0972 or BT_2380)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAR5M6	BTh[c] + BTnadph[c] + BT5m3ohexACP[c] <=> BTnadp[c] + BT5m3hhexACP[c]	-1000	1000	(BT_0972 or BT_2380)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAR60	BTh[c] + BTnadph[c] + BT3ohexACP[c] <=> BTnadp[c] + BT3hhexACP[c]	-1000	1000	(BT_0972 or BT_2380)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAR6M7	BTh[c] + BTnadph[c] + BT6m3ohepACP[c] <=> BTnadp[c] + BT6m3hheptACP[c]	-1000	1000	(BT_0972 or BT_2380)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAR6M8	BTh[c] + BTnadph[c] + BT6m3ooctACP[c] <=> BTnadp[c] + BT6m3hoctACP[c]	-1000	1000	(BT_0972 or BT_2380)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAR7M8	BTh[c] + BTnadph[c] + BT7m3ooctACP[c] <=> BTnadp[c] + BT7m3hoctACP[c]	-1000	1000	(BT_0972 or BT_2380)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAR80	BTh[c] + BTnadph[c] + BT3ooctACP[c] <=> BTnadp[c] + BT3hoctACP[c]	-1000	1000	(BT_0972 or BT_2380)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAR8M10	BTh[c] + BTnadph[c] + BT8m3oddcaACP[c] <=> BTnadp[c] + BT8m3hddcaACP[c]	-1000	1000	(BT_0972 or BT_2380)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAR8M9	BTh[c] + BTnadph[c] + BT8m3ononACP[c] <=> BTnadp[c] + BT8m3hnonACP[c]	-1000	1000	(BT_0972 or BT_2380)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAR9M10	BTh[c] + BTnadph[c] + BT9m3oddcaACP[c] <=> BTnadp[c] + BT9m3hddcaACP[c]	-1000	1000	(BT_0972 or BT_2380)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction

BT3OAS100	BTh[c] + BTmalACP[c] + BTocACP[c] -> BTACP[c] + BT3odecACP[c] + BTco2[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAS10M11	BTh[c] + BTmalACP[c] + BT10mundecACP[c] -> BTACP[c] + BT12m3otridecACP[c] + BTco2[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAS10M12	BTh[c] + BTmalACP[c] + BT10mddecACP[c] -> BTACP[c] + BT12m3omyrACP[c] + BTco2[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAS11M12	BTh[c] + BTmalACP[c] + BT11mddecACP[c] -> BTACP[c] + BT13m3omyrACP[c] + BTco2[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAS120	BTh[c] + BTmalACP[c] + BTdcaACP[c] -> BTACP[c] + BT3oddecACP[c] + BTco2[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAS121	BTh[c] + BTmalACP[c] + BTcdec5eACP[c] -> BTACP[c] + BT3ocddec5eACP[c] + BTco2[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAS12M13	BTh[c] + BTmalACP[c] + BT12mtridecACP[c] -> BTACP[c] + BT14m3opentdecACP[c] + BTco2[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAS12M14	BTh[c] + BTmalACP[c] + BT12mmyrsACP[c] -> BTACP[c] + BT14m3opalmACP[c] + BTco2[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAS13M14	BTh[c] + BTmalACP[c] + BT13mmyrsACP[c] -> BTACP[c] + BT15m3opalmACP[c] + BTco2[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAS140	BTh[c] + BTmalACP[c] + BTddcaACP[c] -> BTACP[c] + BT3omrsACP[c] + BTco2[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAS141	BTh[c] + BTmalACP[c] + BTcddec5eACP[c] -> BTACP[c] + BT3ocmrs7eACP[c] + BTco2[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAS160	BTh[c] + BTmalACP[c] + BTmyrsACP[c] -> BTACP[c] + BT3opalmACP[c] + BTco2[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAS161	BTh[c] + BTmalACP[c] + BTdeACP[c] -> BTACP[c] + BT3ocpalm9eACP[c] + BTco2[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAS180	BTh[c] + BTmalACP[c] + BTpalmACP[c] -> BTACP[c] + BT3ooctdACP[c] + BTco2[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAS181	BTh[c] + BTmalACP[c] + BTddeACP[c] -> BTACP[c] + BT3ocvac11eACP[c] + BTco2[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAS2M3	BTh[c] + BTmalACP[c] + BT2mpropACP[c] -> BTACP[c] + BT4m3opentACP[c] + BTco2[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAS3M4	BTh[c] + BTmalACP[c] + BT3mbutACP[c] -> BTACP[c] + BT5m3ohexACP[c] + BTco2[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAS4M3O6	BTh[c] + BT2mbutACP[c] + BTmalACP[c] -> BTACP[c] + BT4m3ohexACP[c] + BTco2[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAS4M5	BTh[c] + BTmalACP[c] + BT4mpentACP[c] -> BTACP[c] + BT6m3ohexACP[c] + BTco2[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAS4M6	BTh[c] + BTmalACP[c] + BT4mhexACP[c] -> BTACP[c] + BT6m3ooctACP[c] + BTco2[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAS5M6	BTh[c] + BTmalACP[c] + BT5mhexACP[c] -> BTACP[c] + BT7m3ooctACP[c] + BTco2[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAS60	BTh[c] + BTmalACP[c] + BTbutACP[c] -> BTACP[c] + BT3ohexACP[c] + BTco2[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAS6M7	BTh[c] + BTmalACP[c] + BT6mheptACP[c] -> BTACP[c] + BT8m3ononACP[c] + BTco2[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAS6M8	BTh[c] + BTmalACP[c] + BT6mocACP[c] -> BTACP[c] + BT8m3oddcaACP[c] + BTco2[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAS7M8	BTh[c] + BTmalACP[c] + BT7mocACP[c] -> BTACP[c] + BT9m3oddcaACP[c] + BTco2[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAS80	BTh[c] + BTmalACP[c] + BT8mcACP[c] -> BTACP[c] + BT3ooctACP[c] + BTco2[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAS8M10	BTh[c] + BTmalACP[c] + BT8mdcaACP[c] -> BTACP[c] + BT10m3oddcaACP[c] + BTco2[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAS8M9	BTh[c] + BTmalACP[c] + BT8mnonACP[c] -> BTACP[c] + BT10m3ounedecACP[c] + BTco2[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3OAS9M10	BTh[c] + BTmalACP[c] + BT9mdcaACP[c] -> BTACP[c] + BT11m3oddcaACP[c] + BTco2[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT3POPDC	BTh[c] + BT3pop[c] -> BTpald[c] + BTco2[c]	0	1000	BT_1719	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT4HTHRS	BTh2o[c] + BTphthr[c] -> BT4thhr[c] + BTpl[c]	0	1000	BT_2401	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT5DOAN	BTh2o[c] + BTdad-5[c] -> BT5drib[c] + BTade[c]	0	1000	BT_4451	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT7AHSDH	BTcholate[c] + BTnad[c] <=> BTh[c] + BT7ocholate[c] + BTnadh[c]	-1000	1000	BT_1911	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT7OCHOLATEt2	BT7ocholate[c] + 2 BTna1[c] -> BT7ocholate[e] + 2 BTna1[e]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTA5PISO	BTru5p-D[c] <=> BTara5p[c]	-1000	1000	BT_3306	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTACCOAC	BTaccoa[c] + BTatp[c] + BThco3[c] -> BTh[c] + BTpi[c] + BTadp[c] + BTmalcoa[c]	0	1000	((BT_1915 and BT_1916 and BT_2238) or (BT_1448 and BT_1449 and BT_2238))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTACETOLt	BTacetol[e] <=> BTacetol[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTACGALK3	BTatp[c] + BTacgal[c] -> BTh[c] + BTadp[c] + BTacgal6p[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTACGALr	2 BTh[e] + BTacgal[e] <=> 2 BTh[c] + BTacgal[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTACGAM2E	BTacgam[c] <=> BTacmana[c]	-1000	1000	(BT_0437 or BT_0453 or BT_3605)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTACGAMK	BTatp[c] + BTacgam[c] -> BTh[c] + BTadp[c] + BTacgam6p[c]	0	1000	(BT_2493 or BT_4654)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTACGAMPM	BTacgam6p[c] <=> BTacgam1p[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTACGAMT	BTuacgam[c] + BTudcpp[c] -> BTump[c] + BTunagp[c]	0	1000	(BT_1339 or BT_2888)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTACGAMtr	2 BTh[e] + BTacgam[e] <=> 2 BTh[c] + BTacgam[c]	-1000	1000	(BT_3180 or BT_3619)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTACGK	BTatp[c] + BTacglk[c] -> BTadp[c] + BTacg5p[c]	0	1000	BT_3395	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTACGS	BTglu-L[c] + BTaccoa[c] -> BTh[c] + BTcoa[c] + BTacglu[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTACHBS	BTh[c] + BTpyr[c] + BT2obut[c] -> BTco2[c] + BT2ahbut[c]	0	1000	(BT_2076 and BT_2077)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTACKr	BTatp[c] + BTac[c] <=> BTadp[c] + BTactp[c]	-1000	1000	BT_3693	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTACLS	BTh[c] + 2 BTpyr[c] -> BTco2[c] + BTalac-S[c]	0	1000	(BT_2076 and BT_2077)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTACNAM9PL2	BTh2o[c] + BTmanl6p[c] + BTpep[c] -> BTp[c] + BTkdnp[c]	0	1000	BT_1714	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTACNAMt2r	BTh[e] + BTacnam[e] -> BTh[c] + BTacnam[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTACOAAGPAT140	BT1tdecg3p[c] + BTtdcoa[c] -> BTcoa[c] + BTpa140[c]	0	1000	(BT_0243 or BT_4462)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTACOAAGPAT160	BTpmtcoa[c] + BT1hdecg3p[c] -> BTcoa[c] + BTpa160[c]	0	1000	(BT_0243 or BT_4462)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTACOAAGPAT180	BTstcoa[c] + BT1odecg3p[c] -> BTcoa[c] + BTpa180[c]	0	1000	(BT_0243 or BT_4462)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTACOAAGPATA115	BT1aipdecg3p[c] + BTaipdcoa[c] -> BTh[c] + BTcoa[c] + BTpaai15[c]	0	1000	(BT_0243 or BT_4462)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTACOAAGPATA117	BTaihpdcoa[c] + BT1aihpdecg3p[c] -> BTcoa[c] + BTpaai17[c]	0	1000	(BT_0243 or BT_4462)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTACOAAGPATI14	BTidcoa[c] + BT1idecg3p[c] -> BTh[c] + BTcoa[c] + BTpaii14[c]	0	1000	(BT_0243 or BT_4462)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTACOAAGPATI15	BTipdcoa[c] + BT1ipdecg3p[c] -> BTh[c] + BTcoa[c] + BTpaii15[c]	0	1000	(BT_0243 or BT_4462)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTACOAAGPATI16	BThdcoa[c] + BT1hdecg3p[c] -> BTh[c] + BTcoa[c] + BTpaii16[c]	0	1000	(BT_0243 or BT_4462)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTACOAAGPATI17	BThpdcoa[c] + BT1hpdecg3p[c] -> BTcoa[c] + BTpaii17[c]	0	1000	(BT_0243 or BT_4462)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTACOATA	BTACP[c] + BTaccoa[c] <=> BTcoa[c] + BTacACP[c]	-1000	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTACODA	BTh2o[c] + BTacorn[c] -> BTac[c] + BTorn[c]	0	1000	BT_3549	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTACONTa	BTcit[c] <=> BTh2o[c] + BTacon-C[c]	-1000	1000	BT_2072	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTACONTb	BTh2o[c] + BTacon-C[c] <=> BTicit[c]	-1000	1000	BT_2072	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTACOTA	BTakg[c] + BTacorn[c] <=> BTglu-L[c] + BTacg5sa[c]	-1000	1000	BT_3758	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTACPS1	BTcoa[c] + BTapoACP[c] -> BTh[c] + BTACP[c] + BTpap[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTACS	BTcoa[c] + BTatp[c] + BTac[c] -> BTaccoa[c] + BTamp[c] + BTppi[c]	0	1000	BT_2924	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTACS2	BTcoa[c] + BTatp[c] + BTppa[c] -> BTamp[c] + BTppi[c] + BTppcoa[c]	0	1000	BT_2924	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTACTNDH	BTcoa[c] + BTnad[c] + BTactn-R[c] <=> BTh[c] + BTnadh[c] + BTaccoa[c] + BTacald[c]	-1000	1000	(BT_0309 and BT_0311 and BT_0312)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTACtr	BTac[e] <=> BTac[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTADCL	BT4adcho[c] -> BTh[c] + BTpyr[c] + BT4abut[c]	0	1000	BT_0768	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTADK1	BTatp[c] + BTamp[c] <=> 2 BTadp[c]	-1000	1000	BT_4387	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTADK2	BTamp[c] + BTpppi[c] <=> BTadp[c] + BTppi[c]	-1000	1000	BT_4387	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTADNUC	BTh2o[c] + BTadn[c] -> BTade[c] + BTrib-D[c]	0	1000	BT_2808	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTADNt2	BTh[e] + BTadn[e] -> BTh[c] + BTadn[c]	0	1000	BT_4330	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTADOCBLabc	BTh2o[c] + BTatp[c] + BTadocbl[e] -> BTh[c] + BTpi[c] + BTadp[c] + BTadocbl[c]	0	1000	(BT_1799 or BT_1489)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTADPT	BTade[c] + BTpppi[c] -> BTamp[c] + BTppi[c]	0	1000	BT_3267	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTADSK	BTatp[c] + BTaps[c] -> BTh[c] + BTadp[c] + BTpaps[c]	0	1000	BT_0413	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTADSL1r	BTdcamp[c] <=> BTamp[c] + BTlum[c]	-1000	1000	BT_3871	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTADSL2r	BT25aics[c] <=> BTlum[c] + BTaicar[c]	-1000	1000	BT_3871	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTADSS	BTasp-L[c] + BTgtp[c] + BTimp[c] -> 2 BTh[c] + BTpi[c] + BTdcamp[c] + BTdpd[c]	0	1000	BT_1843	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAGDC	BTh2o[c] + BTacgam6p[c] -> BTac[c] + BTgam6p[c]	0	1000	(BT_0675 or BT_0676 or BT_3588)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAGDC2	BTh2o[c] + BTacgalf6p[c] -> BTac[c] + BTgalam6p[c]	0	1000	(BT_0675 or BT_0676 or BT_3588)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAGMD	BTh2o[c] + BTagmt[c] -> BTnbtd[c] + BTncptrc[c]	0	1000	BT_0876	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAGMHE	BTadphep-DD[c] -> BTadphep-LD[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction

BTAGPAT120	BTddcaACP[c] + BT1ddecg3p[c] -> BTACP[c] + BTpa120[c]	0	1000	(BT_0243 or BT_4462)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAGPAT140	BTmyrsACP[c] + BT1tdecg3p[c] -> BTACP[c] + BTpa140[c]	0	1000	(BT_0243 or BT_4462)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAGPAT160	BTpalmACP[c] + BT1hdecg3p[c] -> BTACP[c] + BTpa160[c]	0	1000	(BT_0243 or BT_4462)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAGPAT180	BT1odecg3p[c] + BTocdcaACP[c] -> BTACP[c] + BTpa180[c]	0	1000	(BT_0243 or BT_4462)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAGPAT181	BT1odec11eg3p[c] + BTocteACP[c] -> BTACP[c] + BTpa181[c]	0	1000	(BT_0243 or BT_4462)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAGPR	BTnadp[c] + BTp[c] + BTacgGsa[c] <=> BTh[c] + BTnadph[c] + BTacg6p[c]	-1000	1000	BT_3759	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAHC	BTh2o[c] + BTahcys[c] <=> BTadn[c] + BThcys-L[c]	-1000	1000	BT_2797	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAHCYSNS_r	BTh2o[c] + BTahcys[c] <=> BTade[c] + BThcys[c]	-1000	1000	BT_4451	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAHEXASE2e	BTh2o[e] + BTs2f2n2m2m[e] -> BTacgam[e] + BTs2f2n2m2mn[e]	0	1000	(BT_4394 or BT_4395 or BT_4337 or BT_3598 or BT_1627 or BT_3868 or BT_0459 or BT_0460 or BT_0506 or BT_4681 or BT_1621 or BT_3178 or BT_0456 or BT_1051 or BT_2459)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAHEXASE3e	BTh2o[e] + BTchtbs[e] -> 2 BTacgam[e]	0	1000	(BT_4394 or BT_4395 or BT_4337 or BT_3598 or BT_1627 or BT_3868 or BT_0459 or BT_0460 or BT_0506 or BT_4681 or BT_1621 or BT_3178 or BT_0456 or BT_1051 or BT_2459)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAHEXASEe	2 BTh2o[e] + BTn2m2mn[e] -> 2 BTacgam[e] + BTm2mn[e]	0	1000	(BT_4394 or BT_4395 or BT_4337 or BT_3598 or BT_1627 or BT_3868 or BT_0459 or BT_0460 or BT_0506 or BT_4681 or BT_1621 or BT_3178 or BT_0456 or BT_1051 or BT_2459)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAHMMPS	2 BTh[c] + BTair[c] -> BTpi[c] + BT4ahmmp[c] + BTgcald[c]	0	1000	BT_0650	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAHSERL2	BTachms[c] + BTh2s[c] -> BTh[c] + BTac[c] + BThcys-L[c]	0	1000	(BT_1923 or BT_2387)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAHSERL3	BTachms[c] + BTrdrd[c] + BTnad[c] <=> BTh[c] + BTac[c] + BThcys-L[c] + BTrdox[c] + BTnox3[c]	-1000	1000	(BT_1923 or BT_2387)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAICART	BTaicar[c] + BT10fthf[c] <=> BTpora[c] + BTthf[c]	-1000	1000	BT_3812	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAIHPDCOATA	BTcoa[c] + BT14mpalmACP[c] <=> BTACP[c] + BTahpdcoa[c]	-1000	1000	BT_0789	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAIPDCOATA	BTcoa[c] + BT12mmyrsACP[c] <=> BTACP[c] + BTaipdcoa[c]	-1000	1000	BT_0789	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAIRC2	BTaip[c] + BThco3[c] + BTair[c] -> BTh[c] + BTpi[c] + BTadp[c] + BTcsair[c]	0	1000	BT_2518	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAIRC3	BTsairc[c] <=> BTcsair[c]	-1000	1000	BT_2518	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAIRCr	BTco2[c] + BTair[c] <=> BTh[c] + BTsairc[c]	-1000	1000	BT_2518	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAKP1	3 BTh2o[c] + BTahdf[c] -> 2 BTh[c] + 3 BTp[c] + BTdhnpt[c]	0	1000	(BT_0028 or BT_3708 or BT_4363)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTALAALA	BTatp[c] + 2 BTala-D[c] -> BTh[c] + BTpi[c] + BTadp[c] + BTalaala[c]	0	1000	BT_3713	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTALAALADe	BTh2o[e] + BTalaala[e] -> 2 BTala-D[e]	0	1000	(BT_3007 or BT_3187)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTALAASP1c	BTh2o[c] + BTalaasp[c] <=> BTala-L[c] + BTasp-L[c]	-1000	1000	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314 or BT_1838)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTALAASPt	BTh[e] + BTalaasp[e] -> BTh[c] + BTalaasp[c]	0	1000	(BT_0580 or BT_4385 or BT_1086)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTALAD_R	BTh2o[c] + BTala-L[c] + BTnad[c] <=> BTh[c] + BTpyr[c] + BTnadh[c] + BTnhd[c]	-1000	1000	BT_1554	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTALAGLN1c	BTh2o[c] + BTalagln[c] <=> BTala-L[c] + BTgln-L[c]	-1000	1000	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314 or BT_1838)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTALAGLNt	BTh[e] + BTalagln[e] -> BTh[c] + BTalagln[c]	0	1000	(BT_0580 or BT_4385 or BT_1086)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTALAGLU1c	BTh2o[c] + BTalaglu[c] <=> BTglu-L[c] + BTala-L[c]	-1000	1000	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314 or BT_1838)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTALAGLUt	BTh[e] + BTalaglu[e] -> BTh[c] + BTalaglu[c]	0	1000	(BT_0580 or BT_4385 or BT_1086)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTALAGLY1c	BTh2o[c] + BTalagly[c] <=> BTala-L[c] + BTgly[c]	-1000	1000	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314 or BT_1838)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTALAGLYt	BTh[e] + BTalagly[e] -> BTh[c] + BTalagly[c]	0	1000	(BT_0580 or BT_4385 or BT_1086)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTALAHIS1c	BTh2o[c] + BTalahis[c] <=> BTala-L[c] + BThis-L[c]	-1000	1000	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314 or BT_1838)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTALAHISt	BTh[e] + BTalahis[e] -> BTh[c] + BTalahis[c]	0	1000	(BT_0580 or BT_4385 or BT_1086)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTALALEU1c	BTh2o[c] + BTalaleu[c] <=> BTala-L[c] + BTleu-L[c]	-1000	1000	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314 or BT_1838)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTALALEUt	BTh[e] + BTalaleu[e] -> BTh[c] + BTalaleu[c]	0	1000	(BT_0580 or BT_4385 or BT_1086)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTALAR	BTala-L[c] <=> BTala-D[c]	-1000	1000	BT_4101	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTALATHR1c	BTh2o[c] + BTalathr[c] <=> BTala-L[c] + BThr-L[c]	-1000	1000	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314 or BT_1838)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTALATHRt	BTh[e] + BTalathr[e] -> BTh[c] + BTalathr[c]	0	1000	(BT_0580 or BT_4385 or BT_1086)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTALAt4r	BTna1[e] + BTala-L[e] <=> BTala-L[c] + BTna1[c]	-1000	1000	BT_4476	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTALCD19	BTh[c] + BTnadh[c] + BTglyald[c] <=> BTnad[c] + BTglyc[c]	-1000	1000	(BT_0535 or BT_4512)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTALCD2x	BTnad[c] + BTetoh[c] <=> BTh[c] + BTnadh[c] + BTacald[c]	-1000	1000	(BT_0535 or BT_4512)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTALKP	BTh2o[c] + BTdhap[c] -> BTpi[c] + BTdha[c]	0	1000	(BT_0028 or BT_3708 or BT_4363)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTALR2	BTh[c] + BTnadph[c] + BTmthgxl[c] -> BTnadp[c] + BTacetol[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTALR4x	BTh[c] + BTnadh[c] + BTacetol[c] -> BT12ppd-R[c] + BTnad[c]	0	1000	(BT_3617 or BT_4424)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTALTRH	BTaltru[c] -> BTh2o[c] + BT2ddglcn[c]	0	1000	BT_0486	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAMAA	BTh2o[c] + BTacmamu[c] -> BTala-L[c] + BTacmam[c]	0	1000	(BT_1991 or BT_2027 or BT_2141 or BT_3200 or BT_4736 or BT_0706 or BT_1168 or BT_1519 or BT_1641 or BT_1706 or BT_4031)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAMALT1	BTmalt[c] + BTmaltn[c] -> BTglc-D[c] + BTmaltr[c]	0	1000	BT_2146	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAMALT2	BTmalt[c] + BTmaltrr[c] -> BTglc-D[c] + BTmaltp[c]	0	1000	BT_2146	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAMALT3	BTmalt[c] + BTmaltp[c] -> BTglc-D[c] + BTmalths[c]	0	1000	BT_2146	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAMALT4	BTmalt[c] + BTmalths[c] -> BTglc-D[c] + BTmalthp[c]	0	1000	BT_2146	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAMANNANASEe	139 BTh2o[e] + BTamannan140[e] <=> 140 BTman[e]	-1000	1000	((BT_3990 or BT_2629 or BT_2199 or BT_3784 or BT_3962 or BT_4092) and (BT_3991 or BT_3858 or BT_1769 or BT_1878 or BT_3130 or BT_3773) and (BT_3994 or BT_3792 or BT_2623 or BT_2949 or BT_3501 or BT_1883 or BT_3524 or BT_3301 or BT_3521) and ((BT_2625 and BT_2626) or (BT_3788 and BT_3789) or (BT_3854 and BT_3855)))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAMAOTr	BTBaorn[c] + BTamet[c] <=> BTamoh[c] + BTdasn[c]	-1000	1000	BT_1442	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAMMQLT8	BTamet[c] + BT2dmmq8[c] -> BTh[c] + BTahcys[c] + BTmqI8[c]	0	1000	(BT_0853 or BT_4216)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAMMQT10	BTh[c] + BTamet[c] + BT2dmmq10[c] -> BTahcys[c] + BTmqI10[c]	0	1000	(BT_0853 or BT_4216)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAMMQT11	BTh[c] + BTamet[c] + BT2dmmq11[c] -> BTahcys[c] + BTmqI11[c]	0	1000	(BT_0853 or BT_4216)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAMMQT7	BTh[c] + BTamet[c] + BT2dmmq7[c] -> BTahcys[c] + BTmqI7[c]	0	1000	(BT_0853 or BT_4216)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAMMQT8	BTh[c] + BTamet[c] + BT2dmmq8[c] -> BTahcys[c] + BTmqI8[c]	0	1000	(BT_0853 or BT_4216)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAMMQT9	BTh[c] + BTamet[c] + BT2dmmq9[c] -> BTahcys[c] + BTmqI9[c]	0	1000	(BT_0853 or BT_4216)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAMPN	BTh2o[c] + BTamp[c] -> BTade[c] + BTr5p[c]	0	1000	BT_0888	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAMPTASECG	BTh2o[c] + BTcgly[c] -> BTgly[c] + BTcys-L[c]	0	1000	(BT_0638 or BT_1615 or BT_2706 or BT_4045)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAMPTASEPG	BTh2o[c] + BTprogly[c] -> BTgly[c] + BTpro-L[c]	0	1000	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAMPTASEPGe	BTh2o[e] + BTprogly[e] -> BTpro-L[e] + BTgly[e]	0	1000	BT_0587	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAMY1e	8 BTh2o[e] + BTstrch1[e] -> 8 BTglc-D[e] + BTstrch2[e]	0	1000	((BT_3698 and BT_3701 and BT_3702) or (BT_0773 and BT_3701 and BT_3702) or (BT_4305 and BT_3701 and BT_3702))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAMYLe	199 BTh2o[e] + BTamylose300[e] -> 100 BTglc-D[e] + 100 BTmalt[e]	0	1000	((BT_3698 and BT_3701 and BT_3702) or (BT_0773 and BT_3701 and BT_3702) or (BT_4305 and BT_3701 and BT_3702))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAMYe	499 BTh2o[e] + BTstarch1200[e] -> 100 BTglc-D[e] + 100 BTmalt[e] + 300 BTmaltr[e]	0	1000	((BT_3698 and BT_3701 and BT_3702) or (BT_0773 and BT_3701 and BT_3702) or (BT_4305 and BT_3701 and BT_3702))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTANPRT	BTprpp[c] + BTanth[c] -> BTppi[c] + BTpran[c]	0	1000	BT_0530	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTANS	BTgln-L[c] + BTchor[c] -> BTh[c] + BTglu-L[c] + BTpyr[c] + BTanth[c]	0	1000	(BT_0531 and BT_0532)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTANS2	BTnh4[c] + BTchor[c] -> BTh2o[c] + BTh[c] + BTpyr[c] + BTanth[c]	0	1000	(BT_0531 and BT_0532)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAOBUTDs	BTh[c] + BT2aobut[c] -> BTco2[c] + BTact[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAOXSr	BTh[c] + BTala-L[c] + BTpmcoa[c] <=> BTcoa[c] + BTco2[c] + BTBaorn[c]	-1000	1000	(BT_0870 or BT_1443)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAOXSr2	BTh[c] + BTala-L[c] + BTpmACP[c] <=> BTACP[c] + BTco2[c] + BTBaorn[c]	-1000	1000	(BT_0870 or BT_1443)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAPRAUR	BTh[c] + BTnadph[c] + BTSapru[c] -> BTnadp[c] + BTSaprbu[c]	0	1000	BT_3728	*B. thetaiotaomicron* metabolic/ transport/ demand reaction

BTARABASE3e	2 BTh2o[e] + BTarabtr[e] -> 3 BTarab-L[e]	0	1000	(BT_0348 or BT_3096 or BT_3657)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTARABINANASEe	100 BTh2o[e] + BTarabinan101[e] <=> 97 BTarab-L[e] + BTgal[e] + BTrnm[e] + 2 BTgalur[e]	-1000	1000	((BT_0360 or BT_0367 or BT_0368 or BT_0369) and (BT_4152 or BT_4667 or BT_4668) and (BT_4153 or BT_4170) and (BT_4175 or BT_4176) and ((BT_0361 and BT_0362) or (BT_4164 and BT_4165) or (BT_0363 and BT_0364) or (BT_4670 and BT_4671) or (BT_3680 and BT_3681)))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTARABINOGALASEe	659 BTh2o[e] + BTarabinogal[e] -> 15 BTh[e] + 92 BTarab-L[e] + 552 BTgal[e] + 15 BTglcur[e]	0	1000	((BT_0348 or BT_0265 or BT_3675 or BT_3685) and BT_0290 and BT_3687 and ((BT_3045 and BT_3046) or (BT_0268 and BT_0269) or (BT_0272 and BT_0273) or (BT_3680 and BT_3681)))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTARAI	BTarab-L[c] <=> BTrbl-L[c]	-1000	1000	BT_0351	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTARBt2r	BTh[e] + BTarab-L[e] <=> BTh[c] + BTarab-L[c]	-1000	1000	BT_0454	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTARGARG1c	BTh2o[c] + BTargarg[c] <=> 2 BTarg-L[c]	-1000	1000	BT_1846	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTARGARGt	BTh[e] + BTargarg[e] <=> BTh[c] + BTargarg[c]	-1000	1000	(BT_0580 or BT_4385 or BT_1086)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTARGDC	BTh[c] + BTarg-L[c] -> BTco2[c] + BTagm[c]	0	1000	BT_3394	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTARGN	BTh2o[c] + BTarg-L[c] -> BTorn[c] + BTurea[c]	0	1000	BT_1099	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTARGSL	BTargsuc[c] <=> BTsuc[c] + BTarg-L[c]	-1000	1000	BT_3733	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTARGSSr	BTatp[c] + BTasp-L[c] + BTcitr-L[c] <=> BTh[c] + BTamp[c] + BTppi[c] + BTargsuc[c]	-1000	1000	BT_3760	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTARGabc	BTh2o[c] + BTatp[c] + BTarg-L[e] -> BTh[c] + BTpi[c] + BTadp[c] + BTarg-L[c]	0	1000	BT_4049	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAROH	BTLargir[c] -> BTh2o[c] + BTco2[c] + BTphe-L[c]	0	1000	BT_3936	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAS3TASE_HS1	BTh2o[e] + BThspg_degr_4[e] -> BTh[e] + BThspg_degr_5[e] + BTso4[e]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAS3TASE_HS2	BTh2o[e] + BThspg_degr_5[e] -> BTh[e] + BTso4[e] + BThspg_degr_10[e]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAS6TASE_HS1	2 BTh2o[e] + BThspg_degr_3[e] -> 2 BTh[e] + BThspg_degr_4[e] + 2 BTso4[e]	0	1000	(BT_4656 and BT_0238)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTAS6TASE_HS2	BTh2o[e] + BThspg_degr_8[e] -> BTh[e] + BTso4[e] + BThspg_degr_9[e]	0	1000	(BT_4656 and BT_0238)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTASADi	BTh[c] + BTnadph[c] + BT4pasp[c] -> BTnadp[c] + BTpi[c] + BTaspsa[c]	0	1000	BT_3636	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTASNN	BTh2o[c] + BTasn-L[c] -> BTasp-L[c] + BTnh4[c]	0	1000	(BT_0526 or BT_2404 or BT_2757)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTASNS1	BTh2o[c] + BTatp[c] + BTasp-L[c] + BTglu-L[c] -> BTh[c] + BTglu-L[c] + BTamp[c] + BTppi[c] + BTasn-L[c]	0	1000	BT_0551	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTASNS2	BTatp[c] + BTasp-L[c] + BTnh4[c] -> BTh[c] + BTamp[c] + BTppi[c] + BTasn-L[c]	0	1000	BT_2129	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTASNt2r	BTh[e] + BTasn-L[e] <=> BTh[c] + BTasn-L[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTASP1DC	BTh[c] + BTasp-L[c] -> BTco2[c] + BTala-B[c]	0	1000	BT_4309	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTASPCT	BTasp-L[c] + BTchp[c] -> BTh[c] + BTpi[c] + BTchasp[c]	0	1000	(BT_0741 and BT_0742)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTASPK	BTatp[c] + BTasp-L[c] <=> BTadp[c] + BT4pasp[c]	-1000	1000	(BT_1375 or BT_1901 or BT_2403)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTASPO1	BTh2o[c] + BTasp-L[c] + BTo2[c] -> BTnh4[c] + BTh2o2[c] + BToaa[c]	0	1000	BT_3184	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTASPO5	BThum[c] + BTasp-L[c] -> BTh[c] + BTiasp[c] + BTsucc[c]	0	1000	BT_3184	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTASPO6	BTasp-L[c] + BTo2[c] -> BTh[c] + BTh2o2[c] + BTiasp[c]	0	1000	BT_3184	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTASPT	BTasp-L[c] -> BThum[c] + BTnh4[c]	0	1000	BT_2755	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTASPTA	BTakg[c] + BTasp-L[c] <=> BTglu-L[c] + BToaa[c]	-1000	1000	(BT_3935 or BT_3720 or BT_3375 or BT_0666 or BT_1077 or BT_1476 or BT_2415)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTASPt2r	BTh[e] + BTasp-L[e] <=> BTh[c] + BTasp-L[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTATPM	BTh2o[c] + BTatp[c] -> BTh[c] + BTpi[c] + BTadp[c]	8,43	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTATPPRT	BTatp[c] + BTpprpp[c] -> BTppi[c] + BTprbatp[c]	0	1000	BT_0200	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTATPS4	BTpi[c] + BTadp[c] + 4 BTh[e] -> BTh2o[c] + 3 BTh[c] + BTatp[c]	0	1000	(BT_0711 and BT_0712 and BT_0714 and BT_0715 and BT_0716 and BT_0717 and BT_0718 and BT_0719)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTA_MANASEe	2 BTh2o[e] + BTm2mn[e] -> 2 BTman[e] + BTmn[e]	0	1000	(BT_3774 or BT_3990 or BT_2199 or BT_2105 or BT_4072 or BT_4092 or BT_3784 or BT_3527 or BT_3530 or BT_3962)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTBACCL	BTh[c] + BTatp[c] + BTbtn[c] -> BTppi[c] + BTbtamp[c]	0	1000	BT_2238	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTBGLA	BTh2o[c] + BTcellb[c] -> 2 BTglc-D[c]	0	1000	(BT_3009 or BT_3300 or BT_3314 or BT_1778)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTBPNT	BTh2o[c] + BTpap[c] -> BTpi[c] + BTamp[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTBTNPL	BTbtamp[c] + BTapoC_Lys[c] -> BTh[c] + BTamp[c] + BTapoC_Lys_btn[c]	0	1000	(BT_1450 or BT_1917)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTBTN2	BTh[e] + BTbtn[e] <=> BTh[c] + BTbtn[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTBTS4	BTamet[c] + BTdtbt[c] + BTs[c] -> BTh[c] + BTdad-5[c] + BTbtn[c] + BTmet-L[c]	0	1000	BT_1442	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTBUTK	BTatp[c] + BTbut[c] -> BTadp[c] + BTbutp[c]	0	1000	BT_2552	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTB_MANNASEe	BTh2o[e] + BTmn[e] -> BTacgam[e] + BTman[e]	0	1000	(BT_0458 or BT_2855 or BT_4074 or BT_2432 or BT_3599)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTBiomass_BT_v2	34.7965 BTh2o[c] + 0.25601 BTglu-L[c] + 0.50006 BTala-L[c] + 0.004668 BTACP[c] + 0.004668 BTcoa[c] + 0.004668 BTnadp[c] + 0.004668 BTnadl[c] + 0.004668 BTna1[c] + 40.1701 BTatp[c] + 0.004668 BTadocbl[c] + 0.23468 BTasp-L[c] + 0.2091 BTgtp[c] + 0.004668 BT10fthf[c] + 0.004668 BTthf[c] + 0.25601 BTglu-L[c] + 0.5958 BTgly[c] + 0.092623 BThis-L[c] + 0.43866 BTleu-L[c] + 0.24665 BTthr-L[c] + 0.004668 BTamet[c] + 0.004668 BTmlthf[c] + 0.004668 BTmql10[c] + 0.004668 BTmqll1[c] + 0.004668 BTmql7[c] + 0.004668 BTmql8[c] + 0.08898 BTcys-L[c] + 0.21543 BTpro-L[c] + 0.28828 BTarg-L[c] + 0.18056 BTphe-L[c] + 0.23468 BTasn-L[c] + 0.004668 BTbmt[c] + 0.14934 BTorn-L[c] + 0.004668 BTca2[c] + 0.12988 BTcpp[c] + 0.010648 BTpgl40[c] + 0.010648 BTclpn140[c] + 0.010648 BTpg160[c] + 0.010648 BTclpn160[c] + 0.010648 BTpg180[c] + 0.010648 BTclpn180[c] + 0.010648 BTclpna15[c] + 0.010648 BTpgal17[c] + 0.010648 BTclpna17[c] + 0.010648 BTcpn140[c] + 0.010648 BTcpn150[c] + 0.010648 BTcpn160[c] + 0.010648 BTcpgal17[c] + 0.010648 BTclpn17[c] + 0.004668 BTcobalt2[c] + 0.004668 BTcps_bt[e] + 0.004668 BTspmd[c] + 0.14027 BTutp[c] + 0.33355 BThys-L[c] + 0.01945 BTips_bt[e] + 0.004668 BTpe_cer1_bt[e] + 0.004668 BTsphmyln_bt[e] + 0.004668 BTfe2[c] + 0.004668 BTfe3[c] + 0.004668 BTadf[c] + 0.023503 BTdttp[c] + 0.2097 BTser-L[c] + 0.023503 BTdatp[c] + 0.004668 BTpheme[c] + 0.28255 BTile-L[c] + 0.004668 BTk[c] + 0.004668 BTsmbt[c] + 0.004668 BTmg2[c] + 0.004668 BTmn2[c] + 0.023503 BTdgtp[c] + 0.023503 BTdctp[c] + 0.004668 BTpedv5p[c] + 0.010648 BTpe160[c] + 0.010648 BTpgl120[c] + 0.010648 BTpgl181[c] + 0.092476 BTpeptido_EC[c] + 0.092476 BTudcpdp[c] + 0.010648 BTpe120[c] + 0.010648 BTpe140[c] + 0.010648 BTpe180[c] + 0.010648 BTpe181[c] + 0.010648 BTpeai15[c] + 0.010648 BTpeai17[c] + 0.010648 BTpei14[c] + 0.010648 BTpei15[c] + 0.010648 BTpei16[c] + 0.010648 BTpei17[c] + 0.004668 BTrbflv[c] + 0.004668 BThtrnpg[c] + 0.13425 BTtyr-L[c] + 0.055157 BTrtp-L[c] + 0.4116 BTval-L[c] + 0.004668 BTzn2[c] -> 40 BTh[c] + 39.9953 BTpi[c] + 40 BTadp[c] + 0.004668 BTapoACP[c] + 0.60238 BTppi[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCA2abc	BTh2o[c] + BTatp[c] + BTca2[e] -> BTh[c] + BTpi[c] + BTadp[c] + BTca2[c]	0	1000	BT_2541	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCARNCNc	BTh2o[c] + BTcarn[c] <=> BThis-L[c] + BTala-B[c]	-1000	1000	(BT_4045 or BT_1615)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCARPEPT1tr	BTh[e] + BTcarn[e] <=> BTh[c] + BTcarn[c]	-1000	1000	(BT_4385 or BT_0580)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCAT	2 BTh2o2[c] -> 2 BTh2o[c] + BTo2[c]	0	1000	BT_1971	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCAt7r	3 BTna1[e] + BTca2[c] <=> 3 BTna1[c] + BTca2[e]	-1000	1000	BT_3019	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCBL1abc	BTh2o[c] + BTatp[c] + BTcbl1[e] -> BTh[c] + BTpi[c] + BTadp[c] + BTcbl1[c]	0	1000	(BT_1799 or BT_1489)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCBLAT	BTh[c] + BTatp[c] + BTcbl1[c] <=> BTppp[c] + BTadocbl[c]	-1000	1000	BT_2760	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCBPS	BTh2o[c] + 2 BTatp[c] + BThco3[c] + BTgln-L[c] -> 2 BTh[c] + BTglu-L[c] + BTpi[c] + 2 BTadp[c] + BTchp[c]	0	1000	(BT_0556 and BT_0557 and BT_3866)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCCP	2 BTh[c] + BTh2o2[c] + 2 BTficytcc553[c] -> 2 BTh2o[c] + 2 BTficytcc553[c]	0	1000	BT_1606	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCD2abc1	BTh2o[c] + BTatp[c] + BTcd2[c] -> BTh[c] + BTpi[c] + BTadp[c] + BTcd2[e]	0	1000	BT_1091	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCDPGHL	BTcdpgk[c] -> BTh2o[c] + BTcdpddg[c]	0	1000	BT_1350	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCDPMEK	BTatp[c] + BT4c2me[c] -> BTh[c] + BTadp[c] + BT2p4c2me[c]	0	1000	BT_0624	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCEPTC_BT	BTcdpcho1[c] + BTcer1_bt[c] -> BTh[c] + BTcmp[c] + BTsphrmyln_bt[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCEPTE_BT	BTcer1_bt[c] + BTcdpea[c] -> BTh[c] + BTcmp[c] + BTpe_cer1_bt[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCERS_BT	BTsphgn[c] + BTihpdcoa[c] -> BTh[c] + BTcoa[c] + BTcer1_bt[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCGLYt3_2_	2 BTh[e] + BTcgly[e] -> 2 BTh[c] + BTcgly[c]	0	1000	(BT_0580 or BT_4385 or BT_1086)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCHLPCTD	BTh[c] + BTcp[c] + BTcholp[c] -> BTppi[c] + BTclpcho[c]	0	1000	BT_1721	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCHOLK	BTatp[c] + BTchol[c] -> BTh[c] + BTadp[c] + BTcholp[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCHOLSH	BTh2o[c] + BTchols[c] -> BTh[c] + BTchol[c] + BTso4[c]	0	1000	(BT_1918 or BT_3349)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction

BTCHORM	BTchor[c] -> BTpphn[c]	0	1000	BT_3934	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCHORS	BT3psme[c] -> BTpi[c] + BTchor[c]	0	1000	BT_2084	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCITRAMALS	BTh2o[c] + BTpyr[c] + BTaccoa[c] <=> BTh[c] + BTcoa[c] + BT2mmal[c]	-1000	1000	BT_1858	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCKDNS	BTcip[c] + BTkdn[c] -> BTpp[c] + BTckdn[c]	0	1000	BT_1715	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCLPNS140	2 BTpg140[c] <=> BTglyc[c] + BTclpn140[c]	-1000	1000	(BT_2046 or BT_2382 or BT_3978)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCLPNS160	2 BTpg160[c] <=> BTglyc[c] + BTclpn160[c]	-1000	1000	(BT_2046 or BT_2382 or BT_3978)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCLPNS180	2 BTpg180[c] <=> BTglyc[c] + BTclpn180[c]	-1000	1000	(BT_2046 or BT_2382 or BT_3978)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCLPNSAI15	2 BTpgai15[c] <=> BTglyc[c] + BTclpnai15[c]	-1000	1000	(BT_2046 or BT_2382 or BT_3978)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCLPNSAI17	2 BTpgai17[c] <=> BTglyc[c] + BTclpnai17[c]	-1000	1000	(BT_2046 or BT_2382 or BT_3978)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCLPNSI14	2 BTpgi14[c] <=> BTglyc[c] + BTclpni14[c]	-1000	1000	(BT_2046 or BT_2382 or BT_3978)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCLPNSI15	2 BTpgi15[c] <=> BTglyc[c] + BTclpni15[c]	-1000	1000	(BT_2046 or BT_2382 or BT_3978)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCLPNSI16	2 BTpgi16[c] <=> BTglyc[c] + BTclpni16[c]	-1000	1000	(BT_2046 or BT_2382 or BT_3978)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCLPNSI17	2 BTpgi17[c] <=> BTglyc[c] + BTclpni17[c]	-1000	1000	(BT_2046 or BT_2382 or BT_3978)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCMLDC	BT2c25dho[c] -> BTh[c] + BTco2[c] + BT5odhf2a[c]	0	1000	BT_1393	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCO2t	BTco2[e] <=> BTco2[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCOBALTi5	BTcobalt2[c] <=> BTcobalt2[e]	-1000	1000	BT_4679	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCPSS_BT	BT2ameph[c] + BTckdd[c] + BTgdpfor[c] + BTdhdprnm[c] + BTuacmamu[c] -> BTcps_bt[c]	0	1000	(BT_0033 and BT_0378 and BT_0381 and BT_0382 and BT_0391 and BT_0394 and BT_0598 and BT_1343 and BT_1346 and BT_1355 and BT_1644 and BT_1653 and BT_1708 and BT_1722 and BT_2872)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCPS_BT_ABC	BTh2o[c] + BTatp[c] + BTcps_bt[c] -> BTh[c] + BTpi[c] + BTadp[c] + BTcps_bt[e]	0	1000	(BT_0057 and BT_0398 and BT_0481 and BT_0613 and BT_1356 and BT_2863)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCS	BTh2o[c] + BTaccoa[c] + BToaa[c] -> BTh[c] + BTcoa[c] + BTcit[c]	0	1000	BT_2070	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCS4TASE	BTh2o[e] + BTcspg_a_degr[e] -> BTh[e] + BTso4[e] + BTacgaldcur[e]	0	1000	((BT_0238 and BT_3095) or (BT_0238 and BT_3051) or (BT_0238 and BT_3177))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCS4TASE2	BTh2o[e] + BTcspg_b_degr[e] -> BTh[e] + BTso4[e] + BTacgaldeur2s[e]	0	1000	((BT_0238 and BT_3095) or (BT_0238 and BT_3051) or (BT_0238 and BT_3177))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCS6TASE	BTh2o[e] + BTcspg_c_degr[e] -> BTh[e] + BTso4[e] + BTacgaldcur[e]	0	1000	((BT_0238 and BT_1622) or (BT_3057 and BT_0238) or (BT_4656 and BT_0238) or (BT_3486 and BT_0238))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCSABCASE_A_e	2 BTh2o[e] + BTcspg_a[e] -> 2 BTcspg_a_degr[e] + BTcspg_ab_rest[e]	0	1000	(BT_3331 and BT_3332 and BT_3348)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCSABCASE_B_e	2 BTh2o[e] + BTcspg_b[e] -> BTcspg_a_degr[e] + BTcspg_b_degr[e] + BTcspg_ab_rest[e]	0	1000	(BT_3331 and BT_3332 and BT_3348)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCSABCASE_C_e	2 BTh2o[e] + BTcspg_c[e] -> 2 BTcspg_c_degr[e] + BTcspg_c_rest[e]	0	1000	(BT_3331 and BT_3332 and BT_3348)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCSPMDDC	2 BTh[c] + BTcspmd[c] -> BTco2[c] + BTspmd[c]	0	1000	BT_0674	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCSPMDDH	BTnadph[c] + BTaspsa[c] + BTptrc[c] <=> BTh2o[c] + BTnadp[c] + BTcspmd[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCTBTabc	BTh2o[c] + BTatp[c] + BTctbt[e] -> BTh[c] + BTpi[c] + BTadp[c] + BTctbt[c]	0	1000	(BT_1749 and BT_1750 and BT_1751)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCTPS1	BTatp[c] + BTnh4[c] + BTutp[c] -> 2 BTh[c] + BTpi[c] + BTadp[c] + BTctp[c]	0	1000	BT_0590	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCTPS2	BTh2o[c] + BTatp[c] + BTglx-L[c] + BTutp[c] -> 2 BTh[c] + BTglu-L[c] + BTi[c] + BTadp[c] + BTctp[c]	0	1000	BT_0590	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCYSD5	BTh2o[c] + BTcys-L[c] -> BTpyr[c] + BTnh4[c] + BTh2s[c]	0	1000	(BT_1923 or BT_2387)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCYSS	BTh2s[c] + BTacser[c] -> BTh[c] + BTac[c] + BTcys-L[c]	0	1000	(BT_1852 or BT_3080)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCYSS3r	BTrdrd[c] + BTnsul[c] + BTacser[c] <=> BTh[c] + BTac[c] + BTmdox[c] + BTso3[c] + BTcys-L[c]	-1000	1000	(BT_1852 or BT_3080)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCYSt2r	BTh[e] + BTcys-L[e] <=> BTh[c] + BTcys-L[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCYTBD	2 BTh[c] + 0.5 BTo2[c] + BTql8h2[c] -> BTh2o[c] + 2 BTh[e] + BTql8[c]	0	1000	(BT_3053 or (BT_1209 and BT_1210))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCYTBD2	2 BTh[c] + BTmql8[c] + 0.5 BTo2[c] -> BTh2o[c] + 2 BTh[e] + BTmqn8[c]	0	1000	(BT_3053 or (BT_1209 and BT_1210))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCYTD	BTh2o[c] + BTh[c] + BTcytd[c] -> BTnh4[c] + BTuri[c]	0	1000	BT_1539	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCYTDK1	BTatp[c] + BTcytd[c] -> BTh[c] + BTadp[c] + BTcmp[c]	0	1000	(BT_0184 or BT_2527)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCYTDK2	BTgtp[c] + BTcytd[c] -> BTh[c] + BTgdp[c] + BTcmp[c]	0	1000	(BT_0184 or BT_2527)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCYTDK3	BTcytd[c] + BTdp[c] -> BTh[c] + BTcmp[c] + BTdp[c]	0	1000	(BT_2060 or BT_2093)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCYTDK4	BTutp[c] + BTcytd[c] -> BTh[c] + BTcmp[c] + BTudp[c]	0	1000	(BT_0184 or BT_2527)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCYTDt2r	BTh[e] + BTcytd[e] <=> BTh[c] + BTcytd[c]	-1000	1000	BT_4330	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCYTK1	BTatp[c] + BTcmp[c] <=> BTadp[c] + BTcdp[c]	-1000	1000	(BT_2060 or BT_2093)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCYTK2	BTatp[c] + BTdcmp[c] <=> BTadp[c] + BTdcdp[c]	-1000	1000	(BT_2060 or BT_2093)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCIt	BTci[e] <=> BTci[c]	-1000	1000	BT_3944	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCuabc	BTh2o[c] + BTatp[c] + BTcu2[e] -> BTh[c] + BTpi[c] + BTadp[c] + BTcu2[c]	0	1000	BT_1091	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTCut1	BTh2o[c] + BTatp[c] + BTcu2[c] -> BTh[c] + BTpi[c] + BTadp[c] + BTcu2[e]	0	1000	BT_1091	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDADK	BTatp[c] + BTdamp[c] <=> BTadp[c] + BTdadp[c]	-1000	1000	BT_4387	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDADN2r	BTh[e] + BTdad-2[e] <=> BTh[c] + BTdad-2[c]	-1000	1000	BT_4330	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDAGK160	BTatp[c] + BT12dgr160[c] -> BTh[c] + BTadp[c] + BTpa160[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDALAt2r	BTh[e] + BTala-D[e] <=> BTh[c] + BTala-D[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDAPDC	BTh[c] + BT26dap-M[c] -> BTco2[c] + BTlys-L[c]	0	1000	BT_1374	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDAPE	BT26dap-LL[c] <=> BT26dap-M[c]	-1000	1000	BT_0548	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDAPMDH	BTh2o[c] + BTnadp[c] + BT26dap-M[c] <=> BTh[c] + BTnadph[c] + BTnh4[c] + BTL2a6o[c]	-1000	1000	BT_1979	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDASYN120	BTh[c] + BTpa120[c] + BTctp[c] -> BTppi[c] + BTcdpddecg[c]	0	1000	(BT_4006 or BT_4463)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDASYN140	BTh[c] + BTpa140[c] + BTctp[c] -> BTppi[c] + BTcdpdtdecg[c]	0	1000	(BT_4006 or BT_4463)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDASYN160	BTh[c] + BTpa160[c] + BTctp[c] -> BTppi[c] + BTcdpdhdecg[c]	0	1000	(BT_4006 or BT_4463)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDASYN180	BTh[c] + BTpa180[c] + BTctp[c] -> BTppi[c] + BTcdpdodecg[c]	0	1000	(BT_4006 or BT_4463)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDASYN181	BTh[c] + BTpa181[c] + BTctp[c] -> BTppi[c] + BTcdpdodec11eg[c]	0	1000	(BT_4006 or BT_4463)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDASYNAI15	BTh[c] + BTpaai15[c] + BTctp[c] -> BTppi[c] + BTcdpdaipdecg[c]	0	1000	(BT_4006 or BT_4463)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDASYNAI17	BTh[c] + BTpaai17[c] + BTctp[c] -> BTppi[c] + BTcdpdaihpdecg[c]	0	1000	(BT_4006 or BT_4463)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDASYNI14	BTh[c] + BTpai14[c] + BTctp[c] -> BTppi[c] + BTcdpditdecg[c]	0	1000	(BT_4006 or BT_4463)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDASYNI15	BTh[c] + BTpai15[c] + BTctp[c] -> BTppi[c] + BTcdpdipdecg[c]	0	1000	(BT_4006 or BT_4463)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDASYNI16	BTh[c] + BTpai16[c] + BTctp[c] -> BTppi[c] + BTcdpdihdecg[c]	0	1000	(BT_4006 or BT_4463)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDASYNI17	BTh[c] + BTpai17[c] + BTctp[c] -> BTppi[c] + BTcdpdihpdecg[c]	0	1000	(BT_4006 or BT_4463)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDB4PS	BTru5p-D[c] -> BTh[c] + BTdb4p[c] + BTfor[c]	0	1000	BT_2416	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDBTS	BTco2[c] + BTatp[c] + BTdamn[c] -> 3 BTh[c] + BTpi[c] + BTadp[c] + BTdtbt[c]	0	1000	BT_1446	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDCMPDA	BTh2o[c] + BTh[c] + BTdcmp[c] <=> BTnh4[c] + BTdump[c]	-1000	1000	BT_4260	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDCYTD	BTh2o[c] + BTh[c] + BTdcyt[c] -> BTnh4[c] + BTdur[c]	0	1000	BT_1539	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDCYTt2r	BTh[e] + BTdcyt[e] <=> BTh[c] + BTdcyt[c]	-1000	1000	BT_4330	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDDGLKr	BTatp[c] + BT2ddglcn[c] <=> BTh[c] + BTadp[c] + BT2ddg6p[c]	-1000	1000	BT_0488	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDDPA	BTh2o[c] + BTpep[c] + BTe4p[c] -> BTpi[c] + BT2dda7p[c]	0	1000	BT_3934	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDDPGA	BT4h2ogb[c] <=> BTpyr[c] + BTgb[c]	-1000	1000	BT_0489	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDEXTRAN40e	40 BTh2o[e] + BTdextran40[e] -> 40 BTmal[e]	0	1000	(BT_1663 or BT_4689)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDGC3D	BTnad[c] + BT2dglcn[c] -> BTh[c] + BTnadh[c] + BT3ddglc[c]	0	1000	(BT_3232 or BT_1015)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDGC3D2	BTnad[c] + BT2ddglcn[c] <=> BTh[c] + BTnadh[c] + BTdkdglcn[c]	-1000	1000	(BT_3232 or BT_1015)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDGK1	BTatp[c] + BTdgmp[c] <=> BTadp[c] + BTdgdp[c]	-1000	1000	BT_2009	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDGSN2	BTh[e] + BTdgsn[e] -> BTh[c] + BTdgsn[c]	0	1000	BT_4330	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDHAD1	BT23dhmb[c] -> BTh2o[c] + BT3mob[c]	0	1000	BT_2078	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDHAD2	BT23dhmp[c] -> BTh2o[c] + BT3mop[c]	0	1000	BT_2078	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDHDPRy	BTh[c] + BTnadph[c] + BT23dhdp[c] -> BTthdp[c] + BTnadp[c]	0	1000	BT_3320	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDHDPS	BTpyr[c] + BTaspsa[c] -> 2 BTh2o[c] + BTh[c] + BT23dhdp[c]	0	1000	(BT_0895 or BT_2814)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDHFR	BTh[c] + BTnadph[c] + BTdhf[c] <=> BTnadp[c] + BTthf[c]	-1000	1000	(BT_0106 or BT_2048)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDHFS	BTglu-L[c] + BTatp[c] + BTdhpt[c] -> BTh[c] + BTpi[c] + BTadp[c] + BTdhf[c]	0	1000	BT_1335	*B. thetaiotaomicron* metabolic/ transport/ demand reaction

BTDHNAOT10	BTdhna[c] + BTocidp[c] -> BTh[c] + 2 BTco2[c] + BTpp[c] + BT2dmmq10[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDHNAOT11	BTdhna[c] + BTocidp[c] -> BTh[c] + 8 BTco2[c] + BTpp[c] + BT2dmmq11[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDHNAOT4	BTh[c] + BTdhna[c] + BTocidp[c] -> BTco2[c] + BTpp[c] + BT2dmmq8[c]	0	1000	(BT_2014 or BT_2015)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDHNAOT7	BTdhna[c] + BTocidp[c] -> BTh[c] + BTco2[c] + BTpp[c] + BT2dmmq7[c]	0	1000	(BT_2014 or BT_2015)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDHNAOT9	BTdhna[c] + BTocidp[c] -> BTh[c] + BTco2[c] + BTpp[c] + BT2dmmq9[c]	0	1000	(BT_2014 or BT_2015)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDHNPA	BTdhnpt[c] -> BTh[c] + BTgcald[c] + BT2ahhmp[c]	0	1000	BT_2149	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDHORDfum	BTfum[c] + BTdhor-S[c] -> BTsucc[c] + BTorot[c]	0	1000	(BT_1009 or (BT_0891 and BT_0892))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDHORDi	BTo2[c] + BTdhor-S[c] -> BTh2o2[c] + BTorot[c]	0	1000	(BT_1009 or (BT_0891 and BT_0892))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDHORTS	BTh2o[c] + BTdhor-S[c] <=> BTh[c] + BTcbasp[c]	-1000	1000	BT_0250	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDHPPDA	BTh2o[c] + BTh[c] + BT25dhpp[c] -> BTrib4[c] + BT5aprua[c]	0	1000	BT_3728	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDHPS	BT4ahd[c] + BT2ahhmp[c] -> BTh2o[c] + BTdhpt[c]	0	1000	BT_3646	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDHPS3	BT6hmhptpp[c] + BTBrfap[c] -> BTpp[c] + BTdhrfap[c]	0	1000	BT_1410	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDHQS	BT2dda7p[c] -> BTp[c] + BT3dhq[c]	0	1000	BT_3975	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDHQTi	BT3dhq[c] -> BTh2o[c] + BT3dhsk[c]	0	1000	BT_2842	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDINSi2	BTh[e] + BTdin[e] -> BTh[c] + BTdin[c]	0	1000	BT_4330	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDMATT	BTdmpp[c] + BTipdp[c] -> BTppi[c] + BTgrdp[c]	0	1000	(BT_3261 or BT_2058)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDMPPS	BTh[c] + BTnadh[c] + BTh2mb4p[c] -> BTh2o[c] + BTnad[c] + BTdmpp[c]	0	1000	BT_2061	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDMPPS2	BTh[c] + BTnadph[c] + BTh2mb4p[c] -> BTh2o[c] + BTnadp[c] + BTdmpp[c]	0	1000	BT_2061	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDMQMT	BTamet[c] + BT2omhmbb[c] -> BTh[c] + BTahcys[c] + BTqdh2[c]	0	1000	BT_3209	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDM_4HBA	BT4hba[c] ->	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDM_5DRIB	BT5drib[c] ->	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDM_AMOB	BTamob[c] ->	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDPCOAK	BTatp[c] + BTdpcoa[c] -> BTh[c] + BTcoa[c] + BTadp[c]	0	1000	BT_4594	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDPR	BTh[c] + BTnadph[c] + BT2dhp[c] -> BTnadp[c] + BTpant-R[c]	0	1000	(BT_2074 or BT_3117)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDRBKr	BTh[c] + BTadp[c] + BT2dr5p[c] <=> BTatp[c] + BTdrib[c]	-1000	1000	(BT_2799 or BT_3576 or (BT_2803 and BT_2804))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDRPAr	BT2dr5p[c] <=> BTacald[c] + BTg3p[c]	-1000	1000	(BT_3263 or BT_4425)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDT5HSUt2r	BTh[e] + BTdt5hsu[e] <=> BTh[c] + BTdt5hsu[c]	-1000	1000	BT_4105	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDTMPK	BTatp[c] + BTdtmp[c] <=> BTadp[c] + BTdtdp[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDURIK1	BTatp[c] + BTdur[c] -> BTh[c] + BTadp[c] + BTdump[c]	0	1000	BT_2275	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDURIPP	BTpi[c] + BTdur[c] <=> BT2dr1p[c] + BTura[c]	-1000	1000	(BT_1881 or BT_4554)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDURIt2	BTh[e] + BTdur[e] -> BTh[c] + BTdur[c]	0	1000	BT_4330	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDUTPDP	BTh2o[c] + BTdutp[c] -> BTh[c] + BTppi[c] + BTdump[c]	0	1000	(BT_3461 or BT_4350)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDXPRIi	BTh[c] + BTnadph[c] + BTdxyl5p[c] -> BTnadp[c] + BT2me4p[c]	0	1000	BT_2002	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTDXPS	BTh[c] + BTpyr[c] + BTg3p[c] -> BTco2[c] + BTdxyl5p[c]	0	1000	(BT_1403 or BT_4099)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTD_LAC2	BTh[e] + BTlac-D[e] <=> BTh[c] + BTlac-D[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTE4PD	BTh2o[c] + BTnad[c] + BTe4p[c] <=> 2 BTh[c] + BTnadh[c] + BT4pe[c]	-1000	1000	BT_4263	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTEACPR1	BTh[c] + BTnadph[c] + BTtgACPm[c] -> BTnadp[c] + BTgACPm[c]	0	1000	BT_4188	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTEACPR2	BTh[c] + BTnadph[c] + BTepACPm[c] -> BTnadp[c] + BTpmACPm[c]	0	1000	BT_4188	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTEAR100x	BTh[c] + BTdec2eACP[c] + BTnadh[c] -> BTdcaACP[c] + BTnad[c]	0	1000	BT_4188	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTEAR10M11x	BTh[c] + BT10mtdec2eACP[c] + BTnadh[c] -> BT10mtdecACP[c] + BTnad[c]	0	1000	BT_4188	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTEAR10M12x	BTh[c] + BT10mtddec2eACP[c] + BTnadh[c] -> BT10mtddcaACP[c] + BTnad[c]	0	1000	BT_4188	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTEAR11M12x	BTh[c] + BT11mtddec2eACP[c] + BTnadh[c] -> BT11mtddcaACP[c] + BTnad[c]	0	1000	BT_4188	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTEAR120x	BTh[c] + BTddec2eACP[c] + BTnadh[c] -> BTddcaACP[c] + BTnad[c]	0	1000	BT_4188	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTEAR121x	BTh[c] + BTd3c5ddeceACP[c] + BTnadh[c] -> BTcddec5eACP[c] + BTnad[c]	0	1000	BT_4188	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTEAR12M13x	BTh[c] + BT12mtdec2eACP[c] + BTnadh[c] -> BT12mtdecACP[c] + BTnad[c]	0	1000	BT_4188	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTEAR12M14x	BTh[c] + BT12mtmrs2eACP[c] + BTnadh[c] -> BT12mmyrsACP[c] + BTnad[c]	0	1000	BT_4188	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTEAR13M14x	BTh[c] + BT13mtmrs2eACP[c] + BTnadh[c] -> BT13mmyrsACP[c] + BTnad[c]	0	1000	BT_4188	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTEAR140x	BTh[c] + BTmrs2eACP[c] + BTnadh[c] -> BTmyrsACP[c] + BTnad[c]	0	1000	BT_4188	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTEAR141x	BTh[c] + BT3c7mrseACP[c] + BTnadh[c] -> BTtdeACP[c] + BTnad[c]	0	1000	BT_4188	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTEAR14M15x	BTh[c] + BT14mtpentdec2eACP[c] + BTnadh[c] -> BTnad[c] + BT14mpentdecACP[c]	0	1000	BT_4188	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTEAR14M16x	BTh[c] + BT14mtpalm2eACP[c] + BTnadh[c] -> BTnad[c] + BT14mpalmACP[c]	0	1000	BT_4188	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTEAR15M16x	BTh[c] + BT15mtpalm2eACP[c] + BTnadh[c] -> BTnad[c] + BT15mpalmACP[c]	0	1000	BT_4188	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTEAR160x	BTh[c] + BTtpalm2eACP[c] + BTnadh[c] -> BTpalmACP[c] + BTnad[c]	0	1000	BT_4188	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTEAR161x	BTh[c] + BT3c9palmeACP[c] + BTnadh[c] -> BTtdeACP[c] + BTnad[c]	0	1000	BT_4188	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTEAR180x	BTh[c] + BTtoctd2eACP[c] + BTnadh[c] -> BTnad[c] + BTocdcaACP[c]	0	1000	BT_4188	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTEAR181x	BTh[c] + BT3c11vaceACP[c] + BTnadh[c] -> BTnad[c] + BTocteACP[c]	0	1000	BT_4188	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTEAR40x	BTh[c] + BTbut2eACP[c] + BTnadh[c] -> BTbutACP[c] + BTnad[c]	0	1000	BT_4188	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTEAR4M5x	BTh[c] + BT4mtpent2eACP[c] + BTnadh[c] -> BT4mpentACP[c] + BTnad[c]	0	1000	BT_4188	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTEAR4M6x	BTh[c] + BT4mthex2eACP[c] + BTnadh[c] -> BT4mhexACP[c] + BTnad[c]	0	1000	BT_4188	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTEAR5M6x	BTh[c] + BT5mthex2eACP[c] + BTnadh[c] -> BT5mhexACP[c] + BTnad[c]	0	1000	BT_4188	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTEAR60x	BTh[c] + BThex2eACP[c] + BTnadh[c] -> BThexACP[c] + BTnad[c]	0	1000	BT_4188	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTEAR6M7x	BTh[c] + BT6mthept2eACP[c] + BTnadh[c] -> BT6mheptACP[c] + BTnad[c]	0	1000	BT_4188	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTEAR6M8x	BTh[c] + BT6mtoct2eACP[c] + BTnadh[c] -> BT6mocACP[c] + BTnad[c]	0	1000	BT_4188	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTEAR7M8x	BTh[c] + BT7mtoct2eACP[c] + BTnadh[c] -> BT7mocACP[c] + BTnad[c]	0	1000	BT_4188	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTEAR80x	BTh[c] + BTtoct2eACP[c] + BTnadh[c] -> BTocACP[c] + BTnad[c]	0	1000	BT_4188	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTEAR8M10x	BTh[c] + BT8mtdec2eACP[c] + BTnadh[c] -> BT8mdcaACP[c] + BTnad[c]	0	1000	BT_4188	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTEAR8M9x	BTh[c] + BT8mmon2eACP[c] + BTnadh[c] -> BT8mnonACP[c] + BTnad[c]	0	1000	BT_4188	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTEAR9M10x	BTh[c] + BT9mtdec2eACP[c] + BTnadh[c] -> BT9mdcaACP[c] + BTnad[c]	0	1000	BT_4188	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTEDA_R	BT2ddg6p[c] <=> BTpyr[c] + BTg3p[c]	-1000	1000	BT_0489	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTEDTXS1_BT	BTddcaACP[c] + BTkdolipid4_bt[c] -> BTACP[c] + BTkdolipid4L_bt[c]	0	1000	BT_2152	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTEHGLAT	BTakg[c] + BTe4hgh[c] -> BTglu-L[c] + BTd4h2ogh[c]	0	1000	(BT_0666 or BT_1077 or BT_1476 or BT_2415 or BT_3375 or BT_3720 or BT_3935)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTENO	BT2pg[c] <=> BTh2o[c] + BTpep[c]	-1000	1000	BT_4572	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTETOHt	BTetoh[e] <=> BTetoh[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTF1PGT	BTh[c] + BTgtp[c] + BTfuc1p-L[c] <=> BTpp[c] + BTgtpfuc[c]	-1000	1000	BT_2128	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFACOAL140	BTcoa[c] + BTatp[c] + BThdca[c] <=> BThdcoa[c] + BTamp[c] + BTppi[c]	-1000	1000	(BT_0684 or BT_1226 or BT_2154 or BT_2782 or BT_3550)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFACOAL160	BTcoa[c] + BTatp[c] + BThdcad[c] <=> BTpmtcoa[c] + BTamp[c] + BTppi[c]	-1000	1000	(BT_0684 or BT_1226 or BT_2154 or BT_2782 or BT_3550)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFACOAL161	BTcoa[c] + BTatp[c] + BThdcea[c] <=> BTamp[c] + BTppi[c] + BThdcoa[c]	-1000	1000	(BT_0684 or BT_1226 or BT_2154 or BT_2782 or BT_3550)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFACOAL180	BTcoa[c] + BTatp[c] + BTocdcac[c] <=> BTstcoa[c] + BTamp[c] + BTppi[c]	-1000	1000	(BT_0684 or BT_1226 or BT_2154 or BT_2782 or BT_3550)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFACOAL181	BTcoa[c] + BTatp[c] + BTocdcea[c] <=> BTamp[c] + BTppi[c] + BTodecoa[c]	-1000	1000	(BT_0684 or BT_1226 or BT_2154 or BT_2782 or BT_3550)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFACOALAI15	BTcoa[c] + BTatp[c] + BTla4[c] <=> BTaipdcoa[c] + BTamp[c] + BTppi[c]	-1000	1000	(BT_0684 or BT_1226 or BT_2154 or BT_2782 or BT_3550)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFACOALAI17	BTcoa[c] + BTatp[c] + BTla12[c] <=> BTahpdcoa[c] + BTamp[c] + BTppi[c]	-1000	1000	(BT_0684 or BT_1226 or BT_2154 or BT_2782 or BT_3550)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFACOALI14	BTcoa[c] + BTatp[c] + BTla1[c] <=> BTtdcoa[c] + BTamp[c] + BTppi[c]	-1000	1000	(BT_0684 or BT_1226 or BT_2154 or BT_2782 or BT_3550)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFACOALI15	BTcoa[c] + BTatp[c] + BTa3[c] <=> BTpdcoa[c] + BTamp[c] + BTppi[c]	-1000	1000	(BT_0684 or BT_1226 or BT_2154 or BT_2782 or BT_3550)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFACOALI16	BTcoa[c] + BTatp[c] + BTla6[c] <=> BThdcoa[c] + BTamp[c] + BTppi[c]	-1000	1000	(BT_0684 or BT_1226 or BT_2154 or BT_2782 or BT_3550)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFACOALI17	BTcoa[c] + BTatp[c] + BTla11[c] <=> BTtpdcoa[c] + BTamp[c] + BTppi[c]	-1000	1000	(BT_0684 or BT_1226 or BT_2154 or BT_2782 or BT_3550)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction

BTFBA	BTfdp[c] <=> BTdhap[c] + BTg3p[c]	-1000	1000	(BT_1106 or BT_1659 or BT_1691)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFBA2	BTfp[c] <=> BTglyald[c] + BTdhap[c]	-1000	1000	(BT_1106 or BT_1659 or BT_1691)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFBA3	BTs17bp[c] <=> BTdhap[c] + BTe4p[c]	-1000	1000	(BT_1106 or BT_1659 or BT_1691)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFBP	BTh2o[c] + BTfdp[c] -> BTpi[c] + BTf6p[c]	0	1000	BT_1228	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFCI	BTfuc-L[c] <=> BTfcl-L[c]	-1000	1000	BT_1273	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFCLK	BTatp[c] + BTfcl-L[c] -> BTh[c] + BTadp[c] + BTfc1p[c]	0	1000	BT_1275	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFCLPA	BTfc1p[c] <=> BTdhap[c] + BTald-L[c]	-1000	1000	BT_1274	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFDNADOX	BTnad[c] + BTfdxrd[c] <=> BTh[c] + BTnadh[c] + BTfdxox[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFE2abc	BTh2o[c] + BTatp[c] + BTfe2[e] -> BTh[c] + BTpi[c] + BTadp[c] + BTfe2[c]	0	1000	(BT_1592 or (BT_2098 and BT_2099) or (BT_1950 and BT_1952))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFE3DCITabc	BTh2o[c] + BTatp[c] + BTfe3dcit[e] -> BTh[c] + BTpi[c] + BTadp[c] + 2 BTcit[c] + BTfe3[c]	0	1000	BT_1951	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFE3abc	BTh2o[c] + BTatp[c] + BTfe3[e] -> BTh[c] + BTpi[c] + BTadp[c] + BTfe3[c]	0	1000	((BT_2098 and BT_2099) or (BT_1950 and BT_1952))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFEDCabc	BTh2o[c] + BTatp[c] + 2 BTcit[e] + BTfe3[e] -> BTh[c] + BTpi[c] + BTadp[c] + 2 BTcit[c] + BTfe3[c]	0	1000	BT_1951	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFERO	4 BTh[c] + BTo2[c] + 4 BTfe2[c] -> 2 BTh2o[c] + 4 BTfe3[c]	0	1000	BT_4715	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFK	BTatp[c] + BTfuc-L[c] -> BTh[c] + BTadp[c] + BTfuc1p-L[c]	0	1000	BT_2128	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFMNAT	BTh[c] + BTatp[c] + BTfmn[c] -> BTppi[c] + BTfad[c]	0	1000	BT_2543	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFOLD3	BT4abz[c] + BT2ahhmd[c] -> BTppi[c] + BTdhpt[c]	0	1000	BT_3646	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFOLR	2 BTnadp[c] + BTthf[c] <=> BTh[c] + 2 BTnadph[c] + BTfolr[c]	-1000	1000	(BT_0106 or BT_2048)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFOLt	BTh[e] + BTfolr[e] <=> BTh[c] + BTfolr[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFOMETR	BTh[c] + BT5thf[c] <=> BTh2o[c] + BTmethf[c]	-1000	1000	BT_4584	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFORt	BTfor[c] <=> BTfor[e]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFPGS7	4 BTglu-L[c] + 4 BTatp[c] + BT10fthf[c] -> 4 BTh[c] + 4 BTpi[c] + 4 BTadp[c] + BT10fthf5glu[c]	0	1000	BT_1335	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFPGS_tm	BTglu-L[c] + BTatp[c] + BTthf[c] -> BTh[c] + BTpi[c] + BTadp[c] + BTthfglu[c]	0	1000	BT_1335	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFRD10	BTfum[c] + BTmql10[c] -> BTsucc[c] + BTmqn10[c]	0	1000	(BT_3054 and BT_3055)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFRD11	BTfum[c] + BTmql11[c] -> BTsucc[c] + BTmqn11[c]	0	1000	(BT_3054 and BT_3055)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFRD2	BTfum[c] + BTmql8[c] -> BTsucc[c] + BTmqn8[c]	0	1000	(BT_3054 and BT_3055)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFRD3	BTfum[c] + BT2dmmql8[c] -> BT2dmmql8[c] + BTsucc[c]	0	1000	(BT_3054 and BT_3055)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFRD8	BTfum[c] + BTmql7[c] -> BTsucc[c] + BTmqn7[c]	0	1000	(BT_3054 and BT_3055)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFRD9	BTfum[c] + BTmql8[c] -> BTsucc[c] + BTmqn9[c]	0	1000	(BT_3054 and BT_3055)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFRTT	BTtpdp[c] + BTfrdp[c] -> BTppi[c] + BTggdp[c]	0	1000	(BT_3261 or BT_2058)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFRUASE3	BTh2o[c] + BTfevanh[c] -> 2 BTfru[c]	0	1000	BT_1765	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFRUt2r	BTh[e] + BTfru[e] <=> BTh[c] + BTfru[c]	-1000	1000	BT_1758	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFTCD_r	2 BTh[c] + BT5fortht[c] <=> BTnh4[c] + BTmethf[c]	-1000	1000	BT_2691	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFTHFCL	BTatp[c] + BT5thf[c] -> BTpi[c] + BTadp[c] + BTmethf[c]	0	1000	BT_4258	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFTHFD	BTh2o[c] + BT10thf[c] -> BTh[c] + BTthf[c] + BTfor[c]	0	1000	BT_1381	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFTHFLi	BTatp[c] + BTthf[c] + BTfor[c] -> BTpi[c] + BTadp[c] + BT10fthf[c]	0	1000	BT_0737	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFUCASEe	BTh2o[e] + BTs2f2fn2m2mass6[e] -> BTfuc-L[e] + BTs2f2n2m2mass6[e]	0	1000	(BT_1842 or BT_2970 or BT_3665)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFUCNEULACNHX_DEGe	8 BTh2o[e] + 2 BTfucneulacnhx6[e] -> 2 BTfuc-L[e] + 2 BTacgam6[e] + 2 BTacnam[e] + 2 BTgal6[e] + BTacnntr[e] + BTacntr[e]	0	1000	((BT_1625 or BT_4136) and (BT_0455 or BT_2194 or BT_2892) and (BT_1626 or BT_0461) and (BT_1627 or BT_1632 or BT_4132 or BT_0459 or BT_0460 or BT_1038 or BT_1044 or BT_1048 or BT_1051 or BT_4295 or BT_2825) and ((BT_1630 and BT_1631) or (BT_4134 and BT_4135) or (BT_1039 and BT_1040) or (BT_1042 and BT_1043) or (BT_1046 and BT_1047) or (BT_4297 and BT_4298) or (BT_2818 and BT_2819) or (BT_2820 and BT_2821)))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFUCt	BTfuc-L[e] + BTh[e] <=> BTh[c] + BTfuc-L[c]	-1000	1000	(BT_1277 or BT_3616)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFUM	BTh2o[c] + BTfum[c] <=> BTmal-L[c]	-1000	1000	BT_2256	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTFUMt2r	BTh[e] + BTfum[e] <=> BTh[c] + BTfum[c]	-1000	1000	BT_2756	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTG1PACT	BTaccoa[c] + BTgam1p[c] -> BTh[c] + BTcoa[c] + BTacgam1p[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTG1PCT	BTh[c] + BTctp[c] + BTg1p[c] <=> BTppi[c] + BTcdpgl[c]	-1000	1000	BT_1351	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTG1PTT	BTh[c] + BTdtp[c] + BTg1p[c] -> BTppi[c] + BTdtdpglu[c]	0	1000	(BT_0463 or BT_2017)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTG3PAT120	BTddcaACP[c] + BTglyc3p[c] -> BTACP[c] + BT1ddecg3p[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTG3PAT140	BTmyrsACP[c] + BTglyc3p[c] -> BTACP[c] + BT1tdecg3p[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTG3PAT160	BTpalmACP[c] + BTglyc3p[c] -> BTACP[c] + BT1hdecg3p[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTG3PAT180	BTocdcaACP[c] + BTglyc3p[c] -> BTACP[c] + BT1odecg3p[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTG3PAT181	BTocteACP[c] + BTglyc3p[c] -> BTACP[c] + BT1odec11eg3p[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTG3PATA115	BTh[c] + BTaipdcoa[c] + BTglyc3p[c] -> BTcoa[c] + BT1aipdecg3p[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTG3PATA117	BTahpdcoa[c] + BTglyc3p[c] -> BTcoa[c] + BT1ahpdecg3p[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTG3PATI14	BTh[c] + BTitdcoa[c] + BTglyc3p[c] -> BTcoa[c] + BT1itdecg3p[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTG3PATI15	BTih[c] + BTipdcoa[c] + BTglyc3p[c] -> BTcoa[c] + BT1ipdecg3p[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTG3PATI16	BTih[c] + BTihdcoa[c] + BTglyc3p[c] -> BTcoa[c] + BT1ihdecg3p[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTG3PATI17	BTihpdcoa[c] + BTglyc3p[c] -> BTcoa[c] + BT1ihpdecg3p[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTG3PD1	BTnad[c] + BTglyc3p[c] <=> BTh[c] + BTnadh[c] + BTdhap[c]	-1000	1000	BT_2123	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTG5SADs	BTglu6sa[c] <=> BTh2o[c] + BTh[c] + BT1pyr5c[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTG5SD	BTh[c] + BTnadph[c] + BTglu5p[c] -> BTnadp[c] + BTp[c] + BTglu6sa[c]	0	1000	BT_3718	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTG6PBDH	BTnadp[c] + BTg6p- B[c] <=> BTh[c] + BTnadph[c] + BT6pgl[c]	-1000	1000	BT_1221	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTG6PDA	BTh2o[c] + BTgam6p[c] -> BTnh4[c] + BT6p[c]	0	1000	(BT_0258 or BT_3587 or BT_3601 or BT_4127)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTG6PDH2r	BTnadp[c] + BTg6p[c] <=> BTh[c] + BTnadph[c] + BT6pgl[c]	-1000	1000	BT_1221	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTG6PI	BTg6p[c] <=> BTg6p- B[c]	-1000	1000	BT_2124	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTG6PI3	BTg6p- B[c] <=> BTf6p[c]	-1000	1000	BT_2124	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGACPCD	BTh[c] + BTmalACP[c] + BTgACPm[c] -> BTACP[c] + BT3opACPm[c] + BTco2[c]	0	1000	BT_3358	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGALAM6PDA	BTh2o[c] + BTgalam6p[c] -> BTnh4[c] + BTgglp- D[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGALAMt2r	BTh[e] + BTgalam[e] <=> BTh[c] + BTgalam[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGALASE1e	2 BTh2o[e] + BTl2n2m2mn[e] -> BTn2m2mn[e] + 2 BTgal[e]	0	1000	(BT_0290 or BT_0461 or BT_0757 or BT_0983 or BT_0992 or BT_0993 or BT_0996 or BT_1626 or BT_2190 or BT_2680 or BT_2922 or BT_2969 or BT_3092 or BT_3114 or BT_3179 or BT_3293 or BT_3340 or BT_3513 or BT_3654 or BT_4050 or BT_4152 or BT_4156 or BT_4160 or BT_4181 or BT_4241 or BT_4667 or BT_4684)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGALASE_HSe	2 BTh2o[e] + BThspg_degr_15[e] -> 2 BTgal[e] + BThspg_rest[e]	0	1000	(BT_0290 or BT_0461 or BT_0757 or BT_0983 or BT_0992 or BT_0993 or BT_0996 or BT_1626 or BT_2190 or BT_2680 or BT_2922 or BT_2969 or BT_3092 or BT_3114 or BT_3179 or BT_3293 or BT_3340 or BT_3513 or BT_3654 or BT_4050 or BT_4152 or BT_4156 or BT_4160 or BT_4181 or BT_4241 or BT_4667 or BT_4684)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGALASE_OGLYCAN1e	BTh2o[e] + BTfla[e] -> BTgal[e] + BTcore6[e]	0	1000	BT_4241 and BT_4246 and BT_4247	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGALASE_OGLYCAN2e	BTh2o[e] + BTT_antigen[e] -> BTgal[e] + BTTn_antigen[e]	0	1000	BT_4241 and BT_4246 and BT_4247	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGALASE_OGLYCAN3e	BTh2o[e] + BTcore8[e] -> BTgal[e] + BTTn_antigen[e]	0	1000	BT_4241 and BT_4246 and BT_4247	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGALK	BTatp[c] + BTgal[c] -> BTh[c] + BTadp[c] + BTgal1p[c]	0	1000	BT_0370	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGALM1r	BTglc-bD[c] <=> BTglc-D[c]	-1000	1000	(BT_0372 or BT_0356 or BT_2849 or BT_3529 or BT_3532)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGALNACASE_OGLYCAN1e	BTh2o[e] + BTTn_antigen[e] -> BTacgal[e] + BTSer_Thr[e]	0	1000	BT_0065	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGALNACASE_OGLYCAN2e	BTh2o[e] + BTcore5[e] -> BTacgal[e] + BTTn_antigen[e]	0	1000	BT_0065	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGALNACASE_OGLYCAN3e	BTh2o[e] + BTcore7[e] -> BTacgal[e] + BTTn_antigen[e]	0	1000	BT_0065	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGALOX	BTh2o[c] + BTo2[c] + BTgal[c] <=> BTh[c] + BTh2o2[c] + BTgalctn-D[c]	-1000	1000	BT_4040 or BT_4632	*B. thetaiotaomicron* metabolic/ transport/ demand reaction

BTGALS3	BTh2o[c] + BTmelib[c] -> BTglc-D[c] + BTgal[c]	0	1000	(BT_1871 or BT_2851 or BT_3065 or BT_3131 or BT_3133 or BT_3410)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGALURt2r	BTh[c] + BTgalur[c] <=> BTh[e] + BTgalur[e]	-1000	1000	BT_4105	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGALUi	BTh[c] + BTutp[c] + BTg1p[c] -> BTppi[c] + BTudpg[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGALt2_2	BTh[e] + BTgal[e] <=> BTh[c] + BTgal[c]	-1000	1000	(BT_3589 or BT_1758 or BT_0371 or BT_4311 or BT_4653)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGAM2STASE_HS1	2 BTh2o[e] + BTgam26s[e] -> BTh[e] + 2 BTso4[e] + BTgam[e]	0	1000	((BT_1624 and BT_0238) or (BT_3796 and BT_0238))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGAM2STASE_HS2	2 BTh2o[e] + BThspg_degr_5[e] -> 2 BTh[e] + 2 BTso4[e] + BThspg_degr_6[e]	0	1000	((BT_1624 and BT_0238) or (BT_3796 and BT_0238))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGAM2STASE_HS3	BTh2o[e] + BThspg_degr_10[e] -> BTh[e] + BTso4[e] + BThspg_degr_11[e]	0	1000	((BT_1624 and BT_0238) or (BT_3796 and BT_0238))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGAMt2r	BTh[e] + BTgam[e] <=> BTh[c] + BTgam[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGAPD	BTg3p[c] + BTnad[c] + BTg3p[c] <=> BTh[c] + BTnadh[c] + BT13dpg[c]	-1000	1000	BT_4263	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGARFTi	BT10fthf[c] + BTgar[c] -> BTh[c] + BTthf[c] + BTfgam[c]	0	1000	(BT_2883 or BT_3360)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGART	BTatp[c] + BTfor[c] + BTgar[c] -> BTh[c] + BTp[c] + BTadp[c] + BTfgam[c]	0	1000	BT_0704	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGCCa	BTh[c] + BTgly[c] + BTpro[c] -> BTco2[c] + BTalpro[c]	0	1000	BT_1147	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGCCb	BThthf[c] + BTalpro[c] -> BTnh4[c] + BThthpro[c] + BTmthf[c]	0	1000	(BT_2519 and BT_4584)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGCCc	BTnad[c] + BThthpro[c] -> BTh[c] + BTnadh[c] + BTprpc[c]	0	1000	(BT_2519 or BT_3186 or (BT_1147 and BT_2519))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGCHOLAH	BTh2o[c] + BTgchola[c] -> BTh[c] + BTcholate[c] + BTgly[c]	0	1000	(BT_1259 or BT_2086)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGCHOLAt2	2 BTna1[e] + BTgchola[e] -> 2 BTna1[c] + BTgchola[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGF6PTAr	BTglu-L[c] + BTf6p[c] <=> BTglu-L[c] + BTgam6p[c]	-1000	1000	BT_0554	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGFUCS	BTh[c] + BTnadph[c] + BTgalpddmun[c] -> BTnadp[c] + BTgdpfuc[c]	0	1000	BT_1225	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGGTT	BTpedp[c] + BTggdp[c] -> BTppi[c] + BTpendp[c]	0	1000	(BT_3261 or BT_2058)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGHMT2r	BThthf[c] + BTser-L[c] <=> BTh2o[c] + BTgly[c] + BTmthf[c]	-1000	1000	BT_0738	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGK1	BTatp[c] + BTgmp[c] <=> BTadp[c] + BTgdp[c]	-1000	1000	BT_2009	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGK2	BTdatp[c] + BTgmp[c] <=> BTgdp[c] + BTdadp[c]	-1000	1000	BT_2009	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLCAASE8e	BTh2o[e] + BTha[e] -> BTglcur[e] + BTha_deg1[e]	0	1000	(BT_3292 or BT_4151)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLCAASE9e	2 BTh2o[e] + BTha_pre1[e] -> BTacgam[e] + BTglcur[e]	0	1000	(BT_3292 or BT_4151)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLCAASE_HSe	BTh2o[e] + BThspg_degr_12[e] -> BTglcur[e] + BThspg_degr_13[e]	0	1000	(BT_3292 or BT_4151)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLCAASEe	BTh2o[e] + BTacgalglcur[e] -> BTacgal[e] + BTglcur[e]	0	1000	(BT_3292 or BT_4151 or BT_3324 or BT_3350)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLCNACASE_HS1	2 BTh2o[e] + 2 BTh[e] + BThspg_degr_6[e] -> 2 BTacgam[e] + BTglcur[e]	0	1000	(BT_0438 or BT_3590 or BT_4359)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLCNACASE_HS2	BTh2o[e] + BTh[e] + BThspg_degr_11[e] -> BTgam[e] + BThspg_degr_12[e]	0	1000	(BT_0438 or BT_3590 or BT_4359)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLCNACASE_HS3	BTh2o[e] + BThspg_degr_13[e] -> BTacgam[e] + BThspg_degr_14[e]	0	1000	(BT_0438 or BT_3590 or BT_4359)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLCNACASE_OGLYCAN1e	BTh2o[e] + BTcore6[e] -> BTacgam[e] + BTTn_antigen[e]	0	1000	((BT_2825 or BT_1038 or BT_1044 or BT_1048 or BT_0865 or BT_1282 or BT_3753 or BT_4132 or BT_4406 or BT_3985 or BT_3987) and ((BT_1039 and BT_1040) or (BT_1042 and BT_1043) or (BT_1046 and BT_1047) or (BT_4134 and BT_4135) or (BT_4404 and BT_4405) or (BT_3983 and BT_3984) or BT_0866 and BT_0867) or (BT_3751 and BT_3752) or (BT_1280 and BT_1281) or (BT_3958 and BT_3959) or (BT_4633 and BT_4634) or (BT_2818 and BT_2819) or (BT_2820 and BT_2821)))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLCNACASE_OGLYCAN2e	BTh2o[e] + BTgncore2[e] -> BTacgam[e] + BTcore2[e]	0	1000	((BT_2825 or BT_1038 or BT_1044 or BT_1048 or BT_0865 or BT_1282 or BT_3753 or BT_4132 or BT_4406 or BT_3985 or BT_3987) and ((BT_1039 and BT_1040) or (BT_1042 and BT_1043) or (BT_1046 and BT_1047) or (BT_4134 and BT_4135) or (BT_4404 and BT_4405) or (BT_3983 and BT_3984) or BT_0866 and BT_0867) or (BT_3751 and BT_3752) or (BT_1280 and BT_1281) or (BT_3958 and BT_3959) or (BT_4633 and BT_4634) or (BT_2818 and BT_2819) or (BT_2820 and BT_2821)))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLCNACASE_OGLYCAN3e	BTh2o[e] + BTcore2[e] -> BTacgam[e] + BTT_antigen[e]	0	1000	((BT_2825 or BT_1038 or BT_1044 or BT_1048 or BT_0865 or BT_1282 or BT_3753 or BT_4132 or BT_4406 or BT_3985 or BT_3987) and ((BT_1039 and BT_1040) or (BT_1042 and BT_1043) or (BT_1046 and BT_1047) or (BT_4134 and BT_4135) or (BT_4404 and BT_4405) or (BT_3983 and BT_3984) or BT_0866 and BT_0867) or (BT_3751 and BT_3752) or (BT_1280 and BT_1281) or (BT_3958 and BT_3959) or (BT_4633 and BT_4634) or (BT_2818 and BT_2819) or (BT_2820 and BT_2821)))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLCNACASE_OGLYCAN4e	BTh2o[e] + BTgncore1[e] -> BTacgam[e] + BTT_antigen[e]	0	1000	((BT_2825 or BT_1038 or BT_1044 or BT_1048 or BT_0865 or BT_1282 or BT_3753 or BT_4132 or BT_4406 or BT_3985 or BT_3987) and ((BT_1039 and BT_1040) or (BT_1042 and BT_1043) or (BT_1046 and BT_1047) or (BT_4134 and BT_4135) or (BT_4404 and BT_4405) or (BT_3983 and BT_3984) or BT_0866 and BT_0867) or (BT_3751 and BT_3752) or (BT_1280 and BT_1281) or (BT_3958 and BT_3959) or (BT_4633 and BT_4634) or (BT_2818 and BT_2819) or (BT_2820 and BT_2821)))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLCNACASE_OGLYCAN5e	BTh2o[e] + BTcore4[e] -> BTacgam[e] + BTcore3[e]	0	1000	((BT_2825 or BT_1038 or BT_1044 or BT_1048 or BT_0865 or BT_1282 or BT_3753 or BT_4132 or BT_4406 or BT_3985 or BT_3987) and ((BT_1039 and BT_1040) or (BT_1042 and BT_1043) or (BT_1046 and BT_1047) or (BT_4134 and BT_4135) or (BT_4404 and BT_4405) or (BT_3983 and BT_3984) or BT_0866 and BT_0867) or (BT_3751 and BT_3752) or (BT_1280 and BT_1281) or (BT_3958 and BT_3959) or (BT_4633 and BT_4634) or (BT_2818 and BT_2819) or (BT_2820 and BT_2821)))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLCNACASE_OGLYCAN6e	BTh2o[e] + BTcore3[e] -> BTacgam[e] + BTTn_antigen[e]	0	1000	((BT_2825 or BT_1038 or BT_1044 or BT_1048 or BT_0865 or BT_1282 or BT_3753 or BT_4132 or BT_4406 or BT_3985 or BT_3987) and ((BT_1039 and BT_1040) or (BT_1042 and BT_1043) or (BT_1046 and BT_1047) or (BT_4134 and BT_4135) or (BT_4404 and BT_4405) or (BT_3983 and BT_3984) or BT_0866 and BT_0867) or (BT_3751 and BT_3752) or (BT_1280 and BT_1281) or (BT_3958 and BT_3959) or (BT_4633 and BT_4634) or (BT_2818 and BT_2819) or (BT_2820 and BT_2821)))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLCP	BTp[c] + BTglycogen[c] -> BTg1p[c]	0	1000	(BT_1100 or BT_1293)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLCS2	BTudpg[c] -> BTh[c] + BTudp[c] + BTglycogen[c]	0	1000	(BT_1294 or BT_4307)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLCURt2r	BTh[e] + BTglcur[e] <=> BTh[c] + BTglcur[c]	-1000	1000	BT_4105	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLCt2r	BTh[e] + BTglc-D[e] <=> BTh[c] + BTglc-D[c]	-1000	1000	(BT_3589 or BT_1758 or BT_0371 or BT_4311 or BT_4653)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLCt4	BTna1[e] + BTglc-D[e] <=> BTna1[c] + BTglc-D[c]	-1000	1000	BT_0355	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLNS	BTglu-L[c] + BTatp[c] + BTnh4[c] -> BTh[c] + BTp[c] + BTadp[c] + BTgln-L[c]	0	1000	(BT_0453 or BT_0543 or BT_0785 or BT_4339)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLNt2r	BTh[e] + BTgln-L[e] <=> BTh[c] + BTgln-L[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLU5K	BTglu-L[c] + BTatp[c] -> BTadp[c] + BTglu5p[c]	0	1000	BT_3719	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLUABUTt7	BTglu-L[e] + BT4abut[c] <=> BTglu-L[c] + BT4abut[e]	-1000	1000	BT_2573	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLUDC	BTh[c] + BTglu-L[c] -> BTco2[c] + BT4abut[c]	0	1000	BT_2570	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLUDxi	BTh2o[c] + BTglu-L[c] + BTnad[c] -> BTh[c] + BTakg[c] + BTnadh[c] + BTnh4[c]	0	1000	(BT_1970 or BT_1973)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLUDy	BTh2o[c] + BTglu-L[c] + BTnadp[c] <=> BTh[c] + BTakg[c] + BTnadph[c] + BTnh4[c]	-1000	1000	BT_1970	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLUFORT	BTglu-L[c] + BT5forthf[c] <=> BTh[c] + BThf[c] + BTforglu[c]	-1000	1000	BT_2693	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLUN	BTh2o[c] + BTgln-L[c] -> BTglu-L[c] + BTnh4[c]	0	1000	BT_2571	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLUPRT	BTh2o[c] + BTprpp[c] + BTgln-L[c] -> BTglu-L[c] + BTppi[c] + BTpram[c]	0	1000	(BT_0555 or BT_4582)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLUR	BTglu-D[c] <=> BTglu-L[c]	-1000	1000	BT_3722	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLUSy	BTh[c] + BTakg[c] + BTnadph[c] + BTgln-L[c] -> 2 BTglu-L[c] + BTnadp[c]	0	1000	(BT_0552 and BT_0553)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLYASN1c	BTh2o[c] + BTglyasn[c] <=> BTgly[c] + BTasn-L[c]	-1000	1000	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLYASNt	BTh[e] + BTglyasn[e] -> BTh[c] + BTglyasn[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLYASP1c	BTh2o[c] + BTglyasp[c] <=> BTasp-L[c] + BTgly[c]	-1000	1000	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLYASPt	BTh[e] + BTglyasp[e] -> BTh[c] + BTglyasp[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLYAT	BTaccoa[c] + BTgly[c] <=> BTcoa[c] + BT2aobut[c]	-1000	1000	BT_1371	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLYBabc	BTh2o[c] + BTatp[c] + BTglyb[e] -> BTh[c] + BTp[c] + BTadp[c] + BTglyb[c]	0	1000	(BT_1749 and BT_1750 and BT_1751)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLYCK	BTatp[c] + BTglyc-R[c] -> BTh[c] + BTadp[c] + BT3pg[c]	0	1000	BT_1437	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLYCOe	1124 BTh2o[e] + BTglycogen1500[e] -> 750 BTglc-D[e] + 375 BTmal[e]	0	1000	(BT_3698 and BT_3701 and BT_3702)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction

BTGLYD	BTh[c] + BTnadh[c] + BThpyr[c] <=> BTnad[c] + BTglyc-R[c]	-1000	1000	BT_1207	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLYGLN1c	BTh2o[c] + BTglygln[c] <=> BTgln-L[c] + BTgly[c]	-1000	1000	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLYGLNt	BTh[e] + BTglygln[e] -> BTh[c] + BTglygln[c]	0	1000	(BT_0580 or BT_4385 or BT_1086)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLYGLU1c	BTh2o[c] + BTglygln[c] <=> BTgln-L[c] + BTgly[c]	-1000	1000	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLYGLUt	BTh[e] + BTglygln[e] -> BTh[c] + BTglygln[c]	0	1000	(BT_0580 or BT_4385 or BT_1086)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLYGLYHyi	BTh2o[c] + BTglygly[c] -> 2 BTgly[c]	0	1000	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLYGLYt	BTh[e] + BTglygly[e] <=> BTh[c] + BTglygly[c]	-1000	1000	(BT_0580 or BT_4385 or BT_1086)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLYKr	BTatp[c] + BTglyc[c] <=> BTh[c] + BTadp[c] + BTglyc3p[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLYLEUHYDROc	BTh2o[c] + BTglyleu[c] <=> BTgly[c] + BTleu-L[c]	-1000	1000	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLYLEUHYDROe	BTh2o[e] + BTglyleu[e] -> BTgly[e] + BTleu-L[e]	0	1000	BT_2548	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLYLEUPEPT1t	BTh[e] + BTglyleu[e] -> BTh[c] + BTglyleu[c]	0	1000	(BT_0580 or BT_4385 or BT_1086)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLYMET1c	BTh2o[c] + BTglymet[c] <=> BTgly[c] + BTmet-L[c]	-1000	1000	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLYMETt	BTh[e] + BTglymet[e] -> BTh[c] + BTglymet[c]	0	1000	(BT_0580 or BT_4385 or BT_1086)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLYPHEHYi	BTh2o[c] + BTglyphe[c] -> BTgly[c] + BTphe-L[c]	0	1000	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLYPHEt	BTh[e] + BTglyphe[e] <=> BTh[c] + BTglyphe[c]	-1000	1000	(BT_0580 or BT_4385 or BT_1086)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLYPROPRO1c	BTh2o[c] + BTglypro[c] <=> BTgly[c] + BTpro-L[c]	-1000	1000	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLYPROPRO1e	BTh2o[e] + BTglypro[e] -> BTpro-L[e] + BTgly[e]	0	1000	BT_0587	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLYPROt	BTh[e] + BTglypro[e] -> BTh[c] + BTglypro[c]	0	1000	(BT_0580 or BT_4385 or BT_1086)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLYTYR1c	BTh2o[c] + BTglytyr[c] <=> BTgly[c] + BTtyr-L[c]	-1000	1000	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLYTYRt	BTh[e] + BTglytyr[e] -> BTh[c] + BTglytyr[c]	0	1000	(BT_0580 or BT_4385 or BT_1086)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGLYt2r	BTH[e] + BTgly[e] <=> BTh[c] + BTgly[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGMAND	BTgdpmann[c] -> BTh2o[c] + BTglpddmun[c]	0	1000	BT_1224	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGMHEPAT	BTh[c] + BTatp[c] + BTgmhep1p[c] -> BTpp[c] + BTadphep-DD[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGMHEPK	BTatp[c] + BTgmhep7p[c] -> BTh[c] + BTadp[c] + BTgmhep17bp[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGMHEPPA	BTh2o[c] + BTgmhep17bp[c] -> BTpi[c] + BTgmhep1p[c]	0	1000	BT_0477	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGMPS2	BTh2o[c] + BTatp[c] + BTglu-L[c] + BTump[c] -> 2 BTh[c] + BTglu-L[c] + BTamp[c] + BTppi[c] + BTgmp[c]	0	1000	(BT_2419 or BT_4265)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGND	BTnadp[c] + BT6pgc[c] -> BTnadph[c] + BTco2[c] + BTru5p-D[c]	0	1000	BT_1222	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGNNUC	BTh2o[c] + BTgsn[c] -> BTrib-D[c] + BTgua[c]	0	1000	BT_2808	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGPDDA1	BTh2o[c] + BTg3pc[c] -> BTH[c] + BTchol[c] + BTglyc3p[c]	0	1000	(BT_0442 or BT_0550 or BT_0195 or BT_3162 or BT_4727)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGPDDA2	BTh2o[c] + BTg3pe[c] -> BTH[c] + BTglyc3p[c] + BTetha[c]	0	1000	(BT_0442 or BT_0550 or BT_0195 or BT_3162 or BT_4727)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGPDDA4	BTh2o[c] + BTg3pg[c] -> BTH[c] + BTglyc[c] + BTglyc3p[c]	0	1000	(BT_0442 or BT_0550 or BT_0195 or BT_3162 or BT_4727)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGRTT	BTpdp[c] + BTgrdp[c] -> BTpp[c] + BTrdp[c]	0	1000	(BT_3261 or BT_2058)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGSNt2r	BTh[e] + BTgsn[e] <=> BTh[c] + BTgsn[c]	-1000	1000	BT_4330	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGTPCI	BTh2o[c] + BTgtp[c] -> BTH[c] + BTahtd[c] + BTfor[c]	0	1000	BT_3931	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGTPCII	3 BTh2o[c] + BTgtp[c] -> 2 BTH[c] + BTppi[c] + BTfor[c] + BT25dhpg[c]	0	1000	BT_2416	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGTPDPDP	BTh2o[c] + BTgdptp[c] -> BTH[c] + BTpi[c] + BTppgpp[c]	0	1000	BT_0540	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGTPDPK	BTatp[c] + BTgtp[c] -> BTH[c] + BTamp[c] + BTgdptp[c]	0	1000	(BT_0700 or BT_3998)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGUAPRT	BTprpp[c] + BTgua[c] -> BTppi[c] + BTgmp[c]	0	1000	BT_4386	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGUI1	BTglcur[c] <=> BTruur[c]	-1000	1000	BT_0823	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTGUI2	BTgalur[c] <=> BTtagur[c]	-1000	1000	BT_0823	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTH2Ot	BTh2o[e] <=> BTh2o[c]	-1000	1000	BT_4718	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTH2St	BTh2s[e] <=> BTh2s[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTH2td	BTh2[c] <=> BTh2[e]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTHCO3E	BTh2o[c] + BTco2[c] <=> BTH[c] + BThco3[c]	-1000	1000	BT_1681	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTHCYSMT	BThcys-L[c] + BTamet[c] -> BTH[c] + BTahcys[c] + BTmet-L[c]	0	1000	BT_0180	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTHEMEti	BTh2o[c] + BTatp[c] + BTpheme[e] -> BTH[c] + BTpi[c] + BTadp[c] + BTpheme[c]	0	1000	((BT_0491 and BT_0492 and BT_0493 and BT_0494 and BT_0495 and BT_0496 and BT_0497 and BT_0498 and BT_0499) or (BT_1950 and BT_1951 and BT_1952))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTHEPARL1_e	2 BTh2o[e] + BThspg[e] -> 2 BTH[e] + BTgam26g[e] + BThspg_degr_1[e] + BThspg_degr_2[e]	0	1000	BT_4675	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTHETT	BTipdp[c] + BThepdp[c] -> BTpp[c] + BToctdp[c]	0	1000	(BT_3261 or BT_2058)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTHEX1	BTatp[c] + BTglc-D[c] -> BTH[c] + BTadp[c] + BTg6p[c]	0	1000	(BT_2430 or BT_2493 or BT_4654)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTHEX10	BTatp[c] + BTgam[c] -> BTH[c] + BTadp[c] + BTgam6p[c]	0	1000	BT_2430	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTHEX11	BTatp[c] + BTgalam[c] -> BTH[c] + BTadp[c] + BTgalam6p[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTHEX4	BTatp[c] + BTman[c] -> BTH[c] + BTadp[c] + BTman6p[c]	0	1000	(BT_2430 or BT_2493 or BT_4654)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTHEX7	BTatp[c] + BTfru[c] -> BTH[c] + BTadp[c] + BTf6p[c]	0	1000	(BT_1757 or BT_3305)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTHEXTT	BTipdp[c] + BThexdp[c] -> BTpp[c] + BThepdp[c]	0	1000	(BT_3261 or BT_2058)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTHEXb	BTatp[c] + BTglc-bD[c] -> BTH[c] + BTadp[c] + BTg6p-B[c]	0	1000	(BT_2430 or BT_2493 or BT_4654)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTHG2abc	BTh2o[c] + BTatp[c] + BThg2[c] -> BTh[c] + BTpi[c] + BTadp[c] + BThg2[e]	0	1000	BT_1091	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTHISD	BThis-L[c] -> BTnh4[c] + BTurcan[c]	0	1000	BT_2690	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTHISTD	BTh2o[c] + 2 BTnad[c] + BThist[c] -> 3 BTH[c] + 2 BTnadh[c] + BThis-L[c]	0	1000	BT_0201	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTHISTP	BTh2o[c] + BThisp[c] -> BTpi[c] + BThistd[c]	0	1000	(BT_0203 or BT_1478 or BT_4257)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTHISt2r	BTh[e] + BThis-L[e] <=> BTh[c] + BThis-L[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTHMPK1	BTatp[c] + BT4ahmmp[c] -> BTH[c] + BTadp[c] + BT4ampm[c]	0	1000	BT_0790	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTHOMOGALASEe	100 BTh2o[e] + BThomogal[e] -> 20 BTac[e] + 100 BTgalur[e] + 20 BTmeoh[e]	0	1000	((BT_4146 or BT_4149 or BT_4153 or BT_4155 or BT_4170 or BT_4183 or BT_4115 or BT_4116 or BT_4119 or BT_4123) and BT_4150 and BT_4175 and (BT_4109 or BT_4110) and ((BT_4670 and BT_4671) or (BT_4164 and BT_4165) or (BT_4113 and BT_4114) or (BT_4121 and BT_4122) or (BT_3680 and BT_3681)))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTHPPK	BTatp[c] + BT2ahhmp[c] -> BTh[c] + BTamp[c] + BT2ahhmd[c]	0	1000	BT_3216	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTHSDu2	BTh[c] + BTnadh[c] + BTaspsa[c] -> BTnad[c] + BThom-L[c]	0	1000	BT_2403	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTHSDy2	BTh[c] + BTnadph[c] + BTaspsa[c] -> BTnadp[c] + BThom-L[c]	0	1000	BT_2403	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTHSK	BTatp[c] + BThom-L[c] -> BTh[c] + BTadp[c] + BThom[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTHSST	BThom-L[c] + BTsuccoa[c] -> BTcoa[c] + BTsuchms[c]	0	1000	BT_2413	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTHSTPTr	BTakg[c] + BThisp[c] <=> BTglu-L[c] + BTimacp[c]	-1000	1000	BT_0202	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTHXPRT	BTprpp[c] + BThxan[c] -> BTppi[c] + BTimp[c]	0	1000	BT_4386	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTHYD1	2 BTh[c] + BTq8h2[c] + BTh2[c] -> 2 BTH[e] + BTq8h2[c]	0	1000	(BT_1210 or BT_0124 or BT_1834)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTHYD4	BTfdxrd[c] <=> BTfdxox[c] + BTh2[c]	-1000	1000	(BT_1210 or BT_0124 or BT_1834)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTHYPSUCORNS	BTorn[c] + BTsucc[c] -> BTh2o[c] + BTsucorn[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTIBCOATA	BTACP[c] + BTibcoa[c] <=> BTcoa[c] + BT2mpropACP[c]	-1000	1000	BT_0789	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTICDHyr	BTnadp[c] + BTicit[c] <=> BTakg[c] + BTnadph[c] + BTco2[c]	-1000	1000	BT_2071	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTICHORS	BTchor[c] <=> BTichor[c]	-1000	1000	BT_4700	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTIDOURASE	BTh2o[e] + BTacgalidour[e] -> BTacgal[e] + BTidour[e]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTIDOURASE_HS1	BTh2o[e] + BThspg_degr_1[e] -> BThspg_degr_3[e] + BTidour[e]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTIDOURASE_HS2	BTh2o[e] + BThspg_degr_7[e] -> BThspg_degr_8[e] + BTidour[e]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction

BTtDOURASE_HS3	BTh2o[e] + BThspg_degr_14[e] -> BThspg_degr_15[e] + BTtdour[e]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtG3PS	BTglo-L[c] + BTprlp[c] -> BTh[c] + BTglu-L[c] + BTacar[c] + BTeig3p[c]	0	1000	(BT_1378 and BT_1380)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtGPDH	BTeig3p[c] -> BTh2o[c] + BTrnacp[c]	0	1000	BT_0203	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtGPS	BTh[c] + BT2cpr5p[c] -> BTh2o[c] + BTco2[c] + BT3ig3p[c]	0	1000	BT_0529	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtHDCOATA	BTcoa[c] + BT14mpentdecACP[c] <=> BTACP[c] + BTtdcoa[c]	-1000	1000	BT_0789	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtHPDCOATA	BTcoa[c] + BT15mpalmACP[c] <=> BTACP[c] + BThpdcoa[c]	-1000	1000	BT_0789	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtLETA	BTakg[c] + BTile-L[c] <=> BTglu-L[c] + BT3mop[c]	-1000	1000	BT_3892	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtLEt2r	BTh[e] + BTile-L[e] <=> BTh[c] + BTile-L[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtMPC	BTh2o[c] + BTmp[c] <=> BTprica[c]	-1000	1000	BT_3812	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtMPD	BTh2o[c] + BTnad[c] + BTmp[c] -> BTh[c] + BTnadh[c] + BTxmp[c]	0	1000	BT_3845	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtNSH	BTh2o[c] + BTins[c] -> BTrib-D[c] + BThxan[c]	0	1000	BT_2808	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtNSt2	BTh[e] + BTins[e] <=> BTh[c] + BTins[c]	-1000	1000	BT_4330	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtNULINASEe	25 BTh2o[e] + BTinulin[e] -> 25 BTfru[e] + BTkestopt[e]	0	1000	(BT_1759 or BT_3082)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtOR2	BTcoa[c] + 2 BTkhtox[c] + BTphtpyr[c] <=> BTh[c] + BTco2[c] + 2 BTtdred[c] + BTphaccoa[c]	-1000	1000	(BT_0429 and BT_0430)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtPDCOATA	BTcoa[c] + BT13mmyrsACP[c] <=> BTACP[c] + BTpdcoa[c]	-1000	1000	BT_0789	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtPDDI	BTpdp[c] <=> BTdmpp[c]	-1000	1000	BT_3972	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtPDPS	BTh[c] + BTnadh[c] + BTh2mb4p[c] -> BTh2o[c] + BTnad[c] + BTpdp[c]	0	1000	BT_2061	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtPDPS2	BTh[c] + BTnadph[c] + BTh2mb4p[c] -> BTh2o[c] + BTnadp[c] + BTpdp[c]	0	1000	BT_2061	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtPMD2	BTe3mmal[c] + BTnad[c] -> BTco2[c] + BTnadh[c] + BT2obut[c]	0	1000	BT_1857	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtPMDr	BTnad[c] + BT3c2hmp[c] <=> BTh[c] + BTnadh[c] + BT3c4mop[c]	-1000	1000	BT_1857	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtPPMIa	BT3c2tmp[c] <=> BTh2o[c] + BT2ippm[c]	-1000	1000	(BT_1859 and BT_1860)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtPPMIb	BTh2o[c] + BT2ippm[c] <=> BT3c3hmp[c]	-1000	1000	(BT_1859 and BT_1860)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtPPS	BTh2o[c] + BTaccoa[c] + BT3mnob[c] -> BTh[c] + BTcoa[c] + BT3c3hmp[c]	0	1000	BT_1861	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtS2TASE	BTh2o[e] + BTacgalidour2s[e] -> BTh[e] + BTso4[e] + BTacgalidour[e]	0	1000	((BT_0238 and BT_0756) or (BT_0238 and BT_2914))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtS2TASE_HS1	2 BTh2o[e] + BThspg_degr_2[e] -> 4 BTh[e] + 2 BTso4[e] + BThspg_degr_7[e]	0	1000	((BT_0238 and BT_0756) or (BT_0238 and BT_2914))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtSOBUTt2r	BTh[e] + BTisobut[e] <=> BTh[c] + BTisobut[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtSOCAPRt2r	BTh[e] + BTisocapr[e] <=> BTh[c] + BTisocapr[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtSOVALt2r	BTh[e] + BTisoval[e] <=> BTh[c] + BTisoval[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtTDCOATA	BTcoa[c] + BT12mtridecACP[c] <=> BTACP[c] + BTtdcoa[c]	-1000	1000	BT_0789	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtVCOATA	BTACP[c] + BTvccoa[c] <=> BTcoa[c] + BT3mbutACP[c]	-1000	1000	BT_0789	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtZPN	BTh2o[c] + BT4tup[c] -> BTh[c] + BTforglu[c]	0	1000	BT_2692	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtKARA1	BTnadp[c] + BT23dhmb[c] <=> BTh[c] + BTnadph[c] + BTalac-S[c]	-1000	1000	BT_2074	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtKARA2	BTh[c] + BTnadph[c] + BT2ahbut[c] <=> BTnadp[c] + BT23dhmp[c]	-1000	1000	BT_2074	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtKAS1	14 BTh[c] + 10 BTnadph[c] + 5 BTmalcoa[c] + BTibcoa[c] -> 4 BTh2o[c] + 6 BTcoa[c] + 10 BTnadp[c] + 5 BTco2[c] + BTfa11[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtKAS11	17 BTh[c] + 12 BTnadph[c] + 6 BTmalcoa[c] + BTivcoa[c] -> 5 BTh2o[c] + 7 BTcoa[c] + 12 BTnadp[c] + 6 BTco2[c] + BTfa11[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtKAS12	17 BTh[c] + BT2mbcoa[c] + 12 BTnadph[c] + 6 BTmalcoa[c] -> 5 BTh2o[c] + 7 BTcoa[c] + 12 BTnadp[c] + 6 BTco2[c] + BTfa12[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtKAS13	23 BTh[c] + 16 BTnadph[c] + BTaccoa[c] + 8 BTmalcoa[c] -> 7 BTh2o[c] + 9 BTcoa[c] + 16 BTnadp[c] + 8 BTco2[c] + BTocdcac[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtKAS14	BTh[c] + BTmalACP[c] + BTacACP[c] -> BTACP[c] + BTactACP[c] + BTco2[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtKAS2	17 BTh[c] + 12 BTnadph[c] + BTaccoa[c] + 6 BTmalcoa[c] -> 5 BTh2o[c] + 7 BTcoa[c] + 12 BTnadp[c] + 6 BTco2[c] + BTtdcal[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtKAS3	14 BTh[c] + 10 BTnadph[c] + 5 BTmalcoa[c] + BTivcoa[c] -> 4 BTh2o[c] + 6 BTcoa[c] + 10 BTnadp[c] + 5 BTco2[c] + BTfa3[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtKAS4	14 BTh[c] + BT2mbcoa[c] + 10 BTnadph[c] + 5 BTmalcoa[c] -> 4 BTh2o[c] + 6 BTcoa[c] + 10 BTnadp[c] + 5 BTco2[c] + BTfa4[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtKAS6	17 BTh[c] + 12 BTnadph[c] + 6 BTmalcoa[c] + BTibcoa[c] -> 5 BTh2o[c] + 7 BTcoa[c] + 12 BTnadp[c] + 6 BTco2[c] + BTfa6[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtKAS8	20 BTh[c] + 14 BTnadph[c] + BTaccoa[c] + 7 BTmalcoa[c] -> 6 BTh2o[c] + 8 BTcoa[c] + 14 BTnadp[c] + 7 BTco2[c] + BThdca[c]	0	1000	((BT_0122 and BT_3358) or (BT_3358 and BT_3834))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtKDNH	BTh2o[c] + BTkdnp[c] -> BTpi[c] + BTkdn[c]	0	1000	BT_1713	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtKDOCT2	BTctp[c] + BTkdo[c] -> BTpp[c] + BTckdo[c]	0	1000	BT_0745	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtKDOPP	BTh2o[c] + BTkdo8p[c] -> BTpi[c] + BTkdo[c]	0	1000	(BT_1677 or BT_1713)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtKDOPS	BTh2o[c] + BTara5p[c] + BTpep[c] -> BTpi[c] + BTkdo8p[c]	0	1000	BT_4321	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtKDUI	BTdr5hsa[c] -> BTdkdglcn[c]	0	1000	(BT_3231 or BT_4106)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtKESTOASEe	2 BTh2o[e] + BTkesto[e] -> BTglc-D[e] + 2 BTfru[e]	0	1000	(BT_1759 or BT_3082)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtKESTOPTASEe	4 BTh2o[e] + BTkestopt[e] -> BTglc-D[e] + 4 BTfru[e]	0	1000	(BT_1759 or BT_3082)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtKESTOTTRASEe	3 BTh2o[e] + BTkestottr[e] -> BTglc-D[e] + 3 BTfru[e]	0	1000	(BT_1759 or BT_3082)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtKabc	BTh2o[c] + BTatp[c] + BTh[e] -> BTh[c] + BTpi[c] + BTadp[c] + BTh[c]	0	1000	(BT_2423 and BT_2424 and BT_2425)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtKt3r	BTh[e] + BTk[c] <=> BTh[c] + BTk[e]	-1000	1000	((BT_4097 and BT_4098) or (BT_4665 and BT_4666))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtL2A6OD2s	BTh2o[c] + BTh[c] + BTthlp[c] -> BTl2a6o[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtLACDFUCTTR_FUCASEe	BTh2o[e] + BTlacdfuctr[e] -> BT2fuclac[e] + BTfuc-L[e]	0	1000	((BT_1625 or BT_4136) and ((BT_4134 and BT_4135) or (BT_1630 and BT_1631)))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtLACNDFUCHX_FUCASEe	BTh2o[e] + BTlacndfuchx[e] -> BTfuc-L[e] + BTlacnfucp[e]	0	1000	((BT_1625 or BT_4136) and ((BT_4134 and BT_4135) or (BT_1630 and BT_1631)))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtLACNFUCPT_FUCASEe	BTh2o[e] + BTlacnfucp[e] -> BTfuc-L[e] + BTlacntr[e]	0	1000	((BT_1625 or BT_4136) and ((BT_4134 and BT_4135) or (BT_1630 and BT_1631)))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtLACNTTR_DEGe	2 BTh2o[e] + BTlacntr[e] -> BTlcts[e] + BTacgam[e] + BTgal[e]	0	1000	((BT_1626 or BT_0461) and (BT_1627 or BT_1632 or BT_4132 or BT_0459 or BT_0460 or BT_1038 or BT_1044 or BT_1048 or BT_1051 or BT_4295 or BT_2825) and ((BT_1630 and BT_1631) or (BT_4134 and BT_4135) or (BT_1039 and BT_1040) or (BT_1042 and BT_1043) or (BT_1046 and BT_1047) or (BT_4297 and BT_4298) or (BT_2818 and BT_2819) or (BT_2820 and BT_2821)))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtLACZe	BTh2o[e] + BTlcts[e] -> BTglc-D[e] + BTgal[e]	0	1000	(BT_1626 or BT_4050)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtLARGNAT	BTLargn[c] + BToaa[c] <=> BTh[c] + BTasp-L[c] + BTpphn[c]	-1000	1000	BT_3935	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtLCAR2	BTh[c] + BTnadh[c] + BTgcald[c] <=> BT12ethd[c] + BTnad[c]	-1000	1000	BT_3767	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtLCARS	BTh[c] + BTnadh[c] + BTald-L[c] <=> BT12ppd-S[c] + BTnad[c]	-1000	1000	BT_3767	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtLDH_D	BTnad[c] + BTlac-D[c] <=> BTh[c] + BTpyr[c] + BTnadh[c]	-1000	1000	BT_1575	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtLDH_L	BTnad[c] + BTlac-L[c] <=> BTh[c] + BTpyr[c] + BTnadh[c]	-1000	1000	(BT_4455 and BT_4456 and BT_4457)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtLEUGLY1c	BTh2o[c] + BTleugly[c] -> BTgly[c] + BTleu-L[c]	0	1000	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtLEUGLYLAPe	BTh2o[e] + BTleugly[e] -> BTgly[e] + BTleu-L[e]	0	1000	BT_2548	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtLEUGLYt	BTh[e] + BTleugly[e] -> BTh[c] + BTleugly[c]	0	1000	(BT_0580 or BT_4385 or BT_1086)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtLEULEU1c	BTh2o[c] + BTleuleu[c] -> 2 BTleu-L[c]	0	1000	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtLEULEULAPe	BTh2o[e] + BTleuleu[e] -> BTleu-L[e]	0	1000	BT_2548	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtLEULEUt	BTh[e] + BTleuleu[e] -> BTh[c] + BTleuleu[c]	0	1000	(BT_0580 or BT_4385 or BT_1086)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtLEUO	2 BTh2o[c] + 3 BTleu-L[c] -> BTco2[c] + 3 BTtah4[c] + 2 BTisocapr[c] + BTisoval[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtLEUTA	BTakg[c] + BTleu-L[c] <=> BTglu-L[c] + BT4mop[c]	-1000	1000	BT_3892	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtLEUt2r	BTh[e] + BTleu-L[e] <=> BTh[c] + BTleu-L[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtLEVANASE_1e	249 BTh2o[e] + BTlevan1000[e] -> 250 BTlevantr[e]	0	1000	(BT_1760 and BT_1762 and BT_1763)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtLEVANASE_2e	BTh2o[e] + BTlevantr[e] -> BTfru[e] + BTlevanb[e]	0	1000	(BT_1759 or BT_3082 or BT_1760)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTtLEVANASE_3e	BTh2o[e] + BTlevanbt[e] -> BTfru[e] + BTlevanb[e]	0	1000	(BT_1759 or BT_3082 or BT_1760)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction

BTLEVANASE_4e	BTh2o[e] + BTlevanb[e] -> 2 BTfru[e]	0	1000	(BT_1759 or BT_3082 or BT_1760)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTLEVANB_ABC	BTh2o[c] + BTatp[c] + BTlevanb[e] -> BTh[c] + BTp[c] + BTadp[c] + BTlevanb[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTLGTHL	BTmthgxl[c] + BTglthrd[c] -> BTlgt-S[c]	0	1000	BT_1580	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTLMN2e	BTh2o[e] + BTmn2[e] -> 2 BTglc-D[e]	0	1000	(BT_2550 or BT_2824 or BT_3683)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTLMNe	14 BTh2o[e] + BTmn30[e] -> 15 BTmn2[e]	0	1000	(BT_2550 or BT_2824 or BT_3683)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTLPADSS_BT	BTlipidX_b[c] + BTu2ga_b[c] -> 2 BTh[c] + BTudp[c] + BTlipidAds_b[c]	0	1000	BT_4004	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTLPSSYN_BT	2 BTuacgam[c] + BTadphep-DD[c] + 3 BTgdpfuc[c] + BTudpgl[c] + BTcore_lps_b[c] + 2 BTudpga[c] -> BTadp[c] + 3 BTgdp[c] + 5 BTudp[c] + BTlps_b[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTLPS_BTabc	BTh2o[c] + BTatp[c] + BTlps_b[c] -> BTh[c] + BTp[c] + BTadp[c] + BTlps_b[e]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTLYSAM	BTlys-L[c] <=> BT36dalys[c]	-1000	1000	BT_4474	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTLYSDC	BTh[c] + BTlys-L[c] -> BTco2[c] + BT15dap[c]	0	1000	BT_3307	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTLYSt3r	BTh[e] + BTlys-L[c] <=> BTh[c] + BTlys-L[e]	-1000	1000	BT_1732	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTL_LAC2r	BTh[e] + BTlac-L[e] <=> BTh[c] + BTlac-L[c]	-1000	1000	BT_1453	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMALCOACD	BTh[c] + BTmalACP[c] + BTmalcoam[c] -> BTco2[c] + BT3ogACPm[c] + BTco2[c]	0	1000	(BT_0122 or BT_3834)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMALCOAMT	BTmalcoa[c] + BTamet[c] -> BTahcys[c] + BTmalcoam[c]	0	1000	BT_1445	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMALT	BTh2o[c] + BTmalt[c] -> 2 BTglc-D[c]	0	1000	(BT_0132 or BT_0683 or BT_2620 or BT_3163 or BT_3169 or BT_3294 or BT_3299 or BT_3664 or BT_4581)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMALTe	BTh2o[e] + BTmalt[e] -> 2 BTglc-D[e]	0	1000	(BT_3704 or BT_3703)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMALTt2r	BTh[e] + BTmalt[e] <=> BTh[c] + BTmalt[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMAN1PT2r	BTh[c] + BTgdp[c] + BTman1p[c] <=> BTp[c] + BTgdpmann[c]	-1000	1000	BT_0558	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMAN6PI	BTman6p[c] <=> BT6p[c]	-1000	1000	BT_0373	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMANA1e	BTh2o[e] + BTmanb[e] -> 2 BTman[e]	0	1000	(BT_0458 or BT_2855 or BT_4074 or BT_2432 or BT_3599 or BT_1769 or BT_1878 or BT_2199 or BT_3773 or BT_3784 or BT_3858 or BT_3962 or BT_3965 or BT_3990 or BT_3991 or BT_4073 or BT_4092 or BT_4093)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMANA2e	BTh2o[e] + BTmantr[e] -> BTman[e] + BTmanb[e]	0	1000	(BT_0458 or BT_2855 or BT_4074 or BT_2432 or BT_3599)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMANA3e	BTh2o[e] + BTmantrr[e] -> BTman[e] + BTmantr[e]	0	1000	(BT_0458 or BT_2855 or BT_4074 or BT_2432 or BT_3599)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMANA4	BTh2o[c] + BTmantr[c] <=> BTgal[c] + BTmelib[c]	-1000	1000	(BT_1871 or BT_2851 or BT_3065 or BT_3131 or BT_3133 or BT_3410)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMANA4e	BTh2o[e] + BTmanp[e] -> BTman[e] + BTmantr[e]	0	1000	(BT_0458 or BT_2855 or BT_4074 or BT_2432 or BT_3599)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMANAO	BTnad[c] + BTmana[c] <=> BTh[c] + BTnadh[c] + BTfrur[c]	-1000	1000	(BT_0130 or BT_1433)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMANTRabc	BTh2o[c] + BTatp[c] + BTmantr[e] -> BTh[c] + BTp[c] + BTadp[c] + BTmantr[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMANabc	BTh2o[c] + BTatp[c] + BTman[e] -> BTh[c] + BTp[c] + BTadp[c] + BTman[c]	0	1000	BT_1536	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMCOATA	BTACP[c] + BTmalcoa[c] <=> BTcoa[c] + BTmalACP[c]	-1000	1000	BT_0789	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMDH	BTnad[c] + BTmal-L[c] <=> BTh[c] + BTnadh[c] + BToaa[c]	-1000	1000	(BT_2510 or BT_3911)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTME2	BTnadp[c] + BTmal-L[c] -> BTpyr[c] + BTnadph[c] + BTco2[c]	0	1000	BT_1969	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMECDPDH2	BTnadh[c] + BT2mecdp[c] -> BTh2o[c] + BTnad[c] + BTh2mb4p[c]	0	1000	BT_2517	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMECDPS	BT2p4c2me[c] -> BTcmp[c] + BT2mecdp[c]	0	1000	BT_3884	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMELIBabc	BTh2o[c] + BTatp[c] + BTmelib[e] -> BTh[c] + BTp[c] + BTadp[c] + BTmelib[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMEOHt2	BTmeoh[e] <=> BTmeoh[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMEPCT	BTh[c] + BTcip[c] + BT2me4p[c] -> BTpp[c] + BT4c2me[c]	0	1000	(BT_1651 or BT_2881 or BT_3923)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMETALA1c	BTh2o[c] + BTmetala[c] <=> BTala-L[c] + BTmet-L[c]	-1000	1000	(BT_3464 or BT_3926 or BT_3996 or BT_0149 or BT_4193 or BT_3254 or BT_1260 or BT_1261 or BT_1314 or BT_1838)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMETALAt	BTh[e] + BTmetala[e] <=> BTh[c] + BTmetala[c]	0	1000	(BT_0580 or BT_4385 or BT_1086)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMETAT	BTh2o[c] + BTatp[c] + BTmet-L[c] -> BTpi[c] + BTppi[c] + BTamet[c]	0	1000	BT_3219	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMETOX1s	BTh2o2[c] + BTmes-L[c] -> BTh2o[c] + BTmetsox-S-L[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMETSOXR1	BTtrdrd[c] + BTmetsox-S-L[c] -> BTh2o2[c] + BTtrdox[c] + BTmet-L[c]	0	1000	BT_2499	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMETSr	BThcys-L[c] + BT5mthf[c] <=> BTh[c] + BThlf[c] + BTmet-L[c]	-1000	1000	(BT_0180 or BT_0249 or BT_0342)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMETt2r	BTh[e] + BTmet-L[e] <=> BTh[c] + BTmet-L[c]	-1000	1000	BT_1270	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMG2abc	BTh2o[c] + BTatp[c] + BTmg2[e] -> BTh[c] + BTp[c] + BTadp[c] + BTmg2[c]	0	1000	BT_0988	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMGSA	BTdhap[c] -> BTpi[c] + BTmthgxl[c]	0	1000	(BT_1098 or BT_2150)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMGt5	BTmg2[c] <=> BTmg2[e]	-1000	1000	(BT_4042 or BT_4679)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMI1PP	BTh2o[c] + BTmi1p-D[c] -> BTp[c] + BTinost[c]	0	1000	BT_2801	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMI1PS	BTg6p[c] -> BTmi1p-D[c]	0	1000	BT_1526	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMI3PP	BTh2o[c] + BTmi3p-D[c] -> BTp[c] + BTinost[c]	0	1000	BT_2801	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMI4PP	BTh2o[c] + BTmi4p-D[c] -> BTp[c] + BTinost[c]	0	1000	BT_2801	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMK10t	BTmqn10[c] <=> BTmqn10[e]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMK11t	BTmqn11[c] <=> BTmqn11[e]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMK7t	BTmqn7[c] <=> BTmqn7[e]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMK8t	BTmqn8[c] <=> BTmqn8[e]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMK9t	BTmqn9[c] <=> BTmqn9[e]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMLTG1	BTh2o[c] + BTmaltrr[c] -> BTmalt[c] + BTglc-D[c]	0	1000	BT_4690	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMLTG1e	BTh2o[e] + BTmaltrr[e] -> BTglc-D[e] + BTmalt[e]	0	1000	(BT_3703 or BT_3704)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMLTG2	BTh2o[c] + BTmaltrr[c] -> BTmaltr[c] + BTglc-D[c]	0	1000	BT_4690	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMLTG2e	BTh2o[e] + BTmaltrr[e] -> BTglc-D[e] + BTmaltr[e]	0	1000	(BT_3703 or BT_3704)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMLTG3	BTh2o[c] + BTmaltpt[c] -> BTglc-D[c] + BTmaltrr[c]	0	1000	BT_4690	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMLTG3e	BTh2o[e] + BTmaltpt[e] -> BTglc-D[e] + BTmaltrr[e]	0	1000	(BT_3703 or BT_3704)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMLTG4	BTh2o[c] + BTmaltbx[c] -> BTglc-D[c] + BTmaltpt[c]	0	1000	BT_4690	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMLTG4e	BTh2o[e] + BTmaltbx[e] -> BTglc-D[e] + BTmaltpt[e]	0	1000	((BT_3698 and BT_3701 and BT_3702) or (BT_0773 and BT_3701 and BT_3702) or (BT_4305 and BT_3701 and BT_3702))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMLTG5	BTh2o[c] + BTmaltbp[c] -> BTglc-D[c] + BTmaltbx[c]	0	1000	BT_4690	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMLTG5e	BTh2o[e] + BTmaltbp[e] -> BTglc-D[e] + BTmaltbx[e]	0	1000	((BT_3698 and BT_3701 and BT_3702) or (BT_0773 and BT_3701 and BT_3702) or (BT_4305 and BT_3701 and BT_3702))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMMCD	BTh[c] + BTmmcoa-S[c] -> BTco2[c] + BTppcoa[c]	0	1000	(BT_1686 and BT_1689 and BT_4415)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMME	BTmmcoa-R[c] <=> BTmmcoa-S[c]	-1000	1000	BT_1685	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMMM2r	BTsuccoa[c] <=> BTmmcoa-R[c]	-1000	1000	(BT_2090 and BT_2091)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMNNH	BTmana[c] -> BTh2o[c] + BT2ddglcn[c]	0	1000	(BT_0129 or BT_1432)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMNt2	BTh[e] + BTmn2[e] -> BTh[c] + BTmn2[c]	0	1000	BT_0629	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMOAT_BT	BTckdo[c] + BTlipidA_b[c] -> BTh[c] + BTcmp[c] + BTkdolipid4_b[c]	0	1000	BT_2747	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMOHMT	BTh2o[c] + BT3mob[c] + BTmthhf[c] -> BThlf[c] + BT2dhp[c]	0	1000	BT_0698	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMTAN	BTh2o[c] + BT5mta[c] -> BTade[c] + BT5mtr[c]	0	1000	BT_4451	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMTHFC	BTh2o[c] + BTmethf[c] <=> BTh[c] + BT10thf[c]	-1000	1000	(BT_0737 or BT_1607)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMTHFD	BTnadp[c] + BTmthf[c] <=> BTnadph[c] + BTmethf[c]	-1000	1000	BT_1607	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMTHFR2	2 BTh[c] + BTnadh[c] + BTmthf[c] -> BTnad[c] + BT5mthf[c]	0	1000	BT_3821	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMTHFR3	2 BTh[c] + BTnadph[c] + BTmthf[c] -> BTnadp[c] + BT5mthf[c]	0	1000	BT_3821	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTMTHGXLt	BTmthgxl[c] -> BTmthgxl[e]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNACHEX27e	BTh2o[e] + BTha_deg1[e] -> BTacgam[e] + BTha_pre1[e]	0	1000	(BT_4394 or BT_4395 or BT_4337 or BT_3598 or BT_1627 or BT_3868 or BT_0459 or BT_0460 or BT_0506 or BT_4681 or BT_1621 or BT_3178 or BT_0456 or BT_1051 or BT_2459)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNACt	BTnac[c] <=> BTnac[e]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNADDP	BTh2o[c] + BTnad[c] -> 2 BTh[c] + BTamp[c] + BTnmn[c]	0	1000	BT_1544	*B. thetaiotaomicron* metabolic/ transport/ demand reaction

BTNADH10	BTh[c] + BTnadh[c] + BTmqn8[c] -> BTnad[c] + BTmql8[c]	0	1000	BT_1537	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNADH17	4 BTh[c] + BTnadh[c] + BTmqn8[c] -> BTnad[c] + 3 BTh[e] + BTmql8[c]	0	1000	(BT_4058 and BT_4059 and BT_4060 and BT_4061 and BT_4062 and BT_4063 and BT_4064 and BT_4065 and BT_4066 and BT_4067)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNADH5	BTh[c] + BTnadh[c] + BTq8[c] -> BTnad[c] + BTq8h2[c]	0	1000	BT_1537	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNADH9	BTh[c] + BTnadh[c] + BT2dmmql8[c] -> BTnad[c] + BT2dmmql8[c]	0	1000	BT_1537	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNADK	BTnad[c] + BTatp[c] -> BTh[c] + BTnadp[c] + BTadp[c]	0	1000	BT_3917	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNADK2	BTnad[c] + BTdtp[c] -> BTh[c] + BTnadp[c] + BTdtdp[c]	0	1000	BT_3917	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNADS1	BTatp[c] + BTnhs4[c] + BTdnad[c] -> BTh[c] + BTnad[c] + BTamp[c] + BTppi[c]	0	1000	BT_0205	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNADS2	BTh2o[c] + BTatp[c] + BTglu-L[c] + BTdnad[c] -> BTh[c] + BTglu-L[c] + BTnad[c] + BTamp[c] + BTppi[c]	0	1000	BT_0205	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNAMNPP	BTh2o[c] + BTatp[c] + BTpppp[c] + BTnac[c] -> BTp[c] + BTadp[c] + BTppi[c] + BTnicrnt[c]	0	1000	BT_1913	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNARK	BTno2[c] -> BTno2[e]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNAt3_1	BTna1[c] + BTh[e] <=> BTh[c] + BTna1[e]	-1000	1000	(BT_0634 or BT_3638)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNCPTRCA	BTh2o[c] + 2 BTh[c] + BTncptrc[c] -> BTco2[c] + BTnh4[c] + BTptrc[c]	0	1000	BT_0875	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNDPK1	BTatp[c] + BTgdp[c] <=> BTadp[c] + BTgtp[c]	-1000	1000	BT_3925	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNDPK2	BTatp[c] + BTudp[c] <=> BTadp[c] + BTutp[c]	-1000	1000	BT_3925	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNDPK3	BTatp[c] + BTcdp[c] <=> BTadp[c] + BTctp[c]	-1000	1000	BT_3925	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNDPK4	BTatp[c] + BTdtdp[c] <=> BTadp[c] + BTdtp[c]	-1000	1000	BT_3925	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNDPK5	BTatp[c] + BTdgdp[c] <=> BTadp[c] + BTdgtp[c]	-1000	1000	BT_3925	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNDPK6	BTatp[c] + BTdudp[c] <=> BTadp[c] + BTdutp[c]	-1000	1000	BT_3925	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNDPK7	BTatp[c] + BTdcdp[c] <=> BTadp[c] + BTdctp[c]	-1000	1000	BT_3925	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNDPK8	BTatp[c] + BTdadp[c] <=> BTadp[c] + BTdatp[c]	-1000	1000	BT_3925	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNDPK9	BTatp[c] + BTdtp[c] <=> BTadp[c] + BTtp[c]	-1000	1000	BT_3925	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNEULACNTTR_SIASEe	BTh2o[e] + BTneulacnttr[e] -> BTacnam[e] + BTlacntr[e]	0	1000	BT_0455 or BT_2194 or BT_2892	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNH4t	BTnh4[e] <=> BTnh4[c]	-1000	1000	BT_0544	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNMN2r	BTh[c] + BTnmn[c] <=> BTh[e] + BTnmn[e]	-1000	1000	BT_2396	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNNATr	BTh[c] + BTatp[c] + BTnicrnt[c] <=> BTppi[c] + BTdnad[c]	-1000	1000	BT_2011	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNNDPR	2 BTh[c] + BTpppp[c] + BTquh[c] -> BTco2[c] + BTppi[c] + BTnicrnt[c]	0	1000	BT_1560	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNP1_r	BTh[c] + BTnac[c] + BTr1p[c] <=> BTp[c] + BTnicrns[c]	-1000	1000	(BT_1881 or BT_4554)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNPHS	BTsbzcoa[c] -> BTcoa[c] + BTdhna[c]	0	1000	BT_4702	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNT5C	BTh2o[c] + BTnicrnt[c] -> BTp[c] + BTnicrns[c]	0	1000	(BT_1236 or (BT_2440 and BT_2441))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNTD1	BTh2o[c] + BTdamp[c] -> BTp[c] + BTduri[c]	0	1000	(BT_1236 or BT_4003 or (BT_2440 and BT_2441))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNTD10	BTh2o[c] + BTxmp[c] -> BTp[c] + BTxtsn[c]	0	1000	(BT_1236 or (BT_2440 and BT_2441))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNTD11	BTh2o[c] + BTimp[c] -> BTp[c] + BTins[c]	0	1000	(BT_1236 or (BT_2440 and BT_2441))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNTD2	BTh2o[c] + BTump[c] -> BTp[c] + BTur[c]	0	1000	(BT_1236 or (BT_2440 and BT_2441))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNTD3	BTh2o[c] + BTdcmp[c] -> BTp[c] + BTdcyt[c]	0	1000	(BT_1236 or (BT_2440 and BT_2441))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNTD4	BTh2o[c] + BTcmp[c] -> BTp[c] + BTcytd[c]	0	1000	(BT_1236 or (BT_2440 and BT_2441))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNTD5	BTh2o[c] + BTdtmp[c] -> BTp[c] + BThymd[c]	0	1000	(BT_1236 or (BT_2440 and BT_2441))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNTD5_a	BTh2o[c] + BTnmn[c] -> BTp[c] + BTnsrn[c]	0	1000	(BT_1236 or (BT_2440 and BT_2441))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNTD6	BTh2o[c] + BTdamp[c] -> BTp[c] + BTdad-2[c]	0	1000	(BT_1236 or (BT_2440 and BT_2441))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNTD7	BTh2o[c] + BTamp[c] -> BTp[c] + BTadn[c]	0	1000	(BT_1236 or (BT_2440 and BT_2441))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNTD8	BTh2o[c] + BTdgmp[c] -> BTp[c] + BTdgsn[c]	0	1000	(BT_1236 or (BT_2440 and BT_2441))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNTD9	BTh2o[c] + BTgmp[c] -> BTp[c] + BTgsn[c]	0	1000	(BT_1236 or (BT_2440 and BT_2441))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNTP1	BTh2o[c] + BTatp[c] -> BTh[c] + BTp[c] + BTadp[c]	0	1000	BT_3128	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNTPP1	BTh2o[c] + BTdgtp[c] -> BTh[c] + BTppi[c] + BTdgmp[c]	0	1000	BT_4350	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNTPP10	BTh2o[c] + BTditp[c] -> BTh[c] + BTppi[c] + BTdimp[c]	0	1000	BT_4350	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNTPP11	BTh2o[c] + BTxtp[c] -> BTh[c] + BTppi[c] + BTxmp[c]	0	1000	BT_4350	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNTPP2	BTh2o[c] + BTgtp[c] -> BTh[c] + BTppi[c] + BTgmp[c]	0	1000	BT_4350	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNTPP8	BTh2o[c] + BTutp[c] -> BTh[c] + BTump[c] + BTppi[c]	0	1000	BT_4350	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNTPP9	BTh2o[c] + BTtp[c] -> BTh[c] + BTppi[c] + BTmp[c]	0	1000	BT_4350	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNTPTP1	BTh2o[c] + BTdgtp[c] -> BTpppi[c] + BTdgsn[c]	0	1000	(BT_3460 or BT_4208)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTNTRIR5	2 BTh2o[c] + BTnh4[c] + 6 BTfe3cytcc553[c] <=> 8 BTh[c] + 6 BTfe2cytcc553[c] + BTno2[c]	-1000	1000	BT_1417	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTO16G2e	BTh2o[e] + BTstrch2[e] -> BTglc-D[e] + BTmal[e]	0	1000	BT_3299	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTO2t	BTo2[e] <=> BTo2[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTOAADC	BTh[c] + BToaa[c] -> BTpyr[c] + BTco2[c]	0	1000	((BT_1696 and BT_1697 and BT_1698) or BT_1689 or BT_4415)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTOBTFL	BTcoa[c] + BT2obut[c] -> BTppcoa[c] + BTfor[c]	0	1000	((BT_1055 and BT_2955) or (BT_4738 and BT_1055) or (BT_2955 and BT_2956) or (BT_4737 and BT_4738))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTOGALURLe	BTunsdigalur[e] -> 2 BTdt5hsu[e]	0	1000	(BT_4115 or BT_4116)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTOHPBAT	BTglu-L[c] + BTohphb[c] <=> BTakg[c] + BTphthe[c]	-1000	1000	BT_1153	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTOHPHM	BTasne[c] + BT2ohph[c] -> BTh[c] + BTahcys[c] + BT2omph[c]	0	1000	BT_3209	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTOIVD1r	BTcoa[c] + BTnad[c] + BT4mop[c] <=> BTco2[c] + BTnadh[c] + BTbccoa[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTOIVD2	BTcoa[c] + BTnad[c] + BT3mob[c] -> BTco2[c] + BTnadh[c] + BTibccoa[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTOIVD3	BTcoa[c] + BTnad[c] + BT3mop[c] -> BT2mbcoa[c] + BTco2[c] + BTnadh[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTOLIGOFRUASEe	4 BTh2o[e] + BToligofru4[e] -> 4 BTfru[e]	0	1000	(BT_1759 or BT_3082)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTOMCDC	BTh[c] + BT3c4mop[c] -> BTco2[c] + BT4mop[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTOMPDC	BTh[c] + BTorot5p[c] -> BTco2[c] + BTump[c]	0	1000	BT_4209	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTOOR2r	BTco2[c] + BTfdxrd[c] + BTsuccoa[c] <=> BTh[c] + BTakg[c] + BTcoa[c] + BTfdxox[c]	-1000	1000	((BT_0329 and BT_0330 and BT_0331 and BT_0333) or (BT_2836 and BT_2837))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTOOR2r	BTakg[c] + BTcoa[c] + 2 BTfdox[c] <=> BTh[c] + BTco2[c] + BTsuccoa[c] + 2 BTfdred[c]	-1000	1000	((BT_0329 and BT_0330 and BT_0331 and BT_0333) or (BT_2836 and BT_2837))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTORNTA	BTakg[c] + BTorn[c] -> BTglu-L[c] + BTglu5sa[c]	0	1000	BT_3758	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTORNabc	BTh2o[c] + BTatp[c] + BTorn[e] -> BTh[c] + BTp[c] + BTadp[c] + BTorn[c]	0	1000	BT_4049	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTORPT	BTppi[c] + BTorot5p[c] <=> BTpppp[c] + BTorot[c]	-1000	1000	BT_3731	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTP5CD	2 BTh2o[c] + BTnad[c] + BT1pyr5c[c] -> BTh[c] + BTglu-L[c] + BTnadh[c]	0	1000	BT_3115	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTP5CRyr	BTnadp[c] + BTpro-L[c] <=> 2 BTh[c] + BTnadph[c] + BT1pyr5c[c]	-1000	1000	(BT_1902 or BT_3757)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPABB	BTnh4[c] + BTchor[c] -> BTh2o[c] + BT4adchc[c]	0	1000	(BT_0531 or BT_0767)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPACCOALr	BTcoa[c] + BTatp[c] + BTpac[c] <=> BTamp[c] + BTppi[c] + BTphaccoa[c]	-1000	1000	(BT_0428 or BT_0571)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPAC2r	BTh[e] + BTpac[e] <=> BTh[c] + BTpac[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPANTS	BTatp[c] + BTala-B[c] + BTpant-R[c] -> BTh[c] + BTamp[c] + BTppi[c] + BTpnto-R[c]	0	1000	BT_4308	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPAPPT2	BTudcpp[c] + BTuGgla[c] -> BTump[c] + BTuaGgla[c]	0	1000	BT_3451	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPAPPT3	BTudcpp[c] + BTugmda[c] -> BTump[c] + BTuagmda[c]	0	1000	BT_3451	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPBUTT	BTpi[c] + BTbtcoa[c] <=> BTcoa[c] + BTbutpi[c]	-1000	1000	BT_2551	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPBt	BTh2o[c] + BTatp[c] + BTpb[c] -> BTh[c] + BTp[c] + BTadp[c] + BTpb[e]	0	1000	BT_1091	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPC	BTpyr[c] + BTatp[c] + BThco3[c] -> BTh[c] + BTp[c] + BTadp[c] + BToaa[c]	0	1000	BT_1196	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPDHa	BTh[c] + BTpyr[c] + BTlpam[c] -> BTco2[c] + BTadhlam[c]	0	1000	BT_0311	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPDHbr	BTcoa[c] + BTadhlam[c] <=> BTaccoa[c] + BTdhlam[c]	-1000	1000	BT_0311	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPDHcr	BTnad[c] + BTdhlam[c] <=> BTh[c] + BTnadh[c] + BTlpam[c]	-1000	1000	(BT_0309 or BT_1542 or BT_3186)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPDX5POi	BTo2[c] + BTpdx5p[c] -> BTh2o2[c] + BTpydx5p[c]	0	1000	BT_1577	*B. thetaiotaomicron* metabolic/ transport/ demand reaction

BTPDX5PS	BTphthr[c] + BTnad[c] + BTdxy5p[c] -> 2 BTh2o[c] + BTh[c] + BTco2[c] + BTpi[c] + BTnadh[c] + BTpdx5p[c]	0	1000	(BT_3918 and BT_4374)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPECTICGALASEe	99 BTh2o[e] + BTpecticgal[e] -> 2 BTac[e] + 9 BTarab-L[e] + 78 BTgal[e] + 4 BTmnl[e] + 9 BTgalur[e] + 2 BTmeoh[e]	0	1000	((BT_0348 or BT_0360 or BT_0367 or BT_0368 or BT_0369) and (BT_4667 or BT_4668 or BT_4152) and (BT_4146 or BT_4149 or BT_4153 or BT_4155 or BT_4160 or BT_4170 or BT_4183 or BT_4115 or BT_4116 or BT_4119 or BT_4123) and (BT_4150 or BT_4173) and BT_4175 and (BT_4109 or BT_4110) and ((BT_0361 and BT_0362) or (BT_0363 and BT_0364) or (BT_4670 and BT_4671) or (BT_4164 and BT_4165) or (BT_4113 and BT_4114) or (BT_4121 and BT_4122)))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPECTIN_DEG2e	390 BTh[e] + BTpect[e] -> 195 BTmeoh[e] + 195 BTunsdigalur[e]	0	1000	((BT_4115 or BT_4116) and BT_4110)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPECTIN_DEGe	390 BTh2o[e] + BTpect[e] -> 390 BTgalur[e] + 195 BTmeoh[e]	0	1000	((BT_1018 or BT_2378 or BT_4123 or BT_4155 or BT_4187) and BT_4110)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPEPM	BTpep[c] <=> BT3pop[c]	-1000	1000	BT_1720	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPEPT160	BTh[c] + BTpe160[c] + BTcmp[c] -> BTcdpea[c] + BT12dgr160[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPERD	BTnad[c] + BT4per[c] <=> BTh[c] + BTnadh[c] + BTohpb[c]	-1000	1000	BT_3361	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPE_CER1_BTt	BTpe_cer1_bt[c] <=> BTpe_cer1_bt[e]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPFK	BTatp[c] + BTf6p[c] -> BTh[c] + BTadp[c] + BTfdp[c]	0	1000	(BT_1102 or BT_2062 or BT_3356)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPFK(ppi)	BTppi[c] + BTf6p[c] -> BTh[c] + BTpi[c] + BTfdp[c]	0	1000	BT_0307	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPFK_2	BTatp[c] + BTtagfdp-D[c] -> BTh[c] + BTadp[c] + BTtagdp-D[c]	0	1000	(BT_1102 or BT_2062 or BT_3356)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPFK_3	BTatp[c] + BTs7p[c] -> BTh[c] + BTadp[c] + BTs17bp[c]	0	1000	(BT_1102 or BT_2062 or BT_3356)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPFL	BTpyr[c] + BTcoa[c] -> BTaccoa[c] + BTfor[c]	0	1000	((BT_1055 and BT_2955) or (BT_4738 and BT_1055) or (BT_2955 and BT_2956) or (BT_4737 and BT_4738))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPGAMT	BTgam1p[c] <=> BTgam6p[c]	-1000	1000	BT_3950	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPGCDr	BTnad[c] + BT3pg[c] <=> BTh[c] + BTnadh[c] + BT3php[c]	-1000	1000	(BT_1152 or BT_1207)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPGI	BTg6p[c] <=> BTf6p[c]	-1000	1000	BT_2124	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPGK	BTatp[c] + BT3pg[c] <=> BTadp[c] + BT13dpg[c]	-1000	1000	BT_1672	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPGL	BTh2o[c] + BT6pg[c] -> BTh[c] + BT6pgc[c]	0	1000	BT_1220	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPGLYCP	BTh2o[c] + BT2pglyc[c] -> BTpi[c] + BTglycl[c]	0	1000	(BT_4184 or BT_4315)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPGM	BT2pg[c] <=> BT3pg[c]	-1000	1000	(BT_1105 or BT_1660 or BT_3419)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPGMT	BTg1p[c] <=> BTg6p[c]	-1000	1000	(BT_1548 or BT_3950)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPGMT2	BTg1p-B[c] <=> BTg6p-B[c]	-1000	1000	BT_2127	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPGPP120	BTh2o[c] + BTpgp120[c] -> BTpi[c] + BTpgl20[c]	0	1000	BT_1525	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPGPP140	BTh2o[c] + BTpgp140[c] -> BTpi[c] + BTpgl40[c]	0	1000	BT_1525	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPGPP160	BTh2o[c] + BTpgp160[c] -> BTpi[c] + BTpgl160[c]	0	1000	BT_1525	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPGPP180	BTh2o[c] + BTpgp180[c] -> BTpi[c] + BTpgl180[c]	0	1000	BT_1525	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPGPP181	BTh2o[c] + BTpgp181[c] -> BTpi[c] + BTpgl181[c]	0	1000	BT_1525	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPGPPAI15	BTh2o[c] + BTpgpai15[c] -> BTpi[c] + BTpgail15[c]	0	1000	BT_1525	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPGPPAI17	BTh2o[c] + BTpgpai17[c] -> BTpi[c] + BTpgail17[c]	0	1000	BT_1525	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPGPPI14	BTh2o[c] + BTpgpi14[c] -> BTpi[c] + BTpgl14[c]	0	1000	BT_1525	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPGPPI15	BTh2o[c] + BTpgpi15[c] -> BTpi[c] + BTpgl15[c]	0	1000	BT_1525	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPGPPI16	BTh2o[c] + BTpgpi16[c] -> BTpi[c] + BTpgl16[c]	0	1000	BT_1525	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPGPPI17	BTh2o[c] + BTpgpi17[c] -> BTpi[c] + BTpgl17[c]	0	1000	BT_1525	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPGSA120	BTcdpddecg[c] + BTglyc3p[c] -> BTh[c] + BTcmp[c] + BTpgp120[c]	0	1000	(BT_1523 or BT_4464)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPGSA140	BTcdpdtdecg[c] + BTglyc3p[c] -> BTh[c] + BTcmp[c] + BTpgp140[c]	0	1000	(BT_1523 or BT_4464)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPGSA160	BTcdpdhdecg[c] + BTglyc3p[c] -> BTh[c] + BTcmp[c] + BTpgp160[c]	0	1000	(BT_1523 or BT_4464)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPGSA180	BTcdpdodecg[c] + BTglyc3p[c] -> BTh[c] + BTcmp[c] + BTpgp180[c]	0	1000	(BT_1523 or BT_4464)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPGSAI81	BTcdpdodec11eg[c] + BTglyc3p[c] -> BTh[c] + BTcmp[c] + BTpgpi181[c]	0	1000	(BT_1523 or BT_4464)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPGSAAI15	BTcdpdaihpdecg[c] + BTglyc3p[c] -> BTh[c] + BTcmp[c] + BTpgpai15[c]	0	1000	(BT_1523 or BT_4464)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPGSAAI17	BTcdpdaihpdecg[c] + BTglyc3p[c] -> BTh[c] + BTcmp[c] + BTpgpai17[c]	0	1000	(BT_1523 or BT_4464)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPGSAI14	BTcdpdtdecg[c] + BTglyc-3p[c] -> BTh[c] + BTcmp[c] + BTpgpi14[c]	0	1000	(BT_1523 or BT_4464)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPGSAI15	BTcdpdpdecg[c] + BTglyc3p[c] -> BTh[c] + BTcmp[c] + BTpgpi15[c]	0	1000	(BT_1523 or BT_4464)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPGSAI16	BTcdpdhdecg[c] + BTglyc3p[c] -> BTh[c] + BTcmp[c] + BTpgpi16[c]	0	1000	(BT_1523 or BT_4464)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPGSAI17	BTcdpdhhpdecg[c] + BTglyc3p[c] -> BTh[c] + BTcmp[c] + BTpgpi17[c]	0	1000	(BT_1523 or BT_4464)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPHCHGS	BTh2o[c] + BTh[c] + BT1p3h5c[c] <=> BT4hglusa[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPHEARG1c	BTh2o[c] + BTphearg[c] <=> BTarg-L[c] + BTphe-L[c]	-1000	1000	BT_1846	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPHEARGt	BTh[e] + BTphearg[e] <=> BTh[c] + BTphearg[c]	-1000	1000	(BT_0580 or BT_4385 or BT_1086)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPHETA1	BTakg[c] + BTphe-L[c] <=> BTglu-L[c] + BTphpyr[c]	-1000	1000	(BT_0202 or BT_3935)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPHEt2r	BTh[e] + BTphe-L[e] <=> BTh[c] + BTphe-L[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPIabc	BTh2o[c] + BTatp[c] + BTpi[e] -> BTh[c] + 2 BTpi[c] + BTadp[c]	0	1000	((BT_1321 and BT_1322 and BT_1323 and BT_1324) or (BT_1321 and BT_1322 and BT_1323 and BT_0009))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPIt6	BTh[c] + BTpi[c] -> BTh[e] + BTpi[e]	0	1000	BT_4637	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPItli	1.5 BTna1[e] + BTpi[e] -> BTp[c] + 1.5 BTna1[c]	0	1000	BT_2528	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPLPS	BTru5p-D[c] + BTglu-L[c] + BTg3p[c] -> 3 BTh2o[c] + BTh[c] + BTglu-L[c] + BTpi[c] + BTpvds5p[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPMACPME	BTh2o[c] + BTpmACPm[c] -> BTh[c] + BTpmACP[c] + BTmeoh[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPMANM	BTman1p[c] <=> BTman6p[c]	-1000	1000	(BT_3950 or BT_1548)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPMDPHT	BTh2o[c] + BTSaprha[c] -> BTpi[c] + BT4c5au[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPMPK	BTatp[c] + BT4ampm[c] -> BTadp[c] + BT2mahmp[c]	0	1000	BT_0790	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPMTCOATA	BTcoa[c] + BTpalmACP[c] <=> BTACP[c] + BTpmtcoa[c]	-1000	1000	BT_0789	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPNP	BTpi[c] + BTmanr[c] <=> BTh[c] + BTr1p[c] + BTncam[c]	-1000	1000	(BT_1881 or BT_4554)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPNTK	BTatp[c] + BTpnto-R[c] -> BTh[c] + BTadp[c] + BT4ppan[c]	0	1000	BT_4366	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPNTO2	BTh[e] + BTpnto-R[e] <=> BTh[c] + BTpnto-R[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPOR4	BTco2[c] + BTaccoa[c] + BTkhxrd[c] <=> BTh[c] + BTpyr[c] + BTcoa[c] + BTkhxrs[c]	-1000	1000	BT_1747	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPOX	BTh2o[c] + BTpyr[c] + BTq8[c] -> BTco2[c] + BTac[c] + BTq8h2[c]	0	1000	(BT_1820 and BT_1822)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPPAKr	BTadp[c] + BTppap[c] <=> BTatp[c] + BTppa[c]	-1000	1000	BT_3693	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPPA_1	BTh2o[c] + BTppi[c] -> 2 BTpi[c] + BTh[e]	0	1000	BT_3411	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPPAtr	BTppa[e] <=> BTppa[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPPCDC	BTh[c] + BT4ppcys[c] -> BTco2[c] + BTpaas4p[c]	0	1000	BT_1362	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPPCKr	BTatp[c] + BToaa[c] <=> BTco2[c] + BTadp[c] + BTpep[c]	-1000	1000	BT_2790	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPPDK	BTpyr[c] + BTpi[c] + BTatp[c] -> BTh[c] + BTpep[c] + BTamp[c] + BTppi[c]	0	1000	BT_0644	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPPGPPDP	BTh2o[c] + BTppgpp[c] -> BTpp[c] + BTgdp[c]	0	1000	BT_3998	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPPK2	BTatp[c] + BTppi[c] -> BTadp[c] + BTpppi[c]	0	1000	(BT_0541 or BT_2019)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPPNCL2	BTcys-L[c] + BTctp[c] + BT4ppan[c] -> BTh[c] + BTpp[c] + BTcmp[c] + BT4ppcys[c]	0	1000	BT_1362	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPPNCL3	BTatp[c] + BTcys-L[c] + BT4ppan[c] -> BTh[c] + BTamp[c] + BTpp[c] + BT4ppcys[c]	0	1000	BT_1362	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPPND	BTnad[c] + BTpphn[c] -> BTco2[c] + BTnadh[c] + BT34hpp[c]	0	1000	BT_3933	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPPND2	BTnadp[c] + BTpphn[c] -> BTnadph[c] + BTco2[c] + BT34hpp[c]	0	1000	BT_3933	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPPNDH	BTh[c] + BTpphn[c] -> BTh2o[c] + BTco2[c] + BThpyr[c]	0	1000	BT_3936	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPPTGS	BTuagmda[c] -> BTh[c] + BTpeptido_EC[c] + BTudcpdp[c]	0	1000	(BT_3453 or BT_0943 or BT_0162 or BT_2501)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPPTT	BTpdp[c] + BTpendp[c] -> BTpp[c] + BThexdp[c]	0	1000	(BT_3261 or BT_2058)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPRAGS	BTatp[c] + BTgly[c] + BTpram[c] -> BTh[c] + BTpi[c] + BTadp[c] + BTgar[c]	0	1000	BT_3253	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPRAI	BTpram[c] <=> BT2cpr5p[c]	-1000	1000	BT_0528	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPRAIS	BTatp[c] + BTpram[c] -> 2 BTh[c] + BTpi[c] + BTadp[c] + BTair[c]	0	1000	BT_4211	*B. thetaiotaomicron* metabolic/ transport/ demand reaction

BTPRAMPC	BTh2o[c] + BTprbamp[c] -> BTprfp[c]	0	1000	BT_1377	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPRASCSi	BTatp[c] + BTasp-L[c] + BTSaicc[c] -> BTh[c] + BTp[c] + BTadp[c] + BT2Saics[c]	0	1000	BT_4217	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPRATPP	BTh2o[c] + BTprbatp[c] -> BTh[c] + BTppi[c] + BTprbamp[c]	0	1000	BT_1377	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPRFGS	BTh2o[c] + BTatp[c] + BTgln-L[c] + BTgam[c] -> BTh[c] + BTglu-L[c] + BTp[c] + BTadp[c] + BTPram[c]	0	1000	BT_1733	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPRMICI	BTprfp[c] <=> BTprip[c]	-1000	1000	BT_1379	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPRO1x	BTnad[c] + BTpro-L[c] -> 2 BTh[c] + BTnadh[c] + BT1pyr5c[c]	0	1000	(BT_1902 or BT_3757)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPROD2	BTpro-L[c] + BTfad[c] -> BTh[c] + BT1pyr5c[c] + BTfadh2[c]	0	1000	BT_3115	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPROD3	BTfad[c] + BT4hpro-LT[c] <=> BTh[c] + BT1p3h5c[c] + BTfadh2[c]	-1000	1000	BT_3115	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPROGLYt	BTh[e] + BTprogly[e] -> BTh[c] + BTprogly[c]	0	1000	(BT_0580 or BT_4385 or BT_1086)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPROt4r	BTna1[e] + BTpro-L[e] <=> BTna1[c] + BTpro-L[c]	-1000	1000	BT_0182	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPRPPS	BTatp[c] + BTr5p[c] <=> BTh[c] + BTamp[c] + BTprpp[c]	-1000	1000	BT_0748	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPSCVT	BTpep[c] + BTskm5p[c] <=> BTp[c] + BT3psme[c]	-1000	1000	BT_2186	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPSD120	BTh[c] + BTps120[c] -> BTco2[c] + BTpe120[c]	0	1000	BT_2231	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPSD140	BTh[c] + BTps140[c] -> BTco2[c] + BTpe140[c]	0	1000	BT_2231	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPSD160	BTh[c] + BTps160[c] -> BTco2[c] + BTpe160[c]	0	1000	BT_2231	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPSD180	BTh[c] + BTps180[c] -> BTco2[c] + BTpe180[c]	0	1000	BT_2231	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPSD181	BTh[c] + BTps181[c] -> BTco2[c] + BTpe181[c]	0	1000	BT_2231	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPSDAI15	BTh[c] + BTpsai15[c] -> BTco2[c] + BTpeai15[c]	0	1000	BT_2231	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPSDAI17	BTh[c] + BTpsai17[c] -> BTco2[c] + BTpeai17[c]	0	1000	BT_2231	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPSDI14	BTh[c] + BTpsi14[c] -> BTco2[c] + BTpei14[c]	0	1000	BT_2231	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPSDI15	BTh[c] + BTpsi15[c] -> BTco2[c] + BTpei15[c]	0	1000	BT_2231	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPSDI16	BTh[c] + BTpsi16[c] -> BTco2[c] + BTpei16[c]	0	1000	BT_2231	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPSDI17	BTh[c] + BTpsi17[c] -> BTco2[c] + BTpei17[c]	0	1000	BT_2231	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPSERTr	BTakg[c] + BTpser-L[c] <=> BTglu-L[c] + BT3php[c]	-1000	1000	BT_1153	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPSP_L	BTh2o[c] + BTpser-L[c] -> BTp[c] + BTser-L[c]	0	1000	BT_0832	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPSSA120	BTser-L[c] + BTcdpdddecg[c] -> BTh[c] + BTcmp[c] + BTps120[c]	0	1000	BT_2232	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPSSA140	BTser-L[c] + BTcdpdhdecg[c] -> BTh[c] + BTcmp[c] + BTps140[c]	0	1000	BT_2232	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPSSA160	BTser-L[c] + BTcdpdhdecg[c] -> BTh[c] + BTcmp[c] + BTps160[c]	0	1000	BT_2232	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPSSA180	BTser-L[c] + BTcdpdodecg[c] -> BTh[c] + BTcmp[c] + BTps180[c]	0	1000	BT_2232	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPSSA181	BTser-L[c] + BTcdpdodec11eg[c] -> BTh[c] + BTcmp[c] + BTps181[c]	0	1000	BT_2232	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPSSAAI15	BTser-L[c] + BTcdpdaipdecg[c] -> BTh[c] + BTcmp[c] + BTpsail5[c]	0	1000	BT_2232	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPSSAAI17	BTser-L[c] + BTcdpdaihpdecg[c] -> BTh[c] + BTcmp[c] + BTpsail7[c]	0	1000	BT_2232	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPSSAII4	BTser-L[c] + BTcdpditdecg[c] -> BTh[c] + BTcmp[c] + BTpsil4[c]	0	1000	BT_2232	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPSSAII5	BTser-L[c] + BTcdpdipdecg[c] -> BTh[c] + BTcmp[c] + BTpsil5[c]	0	1000	BT_2232	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPSSAII6	BTser-L[c] + BTcdpdihdecg[c] -> BTh[c] + BTcmp[c] + BTpsil6[c]	0	1000	BT_2232	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPSSAII7	BTser-L[c] + BTcdpdihpdecg[c] -> BTh[c] + BTcmp[c] + BTpsil7[c]	0	1000	BT_2232	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPTA2	BTp[c] + BTppcoa[c] -> BTcoa[c] + BTppap[c]	0	1000	BT_3692	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPTAr	BTp[c] + BTaccoa[c] <=> BTcoa[c] + BTactp[c]	-1000	1000	BT_3692	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPTPAT	BTh[c] + BTatp[c] + BTpan4p[c] <=> BTppi[c] + BTdpcoa[c]	-1000	1000	BT_3034	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPTRCabc	BTh2o[c] + BTatp[c] + BTptrc[e] -> BTh[c] + BTp[c] + BTadp[c] + BTptrc[c]	0	1000	(BT_1288 and BT_1289 and BT_1290 and BT_1291)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPTRCtex2	BTptrc[c] -> BTptrc[e]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPULLe	399 BTh2o[e] + BTpulkdun1200[e] -> 400 BTmaltr[e]	0	1000	((BT_3698 and BT_3701 and BT_3702) or (BT_3701 and BT_3702 and BT_4689) or (BT_1663 and BT_3701 and BT_3702))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPUNP1	BTp[c] + BTadn[c] <=> BTade[c] + BT1r1p[c]	-1000	1000	(BT_1881 or BT_4554)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPUNP2	BTp[c] + BTdad-2[c] <=> BTade[c] + BT2dr1p[c]	-1000	1000	(BT_1881 or BT_4554)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPUNP3	BTp[c] + BTgsn[c] <=> BTgua[c] + BTr1p[c]	-1000	1000	(BT_1881 or BT_4554)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPUNP4	BTp[c] + BTdgsn[c] <=> BT2dr1p[c] + BTgua[c]	-1000	1000	(BT_1881 or BT_4554)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPUNP5	BTp[c] + BTins[c] <=> BThxan[c] + BTr1p[c]	-1000	1000	(BT_1881 or BT_4554)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPUNP6	BTp[c] + BTdin[c] <=> BT2dr1p[c] + BThxan[c]	-1000	1000	(BT_1881 or BT_4554)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPUNP7	BTp[c] + BTxtsn[c] <=> BTr1p[c] + BTxan[c]	-1000	1000	(BT_1881 or BT_4554)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPUTA3	BTh2o[c] + BTnad[c] + BTglu5sa[c] -> 2 BTh[c] + BTglu-L[c] + BTnadh[c]	0	1000	BT_3115	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPYAM5PO	BTh2o[c] + BTo2[c] + BTpyam5p[c] -> BTnh4[c] + BTh2o2[c] + BTpydx5p[c]	0	1000	BT_1577	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPYDAMK	BTatp[c] + BTpydam[c] -> BTh[c] + BTadp[c] + BTpyam5p[c]	0	1000	BT_4458	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPYDXK	BTatp[c] + BTpydx[c] -> BTh[c] + BTadp[c] + BTpydx5p[c]	0	1000	BT_4458	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPYDXNK	BTatp[c] + BTpydxn[c] -> BTh[c] + BTadp[c] + BTpdx5p[c]	0	1000	BT_4458	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPYDXNO	BTo2[c] + BTpydxn[c] <=> BTh2o2[c] + BTpydx[c]	-1000	1000	BT_1577	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPYDXNtr	BTpydxn[e] <=> BTpydxn[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPYDXO	2 BTh2o[c] + BTnh4[c] + 0.5 BTo2[c] + BTpydx[c] <=> 2 BTh2o2[c] + BTpydam[c]	-1000	1000	BT_1577	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPYK	BTh[c] + BTadp[c] + BTpep[c] -> BTpyr[c] + BTatp[c]	0	1000	BT_2841	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTPYRt2r	BTh[e] + BTpyr[e] <=> BTh[c] + BTpyr[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTQMO3	BTmqll8[c] + 2 BTo2[c] -> 2 BTh[c] + BTmqnl8[c] + 2 BTo2s[c]	0	1000	(BT_3054 and BT_3055)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTQULNS	BTdhap[c] + BTasp[c] -> 2 BTh2o[c] + BTp[c] + BTquln[c]	0	1000	BT_3164	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTRAFFabc	BTh2o[c] + BTatp[c] + BTraffin[e] -> BTh[c] + BTp[c] + BTadp[c] + BTraffin[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTRAFGH	BTh2o[c] + BTraffin[c] -> BTgal[c] + BTsucr[c]	0	1000	(BT_1871 or BT_2851 or BT_3065 or BT_3131 or BT_3133 or BT_3410)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTRAFH	BTh2o[c] + BTraffin[c] -> BTru[c] + BTmelib[c]	0	1000	BT_1765	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTRBFK	BTatp[c] + BTribfb[c] -> BTh[c] + BTadp[c] + BTrmn[c]	0	1000	BT_2543	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTRBFSa	BTdh4p[c] + BT4r5au[c] -> 2 BTh2o[c] + BTp[c] + BTdrnh[c]	0	1000	BT_4253	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTRBFSb	2 BTdrnh[c] -> BTribfb[c] + BT4r5au[c]	0	1000	BT_1317	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTRBK	BTatp[c] + BTrib-D[c] -> BTh[c] + BTadp[c] + BTr5p[c]	0	1000	(BT_2799 or BT_3576 or (BT_2803 and BT_2804))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTRBK_D	BTatp[c] + BTrbl-D[c] -> BTh[c] + BTru5p-D[c] + BTadp[c]	0	1000	BT_0350	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTRBK_L1	BTatp[c] + BTrbl-L[c] -> BTh[c] + BTadp[c] + BTru5p-L[c]	0	1000	BT_0350	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTRBP4E	BTru5p-L[c] <=> BTxu5p-D[c]	-1000	1000	BT_0353	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTRFAC_HP	BTatp[c] + BTadphep-LD[c] -> BTh[c] + BTadp[c] + BTadphep7p-LD[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTRFA_BT	BTadphep-DD[c] + BTadphep-LD[c] + BTkdolipid4L_bt[c] + 2 BTudpg[c] + BTudpgal[c] + BTadpbep7p-LD[c] -> 3 BTadp[c] + 3 BTudp[c] + BTcore_lps_bt[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTRHAMNOGALURASEe_I	979 BTh2o[e] + BTrhamnogalurI[e] -> 30 BTarab-L[e] + 120 BTgal[e] + 200 BTmnn[e] + 620 BTgalur[e] + 10 BTxyl-D[e]	0	1000	(BT_1021 and BT_3662 and (BT_4152 or BT_0983 or BT_0992 or BT_0993 or BT_0996) and (BT_1001 or BT_1013 or BT_1019) and (BT_4146 or BT_4149 or BT_4153 or BT_4155 or BT_4183 or BT_4115 or BT_4116 or BT_1011 or BT_1018) and (BT_4150 or BT_4173) and BT_4175 and (BT_4109 or BT_4110) and ((BT_4670 and BT_4671) or (BT_4146 or BT_4149 or BT_4153 or BT_4155 or BT_4183 or BT_4115 or BT_4116 or BT_1018) and (BT_4150 or BT_4173) and BT_4175 and (BT_4109 or BT_4110) and ((BT_4670 and BT_4671) or (BT_4164 and BT_4165) or (BT_4113 and BT_4114)) or (BT_1028 and BT_1029) or (BT_1683 and BT_1683)) or (BT_3670 and BT_3671))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTRHAMNOGALURASEe_II	52 BTh2o[e] + BTrhamnogalurII[e] -> 2 BTkac-L[e] + 6 BTarab-L[e] + 3 BTgal[e] + 8 BTmnn[e] + 19 BTgalur[e] + 3 BTglcur1e[e] + 2 BT2comfuc[e] + 2 BT2comxy[e] + 2 BT3ddlfheps[e] + BTacorA[e] + 3 BTapio-D[e] + 2 BTkdo[e]	0	1000	((BT_1021 or BT_0348) and (BT_3662 or BT_3663) and BT_1011 and BT_3664 and BT_3665 and (BT_4152 or BT_0983 or BT_0992 or BT_0993 or BT_0996) and (BT_1001 or BT_1013 or BT_1019) and (BT_4146 or BT_4149 or BT_4153 or BT_4155 or BT_4183 or BT_4115 or BT_4116 or BT_1018) and (BT_4150 or BT_4173) and BT_4175 and (BT_4109 or BT_4110) and ((BT_4670 and BT_4671) or (BT_4164 and BT_4165) or (BT_4113 and BT_4114)) or (BT_1028 and BT_1029) or (BT_1683 and BT_1683)) or (BT_3670 and BT_3671) or (BT_1024 and BT_1025)))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction

BTRIBFLVt2r	BTh[e] + BTribflv[e] <=> BTh[c] + BTribflv[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTRIBt2r	BTh[e] + BTrib-D[e] <=> BTh[c] + BTrib-D[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTRMI	BTrmn[c] <=> BTrmI[c]	-1000	1000	BT_3764	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTRMK	BTatp[c] + BTrmI[c] -> BTh[c] + BTadp[c] + BTrmIl p[c]	0	1000	BT_3763	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTRMK2	BTatp[c] + BTxylu-L[c] <=> BTh[c] + BTadp[c] + BTxu1p-L[c]	-1000	1000	BT_3763	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTRMNt	BTh[e] + BTrmn[e] -> BTh[c] + BTrmn[c]	0	1000	(BT_2953 or BT_3765)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTRMPA	BTrmI1p[c] <=> BTdhap[c] + BTald-L[c]	-1000	1000	BT_3766	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTRNTR1	BTatp[c] + BTrdrdI[c] -> BTh2o[c] + BTrdox[c] + BTdatp[c]	0	1000	(BT_1998 and BT_1999)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTRNTR2	BTgtp[c] + BTrdrdI[c] -> BTh2o[c] + BTrdox[c] + BTdgtp[c]	0	1000	(BT_1998 and BT_1999)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTRNTR3	BTrdrdI[c] + BTctp[c] -> BTh2o[c] + BTrdox[c] + BTdctp[c]	0	1000	(BT_1998 and BT_1999)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTRNTR4	BTrdrdI[c] + BTutp[c] -> BTh2o[c] + BTrdox[c] + BTdutp[c]	0	1000	(BT_1998 and BT_1999)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTRPE	BTru5p-D[c] <=> BTxu5p-D[c]	-1000	1000	BT_3946	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTRPI	BTr5p[c] <=> BTru5p-D[c]	-1000	1000	(BT_0346 or BT_1986)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTS7Plr	BTs7p[c] <=> BTgmhep7p[c]	-1000	1000	BT_0475	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSADT	BTh[c] + BTatp[c] + BTso4[c] -> BTppi[c] + BTaps[c]	0	1000	(BT_0414 and BT_0415)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSADT2	BTh2o[c] + BTatp[c] + BTgtp[c] + BTso4[c] -> BTpi[c] + BTppi[c] + BTaps[c] + BTgtp[c]	0	1000	(BT_0414 and BT_0415)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSEPHCHS	BTh[c] + BTakg[c] + BTchor[c] -> BTco2[c] + BT2s5epchc[c]	0	1000	BT_4701	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSERATi	BTaccoa[c] + BTser-L[c] -> BTcoa[c] + BTacser[c]	0	1000	BT_3256	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSERD_L	BTser-L[c] -> BTpyr[c] + BTnh4[c]	0	1000	BT_4678	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSERPT	BTh[c] + BTpmtcoa[c] + BTser-L[c] -> BTcoa[c] + BT3dsphgn[c] + BTco2[c]	0	1000	BT_0870	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSERt2r	BTh[e] + BTser-L[e] <=> BTh[c] + BTser-L[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSHCHCS3	BT2s5epchc[c] -> BTpyr[c] + BT2shchc[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSHK3Dr	BTh[c] + BTnadph[c] + BT3dhsk[c] <=> BTnadp[c] + BTskm[c]	-1000	1000	BT_4215	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSHKK	BTatp[c] + BTskm[c] -> BTh[c] + BTadp[c] + BTskm5p[c]	0	1000	BT_3393	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSHSL2r	BTh2s[c] + BTsuchms[c] <=> BTh[c] + BTHcys-L[c] + BTsucc[c]	-1000	1000	(BT_1923 or BT_2387)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSERt2r	BTh[e] + BTser-L[e] <=> BTh[c] + BTser-L[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSIAASE_OGLYCAN1e	BTh2o[e] + BTsTn_antigen[e] -> BTacnam[e] + BTTn_antigen[e]	0	1000	BT_0455 or BT_2194 or BT_2892	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSIAASE_OGLYCAN2e	BTh2o[e] + BTdsT_antigen[e] -> BTacnam[e] + BTsT_antigen[e]	0	1000	BT_0455 or BT_2194 or BT_2892	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSIAASE_OGLYCAN3e	BTh2o[e] + BTsT_antigen[e] -> BTacnam[e] + BTT_antigen[e]	0	1000	BT_0455 or BT_2194 or BT_2892	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSIAASEe	2 BTh2o[c] + BTs2f2n2m2m6e[e] -> 2 BTacnam[e] + BTf2n2m2m6e[e]	0	1000	BT_0455 or BT_2194 or BT_2892	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSO4t2	BTh[e] + BTso4[e] <=> BTh[c] + BTso4[c]	-1000	1000	(BT_0412 or BT_3181)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSPHMYLN_BTt	BTsphmyln_bt[c] <=> BTsphmyln_bt[e]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSPMDAT1	BTaccoa[c] + BTspmd[c] -> BTh[c] + BTcoa[c] + BTN1aspmd[c]	0	1000	BT_1079	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSPMDAT2	BTaccoa[c] + BTspmd[c] -> BTh[c] + BTcoa[c] + BTn8aspmd[c]	0	1000	BT_1079	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSPMDabc	BTh2o[c] + BTatp[c] + BTspmd[e] -> BTh[c] + BTpi[c] + BTadp[c] + BTspmd[c]	0	1000	(BT_1288 or BT_1289 or BT_1290 or BT_1291)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSPMDtex2	BTspmd[c] -> BTspmd[e]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSPODM	2 BTh[c] + 2 BTo2s[c] -> BTo2[c] + BTh2o2[c]	0	1000	BT_0655	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSTCOATA	BTcoa[c] + BTocdcaACP[c] <=> BTACP[c] + BTstcoa[c]	-1000	1000	BT_0789	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSTYSGH	BTh2o[c] + BTstys[c] <=> BTgal[c] + BTraffin[c]	-1000	1000	(BT_1871 or BT_2851 or BT_3065 or BT_3131 or BT_3133 or BT_3410)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSTYSabc	BTh2o[c] + BTatp[c] + BTstys[e] -> BTh[c] + BTpi[c] + BTadp[c] + BTstys[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSUCBZL	BTcoa[c] + BTatp[c] + BTsucbzl[c] -> BTamp[c] + BTppi[c] + BTsbzcoa[c]	0	1000	BT_4704	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSUCBZS	BT2shchc[c] -> BTh2o[c] + BTsucbz[c]	0	1000	BT_4703	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSUCCITRDSs	BTh2o[c] + BTsuccitr-L[c] -> BTh[c] + BTcitr-L[c] + BTsucc[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSUCCt2r	BTh[e] + BTsucc[e] <=> BTh[c] + BTsucc[c]	-1000	1000	BT_2756	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSUCD1	BTsucc[c] + BTfad[c] <=> BTfum[c] + BTfadh2[c]	-1000	1000	(BT_3054 and BT_3055)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSUCDi	BTsucc[c] + BTq8[c] -> BTfum[c] + BTq8h2[c]	0	1000	(BT_3054 and BT_3055)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSUCOAS	BTcoa[c] + BTatp[c] + BTsucc[c] <=> BTpi[c] + BTadp[c] + BTsuccoa[c]	-1000	1000	(BT_0787 and BT_0788)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSUCORNTC	BTchp[c] + BTsucorn[c] -> BTpi[c] + BTsucacitr-L[c]	0	1000	BT_3717	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSUCR	BTh2o[c] + BTsucr[c] -> BTglc-D[c] + BTfru[c]	0	1000	BT_1765	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTSUCRt2	BTh[e] + BTsucr[e] -> BTh[c] + BTsucr[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTT2DECAI	BTtdec2eACP[c] <=> BTcdec3eACP[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTAGUR	BTuad[c] + BTaltn[c] <=> BTh[c] + BTuadh[c] + BTtagur[c]	-1000	1000	BT_0825	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTALA	BTg3p[c] + BTs7p[c] <=> BTe4p[c] + BTf6p[c]	-1000	1000	BT_1658	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTAURtex2	BTaur[e] <=> BTaur[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTCHOLAH	BTh2o[c] + BTtchola[c] -> BTh[c] + BTcholate[c] + BTtaur[c]	0	1000	(BT_1259 or BT_2086)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTCHOLAt2	2 BTna1[e] + BTtchola[e] -> 2 BTna1[c] + BTtchola[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTDCOATA	BTcoa[c] + BTmyrsACP[c] <=> BTACP[c] + BTtdcoa[c]	-1000	1000	BT_0789	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTDPDRE	BTtdtdp4d6dgl[c] -> BTtdtdp4d6dm[c]	0	1000	(BT_0464 or BT_0828 or BT_1349 or BT_1338)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTDPDRR	BTh[c] + BTnadph[c] + BTtdtdp4d6dm[c] -> BTnadp[c] + BTtdtdprmn[c]	0	1000	(BT_0725 or BT_0465 or BT_1730)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTDPGDH	BTtdtdpglu[c] -> BTh2o[c] + BTtdtdp4d6dgl[c]	0	1000	(BT_0466 or BT_1350 or BT_2016 or BT_2880)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTDSK_BT	BTatp[c] + BTipidAds_bt[c] -> BTh[c] + BTadp[c] + BTipidA_bt[c]	0	1000	BT_1880	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTGBPA	BTagdp-D[c] <=> BTdhap[c] + BTg3p[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTHIORDXi	BTtrdrd[c] + BTh2o2[c] -> 2 BTh2o[c] + BTrdox[c]	0	1000	(BT_0218 or BT_0677 or BT_1456 or BT_1914 or BT_2229)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTHMDP	2 BTh2o[c] + BThmpp[c] -> BTh[c] + 2 BTpi[c] + BThm[c]	0	1000	BT_3017	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTHMDt2	BTh[e] + BThym[e] -> BTh[c] + BThym[c]	0	1000	BT_4330	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTHMt3	BTh[c] + BThm[e] <=> BTh[e] + BThm[c]	-1000	1000	BT_2396	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTHRAr	BThr-L[c] <=> BTacald[c] + BTgly[c]	-1000	1000	BT_1815	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTHRD	BTuad[c] + BThr-L[c] -> BTh[c] + BTnadh[c] + BT2aobut[c]	0	1000	BT_1370	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTHRS	BTh2o[c] + BTphom[c] -> BTpi[c] + BThr-L[c]	0	1000	BT_2401	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTHRt2r	BTh[e] + BThr-L[e] <=> BTh[c] + BThr-L[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTHZPSN	BTatp[c] + BTcys-L[c] + BTtyr-L[c] + BTdxyl5p[c] -> BTh2o[c] + BTh[c] + BTalu-L[c] + BTco2[c] + BTamp[c] + BTppi[c] + BT4thfu[c] + BT4mpetz[c]	0	1000	((BT_0648 and BT_0651 and BT_0653 and BT_0649) or (BT_0648 and BT_0651 and BT_0653 and BT_1836))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTKT1	BTr5p[c] + BTxu5p-D[c] <=> BTg3p[c] + BTs7p[c]	-1000	1000	BT_0347	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTKT2	BTe4p[c] + BTxu5p-D[c] <=> BTg3p[c] + BTf6p[c]	-1000	1000	BT_0347	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTMDK1	BTatp[c] + BTthym[c] -> BTh[c] + BTadp[c] + BTdmp[c]	0	1000	BT_2275	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTMDPK	BTatp[c] + BTthm[c] -> BTh[c] + BTamp[c] + BThmpp[c]	0	1000	BT_2397	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTMDS	BTdump[c] + BTmlthf[c] -> BTdhf[c] + BTdmp[c]	0	1000	BT_2047	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTMPKr	BTatp[c] + BThmmp[c] <=> BTadp[c] + BThmpp[c]	-1000	1000	BT_1882	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTMPPP	BTh[c] + BT2mahmp[c] + BT4mpetz[c] -> BTppi[c] + BThmmp[c]	0	1000	(BT_0652 or BT_0647)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTPI	BThap[c] <=> BTg3p[c]	-1000	1000	BT_3929	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTRDRr	BTh[c] + BTnadph[c] + BTrdox[c] <=> BTnadp[c] + BTtrdrd[c]	-1000	1000	BT_4336	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTREHe	BTh2o[e] + BTre[e] -> 2 BTglc-D[e]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTRPAS2	BTh2o[c] + BTrp-L[c] <=> BTpyr[c] + BTnh4[c] + BTindole[c]	-1000	1000	BT_1492	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTRPS1	BTser-L[c] + BT3ig3p[c] -> BTh2o[c] + BTrp-L[c] + BTg3p[c]	0	1000	(BT_0527 and BT_0533)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTRPS2	BTser-L[c] + BTindole[c] -> BTh2o[c] + BTrp-L[c]	0	1000	(BT_0533 and BT_0527)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTRPS3r	BT3ig3p[c] <=> BTg3p[c] + BTindole[c]	-1000	1000	(BT_0527 and BT_0533)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction

BTTRPt2r	BTh[e] + BTrp-L[e] <=> BTh[c] + BTrp-L[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTYRTA	BTakg[c] + BTtyr-L[c] <=> BTglu-L[c] + BT34hpp[c]	-1000	1000	(BT_0202 or BT_3935)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTTYRt2r	BTh[e] + BTtyr-L[e] <=> BTh[c] + BTtyr-L[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTU23GAAT_BT	BT15m3hpalmACP[c] + BTu3hga_HP[c] -> BTh[c] + BTACP[c] + BTu23ga_bt[c]	0	1000	BT_4207	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTU2GAAT2_BT	BT15m3hpalmACP[c] + BTu2hga_bt[c] -> BTACP[c] + BTu2ga_bt[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTU2GAAT_BT	BT3hpalmACP[c] + BTugam[c] -> BTACP[c] + BTu2hga_bt[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTUAAGDS	BTatp[c] + BT26dap-M[c] + BTuamag[c] -> BTh[c] + BTpi[c] + BTadp[c] + BTugmd[c]	0	1000	BT_3452	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTUACMAMO	BTh2o[c] + 2 BTnad[c] + BTuacmam[c] -> 3 BTh[c] + 2 BTnadh[c] + BTuacmamn[c]	0	1000	BT_0602	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTUAG2E	BTuacgam[c] <=> BTuacmam[c]	-1000	1000	(BT_0383 or BT_1203 or BT_0601 or BT_2944)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTUAG2EMA	BTh2o[c] + BTuacgam[c] <=> BTh[c] + BTacmana[c] + BTudp[c]	-1000	1000	(BT_0383 or BT_1203 or BT_0601 or BT_2944)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTUAG4E	BTuacgam[c] <=> BTudpacgal[c]	-1000	1000	(BT_0623 or BT_2887)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTUAGAAT_HP	BT3hpalmACP[c] + BTuacgam[c] <=> BTACP[c] + BTu3aga_HP[c]	-1000	1000	(BT_3336 or BT_4205)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTUAGCVT_r	BTuacgam[c] + BTpep[c] <=> BTpi[c] + BTuaccg[c]	-1000	1000	BT_2005	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTUAGDP	BTh[c] + BTacgam1p[c] + BTutp[c] -> BTuacgam[c] + BTpp[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTUAGDP2	BTh[c] + BTutp[c] + BTgam1p[c] -> BTpp[c] + BTugam[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTUAGPT2	BTuacgam[c] + BTuaGgla[c] -> BTh[c] + BTudp[c] + BTuaaGgla[c]	0	1000	BT_3448	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTUAGPT3	BTuacgam[c] + BTuagmda[c] -> BTh[c] + BTudp[c] + BTuaagmda[c]	0	1000	BT_3448	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTUAMAGS	BTatp[c] + BTglu-D[c] + BTuamna[c] -> BTh[c] + BTpi[c] + BTadp[c] + BTuamag[c]	0	1000	BT_3450	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTUAMAS	BTala-L[c] + BTatp[c] + BTuamr[c] -> BTh[c] + BTpi[c] + BTadp[c] + BTuamn[c]	0	1000	BT_3447	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTUAPGR	BTh[c] + BTnadph[c] + BTuaccg[c] -> BTnadp[c] + BTuamr[c]	0	1000	BT_1368	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTUDCPDP	BTh2o[c] + BTudcpdp[c] -> BTh[c] + BTpi[c] + BTudcpp[c]	0	1000	BT_3212	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTUDCPDPS	8 BTipdp[c] + BTfdp[c] -> 8 BTpp[c] + BTudcpdp[c]	0	1000	BT_3726	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTUDPG4E	BTudpg[c] <=> BTudpgal[c]	-1000	1000	(BT_0623 or BT_2887)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTUDPGDr	BTh2o[c] + 2 BTnad[c] + BTudpg[c] <=> 3 BTh[c] + 2 BTnadh[c] + BTudpglcur[c]	-1000	1000	(BT_0379 or BT_0599 or BT_0829 or BT_1341)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTUDPGLCURE	BTudpglcur[c] <=> BTudpidour[c]	-1000	1000	(BT_0600 or BT_1342 or BT_0380)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTUDPGLDC	BTh[c] + BTudpglcur[c] -> BTco2[c] + BTudpxyl[c]	0	1000	BT_1059	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTUGLT	BTgal1p[c] + BTudpg[c] <=> BTg1p[c] + BTudpgal[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTUGMDDS	BTatp[c] + BTalaala[c] + BTugmd[c] -> BTh[c] + BTpi[c] + BTadp[c] + BTugmda[c]	0	1000	(BT_3644 or BT_4101)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTUHGADA_HP	BTh2o[c] + BTu3aga_HP[c] -> BTac[c] + BTu3hga_HP[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTUPPRT	BTprpp[c] + BTura[c] -> BTump[c] + BTppi[c]	0	1000	BT_2791	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTURAt2r	BTh[e] + BTura[e] <=> BTh[c] + BTura[c]	-1000	1000	BT_0686	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTURCN	BTh2o[c] + BTurcan[c] -> BT4izp[c]	0	1000	BT_2694	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTUREAt	BTurea[e] <=> BTurea[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTURFGTT	BTamet[c] + BT2ombz[c] -> BTh[c] + BTahcys[c] + BT2ommb[c]	0	1000	(BT_0853 or BT_4216)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTURIDK1	BTatp[c] + BTump[c] -> BTadp[c] + BTudp[c]	0	1000	BT_2242	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTURIDK2r	BTatp[c] + BTdump[c] <=> BTadp[c] + BTdudp[c]	-1000	1000	BT_2242	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTURIK1	BTatp[c] + BTuri[c] -> BTh[c] + BTadp[c] + BTump[c]	0	1000	(BT_0184 or BT_2527)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTURIK2	BTgtp[c] + BTuri[c] -> BTh[c] + BTump[c] + BTgdp[c]	0	1000	(BT_0184 or BT_2527)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTURIK3	BTuri[c] + BTtp[c] -> BTh[c] + BTump[c] + BTdp[c]	0	1000	(BT_0184 or BT_2527)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTURIt2r	BTh[e] + BTuri[e] <=> BTh[c] + BTuri[c]	-1000	1000	BT_4330	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTUSHD_BT	BTh2o[c] + BTu23ga_bt[c] -> 2 BTh[c] + BTump[c] + BTlpidX_bt[c]	0	1000	BT_3697	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTVALO	4 BTh2o[c] + 5 BTval-L[c] -> BTh[c] + BTco2[c] + 5 BTnh4[c] + 6 BTsohat[c]	0	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTVALTA	BTakg[c] + BTval-L[c] <=> BTglu-L[c] + BT3mob[c]	-1000	1000	BT_3892	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTVALt2r	BTh[e] + BTval-L[e] <=> BTh[c] + BTval-L[c]	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTXANt2r	BTh[e] + BTxan[e] <=> BTh[c] + BTxan[c]	-1000	1000	BT_4473	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTXPPT	BTprpp[c] + BTxan[c] -> BTppi[c] + BTxmp[c]	0	1000	(BT_0427 or BT_4386)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTXTSNH	BTh2o[c] + BTxsn[c] -> BTrib-D[c] + BTxan[c]	0	1000	BT_2808	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTXYLI1	BTxyl-D[c] <=> BTxylu-D[c]	-1000	1000	BT_0793	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTXYLI2	BTglc-D[c] <=> BTfru[c]	-1000	1000	BT_0793	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTXYLKr	BTatp[c] + BTxylu-D[c] <=> BTh[c] + BTadp[c] + BTxu5p-D[c]	-1000	1000	(BT_0792 or BT_4423)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTXYLt2	BTh[e] + BTxyl-D[e] -> BTh[c] + BTxyl-D[c]	0	1000	BT_0794	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTYUMPS	BTr5p[c] + BTura[c] <=> BTh2o[c] + BTpsd5p[c]	-1000	1000	((BT_3872 and BT_4501) or (BT_3213 and BT_4237))	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTZN2t4	BTh[e] + BTm2[c] + BTk[e] <=> BTh[c] + BTk[c] + BTm2[e]	-1000	1000	BT_0499	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTZNabc	BTh2o[c] + BTatp[c] + BTm2[e] -> BTh[c] + BTpi[c] + BTadp[c] + BTzn2[c]	0	1000	(BT_2206 and BT_3248 and BT_3249)	*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTsink_chols	BTchols[c] <=>	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BTsink_s	BTs[c] <=>	-1000	1000		*B. thetaiotaomicron* metabolic/ transport/ demand reaction
BT12ethd[u]tr	BT12ethd[e] <=> 12ethd[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BT12ppd-R[u]tr	BT12ppd-R[e] <=> 12ppd-R[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BT12ppd-S[u]tr	BT12ppd-S[e] <=> 12ppd-S[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BT2fuclac[u]tr	BT2fuclac[e] <=> 2fuclac[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTh2o[u]tr	BTh2o[e] <=> h2o[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTluc-L[u]tr	BTluc-L[e] <=> luc-L[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTlcts[u]tr	BTlcts[e] <=> lcts[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BT3fuclac[u]tr	BT3fuclac[e] <=> 3fuclac[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BT7ocholate[u]tr	BT7ocholate[e] <=> 7ocholate[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTna1[u]tr	BTna1[e] <=> na1[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTacetol[u]tr	BTacetol[e] <=> acetol[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTh[u]tr	BTh[e] <=> h[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTacgal[u]tr	BTacgal[e] <=> acgal[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTacgam[u]tr	BTacgam[e] <=> acgam[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTacnam[u]tr	BTacnam[e] <=> acnam[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTac[u]tr	BTac[e] <=> ac[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTadn[u]tr	BTadn[e] <=> adn[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTadocbl[u]tr	BTadocbl[e] <=> adocbl[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTs2fzn2m2m[u]tr	BTs2fzn2m2m[e] <=> s2fzn2m2m[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTs2fzn2m2mn[u]tr	BTs2fzn2m2mn[e] <=> s2fzn2m2mn[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTchtbs[u]tr	BTchtbs[e] <=> chtbs[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTn2m2mn[u]tr	BTn2m2mn[e] <=> n2m2mn[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTm2mn[u]tr	BTm2mn[e] <=> m2mn[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTalaala[u]tr	BTalaala[e] <=> alaala[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTala-D[u]tr	BTala-D[e] <=> ala-D[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTalaasp[u]tr	BTalaasp[e] <=> alaasp[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTalagln[u]tr	BTalagln[e] <=> alagln[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTalaglu[u]tr	BTalaglu[e] <=> alaglu[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTalagly[u]tr	BTalagly[e] <=> alagly[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen

BTalahis[u]tr	BTalahis[e] <=> alahis[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTalales[u]tr	BTalales[e] <=> alales[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTalathr[u]tr	BTalathr[e] <=> alathr[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTala-L[u]tr	BTala-L[e] <=> ala-L[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTamamnan140[u]tr	BTamamnan140[e] <=> amamnan140[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTmun[u]tr	BTmun[e] <=> mun[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTprogly[u]tr	BTprogly[e] <=> progly[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTpro-L[u]tr	BTpro-L[e] <=> pro-L[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTgly[u]tr	BTgly[e] <=> gly[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTstrch1[u]tr	BTstrch1[e] <=> strch1[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTglc-D[u]tr	BTglc-D[e] <=> glc-D[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTstrch2[u]tr	BTstrch2[e] <=> strch2[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTamylose300[u]tr	BTamylose300[e] <=> amylose300[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTmalt[u]tr	BTmalt[e] <=> malt[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTstarch1200[u]tr	BTstarch1200[e] <=> starch1200[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTmalttr[u]tr	BTmalttr[e] <=> maltrr[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTarabttr[u]tr	BTarabttr[e] <=> arabttr[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTarab-L[u]tr	BTarab-L[e] <=> arab-L[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTarabinan101[u]tr	BTarabinan101[e] <=> arabinan101[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTgal[u]tr	BTgal[e] <=> gal[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTrmn[u]tr	BTrmn[e] <=> rmn[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTgalur[u]tr	BTgalur[e] <=> galur[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTarabinogal[u]tr	BTarabinogal[e] <=> arabinogal[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTglcur[u]tr	BTglcur[e] <=> glcur[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTargarg[u]tr	BTargarg[e] <=> argarg[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTarg-L[u]tr	BTarg-L[e] <=> arg-L[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BThspg_degr_4[u]tr	BThspg_degr_4[e] <=> hspg_degr_4[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BThspg_degr_5[u]tr	BThspg_degr_5[e] <=> hspg_degr_5[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTso4[u]tr	BTso4[e] <=> so4[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BThspg_degr_9[u]tr	BThspg_degr_9[e] <=> hspg_degr_9[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BThspg_degr_10[u]tr	BThspg_degr_10[e] <=> hspg_degr_10[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BThspg_degr_3[u]tr	BThspg_degr_3[e] <=> hspg_degr_3[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BThspg_degr_8[u]tr	BThspg_degr_8[e] <=> hspg_degr_8[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTasn-L[u]tr	BTasn-L[e] <=> asn-L[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTasp-L[u]tr	BTasp-L[e] <=> asp-L[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTrnn[u]tr	BTrnn[e] <=> rnn[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTbtn[u]tr	BTbtn[e] <=> btn[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTcps_bt[u]tr	BTcps_bt[e] <=> cps_bt[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTlps_bt[u]tr	BTlps_bt[e] <=> lps_bt[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTpe_cer1_bt[u]tr	BTpe_cer1_bt[e] <=> pe_cer1_bt[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTsphmyln_bt[u]tr	BTsphmyln_bt[e] <=> sphmyln_bt[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTca2[u]tr	BTca2[e] <=> ca2[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTcarn[u]tr	BTcarn[e] <=> carn[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTcbl1[u]tr	BTcbl1[e] <=> cbl1[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTcd2[u]tr	BTcd2[e] <=> cd2[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTcgly[u]tr	BTcgly[e] <=> cgly[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTcn2[u]tr	BTcn2[e] <=> cn2[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTcobalt2[u]tr	BTcobalt2[e] <=> cobalt2[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTcspg_a_degr[u]tr	BTcspg_a_degr[e] <=> cspg_a_degr[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTacgalglcur[u]tr	BTacgalglcur[e] <=> acgalglcur[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTcspg_b_degr[u]tr	BTcspg_b_degr[e] <=> cspg_b_degr[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTacgalidour2s[u]tr	BTacgalidour2s[e] <=> acgalidour2s[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTcspg_c_degr[u]tr	BTcspg_c_degr[e] <=> cspg_c_degr[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTcspg_a[u]tr	BTcspg_a[e] <=> cspg_a[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTcspg_ab_rest[u]tr	BTcspg_ab_rest[e] <=> cspg_ab_rest[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTcspg_b[u]tr	BTcspg_b[e] <=> cspg_b[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTcspg_c[u]tr	BTcspg_c[e] <=> cspg_c[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTcspg_c_rest[u]tr	BTcspg_c_rest[e] <=> cspg_c_rest[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTctbt[u]tr	BTctbt[e] <=> ctbt[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTcys-L[u]tr	BTcys-L[e] <=> cys-L[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTcytd[u]tr	BTcytd[e] <=> cytd[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTc[u]tr	BTc[e] <=> c[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTcu2[u]tr	BTcu2[e] <=> cu2[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTdad-2[u]tr	BTdad-2[e] <=> dad-2[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTdcyt[u]tr	BTdcyt[e] <=> dcyt[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTdextran40[u]tr	BTdextran40[e] <=> dextran40[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTdgsn[u]tr	BTdgsn[e] <=> dgsn[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTdin[u]tr	BTdin[e] <=> din[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTdt5hsu[u]tr	BTdt5hsu[e] <=> dt5hsu[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTdur[u]tr	BTdur[e] <=> dur[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTlac-D[u]tr	BTlac-D[e] <=> lac-D[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTetoh[u]tr	BTetoh[e] <=> etoh[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BT2omfuc[u]tr	BT2omfuc[e] <=> 2omfuc[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BT2omxyl[u]tr	BT2omxyl[e] <=> 2omxyl[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BT3ddlhept[u]tr	BT3ddlhept[e] <=> 3ddlhept[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BT4abut[u]tr	BT4abut[e] <=> 4abut[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTSer_Thr[u]tr	BTSer_Thr[e] <=> Ser_Thr[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTT_antigen[u]tr	BTT_antigen[e] <=> T_antigen[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTTn_antigen[u]tr	BTTn_antigen[e] <=> Tn_antigen[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTacerA[u]tr	BTacerA[e] <=> acerA[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTacgalidour[u]tr	BTacgalidour[e] <=> acgalidour[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTapio-D[u]tr	BTapio-D[e] <=> apio-D[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTcit[u]tr	BTcit[e] <=> cit[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTcore2[u]tr	BTcore2[e] <=> core2[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTcore3[u]tr	BTcore3[e] <=> core3[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen

BTcore4[u]tr	BTcore4[e] <=> core4[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTcore5[u]tr	BTcore5[e] <=> core5[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTcore6[u]tr	BTcore6[e] <=> core6[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTcore7[u]tr	BTcore7[e] <=> core7[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTcore8[u]tr	BTcore8[e] <=> core8[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTcbsT_antigen[u]tr	BTcbsT_antigen[e] <=> cbsT_antigen[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTf1a[u]tr	BTf1a[e] <=> f1a[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTfe2[u]tr	BTfe2[e] <=> fe2[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTfe3[u]tr	BTfe3[e] <=> fe3[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTfe3dcit[u]tr	BTfe3dcit[e] <=> fe3dcit[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTfol[u]tr	BTfol[e] <=> fol[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTfor[u]tr	BTfor[e] <=> for[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTfru[u]tr	BTfru[e] <=> fru[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTfucneulacnhs[u]tr	BTfucneulacnhs[e] <=> fucneulacnhs[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTfum[u]tr	BTfum[e] <=> fum[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTgalam[u]tr	BTgalam[e] <=> galam[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTgam[u]tr	BTgam[e] <=> gam[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTgam26s[u]tr	BTgam26s[e] <=> gam26s[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTgchola[u]tr	BTgchola[e] <=> gchola[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTgln-L[u]tr	BTgln-L[e] <=> gln-L[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTglu-L[u]tr	BTglu-L[e] <=> glu-L[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTglyasn[u]tr	BTglyasn[e] <=> glyasn[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTglyasp[u]tr	BTglyasp[e] <=> glyasp[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTglyb[u]tr	BTglyb[e] <=> glyb[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTglycogen1500[u]tr	BTglycogen1500[e] <=> glycogen1500[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTglyghr[u]tr	BTglyghr[e] <=> glyghr[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTglygly[u]tr	BTglygly[e] <=> glygly[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTglyleu[u]tr	BTglyleu[e] <=> glyleu[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTglymet[u]tr	BTglymet[e] <=> glymet[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTglyphe[u]tr	BTglyphe[e] <=> glyphe[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTglypro[u]tr	BTglypro[e] <=> glypro[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTglytyr[u]tr	BTglytyr[e] <=> glytyr[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTgncore1[u]tr	BTgncore1[e] <=> gncore1[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTgncore2[u]tr	BTgncore2[e] <=> gncore2[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTgsn[u]tr	BTgsn[e] <=> gsn[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTh2[u]tr	BTh2[e] <=> h2[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTh2s[u]tr	BTh2s[e] <=> h2s[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTha[u]tr	BTha[e] <=> ha[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTha_deg1[u]tr	BTha_deg1[e] <=> ha_deg1[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTha_pre1[u]tr	BTha_pre1[e] <=> ha_pre1[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BThg2[u]tr	BThg2[e] <=> hg2[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BThis-L[u]tr	BThis-L[e] <=> his-L[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BThomogal[u]tr	BThomogal[e] <=> homogal[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BThspg[u]tr	BThspg[e] <=> hspg[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BThspg_degr_1[u]tr	BThspg_degr_1[e] <=> hspg_degr_1[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BThspg_degr_11[u]tr	BThspg_degr_11[e] <=> hspg_degr_11[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BThspg_degr_12[u]tr	BThspg_degr_12[e] <=> hspg_degr_12[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BThspg_degr_13[u]tr	BThspg_degr_13[e] <=> hspg_degr_13[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BThspg_degr_14[u]tr	BThspg_degr_14[e] <=> hspg_degr_14[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BThspg_degr_15[u]tr	BThspg_degr_15[e] <=> hspg_degr_15[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BThspg_degr_2[u]tr	BThspg_degr_2[e] <=> hspg_degr_2[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BThspg_degr_6[u]tr	BThspg_degr_6[e] <=> hspg_degr_6[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BThspg_degr_7[u]tr	BThspg_degr_7[e] <=> hspg_degr_7[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BThspg_rest[u]tr	BThspg_rest[e] <=> hspg_rest[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTidour[u]tr	BTidour[e] <=> idour[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTile-L[u]tr	BTile-L[e] <=> ile-L[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTins[u]tr	BTins[e] <=> ins[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTinulin[u]tr	BTinulin[e] <=> inulin[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTisobut[u]tr	BTisobut[e] <=> isobut[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTisocapr[u]tr	BTisocapr[e] <=> isocapr[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTisoval[u]tr	BTisoval[e] <=> isoval[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTk[u]tr	BTk[e] <=> k[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTkdo[u]tr	BTkdo[e] <=> kdo[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTkesto[u]tr	BTkesto[e] <=> kesto[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTkestopt[u]tr	BTkestopt[e] <=> kestopt[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTkestottr[u]tr	BTkestottr[e] <=> kestottr[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTl2n2m2mn[u]tr	BTl2n2m2mn[e] <=> l2n2m2mn[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTlac-L[u]tr	BTlac-L[e] <=> lac-L[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTlacdifuctr[u]tr	BTlacdifuctr[e] <=> lacdifuctr[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTlacndfucha[u]tr	BTlacndfuchs[e] <=> lacndfuchs[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTlacnfucpt[u]tr	BTlacnfucpt[e] <=> lacnfucpt[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTlacnntr[u]tr	BTlacnntr[e] <=> lacnntr[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTlacntr[u]tr	BTlacntr[e] <=> lacntr[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTleu-L[u]tr	BTleu-L[e] <=> leu-L[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTleugly[u]tr	BTleugly[e] <=> leugly[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTleuleu[u]tr	BTleuleu[e] <=> leuleu[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTlevan1000[u]tr	BTlevan1000[e] <=> levan1000[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTlevanb[u]tr	BTlevanb[e] <=> levanb[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTlevanntr[u]tr	BTlevanntr[e] <=> levanntr[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTlevanttr[u]tr	BTlevanttr[e] <=> levanttr[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTlmn2[u]tr	BTlmn2[e] <=> lmn2[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTlmn30[u]tr	BTlmn30[e] <=> lmn30[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTlys-L[u]tr	BTlys-L[e] <=> lys-L[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTmalthp[u]tr	BTmalthp[e] <=> malthp[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen

BTmaltlx[u]tr	BTmaltlx[e] <=> maltlx[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTmaltpt[u]tr	BTmaltpt[e] <=> maltpt[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTmaltrtr[u]tr	BTmaltrtr[e] <=> maltrtr[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTmanb[u]tr	BTmanb[e] <=> manb[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTmanpt[u]tr	BTmanpt[e] <=> manpt[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTmantr[u]tr	BTmantr[e] <=> mantr[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTmantrr[u]tr	BTmantrr[e] <=> mantrr[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTmelib[u]tr	BTmelib[e] <=> melib[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTmeoh[u]tr	BTmeoh[e] <=> meoh[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTmet-L[u]tr	BTmet-L[e] <=> met-L[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTmetala[u]tr	BTmetala[e] <=> metala[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTmg2[u]tr	BTmg2[e] <=> mg2[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTmn2[u]tr	BTmn2[e] <=> mn2[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTmqn10[u]tr	BTmqn10[e] <=> mqn10[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTmqn11[u]tr	BTmqn11[e] <=> mqn11[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTmqn7[u]tr	BTmqn7[e] <=> mqn7[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTmqn8[u]tr	BTmqn8[e] <=> mqn8[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTmqn9[u]tr	BTmqn9[e] <=> mqn9[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTmthgxl[u]tr	BTmthgxl[e] <=> mthgxl[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTnac[u]tr	BTnac[e] <=> nac[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTneulacntr[u]tr	BTneulacntr[e] <=> neulacntr[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTnh4[u]tr	BTnh4[e] <=> nh4[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTnmn[u]tr	BTnmn[e] <=> nmn[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTno2[u]tr	BTno2[e] <=> no2[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTo2[u]tr	BTo2[e] <=> o2[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BToligofru4[u]tr	BToligofru4[e] <=> oligofru4[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTorn[u]tr	BTorn[e] <=> orn[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTpac[u]tr	BTpac[e] <=> pac[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTpb[u]tr	BTpb[e] <=> pb[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTpect[u]tr	BTpect[e] <=> pect[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTpecticgal[u]tr	BTpecticgal[e] <=> pecticgal[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTphe-L[u]tr	BTphe-L[e] <=> phe-L[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTphearg[u]tr	BTphearg[e] <=> phearg[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTpheme[u]tr	BTpheme[e] <=> pheme[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTpi[u]tr	BTpi[e] <=> pi[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTpnto-R[u]tr	BTpnto-R[e] <=> pnto-R[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTppa[u]tr	BTppa[e] <=> ppa[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTptrc[u]tr	BTptrc[e] <=> ptrc[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTpulkdn1200[u]tr	BTpulkdn1200[e] <=> pulkdn1200[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTpydxn[u]tr	BTpydxn[e] <=> pydxn[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTpyr[u]tr	BTpyr[e] <=> pyr[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTraffin[u]tr	BTraffin[e] <=> raffin[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTrhamnogalurI[u]tr	BTrhamnogalurI[e] <=> rhamnogalurI[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTrhamnogalurII[u]tr	BTrhamnogalurII[e] <=> rhamnogalurII[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTrib-D[u]tr	BTrib-D[e] <=> rib-D[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTribflv[u]tr	BTribflv[e] <=> ribflv[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTs2f6n2m2masn[u]tr	BTs2f6n2m2masn[e] <=> s2f2fn2m2masn[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTs2f2n2m2masn[u]tr	BTs2f2n2m2masn[e] <=> s2f2n2m2masn[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTsT_antigen[u]tr	BTsT_antigen[e] <=> sT_antigen[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTsTn_antigen[u]tr	BTsTn_antigen[e] <=> sTn_antigen[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTser-L[u]tr	BTser-L[e] <=> ser-L[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTspmd[u]tr	BTspmd[e] <=> spmd[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTstys[u]tr	BTstys[e] <=> stys[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTsucc[u]tr	BTsucc[e] <=> succ[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTsucr[u]tr	BTsucr[e] <=> sucr[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTtaur[u]tr	BTtaur[e] <=> taur[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTtchola[u]tr	BTtchola[e] <=> tchola[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTthm[u]tr	BTthm[e] <=> thm[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BThtr-L[u]tr	BThtr-L[e] <=> thr-L[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTthymd[u]tr	BTthymd[e] <=> thymd[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTtre[u]tr	BTtre[e] <=> tre[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTtrp-L[u]tr	BTtrp-L[e] <=> trp-L[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTtyr-L[u]tr	BTtyr-L[e] <=> tyr-L[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTunsdigalur[u]tr	BTunsdigalur[e] <=> unsdigalur[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTura[u]tr	BTura[e] <=> ura[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTurea[u]tr	BTurea[e] <=> urea[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTuri[u]tr	BTuri[e] <=> uri[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTval-L[u]tr	BTval-L[e] <=> val-L[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTxan[u]tr	BTxan[e] <=> xan[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTxyl-D[u]tr	BTxyl-D[e] <=> xyl-D[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
BTzn2[u]tr	BTzn2[e] <=> zn2[u]	-1000	1000		Internal exchange reaction *B. thetaiotaomicron* <=> lumen
MM10FTHF5GLUtl	MM10thf5glu[c] -> MM10thf5glu[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MM10FTHF5GLUtm	MM10thf5glu[m] -> MM10thf5glu[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MM10FTHF6GLUtl	MM10thf6glu[c] -> MM10thf6glu[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MM10FTHF6GLUtm	MM10thf6glu[m] -> MM10thf6glu[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MM10FTHF7GLUtl	MM10thf7glu[c] -> MM10thf7glu[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MM10FTHF7GLUtm	MM10thf7glu[m] -> MM10thf7glu[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MM10FTHFtl	MM10thf[c] <=> MM10thf[l]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MM10FTHFtm	MM10thf[c] <=> MM10thf[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MM11DOCRTSLtm	MM11docrts[c] <=> MM11docrts[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MM11DOCRTSLtr	MM11docrts[c] <=> MM11docrts[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MM11DOCRTSTRNtm	MM11docrstrn[c] <=> MM11docrstrn[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MM11DOCRTSTRNtr	MM11docrstrn[c] <=> MM11docrstrn[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MM13DAMPPOX	MM13dampp[c] + MMh2o[c] + MMo2[c] -> MMbamppaald[c] + MMh2o2[c] + MMnh4[c]	0	1000	237940.1 or 237940.2 or 11754.1 or 76507.1	Mouse metabolic/ transport/ demand reaction
MM1MNCAMti	MMh2o[c] + MM1mncam[c] + MMatp[c] -> MMadp[c] + MMh[c] + MMpi[c] + MM1mncam[e]	0	1000		Mouse metabolic/ transport/ demand reaction

MM1PPDCRp	MM1pipdn2c[x] + MMh[x] + MMnadh[x] -> MML pipecol[x] + MMnad[x]	0	1000		Mouse metabolic/ transport/ demand reaction
MM1a_24_25VITD2Hm	MM2425dhvitd2[m] + MMh[m] + MMnadph[m] + MMo2[m] -> MM1a2425dhvitd2[m] + MMh2o[m] + MMnadp[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MM1a_24_25VITD3Hm	MMh[m] + MMnadph[m] + MMo2[m] + MM2425dhvitd3[m] -> MMh2o[m] + MMnadp[m] + MM1a2425dhvitd3[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MM1a_25VITD2Hm	MMh[m] + MMnadph[m] + MMo2[m] + MM1a25dhvitd2[m] -> MM1a2425dhvitd2[m] + MMh2o[m] + MMnadp[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MM1a_25VITD3Hm	MMh[m] + MMnadph[m] + MMo2[m] + MM1a25dhvitd3[m] -> MMh2o[m] + MMnadp[m] + MM1a2425dhvitd3[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MM24NPHte	MM24nph[e] <=> MM24nph[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MM24_25DHVITD2t	MM2425dhvitd2[c] -> MM2425dhvitd2[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MM24_25DHVITD2tm	MM2425dhvitd2[m] -> MM2425dhvitd2[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MM24_25DHVITD3t	MM2425dhvitd3[c] -> MM2425dhvitd3[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MM24_25DHVITD3tm	MM2425dhvitd3[m] -> MM2425dhvitd3[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MM24_25VITD2Hm	MMh[m] + MMnadph[m] + MMo2[m] + MM25hvitd2[m] -> MM2425dhvitd2[m] + MMh2o[m] + MMnadp[m]	0	1000	13081.1	Mouse metabolic/ transport/ demand reaction
MM24_25VITD3Hm	MMh[m] + MMnadph[m] + MMo2[m] + MM25hvitd3[m] -> MMh2o[m] + MMnadp[m] + MM2425dhvitd3[m]	0	1000	13081.1	Mouse metabolic/ transport/ demand reaction
MM25HVITD2t	MM25hvitd2[c] -> MM25hvitd2[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MM25HVITD2tin	MM25hvitd2[e] -> MM25hvitd2[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MM25HVITD2tin_m	MM25hvitd2[c] -> MM25hvitd2[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MM25HVITD2tm	MM25hvitd2[m] -> MM25hvitd2[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MM25HVITD3t	MM25hvitd3[c] -> MM25hvitd3[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MM25HVITD3te	MM25hvitd3[u] -> MM25hvitd3[c]	0	1000	(14473.1 and 14725.1 and 65969.1)	Mouse metabolic/ transport/ demand reaction
MM25HVITD3tin	MM25hvitd3[e] -> MM25hvitd3[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MM25HVITD3tin_m	MM25hvitd3[c] -> MM25hvitd3[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MM25HVITD3tm	MM25hvitd3[m] -> MM25hvitd3[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MM25VITD2Hm	MMh[m] + MMnadph[m] + MMo2[m] + MM25hvitd2[m] -> MMh2o[m] + MMnadp[m] + MM1a25dhvitd2[m]	0	1000	13115.1	Mouse metabolic/ transport/ demand reaction
MM25VITD3Hm	MMh[m] + MMnadph[m] + MMo2[m] + MM25hvitd3[m] -> MMh2o[m] + MMnadp[m] + MM1a25dhvitd3[m]	0	1000	13115.1	Mouse metabolic/ transport/ demand reaction
MM2AMACHYD	MMh2o[c] + MM2amac[c] -> MMmh4[c] + MMpyr[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MM2AMACSULT	MM2amac[c] + MMnadph[c] + MMpaps[c] -> MMLcys[c] + MMnadp[c] + MMpap[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MM2AMADPTm	MML2aadp[c] + MMakg[m] <=> MMakg[c] + MML2aadp[m]	-1000	1000	217593.1	Mouse metabolic/ transport/ demand reaction
MM2DR1PP	MMh2o[c] + MM2dr1p[c] -> MMp[c] + MMdrib[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MM2Hbt2	MM2hb[e] + MMh[e] <=> MMh[c] + MM2hb[c]	0	1000	20503.1 or 80879.1 or 20501.1	Mouse metabolic/ transport/ demand reaction
MM2HCO3_NAt	2 MMhco3[e] + MMna1[e] <=> 2 MMhco3[c] + MMna1[c]	0	1000	232156.1 or 232156.2 or 232156.3 or 54403.1 or 232156.4	Mouse metabolic/ transport/ demand reaction
MM2MCITt	MM2mcit[c] <=> MM2mcit[e]	-1000	0		Mouse metabolic/ transport/ demand reaction
MM2OXOADOXm	MM2oxoadp[m] + MMcoa[m] + MMnad[m] -> MMco2[m] + MMglutcoa[m] + MMnadh[m]	0	1000	78920.1 or 18293.1 or (27402.1 and 13382.1) or 18293.2	Mouse metabolic/ transport/ demand reaction
MM2OXOADPTm	MMakg[m] + MM2oxoadp[c] <=> MMakg[c] + MM2oxoadp[m]	-1000	1000	217593.1	Mouse metabolic/ transport/ demand reaction
MM34DHOXPEGt	MM34dhoxpeg[c] <=> MM34dhoxpeg[e]	-1000	0		Mouse metabolic/ transport/ demand reaction
MM34DHPHAMT	MM34dhphal[c] + MMamet[c] -> MMh[c] + MMahcys[c] + MMhomoval[c]	0	1000	12846.1 or 12846.2	Mouse metabolic/ transport/ demand reaction
MM34DHPHELAT1tc	MM34dhphe[u] + MMleu-L[c] -> MM34dhphe[c] + MMleu-L[u]	0	1000	(20539.1 and 17254.1)	Mouse metabolic/ transport/ demand reaction
MM34DHPLACOX	MMh2o[c] + MMnad[c] + MM34dhpac[c] -> 2 MMh[c] + MM34dhpha[c] + MMnadh[c]	0	1000	11670.1 or 67689.1 or 56847.1	Mouse metabolic/ transport/ demand reaction
MM34DHPLACOX_NADP_	MMh2o[c] + MMnadp[c] + MM34dhpac[c] <=> 2 MMh[c] + MMnadph[c] + MM34dhpha[c]	-1000	1000	11670.1 or 67689.1 or 56847.1	Mouse metabolic/ transport/ demand reaction
MM34DHXMANDACOX	MMh2o[c] + MMnad[c] + MM34dhmald[c] -> 2 MMh[c] + MMnadh[c] + MM34dhoxmand[c]	0	1000	11670.1 or 67689.1 or 56847.1	Mouse metabolic/ transport/ demand reaction
MM34DHXMANDACOX_NADP_	MMh2o[c] + MMnadp[c] + MM34dhmald[c] <=> 2 MMh[c] + MMnadph[c] + MM34dhoxmand[c]	-1000	1000	11670.1 or 67689.1 or 56847.1	Mouse metabolic/ transport/ demand reaction
MM34HPLFM	MMh[m] + MMnadh[m] + MM34hpp[m] -> MMnad[m] + MM34hpl[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MM34HPPOR	MMo2[c] + MM34hpp[c] -> MMco2[c] + MMhgentis[c]	0	1000	15445.1	Mouse metabolic/ transport/ demand reaction
MM35CGMPtn	MM35cgmp[c] <=> MM35cgmp[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MM3AIBTm	MM2mop[m] + MMglu-L[m] <=> MMakg[m] + MM3aib[m]	-1000	1000	268860.2 or 268860.1	Mouse metabolic/ transport/ demand reaction
MM3AIBt	MM3aib[c] -> MM3aib[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MM3AIBtm	MM2mop[m] + MMglu-L[m] <=> MMakg[m] + MM3aib[m]	-1000	1000	268860.2 or 268860.1	Mouse metabolic/ transport/ demand reaction
MM3DPHBH1	MMh[m] + MMo2[m] + MMnadh[m] + MM3dphb[m] -> MMh2o[m] + MMnad[m] + MM3dpdhb[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MM3DPHBH2	MMh[m] + MMnadph[m] + MMo2[m] + MM3dphb[m] -> MMh2o[m] + MMnadp[m] + MM3dpdhb[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MM3DSPHR	MMh[c] + MMnadph[c] + MM3dsphgn[c] -> MMnadp[c] + MMsphgn[c]	0	1000	70750.1	Mouse metabolic/ transport/ demand reaction
MM3HAO	MMo2[c] + MM3hanthrn[c] -> MMh[c] + MMcmusa[c]	0	1000	107766.1	Mouse metabolic/ transport/ demand reaction
MM3HBCDm	MMh2o[m] + MMh2coa[m] <=> MM3hbcoa- R[m]	-1000	1000	52430.1	Mouse metabolic/ transport/ demand reaction
MM3HBCOAHLm	MMh2o[m] + MM3hbutcoa[m] -> MMh[m] + MMcoa[m] + MM3hmp[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MM3HCO3_NAt	3 MMhco3[e] + MMna1[e] <=> 3 MMhco3[c] + MMna1[c]	0	1000	232156.1 or 232156.2 or 232156.3 or 54403.1 or 232156.4	Mouse metabolic/ transport/ demand reaction
MM3HKYNAKGAT	MMakg[c] + MMhLkynr[c] -> MM42A3HP24DB[c] + MMglu-L[c]	0	1000	23923.1 or 70266.1 or 23923.2	Mouse metabolic/ transport/ demand reaction
MM3HLYTCL	MMh[c] + MM34dhphe[c] -> MMco2[c] + MMdopa[c]	0	1000	13195.1	Mouse metabolic/ transport/ demand reaction
MM3HPCOAHYD	MMh2o[c] + MM3hpcoa[c] -> MMh[c] + MM3hpp[c] + MMcoa[c]	0	1000	227095.1 or 227095.2	Mouse metabolic/ transport/ demand reaction
MM3HPPD	MMnad[c] + MM3hpp[c] <=> MMh[c] + MMnadh[c] + MMmsa[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MM3HXKYNDCL	MMh[c] + MMhLkynr[c] -> MMco2[c] + MM3hxkynam[c]	0	1000	13195.1	Mouse metabolic/ transport/ demand reaction
MM3HXKYNOXDA	MMo2[c] + MM3hxkynam[c] -> MMh2o2[c] + MMmh4[c] + MM48dhoxquin[c]	0	1000	109731.1 or 17161.1	Mouse metabolic/ transport/ demand reaction
MM3M4HDXPAC	MMh2o[c] + MMnad[c] + MM3mox4hpac[c] <=> 2 MMh[c] + MMhomoval[c] + MMnadh[c]	-1000	1000	11670.1 or 67689.1 or 56847.1	Mouse metabolic/ transport/ demand reaction
MM3MLDAt	MM3mlda[c] <=> MM3mlda[e]	-1000	0		Mouse metabolic/ transport/ demand reaction
MM3MOBt2im	MMh[c] + MM3mob[c] -> MMh[m] + MM3mob[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MM3MOPt2im	MMh[c] + MM3mop[c] -> MMh[m] + MM3mop[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MM3MOX4HOXPGALDOX	MMh2o[c] + MMnad[c] + MM3m4hpga[c] -> 2 MMh[c] + MMnadh[c] + MM3mox4hoxm[c]	0	1000	11670.1 or 67689.1 or 56847.1	Mouse metabolic/ transport/ demand reaction
MM3MOX4HOXPGALDOX_NADP_	MMh2o[c] + MMnadp[c] + MM3m4hpga[c] <=> 2 MMh[c] + MMnadph[c] + MM3mox4hoxm[c]	-1000	1000	212647.1 or 212647.2	Mouse metabolic/ transport/ demand reaction
MM3MOXTYROX	MMh2o[c] + MMo2[c] + MM3moxtyr[c] -> MMh2o2[c] + MMmh4[c] + MM3mox4hpac[c]	0	1000	109731.1 or 17161.1	Mouse metabolic/ transport/ demand reaction
MM3NTD7I	MM3amp[l] + MMh2o[l] -> MMadn[l] + MMp[l]	0	1000	11432.1	Mouse metabolic/ transport/ demand reaction
MM3SALAASPm	MMasp-L[c] + MM3sala[m] <=> MM3sala[c] + MMasp-L[m]	-1000	1000	78830.1 or 50799.1	Mouse metabolic/ transport/ demand reaction
MM3SALACBOXL	MMh[c] + MM3sala[c] -> MMco2[c] + MMhyptaur[c]	0	1000	246277.1 or 14415.1 or 14417.1 or 14415.2	Mouse metabolic/ transport/ demand reaction
MM3SALAOX	MMo2[c] + 2 MMh[c] + 2 MM3sala[c] -> 2 MMLcys[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MM3SALATAi	MMh[c] + MMakg[c] + MM3sala[c] -> MMglu-L[c] + MM3supyr[c]	0	1000	14718.1	Mouse metabolic/ transport/ demand reaction
MM3SALATAim	MMh[m] + MMakg[m] + MM3sala[m] -> MMglu-L[m] + MM3supyr[m]	0	1000	14719.1	Mouse metabolic/ transport/ demand reaction
MM3SPYRSP	MMh2o[c] + MM3supyr[c] -> MMh[c] + MMpyr[c] + MMso3[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MM3SPYRSPm	MMh2o[m] + MM3supyr[m] -> MMh[m] + MMpyr[m] + MMso3[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MM41R1H2MAE12BOOX	MMh2o[c] + MMo2[c] + MMadrn[c] -> MMh2o2[c] + MM34dhmald[c] + MMmrna[c]	0	1000	109731.1 or 17161.1	Mouse metabolic/ transport/ demand reaction
MM41R2A1H12BOOX	MMh2o[c] + MMo2[c] + MMnorpphe[c] -> MMh2o2[c] + MMmh4[c] + MM34dhmald[c]	0	1000	109731.1 or 17161.1	Mouse metabolic/ transport/ demand reaction
MM42A12BOOX	MMh2o[c] + MMo2[c] + MMdopa[c] -> MMh2o2[c] + MMmh4[c] + MM34dhpac[c]	0	1000	237940.1 or 109731.1 or 17161.1 or 237940.2 or 11754.1 or 76507.1	Mouse metabolic/ transport/ demand reaction
MM4ABUTtm	MM4abut[c] <=> MM4abut[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MM4HBZCOAFm	MMh2o[m] + MMcoa[m] + MMnad[m] + MMcoucoa[m] -> MMh[m] + MMnadh[m] + MM4hbzcoa[m] + MMaccoa[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MM4HBZFm	MMh2o[m] + MM4hbzcoa[m] -> MMh[m] + MMcoa[m] + MM4hbz[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MM4HDEBRISOQUINEte	MM4hdebrisoquine[e] <=> MM4hdebrisoquine[c]	0	1000		Mouse metabolic/ transport/ demand reaction

MM4HGLSDm	MMh2o[m] + MMnad[m] + MM4hglusa[m] <=> 2 MMh[m] + MMnadh[m] + MMe4hglk[m]	-1000	1000	212647.1 or 212647.2	Mouse metabolic/ transport/ demand reaction
MM4HOXPACDOX_NADP_	MMh2o[c] + MMnadp[c] + MM4hoxpacd[c] <=> 2 MMh[c] + MMnadph[c] + MM4hphac[c]	-1000	1000	212647.1 or 212647.2	Mouse metabolic/ transport/ demand reaction
MM4HPRO_LTt	MMh[e] + MM4hpro-LT[e] <=> MMh[c] + MM4hpro-LT[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MM4MOPt2im	MMh[c] + MM4mop[c] -> MMh[m] + MM4mop[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MM4MPTNLte	MM4mptn[c] <=> MM4mptn[e]	-1000	0		Mouse metabolic/ transport/ demand reaction
MM4MPTNLtm	MM4mptn[c] <=> MM4mptn[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MM4MPTNLtr	MM4mptn[c] <=> MM4mptn[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MM4MTOLBUTAMIDEte	MM4mtolbutamide[e] <=> MM4mtolbutamide[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MM4NPHSFte	MM4nphsf[e] <=> MM4nphsf[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MM4NPHte	MM4nph[e] <=> MM4nph[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MM4OHPROIMINOtc	MM4hpro-LT[u] + 2 MMna1[u] + MMcl[u] -> 2 MMna1[c] + MM4hpro-LT[c] + MMcl[c]	0	1000	(102680.1 and 57394.1)	Mouse metabolic/ transport/ demand reaction
MM4PYRDX	MMh2o[c] + MMatp[c] + MM4pyrdx[c] -> MMadp[c] + MMh[c] + MMpi[c] + MM4pyrdx[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MM5ADTSTSTERONEGLCte	MMh2o[c] + MMatp[c] + MM5adtststeronesgk[c] -> MMadp[c] + MMh[c] + MMpi[c] + MM5adtststeronesgk[e]	0	1000	17250.1	Mouse metabolic/ transport/ demand reaction
MM5ADTSTSTERONEGLCtr	MM5adtststeronesgk[c] <=> MM5adtststeronesgk[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MM5ADTSTSTERONESULT	MMpaps[c] + MM5adtststerone[c] -> MMh[c] + MMpap[c] + MM5adtststerones[c]	0	1000	20859.1	Mouse metabolic/ transport/ demand reaction
MM5ADTSTSTERONESte	MM5adtststerones[c] <=> MM5adtststerones[e]	-1000	0		Mouse metabolic/ transport/ demand reaction
MM5ADTSTSTERONEte	MM5adtststerone[e] <=> MM5adtststerone[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MM5ADTSTSTERONEtr	MM5adtststerone[r] <=> MM5adtststerone[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MM5AOPtm	MM5aop[c] <=> MM5aop[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MM5DHFtl	MM5dhf[c] -> MM5dhf[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MM5FTHFt2	MMoh1[c] + MM5fthf[e] <=> MM5fthf[c] + MMoh1[e]	0	1000	20509.1 or 20509.2	Mouse metabolic/ transport/ demand reaction
MM5HLTDL	MMh[c] + MM5htrp[c] -> MMco2[c] + MM5trtn[c]	0	1000	13195.1	Mouse metabolic/ transport/ demand reaction
MM5HOMEPRAZOLEte	MM5homeprazole[e] <=> MM5homeprazole[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MM5HOXINDACTO2OX	MMh2o[c] + MMo2[c] + MM5hoxindact[c] -> MMh2o2[c] + MMh[c] + MM5hoxindoa[c]	0	1000	11761.1	Mouse metabolic/ transport/ demand reaction
MM5HOXINDACTOX	MMh2o[c] + MMnad[c] + MM5hoxindact[c] -> 2 MMh[c] + MMnadh[c] + MM5hoxindoa[c]	0	1000	19378.1 or 56752.1 or 110695.1 or 11668.1 or 11671.1 or 19378.2 or 19378.3	Mouse metabolic/ transport/ demand reaction
MM5HOXINDACTOXm	MMh2o[m] + MMnad[m] + MM5hoxindact[m] -> 2 MMh[m] + MMnadh[m] + MM5hoxindoa[m]	0	1000	212647.1 or 11669.1 or 212647.2 or 72535.1	Mouse metabolic/ transport/ demand reaction
MM5HOXINOXDA	MMh2o[c] + MMo2[c] + MM5srtn[c] -> MMh2o2[c] + MMnh4[c] + MM5hoxindact[c]	0	1000	109731.1 or 17161.1	Mouse metabolic/ transport/ demand reaction
MM5HTRPDOX	MMo2[c] + MM5htrp[c] -> MM5hoxnfkyn[c]	0	1000	15930.1	Mouse metabolic/ transport/ demand reaction
MM5HTRPVESSEC	2 MMh2o[c] + 2 MMatp[c] + 3 MM5htrp[c] -> 2 MMadp[c] + 2 MMh[c] + 2 MMpi[c] + 3 MM5htrp[e]	0	1000	214084.1 or 110877.1	Mouse metabolic/ transport/ demand reaction
MM5HXKYNDCL	MMh[c] + MM5hxkyn[c] -> MMco2[c] + MM5hxkynam[c]	0	1000	13195.1	Mouse metabolic/ transport/ demand reaction
MM5HXKYNOXDA	MMo2[c] + MM5hxkynam[c] -> MMh2o2[c] + MMnh4[c] + MM46dhoxquin[c]	0	1000	109731.1 or 17161.1	Mouse metabolic/ transport/ demand reaction
MM5MTHFt2	MMoh1[c] + MM5mthf[e] <=> MMoh1[e] + MM5mthf[c]	0	1000	20509.1 or 20509.2	Mouse metabolic/ transport/ demand reaction
MM5MTHFtc	MM5mthf[u] -> MM5mthf[c]	0	1000	(14275.1 or 14276.1)	Mouse metabolic/ transport/ demand reaction
MM5THFtl	MM5thf[c] -> MM5thf[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MM5THFtm	MM5thf[m] -> MM5thf[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MM6DHFtl	MM6dhf[c] -> MM6dhf[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MM6DHFtm	MM6dhf[m] -> MM6dhf[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MM6HTSTSTERONEte	MM6htststerone[c] <=> MM6htststerone[e]	-1000	0		Mouse metabolic/ transport/ demand reaction
MM6HTSTSTERONEtr	MM6htststerone[c] <=> MM6htststerone[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MM6THFtl	MM6thf[c] -> MM6thf[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MM6THFtm	MM6thf[m] -> MM6thf[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MM7DHCHSTEROLtr	MM7dhchsterol[r] <=> MM7dhchsterol[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MM7DHFtl	MM7dhf[c] -> MM7dhf[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MM7DHFtm	MM7dhf[m] -> MM7dhf[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MM7THFtl	MM7thf[c] -> MM7thf[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MM7THFtm	MM7thf[m] -> MM7thf[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMA4GALTc	MMgalgluside_hs[c] + MMudpgal[c] -> MMh[c] + MMtdcrm_hs[c] + MMudp[c]	0	1000	239559.1	Mouse metabolic/ transport/ demand reaction
MMA4GALTg	MMgalgluside_hs[g] + MMudpgal[g] -> MMh[g] + MMtdcrm_hs[g] + MMudp[g]	0	1000	239559.1	Mouse metabolic/ transport/ demand reaction
MMA4GNT1g	MMT_antigen[g] + MMuacgam[g] -> MMh[g] + MMudp[g] + MMgncore1[g]	0	1000	333424.1	Mouse metabolic/ transport/ demand reaction
MMA4GNT2g	MMuacgam[g] + MMcore2[g] -> MMh[g] + MMudp[g] + MMgncore2[g]	0	1000	333424.1	Mouse metabolic/ transport/ demand reaction
MMAACOAT	MMatp[c] + MMcoa[c] + MMacac[c] <=> MMaacoa[c] + MMamp[c] + MMppi[c]	-1000	1000	78894.1	Mouse metabolic/ transport/ demand reaction
MMAACTOOR	MMh2o[c] + MMo2[c] + MMaact[c] -> MMh2o2[c] + MMnh4[c] + MMmthgx[c]	0	1000	11754.1	Mouse metabolic/ transport/ demand reaction
MMAACTtm	MMaact[m] -> MMaact[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMAAPSAS	MMh2o[c] + MMh[c] + MMthp2c[c] -> MML2aadp6sa[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMAASAD3	MMh2o[c] + MMnad[c] + MML2aadp6sa[c] -> 2 MMh[c] + MML2aadp[c] + MMnadh[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMAASAD3m	MMh2o[m] + MMnad[m] + MML2aadp6sa[m] -> 2 MMh[m] + MML2aadp[m] + MMnadh[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMAATAi	MML2aadp[c] + MMakg[c] -> MM2oxoadp[c] + MMglu-L[c]	0	1000	23923.1 or 23923.2	Mouse metabolic/ transport/ demand reaction
MMABTArm	MMakg[m] + MM4abut[m] <=> MMglu-L[m] + MMsucsa[m]	-1000	1000	268860.2 or 268860.1	Mouse metabolic/ transport/ demand reaction
MMABTD	MMnad[c] + MMabt[c] <=> MMh[c] + MMnadh[c] + MMxyla-L[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMABTti	MMabt[c] -> MMabt[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMABUTD	MMh2o[c] + MMnad[c] + MM4abut[c] -> 2 MMh[c] + MMnadh[c] + MM4abut[c]	0	1000	56752.1	Mouse metabolic/ transport/ demand reaction
MMABUTt2r	MMh[e] + MM4abut[e] <=> MMh[c] + MM4abut[c]	0	1000	215335.1	Mouse metabolic/ transport/ demand reaction
MMABUTt2rL	MM4abut[l] + MMh[l] <=> MMh[c] + MM4abut[c]	-1000	1000	215335.1	Mouse metabolic/ transport/ demand reaction
MMABUTt4_2_r	2 MMna1[e] + MM4abut[e] <=> 2 MMna1[c] + MM4abut[c]	0	1000	14412.1 or 14411.1 or 243616.1 or 232333.1	Mouse metabolic/ transport/ demand reaction
MMACACT1	2 MMaccoa[c] -> MMcoa[c] + MMaacoa[c]	0	1000	224530.1	Mouse metabolic/ transport/ demand reaction
MMACACT10m	MMcoa[m] + MM2maacoa[m] <=> MMaccoa[m] + MMppcoa[m]	-1000	1000	110446.1	Mouse metabolic/ transport/ demand reaction
MMACACT1r	2 MMaccoa[c] <=> MMcoa[c] + MMaacoa[c]	-1000	1000	224530.1	Mouse metabolic/ transport/ demand reaction
MMACACT1rm	2 MMaccoa[m] <=> MMcoa[m] + MMaacoa[m]	-1000	1000	110446.1 or 231086.1 or 97212.1	Mouse metabolic/ transport/ demand reaction
MMACACT1x	2 MMaccoa[x] -> MMaacoa[x] + MMcoa[x]	0	1000	224530.1	Mouse metabolic/ transport/ demand reaction
MMACACT4p	MMcoa[x] + MM3odcoa[x] -> MMaccoa[x] + MMoccoa[x]	0	1000	113868.1	Mouse metabolic/ transport/ demand reaction
MMACACT5p	MMcoa[x] + MM3oddcoa[x] -> MMaccoa[x] + MMdcacoa[x]	0	1000	113868.1	Mouse metabolic/ transport/ demand reaction
MMACACT6p	MMcoa[x] + MM3otdcoa[x] -> MMaccoa[x] + MMddcacoa[x]	0	1000	113868.1	Mouse metabolic/ transport/ demand reaction
MMACACT7p	MMcoa[x] + MM3ohdcoa[x] -> MMaccoa[x] + MMtdcoa[x]	0	1000	113868.1	Mouse metabolic/ transport/ demand reaction
MMACACT8p	MMcoa[x] + MM3ohodcoa[x] -> MMaccoa[x] + MMpmtcoa[x]	0	1000	113868.1	Mouse metabolic/ transport/ demand reaction
MMACACT9p	MMcoa[x] + MM3ohxccoa[x] -> MMaccoa[x] + MMttccoa[x]	0	1000	113868.1	Mouse metabolic/ transport/ demand reaction
MMACACt2	MMh[e] + MMacac[e] <=> MMh[c] + MMacac[c]	0	1000	20503.1 or 20501.1	Mouse metabolic/ transport/ demand reaction
MMACACt2m	MMh[c] + MMacac[c] <=> MMh[m] + MMacac[m]	-1000	1000	20501.1	Mouse metabolic/ transport/ demand reaction
MMACACtx	MMacac[c] <=> MMacac[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMACALDt	MMacald[e] <=> MMacald[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMACALDtm	MMacald[m] <=> MMacald[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMACALDtr	MMacald[r] <=> MMacald[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMACALDtx	MMacald[x] <=> MMacald[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMACCOAC	MMatp[c] + MMhco3[c] + MMaccoa[c] -> MMadp[c] + MMh[c] + MMpi[c] + MMmalcoa[c]	0	1000	107476.2 or 107476.1 or 100705.1 and 107476.3 or 100705.1 and 107476.5 or 107476.4 or 100705.1 and 107476.4 or 107476.1 and 100705.1 or 107476.5 or 107476.3 or 100705.1 and 107476.4	Mouse metabolic/ transport/ demand reaction

MMACCOACm	MAaccoa[m] + MAatp[m] + MMhco3[m] -> MMh[m] + MMadp[m] + MMmalcoa[m] + MMpi[m]	0	1000	100705.1	Mouse metabolic/ transport/ demand reaction
MMACCOAL	MMatp[c] + MMcoa[c] + MMppa[c] -> MMadp[c] + MMpi[c] + MMppcoa[c]	0	1000	60525.1 or 60525.2	Mouse metabolic/ transport/ demand reaction
MMACCOALm	MMcoa[m] + MMatp[m] + MMppa[m] -> MMppcoa[m] + MMamp[m] + MMpp[m]	0	1000	68738.1	Mouse metabolic/ transport/ demand reaction
MMACCOAgt	MAaccoa[c] <=> MAaccoa[g]	-1000	1000	11416.1	Mouse metabolic/ transport/ demand reaction
MMACCOAtn	MAaccoa[c] <=> MAaccoa[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMACCOAtr	MAaccoa[c] <=> MAaccoa[r]	-1000	1000	11416.1	Mouse metabolic/ transport/ demand reaction
MMACETONEt2	MMh[e] + MMacetone[e] <=> MMh[c] + MMacetone[c]	0	1000	20503.1 or 80879.1 or 20501.1	Mouse metabolic/ transport/ demand reaction
MMACETONEt2m	MMh[c] + MMacetone[c] <=> MMh[m] + MMacetone[m]	-1000	1000	20501.1	Mouse metabolic/ transport/ demand reaction
MMACGAGBSIDEtg	MMacgagbside_hs[c] <=> MMacgagbside_hs[g]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMACGAGBSIDEtl	MMacgagbside_hs[c] <=> MMacgagbside_hs[l]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMACGALFUCGALACGALFUC12GAL14ACGLCGALGLUSIDEte	MMacgalfucgalacgalfuc12gal14acglcgalglcside_hs[e] <=> MMacgalfucgalacgalfuc12gal14acglcgalglcside_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMACGALFUCGALACGALFUC12GAL14ACGLCGALGLUSIDEtg	MMacgalfucgalacgalfuc12gal14acglcgalglcside_hs[g] <=> MMacgalfucgalacgalfuc12gal14acglcgalglcside_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMACGALFUCGALACGALFUCGALACGLCGAL14ACGLCGALGLUSIDEte	MMacgalfucgalacgalfucgalacglcgal14acglcgalglcside_hs[e] <=> MMacgalfucgalacgalfucgalacglcgal14acglcgalglcside_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMACGALFUCGALACGALFUCGALACGLCGAL14ACGLCGALGLUSIDEtg	MMacgalfucgalacgalfucgalacglcgal14acglcgalglcside_hs[g] <=> MMacgalfucgalacgalfucgalacglcgal14acglcgalglcside_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMACGALK	MMatp[c] + MMacgal[c] -> MMadp[c] + MMh[c] + MMacgal1p[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMACGALK2	MMacgal[c] + MMitp[c] -> MMh[c] + MMacgal1p[c] + MMidp[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMACGALtlg	MMacgal[g] <=> MMacgal[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMACGALtly	MMacgal[l] -> MMacgal[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMACGALtr	MMacgal[c] -> MMacgal[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMACGAM2E	MMacgam[c] <=> MMacmana[c]	-1000	1000	19703.1	Mouse metabolic/ transport/ demand reaction
MMACGAM6PSi	MMaccoa[c] + MMgam6p[c] -> MMh[c] + MMcoa[c] + MMacgam6p[c]	0	1000	54342.1	Mouse metabolic/ transport/ demand reaction
MMACGAMK	MMatp[c] + MMacgam[c] -> MMadp[c] + MMh[c] + MMacgam6p[c]	0	1000	56174.1	Mouse metabolic/ transport/ demand reaction
MMACGAMPM	MMacgam6p[c] <=> MMacgam1p[c]	-1000	1000	109785.1	Mouse metabolic/ transport/ demand reaction
MMACGAMtly	MMacgam[l] -> MMacgam[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMACGBGBSIDEtg	MMacgbgbside_hs[c] <=> MMacgbgbside_hs[g]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMACGBGBSIDEtl	MMacgbgbside_hs[c] <=> MMacgbgbside_hs[l]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMACGPID	MMh2o[c] + MMacggail_hs[c] -> MMac[c] + MMggail_hs[c]	0	1000	327942.1	Mouse metabolic/ transport/ demand reaction
MMACGSm	MMglu-L[m] + MMaccoa[m] -> MMh[m] + MMcoa[m] + MMacglu[m]	0	1000	217214.1	Mouse metabolic/ transport/ demand reaction
MMACHEe	MMach[e] + MMh2o[e] -> MMh[e] + MMac[e] + MMcholl[e]	0	1000	11423.1 or 11423.2	Mouse metabolic/ transport/ demand reaction
MMACHVESSEC	2 MMh2o[c] + 2 MMatp[c] + 3 MMach[c] -> 2 MMadp[c] + 2 MMi[c] + 2 MMpi[c] + 3 MMach[e]	0	1000	20508.1	Mouse metabolic/ transport/ demand reaction
MMACHtn	MMach[n] <=> MMach[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMACITL	MMaip[c] + MMcoa[c] + MMcit[c] -> MMadp[c] + MMpi[c] + MMaccoa[c] + MMoaa[c]	0	1000	104112.1 or 104112.2	Mouse metabolic/ transport/ demand reaction
MMACN13ACNGALGBSIDEte	MMacn13acngalglcside_hs[c] <=> MMacn13acngalglcside_hs[e]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMACN13ACNGALGBSIDEtg	MMacn13acngalglcside_hs[c] <=> MMacn13acngalglcside_hs[g]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMACN23ACNGALGBSIDEte	MMacn23acngalglcside_hs[c] <=> MMacn23acngalglcside_hs[e]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMACN23ACNGALGBSIDEtg	MMacn23acngalglcside_hs[c] <=> MMacn23acngalglcside_hs[g]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMACNACNGAL14ACGLCGALGLUSIDEte	MMacnacngal14acglcgalglcside_hs[e] <=> MMacnacngal14acglcgalglcside_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMACNACNGAL14ACGLCGALGLUSIDEtg	MMacnacngal14acglcgalglcside_hs[g] <=> MMacnacngal14acglcgalglcside_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMACNACNGALGBSIDEte	MMacnacngalglcside_hs[c] <=> MMacnacngalglcside_hs[e]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMACNACNGALGBSIDEtg	MMacnacngalglcside_hs[c] <=> MMacnacngalglcside_hs[g]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMACNAM9PL	MMh2o[c] + MMacmanap[c] + MMpep[c] -> MMpi[c] + MMacramp[c]	0	1000	94181.1	Mouse metabolic/ transport/ demand reaction
MMACNAM9PL2	MMh2o[c] + MMpep[c] + MMman6p[c] -> MMpi[c] + MMkdrnp[c]	0	1000	94181.1	Mouse metabolic/ transport/ demand reaction
MMACNAMPH	MMh2o[c] + MMacramp[c] -> MMpi[c] + MMacnam[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMACNAMt	MMh[c] + MMacnam[c] <=> MMh[l] + MMacnam[l]	-1000	1000	235504.1	Mouse metabolic/ transport/ demand reaction
MMACNAMtn	MMacnam[c] -> MMacnam[n]	0	1000		Mouse metabolic/ transport/ demand reaction
MMACNAMtr	MMacnam[c] -> MMacnam[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMACNGALACGLCGAL14ACGLCGALGLUSIDEte	MMacngalacglcgal14acglcgalglcside_hs[e] <=> MMacngalacglcgal14acglcgalglcside_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMACNGALACGLCGAL14ACGLCGALGLUSIDEtg	MMacngalacglcgal14acglcgalglcside_hs[g] <=> MMacngalacglcgal14acglcgalglcside_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMACNMLr	MMacnam[c] <=> MMpyr[c] + MMacmana[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMACOAD10m	MM2mbcoa[m] + MMfad[m] -> MM2mb2coa[m] + MMfadh2[m]	0	1000	11364.1 or 66885.1	Mouse metabolic/ transport/ demand reaction
MMACOAD1fm	MMfad[m] + MMbtcoa[m] -> MMfb2coa[m] + MMfadh2[m]	0	1000	102632.1 or 66948.1 or 11364.1 or 66885.1 or 11409.1 or 71985.1 or 229211.1	Mouse metabolic/ transport/ demand reaction
MMACOAD8m	MMfad[m] + MMvcoa[m] -> MMfadh2[m] + MM3mb2coa[m]	0	1000	56357.1	Mouse metabolic/ transport/ demand reaction
MMACOAD9m	MMfad[m] + MMibcoa[m] -> MMfadh2[m] + MM2mp2coa[m]	0	1000	66948.1 or 11364.1	Mouse metabolic/ transport/ demand reaction
MMACOAHi	MMh2o[c] + MMaccoa[c] -> MMh[c] + MMcoa[c] + MMac[c]	0	1000	74156.1	Mouse metabolic/ transport/ demand reaction
MMACOAO7p	MMpmtcoa[x] + MMo2[x] -> MMh2o2[x] + MMhdd2coa[x]	0	1000	11430.1 or 11430.2	Mouse metabolic/ transport/ demand reaction
MMACOATA	MMaccoa[c] + MMACP[c] <=> MMcoa[c] + MMacACP[c]	-1000	1000	14104.1	Mouse metabolic/ transport/ demand reaction
MMACODA	MMh2o[c] + MMacorn[c] -> MMac[c] + MMorn[c]	0	1000	109652.1	Mouse metabolic/ transport/ demand reaction
MMACONT	MMcit[c] <=> MMicit[c]	-1000	1000	11428.1 or 64602.1	Mouse metabolic/ transport/ demand reaction
MMACONTm	MMcit[m] <=> MMicit[m]	-1000	1000	11429.1	Mouse metabolic/ transport/ demand reaction
MMACOX22x	0.5 MMo2[x] + MMdhcholoylcoa[x] + MMfadh2[x] -> MMfad[x] + MMthcholoylcoa[x]	0	1000	93732.1	Mouse metabolic/ transport/ demand reaction
MMACOX2x	MMo2[x] + MMfadh2[x] + MMcholcoas[x] -> MMfad[x] + MMcholcoads[x] + 2 MMh2o[x]	0	1000	212647.1 or 212647.2	Mouse metabolic/ transport/ demand reaction
MMACP1_FMN	MMh2o[c] + MMfmn[c] -> MMpi[c] + MMribflv[c]	0	1000	11431.1 or 11431.2 or 11431.3	Mouse metabolic/ transport/ demand reaction
MMACRNtm	MMacrn[c] -> MMacrn[m]	0	1000	57279.1	Mouse metabolic/ transport/ demand reaction
MMACS	MMatp[c] + MMcoa[c] + MMac[c] -> MMamp[c] + MMppi[c] + MMaccoa[c]	0	1000	60525.1 or 78894.1 or 60525.2	Mouse metabolic/ transport/ demand reaction
MMACS2	MMatp[c] + MMcoa[c] + MMppa[c] -> MMamp[c] + MMppi[c] + MMppcoa[c]	0	1000	60525.1 or 78894.1 or 60525.2	Mouse metabolic/ transport/ demand reaction
MMACSm	MMcoa[m] + MMatp[m] + MMac[m] -> MMaccoa[m] + MMamp[m] + MMppi[m]	0	1000	68738.1	Mouse metabolic/ transport/ demand reaction
MMACTLMO	MMo2[c] + MMh[c] + MMnadph[c] + MMacetol[c] -> 2 MMh2o[c] + MMnadp[c] + MMmthgx[c]	0	1000	13106.1	Mouse metabolic/ transport/ demand reaction
MMACTNMO	MMo2[c] + MMh[c] + MMnadph[c] + MMacetone[c] -> MMh2o[c] + MMnadp[c] + MMacetn[c]	0	1000	13106.1	Mouse metabolic/ transport/ demand reaction
MMACYP	MMh2o[c] + MM13dpg[c] -> MMh[c] + MMpi[c] + MM3pg[c]	0	1000	69519.1 or 66204.1 or 66204.2 or 75572.1	Mouse metabolic/ transport/ demand reaction
MMAC2m	MMh[c] + MMac[c] <=> MMh[m] + MMac[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMAC2r	MMh[e] + MMac[e] <=> MMh[c] + MMac[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMACtg	MMac[c] <=> MMac[g]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMADA	MMh2o[c] + MMh[c] + MMadn[c] -> MMnh4[c] + MMins[c]	0	1000	11486.1	Mouse metabolic/ transport/ demand reaction
MMADAe	MMh[e] + MMh2o[e] + MMadn[e] -> MMins[e] + MMnh4[e]	0	1000	11486.1	Mouse metabolic/ transport/ demand reaction
MMADCim	MMh[m] + MMacac[m] -> MMco2[m] + MMacetone[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMADEt	MMade[e] <=> MMade[c]	0	1000	13340.1	Mouse metabolic/ transport/ demand reaction
MMADEtl	MMade[l] <=> MMade[c]	-1000	1000	71279.1	Mouse metabolic/ transport/ demand reaction
MMADHAPtx	MMadhap_hs[c] <=> MMadhap_hs[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMADK1	MMatp[c] + MMamp[c] <=> 2 MMadp[c]	-1000	1000	11636.1 or 229949.1 or 229949.2 or 78801.1	Mouse metabolic/ transport/ demand reaction
MMADK3	MMamp[c] + MMgtp[c] <=> MMadp[c] + MMgdp[c]	-1000	1000	229949.1 or 229949.2	Mouse metabolic/ transport/ demand reaction
MMADK3m	MMamp[m] + MMgtp[m] <=> MMadp[m] + MMgdp[m]	-1000	1000	56248.1	Mouse metabolic/ transport/ demand reaction
MMADKd	MMdamp[c] + MMdatp[c] <=> 2 MMdadp[c]	-1000	1000	229949.1 or 229949.2	Mouse metabolic/ transport/ demand reaction
MMADMDC	MMh[c] + MMamet[c] -> MMco2[c] + MMametam[c]	0	1000	11702.1	Mouse metabolic/ transport/ demand reaction

MMADNCYC	MMatp[c] -> MMppi[c] + MMcamp[c]	0	1000	224129.1 or 11515.1 or 432530.1 or 11512.1 or 104111.1 or 104110.1 or 271639.1 or 11512.2 or 11513.1 or 11514.1 or 271639.1 or 210044.1	Mouse metabolic/ transport/ demand reaction
MMADNK1	MMatp[c] + MMadn[c] -> MMadp[c] + MMh[c] + MMamp[c]	0	1000	11534.1 or 11534.2	Mouse metabolic/ transport/ demand reaction
MMADNK1m	MMatp[m] + MMadn[m] -> MMh[m] + MMadp[m] + MMamp[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMADNt	MMadn[e] <=> MMadn[c]	0	1000	13340.1 or 63959.1	Mouse metabolic/ transport/ demand reaction
MMADNt4	MMna1[e] + MMadn[e] -> MMna1[c] + MMadn[c]	0	1000	114304.1 or 434203.1 or 434203.2 or 269346.1	Mouse metabolic/ transport/ demand reaction
MMADNt5	2 MMna1[e] + MMadn[e] -> 2 MMna1[c] + MMadn[c]	0	1000	114304.1	Mouse metabolic/ transport/ demand reaction
MMADNtl	MMadn[l] <=> MMadn[c]	-1000	1000	71279.1	Mouse metabolic/ transport/ demand reaction
MMADNtm	MMadn[c] <=> MMadn[m]	-1000	1000	63959.1	Mouse metabolic/ transport/ demand reaction
MMADPGLC	MMh2o[c] + MMadpglc[c] -> 2 MMh[c] + MMamp[c] + MMg1p[c]	0	1000	53893.1	Mouse metabolic/ transport/ demand reaction
MMADPMAN	MMh2o[c] + MMadpman[c] -> 2 MMh[c] + MMamp[c] + MMman1p[c]	0	1000	53893.1	Mouse metabolic/ transport/ demand reaction
MMADPRDP	MMh2o[c] + MMadprib[c] -> 2 MMh[c] + MMamp[c] + MMr5p[c]	0	1000	53893.1	Mouse metabolic/ transport/ demand reaction
MMADPRDPm	MMh2o[m] + MMadprib[m] -> 2 MMh[m] + MMamp[m] + MMr5p[m]	0	1000	74167.1 or 74167.2 or 74167.3	Mouse metabolic/ transport/ demand reaction
MMADPRIBt	MMadprib[e] -> MMadprib[c]	0	1000	12494.1	Mouse metabolic/ transport/ demand reaction
MMADPT	MMade[c] + MMprpp[c] -> MMamp[c] + MMppi[c]	0	1000	11821.1	Mouse metabolic/ transport/ demand reaction
MMADPtx	MMadp[c] <=> MMadp[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMADRNCOAtx	MMadrncoa[c] <=> MMadrncoa[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMADRNCPT1	MMadrncoa[c] + MMcrn[c] -> MMcoa[c] + MMadrncrn[c]	0	1000	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	Mouse metabolic/ transport/ demand reaction
MMADRNCPT2	MMcoa[m] + MMadrncrn[m] -> MMadrncoa[m] + MMcrn[m]	0	1000	12896.1	Mouse metabolic/ transport/ demand reaction
MMADRNCRNt	MMadrncrn[c] -> MMadrncrn[m]	0	1000	57279.1	Mouse metabolic/ transport/ demand reaction
MMADRNLPVESSEC	2 MMh2o[c] + 2 MMatp[c] + 3 MMadrnl[c] -> 2 MMadp[c] + 2 MMh[c] + 2 MMpi[c] + 3 MMadrnll[e]	0	1000	214084.1 or 110877.1	Mouse metabolic/ transport/ demand reaction
MMADRNt	MMadrn[e] <=> MMadrn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMADSELK	MMatp[c] + MMadse[c] -> MMadp[c] + MMh[c] + MM3padse[c]	0	1000	23972.1 or 23971.1	Mouse metabolic/ transport/ demand reaction
MMADSK	MMatp[c] + MMaps[c] -> MMadp[c] + MMh[c] + MMpaps[c]	0	1000	23972.1 or 23971.1	Mouse metabolic/ transport/ demand reaction
MMADSL1	MMdcamp[c] -> MMamp[c] + MMfum[c]	0	1000	11564.1 or 11564.2	Mouse metabolic/ transport/ demand reaction
MMADSL2	MM25aics[c] -> MMfum[c] + MMaicar[c]	0	1000	11564.1 or 11564.2	Mouse metabolic/ transport/ demand reaction
MMADSS	MMasp-L[c] + MMgtp[c] + MMimp[c] -> 2 MMh[c] + MMpi[c] + MMgdp[c] + MMdcamp[c]	0	1000	11565.1 or 11565.2 or 11566.1	Mouse metabolic/ transport/ demand reaction
MMAFLATOXINte	MMaflatoxin[e] <=> MMaflatoxin[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMAG13T10g	MMuacgam[g] + MMksi_pre18[g] -> MMh[g] + MMudp[g] + MMksi_pre19[g]	0	1000	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	Mouse metabolic/ transport/ demand reaction
MMAG13T11g	MMuacgam[g] + MMksi_pre21[g] -> MMh[g] + MMudp[g] + MMksi_pre22[g]	0	1000	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	Mouse metabolic/ transport/ demand reaction
MMAG13T12g	MMuacgam[g] + MMksi_pre24[g] -> MMh[g] + MMudp[g] + MMksi_pre25[g]	0	1000	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	Mouse metabolic/ transport/ demand reaction
MMAG13T13g	MMuacgam[g] + MMksi_pre27[g] -> MMh[g] + MMudp[g] + MMksi_pre28[g]	0	1000	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	Mouse metabolic/ transport/ demand reaction
MMAG13T14g	MMuacgam[g] + MMksi_pre30[g] -> MMh[g] + MMudp[g] + MMksi_pre31[g]	0	1000	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	Mouse metabolic/ transport/ demand reaction
MMAG13T15g	MMuacgam[g] + MMksi_pre33[g] -> MMh[g] + MMudp[g] + MMksi_pre34[g]	0	1000	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	Mouse metabolic/ transport/ demand reaction
MMAG13T16g	MMuacgam[g] + MMksii_core4_pre2[g] -> MMh[g] + MMudp[g] + MMksii_core4_pre3[g]	0	1000	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	Mouse metabolic/ transport/ demand reaction
MMAG13T17g	MMuacgam[g] + MMksii_core4_pre4[g] -> MMh[g] + MMudp[g] + MMksi_core4_pre5[g]	0	1000	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	Mouse metabolic/ transport/ demand reaction
MMAG13T18g	MMuacgam[g] + MMksii_core4_pre7[g] -> MMh[g] + MMudp[g] + MMksii_core4_pre8[g]	0	1000	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	Mouse metabolic/ transport/ demand reaction
MMAG13T1g	MMuacgam[g] + MMksii_core2_pre2[g] -> MMh[g] + MMudp[g] + MMksii_core2_pre3[g]	0	1000	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	Mouse metabolic/ transport/ demand reaction
MMAG13T2g	MMuacgam[g] + MMksii_core2_pre4[g] -> MMh[g] + MMudp[g] + MMksii_core2_pre5[g]	0	1000	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	Mouse metabolic/ transport/ demand reaction
MMAG13T3g	MMuacgam[g] + MMksii_core2_pre7[g] -> MMh[g] + MMudp[g] + MMksii_core2_pre8[g]	0	1000	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	Mouse metabolic/ transport/ demand reaction
MMAG13T4g	MMuacgam[g] + MMksi_pre1[g] -> MMh[g] + MMudp[g] + MMksi_pre2[g]	0	1000	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	Mouse metabolic/ transport/ demand reaction
MMAG13T5g	MMuacgam[g] + MMksi_pre3[g] -> MMh[g] + MMudp[g] + MMksi_pre4[g]	0	1000	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	Mouse metabolic/ transport/ demand reaction
MMAG13T6g	MMuacgam[g] + MMksi_pre6[g] -> MMh[g] + MMudp[g] + MMksi_pre7[g]	0	1000	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	Mouse metabolic/ transport/ demand reaction
MMAG13T7g	MMuacgam[g] + MMksi_pre9[g] -> MMh[g] + MMudp[g] + MMksi_pre10[g]	0	1000	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	Mouse metabolic/ transport/ demand reaction
MMAG13T8g	MMuacgam[g] + MMksi_pre12[g] -> MMh[g] + MMudp[g] + MMksi_pre13[g]	0	1000	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	Mouse metabolic/ transport/ demand reaction
MMAG13T9g	MMuacgam[g] + MMksi_pre15[g] -> MMh[g] + MMudp[g] + MMksi_pre16[g]	0	1000	232984.1 or 72297.1 or 53625.1 or 231727.1 or 232984.2 or 227327.1 or 53625.2 or 108902.1 or 210004.1	Mouse metabolic/ transport/ demand reaction
MMAGDC	MMh2o[c] + MMacgam6p[c] -> MMgam6p[c] + MMac[c]	0	1000	245847.1	Mouse metabolic/ transport/ demand reaction
MMAGLPC	MMak2g_hs[c] + MMcdpchol[c] -> MMh2o[c] + MMh[c] + MMak2gchol_hs[c] + MMcmp[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMAGLPED	MMo2[c] + MMh[c] + MMnadph[c] + MMak2gpe_hs[c] -> 2 MMh2o[c] + MMnadp[c] + MMdak2gpe_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMAGLPET	MMh[c] + MMak2g_hs[c] + MMcdpea[c] -> MMh2o[c] + MMcmp[c] + MMak2gpe_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMAGLPH	MMh2o[c] + MMak2gp_hs[c] -> MMpi[c] + MMak2g_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMAGLPR	MMh[c] + MMnadph[c] + MMakdhap_hs[c] -> MMnadp[c] + MMakgp_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMAGLPT	MMh[c] + MMakgp_hs[c] + MMRtotal2[c] -> MMh2o[c] + MMak2gp_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMAGMTm	MMh2o[m] + MMagrn[m] -> MMptrc[m] + MMurea[m]	0	1000	75986.1	Mouse metabolic/ transport/ demand reaction
MMAGPAT1	MMRtotal2coa[c] + MMalpa_hs[c] -> MMcoa[c] + MMpa_hs[c]	0	1000	52123.1 or 28169.1 or 28169.2 or 55979.1 or 67512.1 or 68262.1 or 102247.1	Mouse metabolic/ transport/ demand reaction
MMAGPRim	MMh[m] + MMnadph[m] + MMacg5p[m] -> MMnadp[m] + MMrlp[m] + MMacg5oa[m]	0	1000	56454.1	Mouse metabolic/ transport/ demand reaction
MMAGPSx	MMadhap_hs[x] + MMalkylR1oh[x] -> MMh[x] + MMRtotal[x] + MMakdhap_hs[x]	0	1000	228061.1	Mouse metabolic/ transport/ demand reaction
MMAGPex	MMakdhap_hs[c] <=> MMakdhap_hs[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMAGTim	MMala-L[m] + MMglx[m] -> MMpyr[m] + MMgly[m]	0	1000	268782.1 or 71760.1	Mouse metabolic/ transport/ demand reaction
MMAGTix	MMala-L[x] + MMglx[x] -> MMgly[x] + MMpyr[x]	0	1000	11611.1	Mouse metabolic/ transport/ demand reaction
MMAHANDROSTANGLCte	MMh2o[c] + MMatp[c] + MMahandrostangl[c] -> MMadp[c] + MMh[c] + MMpi[c] + MMahandrostangl[e]	0	1000	17250.1	Mouse metabolic/ transport/ demand reaction
MMAHANDROSTANGLCtr	MMahandrostangl[c] <=> MMahandrostangl[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMAHC	MMh2o[c] + MMahcys[c] <=> MMadn[c] + MMhcys-L[c]	-1000	1000	229709.1 or 229709.2 or 269378.1	Mouse metabolic/ transport/ demand reaction
MMAHCYStn	MMahcys[c] <=> MMahcys[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMAHCYStr	MMahcys[c] <=> MMahcys[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMAHEXASE2ly	3 MMh2o[l] + MMn2m2mm[l] -> 3 MMacgam[l] + MMm2mm[l]	0	1000	(15211.1 or 15212.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMAHEXASEly	2 MMh2o[l] + MMn2m2mm[l] -> 2 MMacgam[l] + MMm2mm[l]	0	1000	(15211.1 or 15212.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMAICART	MM10thf[c] + MMaicar[c] <=> MMfprica[c] + MMthf[c]	-1000	1000	108147.1	Mouse metabolic/ transport/ demand reaction
MMAIRCr	MMco2[c] + MMair[c] <=> MMfp[c] + MMSaize[c]	-1000	1000	67054.1	Mouse metabolic/ transport/ demand reaction
MMAK2LGCHOLt	MMak2lgchol_hs[e] <=> MMak2lgchol_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMAKGDm	MMakg[m] + MMcoa[m] + MMnad[m] -> MMco2[m] + MMnadh[m] + MMsuccoa[m]	0	1000	(78920.1 or 18293.1 or (27402.1 and 13382.1) or 18293.2)	Mouse metabolic/ transport/ demand reaction
MMAKGMALtm	MMakg[m] + MMmal-L[c] <=> MMakg[c] + MMmal-L[m]	-1000	1000	67863.1	Mouse metabolic/ transport/ demand reaction
MMAKGt4_3	3 MMna1[e] + MMakg[e] <=> MMakg[c] + 3 MMna1[c]	0	1000	114644.1 or 114644.2	Mouse metabolic/ transport/ demand reaction
MMAKGtp	MMakg[c] <=> MMakg[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMAKR1C1	MMh[c] + MMnadph[c] + MMprgstrn[c] -> MMnadp[c] + MMprgstrn[c]	0	1000	77337.1	Mouse metabolic/ transport/ demand reaction
MMAKR1C41	MMh[c] + MMnadh[c] + MMxol7ah[c] -> MMnad[c] + MMxol7ah2[c]	0	1000	83702.1	Mouse metabolic/ transport/ demand reaction
MMAKR1C42	MMh[c] + MMnadh[c] + MMxoldioknehl[c] -> MMnad[c] + MMxoltrit[c]	0	1000	83702.1	Mouse metabolic/ transport/ demand reaction
MMAKR1D	MMh[c] + MMnadph[c] + MMxol7aone[c] -> MMnadp[c] + MMxol7ah[c]	0	1000	208665.1	Mouse metabolic/ transport/ demand reaction
MMAKR1D2	MMh[c] + MMnadph[c] + MMxoldioxne[c] -> MMnadp[c] + MMxoldioknehl[c]	0	1000	208665.1	Mouse metabolic/ transport/ demand reaction
MMALAALACNc	MMh2o[c] + MMalaala[c] <=> 2 MMala-L[c]	-1000	1000	(338403.1 or 66054.1)	Mouse metabolic/ transport/ demand reaction
MMALAALAPEPTitc	MMalaala[u] + MMh[u] -> MMh[c] + MMalaala[c]	0	1000	215335.1	Mouse metabolic/ transport/ demand reaction
MMALAASNNaEx	MMna1[e] + MMasn-L[c] + MMala-L[e] -> MMna1[c] + MMala-L[c] + MMasn-L[e]	0	1000	20514.1	Mouse metabolic/ transport/ demand reaction
MMALAATB0tc	2 MMna1[u] + MMc[u] + MMala-L[u] -> 2 MMna1[c] + MMc[c] + MMala-L[c]	0	1000	56774.1	Mouse metabolic/ transport/ demand reaction
MMALACYSNaEx	MMna1[e] + MMala-L[e] + MMcys-L[c] -> MMna1[c] + MMala-L[c] + MMcys-L[e]	0	1000	20514.1 or 55963.1	Mouse metabolic/ transport/ demand reaction

MMALADGLNexR	MMgln-L[c] + MMala-D[e] <=> MMala-D[c] + MMgln-L[e]	-1000	1000	53896.1 or 17254.1	Mouse metabolic/ transport/ demand reaction
MMALADGLYexR	MMala-D[e] + MMgly[c] <=> MMala-D[c] + MMgly[e]	-1000	1000	53896.1 or 17254.1	Mouse metabolic/ transport/ demand reaction
MMALADPATtc	MMh[u] + MMala-D[u] -> MMh[c] + MMala-D[c]	0	1000	215335.1	Mouse metabolic/ transport/ demand reaction
MMALAGLNNaEx	MMna1[e] + MMala-L[e] + MMgln-L[c] -> MMna1[c] + MMala-L[c] + MMgln-L[e]	0	1000	20514.1	Mouse metabolic/ transport/ demand reaction
MMALAGLNNexR	MMala-L[e] + MMgln-L[c] <=> MMala-L[c] + MMgln-L[e]	-1000	1000	53896.1 or 17254.1	Mouse metabolic/ transport/ demand reaction
MMALAGLYexR	MMala-L[e] + MMgly[c] <=> MMala-L[c] + MMgly[e]	-1000	1000	53896.1 or 17254.1	Mouse metabolic/ transport/ demand reaction
MMALAILELAT2tc	MMala-L[e] + MMile-L[c] -> MMala-L[c] + MMile-L[e]	0	1000	(20539.1 and 17254.1)	Mouse metabolic/ transport/ demand reaction
MMALALPATtc	MMh[u] + MMala-L[u] -> MMh[c] + MMala-L[c]	0	1000	215335.1	Mouse metabolic/ transport/ demand reaction
MMALAPHELAT2tc	MMala-L[e] + MMphe-L[c] -> MMala-L[c] + MMphe-L[e]	0	1000	(20539.1 and 17254.1)	Mouse metabolic/ transport/ demand reaction
MMALAR	MMala-L[c] <=> MMala-D[c]	-1000	1000	114863.1	Mouse metabolic/ transport/ demand reaction
MMALASERNaEx	MMna1[e] + MMala-L[e] + MMser-L[c] -> MMna1[c] + MMala-L[c] + MMser-L[e]	0	1000	20514.1 or 55963.1	Mouse metabolic/ transport/ demand reaction
MMALASm	MMh[m] + MMgly[m] + MMsuccoa[m] -> MMcoa[m] + MMco2[m] + MM5aop[m]	0	1000	26912.1 or 11655.1 or 11656.1 or 11655.2	Mouse metabolic/ transport/ demand reaction
MMALATA_L	MMakg[c] + MMala-L[c] <=> MMpyr[c] + MMglu-L[c]	-1000	1000	108682.1 or 76282.1	Mouse metabolic/ transport/ demand reaction
MMALATHRNaEx	MMna1[e] + MMala-L[e] + MMthr-L[c] -> MMna1[c] + MMala-L[c] + MMthr-L[e]	0	1000	20514.1 or 55963.1	Mouse metabolic/ transport/ demand reaction
MMALAt2r	MMh[e] + MMala-L[e] <=> MMh[c] + MMala-L[c]	0	1000	215335.1	Mouse metabolic/ transport/ demand reaction
MMALAt2rL	MMh[l] + MMala-L[l] <=> MMh[c] + MMala-L[c]	-1000	1000	215335.1	Mouse metabolic/ transport/ demand reaction
MMALAt4	MMna1[e] + MMala-L[e] -> MMna1[c] + MMala-L[c]	0	1000	105727.1 or 67760.1 or 69354.1 or 56774.1 or 11989.1 or 11988.1 or 11987.1	Mouse metabolic/ transport/ demand reaction
MMALAt4u	MMna1[u] + MMala-L[u] -> MMna1[c] + MMala-L[c]	0	1000	(70008.1 or (74338.1 and 57394.1))	Mouse metabolic/ transport/ demand reaction
MMALAtN1	MMh[c] + 2 MMna1[e] + MMala-L[e] <=> MMh[e] + 2 MMna1[c] + MMala-L[c]	-1000	1000	209837.1 or 76257.1	Mouse metabolic/ transport/ demand reaction
MMALAyLATtc	MMna1[e] + MMala-L[e] + MMarg-L[c] -> MMna1[c] + MMala-L[c] + MMarg-L[e]	0	1000	(20540.1 or (330836.1 and 17254.1))	Mouse metabolic/ transport/ demand reaction
MMALAyLAThc	MMh[e] + MMala-L[e] + MMarg-L[c] -> MMh[c] + MMala-L[c] + MMarg-L[e]	0	1000	(20540.1 or (330836.1 and 17254.1))	Mouse metabolic/ transport/ demand reaction
MMALCD2yf	MMnadp[c] + MMetoh[c] -> MMh[c] + MMnadph[c] + MMacald[c]	0	1000	58810.1 or 58810.2	Mouse metabolic/ transport/ demand reaction
MMALDD19x	MMh2o[c] + MMnad[c] + MMpacald[c] -> 2 MMh[c] + MMnadh[c] + MMpac[c]	0	1000	11670.1 or 67689.1 or 56847.1	Mouse metabolic/ transport/ demand reaction
MMALDD19x(P)	MMh2o[c] + MMnadp[c] + MMpacald[c] -> 2 MMh[c] + MMnadph[c] + MMpac[c]	0	1000	11670.1 or 67689.1 or 56847.1	Mouse metabolic/ transport/ demand reaction
MMALDD20x	MMh2o[c] + MMnad[c] + MMd3acald[c] -> 2 MMh[c] + MMnadh[c] + MMd3ac[c]	0	1000	19378.1 or 56752.1 or 110695.1 or 11668.1 or 11671.1 or 19378.2 or 19378.3	Mouse metabolic/ transport/ demand reaction
MMALDD20xm	MMh2o[m] + MMnad[m] + MMd3acald[m] -> 2 MMh[m] + MMnadh[m] + MMd3ac[m]	0	1000	212647.1 or 11669.1 or 212647.2 or 72535.1	Mouse metabolic/ transport/ demand reaction
MMALDD21	MMh2o[c] + MMnad[c] + MMpristanal[c] -> 2 MMh[c] + MMnadh[c] + MMpris[c]	0	1000	11671.1	Mouse metabolic/ transport/ demand reaction
MMALDD2x	MMh2o[c] + MMnad[c] + MMacald[c] -> 2 MMh[c] + MMnadh[c] + MMac[c]	0	1000	19378.1 or 56752.1 or 11670.1 or 110695.1 or 67689.1 or 56847.1 or 11668.1 or 11671.1 or 19378.2 or 19378.3	Mouse metabolic/ transport/ demand reaction
MMALDD2xm	MMh2o[m] + MMnad[m] + MMacald[m] -> 2 MMh[m] + MMnadh[m] + MMac[m]	0	1000	11669.1 or 72535.1	Mouse metabolic/ transport/ demand reaction
MMALDD2y	MMh2o[c] + MMnadp[c] + MMacald[c] -> 2 MMh[c] + MMnadph[c] + MMac[c]	0	1000	19378.1 or 56752.1 or 11670.1 or 67689.1 or 11671.1 or 19378.2 or 19378.3	Mouse metabolic/ transport/ demand reaction
MMALDSTRNte	MMaldstrn[c] <=> MMaldstrn[e]	-1000	0		Mouse metabolic/ transport/ demand reaction
MMALDSTRNtm	MMaldstrn[c] <=> MMaldstrn[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMALINOFABPpmtc	MMlnlnca[u] -> MMlnlnca[c]	0	1000	(14719.1 or 12491.1)	Mouse metabolic/ transport/ demand reaction
MMALKP	MMh2o[c] + MMdhap[c] -> MMpi[c] + MMdha[c]	0	1000	11647.1 or 11650.1 or 76768.1	Mouse metabolic/ transport/ demand reaction
MMALOX12	MMo2[c] + MMarachd[c] -> MM12HPET[c]	0	1000	11684.1	Mouse metabolic/ transport/ demand reaction
MMALOX12R	MMo2[c] + MMarachd[c] -> MM12RHPET[c]	0	1000	11686.1	Mouse metabolic/ transport/ demand reaction
MMALOX15	MMo2[c] + MMarachd[c] -> MM15HPET[c]	0	1000	11687.1 or 11688.1	Mouse metabolic/ transport/ demand reaction
MMALOX5	MMo2[c] + MMarachd[c] -> MM5HPET[c]	0	1000	11689.1	Mouse metabolic/ transport/ demand reaction
MMALOX52	MM5HPET[c] -> MMh2o[c] + MMleuktrA4[c]	0	1000	11689.1	Mouse metabolic/ transport/ demand reaction
MMALR	MMh2o[c] + MMnadp[c] + MMmthgxl[c] -> 2 MMh[c] + MMpyr[c] + MMnadph[c]	0	1000	11677.1	Mouse metabolic/ transport/ demand reaction
MMALR2	MMh[c] + MMnadph[c] + MMmthgxl[c] -> MMnadp[c] + MMacetol[c]	0	1000	110198.1 or 58810.2 or 11677.1 or 58810.1	Mouse metabolic/ transport/ demand reaction
MMALR3	MMh[c] + MMnadph[c] + MMacetol[c] -> MMnadp[c] + MM12ppd-S[c]	0	1000	110198.1 or 58810.2 or 11677.1 or 58810.1	Mouse metabolic/ transport/ demand reaction
MMAM6SAD	MMh2o[c] + MMnad[c] + MMamsa[c] -> 2 MMh[c] + MMnadh[c] + MMamuco[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMAMACR2p	0.5 MMo2[x] + MMdhcholestancoa[x] -> MMdhcholoylcoa[x] + MMh2o[x]	0	1000	17117.1 or 17117.2	Mouse metabolic/ transport/ demand reaction
MMAMACR2r	MMdhcholestancoa[r] + 0.5 MMo2[r] -> MMdhcholoylcoa[r] + MMh2o[r]	0	1000	17117.1 or 17117.2	Mouse metabolic/ transport/ demand reaction
MMAMACRp	MMcholcoar[x] -> MMcholcoas[x]	0	1000	17117.1 or 17117.2	Mouse metabolic/ transport/ demand reaction
MMAMACRr	MMcholcoar[r] -> MMcholcoas[r]	0	1000	17117.1 or 17117.2	Mouse metabolic/ transport/ demand reaction
MMAMANK	MMatp[c] + MMacmusa[c] -> MMadp[c] + MMh[c] + MMacmunap[c]	0	1000	50798.1 or 56174.1	Mouse metabolic/ transport/ demand reaction
MMAMCOXO	MMh2o[c] + MMh[c] + MMnadph[c] + MMamuco[c] -> MMnbd[c] + MMnadp[c] + MM2oxoadp[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMAMETr	MMamet[c] <=> MMamet[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMAMETt2m	MMamet[c] + MMahcys[m] <=> MMahcys[c] + MMamet[m]	-1000	1000	67582.1 or 67582.2 or 67582.3	Mouse metabolic/ transport/ demand reaction
MMAMETtn	MMamet[c] <=> MMamet[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMAMPDA	MMh2o[c] + MMh[c] + MMamp[c] -> MMnbd[c] + MMimp[c]	0	1000	109674.1 or 11717.1 or 109674.2 or 229665.1 or 109674.3	Mouse metabolic/ transport/ demand reaction
MMAMPTASECG	MMh2o[c] + MMcgly[c] -> MMcys-L[c] + MMgly[c]	0	1000	16790.1	Mouse metabolic/ transport/ demand reaction
MMAMPTASECGe	MMh2o[e] + MMcgly[c] -> MMcys-L[e] + MMgly[e]	0	1000	16790.1	Mouse metabolic/ transport/ demand reaction
MMAMPtp	MMamp[c] <=> MMamp[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMAMPtr	MMamp[c] <=> MMamp[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMAMY1e	8 MMh2o[e] + MMstrch1[e] -> 8 MMglc-D[e] + MMstrch2[e]	0	1000	100043684.1 or 20532.1 and 30962.1 or 17254.1 or 11722.1 or 100043684.2	Mouse metabolic/ transport/ demand reaction
MMAMY2e	8 MMh2o[e] + MMglygn2[e] -> 8 MMglc-D[e] + MMglygn4[e]	0	1000	100043684.1 or 20532.1 and 30962.1 or 17254.1 or 11722.1 or 100043684.2	Mouse metabolic/ transport/ demand reaction
MMANDRSTRNGLCte	MMh2o[c] + MMatp[c] + MMandrstrngk[c] -> MMadp[c] + MMh[c] + MMpi[c] + MMandrstrngk[e]	0	1000	17250.1	Mouse metabolic/ transport/ demand reaction
MMANDRSTRNGLCtr	MMandrstrngk[c] <=> MMandrstrngk[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMANDRSTRNte	MMandrstrn[e] <=> MMandrstrn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMANDRSTRNtr	MMandrstrn[r] <=> MMandrstrn[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMANTIPYRENEte	MMantipyrene[e] <=> MMantipyrene[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMAOBUTDsm	MMh[m] + MM2aobut[m] -> MMco2[m] + MMaact[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMAP4AH1	MMh2o[c] + MMap4a[c] -> MMatp[c] + 2 MMh[c] + MMamp[c]	0	1000	66401.1 or 66401.2 or 66401.3	Mouse metabolic/ transport/ demand reaction
MMAPAT2rm	MMakg[m] + MMala-B[m] <=> MMglu-L[m] + MMmsa[m]	-1000	1000	268860.2 or 268860.1	Mouse metabolic/ transport/ demand reaction
MMAPNNOXte	MMapnnox[e] <=> MMapnnox[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMAPOCF	MMapoC[c] + MMlys-L[c] -> MMh2o[c] + MMh[c] + MMapoC-Lys[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMAPOCFm	MMapoC[m] + MMlys-L[m] -> MMh[m] + MMh2o[m] + MMapoC-Lys[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMAPOC_LYS_BTNP	MMh2o[c] + MMapoC-Lys_btn[c] -> MMapoC[c] + MMbiocyt[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMAPOC_LYS_BTNPm	MMh2o[m] + MMapoC-Lys_btn[m] -> MMapoC[m] + MMbiocyt[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMAPPNNte	MMappnn[e] <=> MMappnn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMAPRGSTRNte	MMaprgstrn[e] <=> MMaprgstrn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMAPRTO2	MMh2o[c] + MMo2[c] + MMaprut[c] -> MMh2o2[c] + MMnbd[c] + MMoleabutn[c]	0	1000	109731.1 or 17161.1	Mouse metabolic/ transport/ demand reaction
MMAQCOBALt	MMaqcoba[e] <=> MMaqcoba[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARABR	MMh[c] + MMnadph[c] + MMarab-L[c] -> MMnadp[c] + MMabt[c]	0	1000	110198.1 or 58810.2 or 11677.1 or 58810.1	Mouse metabolic/ transport/ demand reaction
MMARAB_Lt	MMarab-L[e] <=> MMarab-L[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMARACHCOAtx	MMarachcoa[c] <=> MMarachcoa[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMARACHCPT1	MMcrn[c] + MMarachcoa[c] -> MMcoa[c] + MMarachcrn[c]	0	1000	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	Mouse metabolic/ transport/ demand reaction
MMARACHCPT2	MMcoa[m] + MMarachcrn[m] -> MMcrn[m] + MMarachcoa[m]	0	1000	12896.1	Mouse metabolic/ transport/ demand reaction
MMARACHCRNt	MMarachcrn[c] -> MMarachcrn[m]	0	1000	57279.1	Mouse metabolic/ transport/ demand reaction
MMARACHDCOAtx	MMarachdcoa[c] <=> MMarachdcoa[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMARACHDt2	MMarachd[e] <=> MMarachd[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARACHDtr	MMarachd[c] <=> MMarachd[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction

MMARACHFABPpmtc	MMarachd[u] -> MMarachd[c]	0	1000	(14719.1 or 12491.1)	Mouse metabolic/ transport/ demand reaction
MMARACHt	MMarach[e] <=> MMarach[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARGALArBATtc	MMala-L[c] + MMarg-L[u] -> MMala-L[u] + MMarg-L[c]	0	1000	(30962.1 and 20532.1)	Mouse metabolic/ transport/ demand reaction
MMARGATB0tc	2 MMna1[u] + MMcit[u] + MMarg-L[u] -> 2 MMna1[c] + MMcit[c] + MMarg-L[c]	0	1000	56774.1	Mouse metabolic/ transport/ demand reaction
MMARGDCm	MMth[m] + MMarg-L[m] -> MMco2[m] + MMagm[m]	0	1000	242669.1	Mouse metabolic/ transport/ demand reaction
MMARGLEUrBATtc	MMleu-L[c] + MMarg-L[u] -> MMleu-L[u] + MMarg-L[c]	0	1000	(30962.1 and 20532.1)	Mouse metabolic/ transport/ demand reaction
MMARGLYSex	MMarg-L[e] + MMlys-L[c] -> MMarg-L[c] + MMlys-L[e]	0	1000	330836.1 and 17254.1	Mouse metabolic/ transport/ demand reaction
MMARGN	MMth2o[c] + MMarg-L[c] -> MMorn[c] + MMurea[c]	0	1000	11846.1	Mouse metabolic/ transport/ demand reaction
MMARGNm	MMth2o[m] + MMarg-L[m] -> MMurea[m] + MMorn[m]	0	1000	11847.1	Mouse metabolic/ transport/ demand reaction
MMARGSL	MMargsuc[c] <=> MMfum[c] + MMarg-L[c]	-1000	1000	109900.1	Mouse metabolic/ transport/ demand reaction
MMARGSS	MMatp[c] + MMasp-L[c] + MMcitr-L[c] -> MMh[c] + MMamp[c] + MMppi[c] + MMargsuc[c]	0	1000	11898.1 or 11898.2	Mouse metabolic/ transport/ demand reaction
MMARGt4	MMna1[e] + MMarg-L[e] -> MMna1[c] + MMarg-L[c]	0	1000	56774.1	Mouse metabolic/ transport/ demand reaction
MMARGt5r	MMarg-L[e] <=> MMarg-L[c]	-1000	1000	11987.1	Mouse metabolic/ transport/ demand reaction
MMARGtiDF	MMarg-L[e] -> MMarg-L[c]	0	1000	69354.1 or 11989.1 or 11988.1 or 11987.1	Mouse metabolic/ transport/ demand reaction
MMARGtm	MMth[m] + MMarg-L[c] <=> MMh[c] + MMarg-L[m]	-1000	1000	18408.1 or 83885.1	Mouse metabolic/ transport/ demand reaction
MMARSA	MMth2o[l] + MMsgalside_hs[l] -> MMh[l] + MMgalside_hs[l] + MMso4[l]	0	1000	11883.1	Mouse metabolic/ transport/ demand reaction
MMARTCOAL1	MMcoa[c] + MMRtota[c] <=> MMRtotalcoa[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMARTCOAL2	MMcoa[c] + MMRtotaI2[c] <=> MMRtotal2coa[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMARTCOAL3	MMcoa[c] + MMRtotaI3[c] <=> MMRtotal3coa[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMARTFR11	MMpmtcoa[c] -> MMR1coa_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARTFR12	MMfadh2[m] + MMhdcoa[c] -> MMfad[m] + MMR1coa_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARTFR13	MMtdcoa[c] -> 0.875 MMR1coa_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARTFR202	MMth[m] + MMnadph[m] + 2 MMfadh2[m] + MMlnlncacoa[c] -> MMnadp[m] + 2 MMfad[m] + 1.125 MMR2coa_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARTFR203	MMth[m] + MMnadph[m] + 2 MMfadh2[m] + MMlnlncgcoa[c] -> MMnadp[m] + 2 MMfad[m] + 1.125 MMR2coa_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARTFR204	2 MMth[m] + 2 MMnadph[m] + 2 MMfadh2[m] + MMstrdnccoa[c] -> 2 MMnadp[m] + 2 MMfad[m] + 1.125 MMR2coa_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARTFR205	MMth[m] + MMnadph[m] + 2 MMfadh2[m] + MMdnlncgcoa[c] -> MMnadp[m] + 2 MMfad[m] + 1.25 MMR2coa_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARTFR206	2 MMth[m] + 2 MMnadph[m] + 2 MMfadh2[m] + MMarachdcoa[c] -> 2 MMnadp[m] + 2 MMfad[m] + 1.25 MMR2coa_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARTFR207	MMarachcoa[c] -> 1.25 MMR2coa_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARTFR208	2 MMth[m] + 2 MMnadph[m] + 3 MMfadh2[m] + MMtrnndncoa[c] -> 2 MMnadp[m] + 3 MMfad[m] + 1.25 MMR2coa_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARTFR209	2 MMth[m] + 2 MMnadph[m] + 2 MMfadh2[m] + MMadrncoa[c] -> 2 MMnadp[m] + 2 MMfad[m] + 1.375 MMR2coa_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARTFR210	MMth[m] + MMnadph[m] + MMfadh2[m] + MMlnlccoa[c] -> MMnadp[m] + MMfad[m] + 1.125 MMR2coa_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARTFR211	2 MMth[m] + 2 MMnadph[m] + 3 MMfadh2[m] + MMclpndcoa[c] -> 2 MMnadp[m] + 3 MMfad[m] + 1.375 MMR2coa_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARTFR212	2 MMth[m] + 2 MMnadph[m] + 3 MMfadh2[m] + MMdcsptn1coa[c] -> 2 MMnadp[m] + 3 MMfad[m] + 1.375 MMR2coa_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARTFR213	3 MMth[m] + 3 MMnadph[m] + 3 MMfadh2[m] + MMc226coa[c] -> 3 MMnadp[m] + 3 MMfad[m] + 1.375 MMR2coa_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARTFR31	MMstcoa[c] -> 1.125 MMR3coa_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARTFR32	MMfadh2[m] + MModecoa[c] -> MMfad[m] + 1.125 MMR3coa_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARTFR33	MMfadh2[m] + MMvaccoa[c] -> MMfad[m] + 1.125 MMR3coa_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARTFR34	2 MMfadh2[m] + MMhexdccoa[c] -> 2 MMfad[m] + 1.125 MMR3coa_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARTFR41	MMfadh2[m] + MMhdcoa[c] -> MMfad[m] + MMR4coa_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARTFR42	MMfadh2[m] + MModecoa[c] -> MMfad[m] + 1.125 MMR4coa_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARTFR43	MMfadh2[m] + MMvaccoa[c] -> MMfad[m] + 1.125 MMR4coa_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARTFR44	2 MMfadh2[m] + MMhexddccoa[c] -> 2 MMfad[m] + 1.125 MMR4coa_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARTFR45	MMfadh2[m] + MMtrvaccoa[c] -> MMfad[m] + 1.5 MMR4coa_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARTFR46	MMfadh2[m] + MMod2coa[c] -> MMfad[m] + 1.125 MMR4coa_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARTFR51	MMtgnccoa[c] -> 1.5 MMR5coa_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARTFR52	MMhexccoa[c] -> 1.625 MMR5coa_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARTFR53	2 MMth[m] + 2 MMnadph[m] + 2 MMfadh2[m] + MMeicosetccoa[c] -> 2 MMnadp[m] + 2 MMfad[m] + 1.25 MMR5coa_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARTFR54	2 MMth[m] + 2 MMnadph[m] + 3 MMfadh2[m] + MMtetpent6coa[c] -> 2 MMnadp[m] + 3 MMfad[m] + 1.5 MMR5coa_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARTFR55	2 MMth[m] + 2 MMnadph[m] + 3 MMfadh2[m] + MMtetpent3coa[c] -> 2 MMnadp[m] + 3 MMfad[m] + 1.5 MMR5coa_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARTFR56	2 MMth[m] + 2 MMnadph[m] + 2 MMfadh2[m] + MMtetter6coa[c] -> 2 MMnadp[m] + 2 MMfad[m] + 1.5 MMR5coa_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARTFR57	3 MMth[m] + 3 MMnadph[m] + 3 MMfadh2[m] + MMtethex3coa[c] -> 3 MMnadp[m] + 3 MMfad[m] + 1.5 MMR5coa_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARTFR61	MMfadh2[m] + MMhtd2coa[c] -> MMfad[m] + MMR6coa_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMARTPLM1	MMRtotalcoa[c] <=> MMpmtcoa[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMARTPLM1m	MMRtotalcoa[m] <=> MMpmtcoa[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMARTPLM2	MMRtotal2coa[c] <=> MMpmtcoa[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMARTPLM2m	MMRtotal2coa[m] <=> MMpmtcoa[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMARTPLM3	MMRtotal3coa[c] <=> MMpmtcoa[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMARTPLM3m	MMRtotal3coa[m] <=> MMpmtcoa[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMASAH1	MMh2o[l] + MMcrm_hs[l] -> MMRtota[l] + MMsphings[l]	0	1000	11886.1 or 11886.2	Mouse metabolic/ transport/ demand reaction
MMASCBOX	2 MMh[c] + MMascb-L[c] + 2 MMo2s[c] -> 2 MMh2o2[c] + MMdhdascb[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMASCBSVCTtc	MMh2o[c] + MMatp[c] + 2 MMna1[u] + MMascb-L[u] -> MMadp[c] + MMh[c] + MMpi[c] + 2 MMna1[c] + MMascb-L[c]	0	1000	20522.1 or 54338.1	Mouse metabolic/ transport/ demand reaction
MMASCBt	MMascb-L[e] <=> MMascb-L[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMASCBt4	MMna1[e] + MMascb-L[e] <=> MMna1[c] + MMascb-L[c]	0	1000	54338.2 or 20522.1 or 20522.2 or 54338.1	Mouse metabolic/ transport/ demand reaction
MMASNALANaEx	MMna1[e] + MMala-L[c] + MMasn-L[e] -> MMna1[c] + MMasn-L[c] + MMala-L[e]	0	1000	20514.1	Mouse metabolic/ transport/ demand reaction
MMASNATB0tc	2 MMna1[u] + MMcit[u] + MMasn-L[u] -> 2 MMna1[c] + MMcit[c] + MMasn-L[c]	0	1000	56774.1	Mouse metabolic/ transport/ demand reaction
MMASNB0AT1tc	MMna1[u] + MMasn-L[u] -> MMna1[c] + MMasn-L[c]	0	1000	(70008.1 or (74338.1 and 57394.1))	Mouse metabolic/ transport/ demand reaction
MMASNCYSNaEx	MMna1[e] + MMasn-L[e] + MMcys-L[c] -> MMna1[c] + MMasn-L[c] + MMcys-L[e]	0	1000	20514.1	Mouse metabolic/ transport/ demand reaction
MMASNGLNNaEx	MMna1[e] + MMasn-L[e] + MMgln-L[c] -> MMna1[c] + MMasn-L[c] + MMgln-L[e]	0	1000	20514.1	Mouse metabolic/ transport/ demand reaction
MMASNILELAT2tc	MMasn-L[e] + MMile-L[c] -> MMasn-L[c] + MMile-L[e]	0	1000	(20539.1 and 17254.1)	Mouse metabolic/ transport/ demand reaction
MMASNNm	MMh2o[m] + MMasn-L[m] -> MMasp-L[m] + MMnh4[m]	0	1000	66514.1	Mouse metabolic/ transport/ demand reaction
MMASNPHELAT2tc	MMasn-L[e] + MMphe-L[c] -> MMasn-L[c] + MMphe-L[e]	0	1000	(20539.1 and 17254.1)	Mouse metabolic/ transport/ demand reaction
MMASNS1	MMh2o[c] + MMatp[c] + MMasp-L[c] + MMgln-L[c] -> MMh[c] + MMglu-L[c] + MMamp[c] + MMppi[c] + MMasn-L[c]	0	1000	27053.1 or 27053.2 or 27053.3	Mouse metabolic/ transport/ demand reaction
MMASNSERNaEx	MMna1[e] + MMasn-L[e] + MMser-L[c] -> MMna1[c] + MMasn-L[c] + MMser-L[e]	0	1000	20514.1	Mouse metabolic/ transport/ demand reaction
MMASNTHRNaEx	MMna1[e] + MMasn-L[e] + MMthr-L[c] -> MMna1[c] + MMasn-L[c] + MMthr-L[e]	0	1000	20514.1	Mouse metabolic/ transport/ demand reaction
MMASN_X_SER_THRtr	MMAsn_X_Ser_Thr[r] <=> MMAsn_X_Ser_Thr[l]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMASNt4	MMna1[e] + MMasn-L[e] -> MMna1[c] + MMasn-L[c]	0	1000	105727.1 or 67760.1 or 69354.1 or 56774.1	Mouse metabolic/ transport/ demand reaction

MMASNtN1	MMh[c] + 2 MMna1[e] + MMasn-L[e] <=> MMh[e] + 2 MMna1[c] + MMasn-L[c]	0	1000	209837.1 or 76257.1	Mouse metabolic/ transport/ demand reaction
MMASNtm	MMasn-L[c] -> MMasn-L[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMASP1DC	MMh[c] + MMasp-L[c] -> MMco2[c] + MMala-B[c]	0	1000	14415.1 or 14415.2	Mouse metabolic/ transport/ demand reaction
MMASPCTr	MMasp-L[c] + MMcbp[c] <=> MMh[c] + MMpi[c] + MMcbasp[c]	-1000	1000	69719.1	Mouse metabolic/ transport/ demand reaction
MMASPDt6	MMh[e] + 3 MMna1[e] + MMk[c] + MMasp-D[e] -> MMh[c] + 3 MMna1[c] + MMasp-D[c] + MMk[e]	0	1000	242607.1 or 20511.1 or 20513.1 or 20510.1 or 20512.1	Mouse metabolic/ transport/ demand reaction
MMASPDxt	MMasp-D[x] <=> MMasp-D[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMASPGLUm	MMh[c] + MMglu-L[c] + MMasp-L[m] <=> MMh[m] + MMglu-L[m] + MMasp-L[c]	-1000	1000	78830.1 or 50799.1	Mouse metabolic/ transport/ demand reaction
MMASPNATm	MMasp-L[m] + MMaccoa[m] -> MMh[m] + MMcoa[m] + MMNacasp[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMASPTA	MMakg[c] + MMasp-L[c] <=> MMglu-L[c] + MMoaa[c]	-1000	1000	14718.1	Mouse metabolic/ transport/ demand reaction
MMASPTAm	MMakg[m] + MMasp-L[m] <=> MMglu-L[m] + MMoaa[m]	-1000	1000	14719.1	Mouse metabolic/ transport/ demand reaction
MMASPt6	MMh[e] + 3 MMna1[e] + MMk[c] + MMasp-L[e] -> MMh[c] + 3 MMna1[c] + MMasp-L[c] + MMk[e]	0	1000	242607.1 or 20511.1 or 20513.1 or 20510.1 or 20512.1	Mouse metabolic/ transport/ demand reaction
MMATP1ter	MMatp[c] + MMadp[r] <=> MMadp[c] + MMatp[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMATP2ter	MMatp[c] + MMamp[r] <=> MMamp[c] + MMatp[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMATPH1e	2 MMh2o[e] + MMatp[e] -> 2 MMh[e] + MMamp[e] + 2 MMpi[e]	0	1000	12495.1 or 12496.2 or 12497.1 or 12499.1 or 215446.1 or 12496.1	Mouse metabolic/ transport/ demand reaction
MMATPH2e	MMh2o[e] + MMadp[e] -> MMh[e] + MMamp[e] + MMpi[e]	0	1000	12495.1 or 12496.2 or 12497.1 or 12499.1 or 215446.1 or 12496.1	Mouse metabolic/ transport/ demand reaction
MMATPM	MMh2o[c] + MMatp[c] -> MMadp[c] + MMh[c] + MMpi[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMATPS4m	4 MMh[c] + MMadp[m] + MMpi[m] -> 3 MMh[m] + MMh2o[m] + MMatp[m]	0	1000	11947.1 and 11946.1 and 67126.1 and 11949.1 and 66043.1 or 11947.1 and 11949.2 and 66043.2 and 11946.3 and 67126.2 or 11947.1 and 11946.1 and 67126.1 and 66043.1 and 11949.2 or 11947.1 and 11949.2 and 66043.1 and 67126.2 and 11946.3 or 11947.1 and 11949.2 and 66043.2 and 11946.2 and 67126.2 or 11947.1 and 11946.1 and 67126.1 and 11949.2 and 66043.2 or 11947.1 and 66043.1 and 11949.2 and 11946.2 and 67126.2 or 11947.1 and 11949.1 and 66043.2 and 67126.2 and 11946.3 or 11947.1 and 11946.1 and 11949.1 and 66043.2 and 67126.2 or 11947.1 and 11949.1 and 11946.2 and 66043.2 and 67126.2 or 11947.1 and 67126.1 and 66043.1 and 11949.2 and 11946.3 or 11947.1 and 67126.1 and 11949.1 and 66043.1 and 11946.3 or 11947.1 and 67126.1 and 11949.1 and 66043.1 and 11946.2 or 11947.1 and 67126.1 and 11949.1 and 11946.2 and 66043.2 or 11947.1 and 11946.1 and 11949.1 and 66043.1 and 67126.2 or 11947.1 and 11946.1 and 11949.2 and 66043.1 and 67126.2 or 11947.1 and 67126.1 and 11949.1 and 66043.2 and 11946.3 or 11947.1 and 67126.1 and 66043.1 and 11949.2 and 11946.2 or 11947.1 and 11949.1 and 66043.1 and 11946.2 and 67126.2 or 11947.1 and 67126.1 and 11949.2 and 66043.2 and 11946.3 or 11947.1 and 11946.1 and 67126.1 and 11949.1 and 66043.2 or 11947.1 and 11946.1 and 11949.2 and 66043.2 and 67126.2 or 11947.1 and 11949.1 and 66043.1 and 67126.2 and 11946.3 or 11947.1 and 67126.1 and 11949.2 and 11946.2 and 66043.2 or 71679.2 and 11957.2 and 11958.1 and 11950.2 and 18195.1 and 57423.2 and 627998.1 and 228033.3 or 11957.2 and 71679.2 and 11950.1 and 11958.1 and 57423.2 and 18195.1 and 228033.3 and 627998.1 or 71679.2 and 11950.3 and 100039108.2 and 11958.1 and 18195.1 and 57423.2 and 627998.1 and 11957.3 or 71679.1 and 100039108.2 and 11958.1 and 11950.2 and 18195.1 and 627998.1 and 57423.3 and 11957.3 or 71679.2 and 11957.2 and 11950.1 and 228033.1 and 11958.1 and 57423.2 and 18195.1 and 627998.1 or 71679.2 and 100039108.1 and 11950.1 and 11957.1 and 11958.1 and 57423.2 and 18195.1 and 627998.1 or 71679.2 and 11950.1 and 11951.1 and 11957.4 and 11958.1 and 18195.1 and 627998.1 and 57423.3 or 71679.2 and 11957.1 and 11958.1 and 11950.2 and 18195.1 and 57423.2 and 228033.2 and 627998.1 or 71679.2 and 57423.1 and 11950.3 and 228033.1 and 11958.1 and 11957.4 and 18195.1 and 627998.1 or 71679.1 and 11951.1 and 11957.4 and 11958.1 and 11950.2 and 57423.2 and 18195.1 and 627998.1 or 11950.1 and 228033.1 and 71679.1 and 11958.1 and	Mouse metabolic/ transport/ demand reaction
MMATPasel	MMh2o[c] + MMatp[c] + 3 MMh[c] -> MMadp[c] + MMpi[c] + 4 MMh[l]	0	1000	2 and 18195.1 and 627998.1 and 57423.3 and 11951.2 or 11950.3 and 71679.1 and 11951.1 and 11958.1 and 11957.4 and 18195.1 and 627998.1 and 57423.3 or 71679.2 and 100039108.1 and 11957.1 and 11958.1 and 11950.2 and 18195.1 and 57423.2 and 627998.1 or 71679.1 and 228033.1 and 11957.5 and 11958.1 and 11950.2 and 18195.1 and 627998.1 and 57423.3 or 100039108.1 and 57423.1 and 71679.1 and 11958.1 and 11950.2 and 11957.4 and 18195.1 and 627998.1 or 71679.1 and 228033.1 and 11958.1 and 11950.2 and 18195.1 and 627998.1 and 57423.3 and 11957.3 or 71679.2 and 11950.1 and 11957.1 and 11951.1 and 11958.1 and 57423.2 and 18195.1 and 627998.1 or 71679.2 and 11950.3 and 11958.1 and 18195.1 and 57423.2 and 627998.1 and 228033.3 and 11957.3 or 11950.3 and 71679.1 and 11957.5 and 11958.1 and 18195.1 and 57423.2 and 627998.1 and 11951.2 or 71679.2 and 11957.2 and 100039108.1 and 11950.1 and 11958.1 and 57423.2 and 18195.1 and 627998.1 or 71679.2 and 57423.1 and 11958.1 and 11957.4 and 11950.2 and 18195.1 and 228033.2 and 627998.1 or 71679.2 and 57423.1 and 11957.1 and 11950.3 and 228033.1 and 11958.1 and 18195.1 and 627998.1 or 71679.2 and 11958.1 and 11950.2 and 18195.1 and 57423.2 and 627998.1 and 228033.3 and 11957.3 or 100039108.1 and 57423.1 and 11950.3 and 71679.1 and 11958.1 and 11957.4 and 18195.1 and 627998.1 or 71679.2 and 11950.3 and 100039108.2 and 11958.1 and 11957.4 and 18195.1 and 627998.1 and 57423.3 or 71679.2 and 11950.1 and 11957.5 and 11958.1 and 18195.1 and 627998.1 and 228033.3 and 57423.3 or 11957.2 and 71679.2 and 11950.1 and 100039108.2 and 11958.1 and 57423.2 and 18195.1 and 627998.1 or 11957.2 and 11950.3 and 71679.1 and 100039108.2 and 11958.1 and 18195.1 and 57423.2 and 627998.1 or 71679.2 and 11957.2 and 11958.1 and 11950.2 and 18195.1 and 627998.1 and 228033.3 and 57423.3 or 71679.2 and 11950.3 and 11957.5 and 11958.1 and 57423.2 and 18195.1 and 627998.1 and 228033.3 or 71679.2 and 11950.3 and 11957.5 and 11951.1 and 11958.1 and 18195.1 and 627998.1 and 57423.3 or 71679.2 and 57423.1 and 11957.5 and 11958.1 and 11950.2 and 18195.1 and 228033.2 and 627998.1 or 71679.2 and 57423.1 and 11957.1 and 11951.1 and 11958.1 and 11950.2 and 18195.1 and 627998.1 or 11957.2 and 71679.2 and 57423.1 and 11950.1 and 100039108.2 and 11958.1 and 18195.1 and 627998.1 or 71679.1 and 11951.1 and 11958.1 and 11950.2 and 57423.2 and 18195.1 and 627998.1 and 11957.2 or 71679.2 and 11950.1 and 228033.1 and	Mouse metabolic/ transport/ demand reaction
MMATPtm	MMadp[c] + MMatp[m] -> MMatp[c] + MMadp[m]	0	1000	11984.1 and 11974.1 and 140494.2 and 242341.1 and 114143.1 or 11984.1 and 11974.1 and 11972.1 and 140494.2 and 114143.1 or 11984.1 and 11974.1 and 11975.1 and 242341.1 and 114143.1 or 11984.1 and 11974.1 and 242341.1 and 114143.1 and 21871.1 or 11984.1 and 11974.1 and 140494.3 and 242341.1 and 114143.1 or 11984.1 and 27060.1 and 11974.1 and 242341.1 and 114143.1 or 11984.1 and 140494.1 and 11974.1 and 242341.1 and 114143.1 or 11984.1 and 11974.1 and 11972.1 and 140494.3 and 114143.1 or 11984.1 and 27060.1 and 11974.1 and 11972.1 and 114143.1 or 11984.1 and 11974.1 and 27060.2 and 11972.1 and 114143.1 or 11984.1 and 11974.1 and 27060.2 and 242341.1 and 114143.1 or 11984.1 and 140494.1 and 11974.1 and 11972.1 and 114143.1 or 11984.1 and 11974.1 and 11972.1 and 114143.1 and 21871.1 or 11984.1 and 11974.1 and 11972.1 and 11975.1 and 114143.1 or 66335.1 and 108664.2 and 338375.2 and 66144.1 and 11964.1 and 73834.1 and 74915.1 and 110935.1 or 66335.1 and 108664.3 and 66144.1 and 11964.1 and 11973.1 and 73834.1 and 66290.1 and 110935.1 or 108664.1 and 66144.1 and 11964.1 and 11973.1 and 73834.1 and 66237.1 and 66335.2 and 110935.1 or 108664.1 and 338375.2 and 66144.1 and 11964.1 and 11973.1 and 73834.1 and 66335.2 and 110935.1 or 11966.1 and 108664.1 and 66144.1 and 11964.1 and 68775.1 and 73834.1 and 66290.1 and 74915.1 or 11966.1 and 108664.1 and 338375.2 and 66144.1 and 11964.1 and 73834.1 and 68775.1 and 74915.1 or 11966.1 and 66237.2 and 66335.1 and 108664.2 and 66144.1 and 11964.1 and 73834.1 and 74915.1 or 11966.1 and 338375.1 and 108664.2 and 66144.1 and 11964.1 and 11973.1 and 68775.1 and 73834.1 or 11966.1 and 66335.1 and 108664.2 and 66144.1 and 11964.1 and 11973.1 and 73834.1 and 66237.1 or 11966.1 and 338375.1 and 108664.3 and 66144.1 and 11964.1 and 73834.1 and 74915.1 and 66335.2 or 66237.2 and 108664.3 and 66144.1 and 11964.1 and 68775.1 and 73834.1 and 74915.1 and 110935.1 or 66237.2 and 108664.1 and 66144.1 and 11964.1 and 73834.1 and 74915.1 and 66335.2 and 110935.1 or 11966.1 and 66237.2 and 66335.1 and 108664.3 and 66144.1 and 11964.1 and 11973.1 and 73834.1 or 108664.2 and 338375.2 and 66144.1 and 11964.1 and 73834.1 and 68775.1 and 74915.1 and 110935.1 or 338375.1 and 108664.1 and 66144.1 and 11964.1 and 73834.1 and 68775.1 and 74915.1 and 110935.1 or 66237.2 and 108664.3 and 66144.1 and 11964.1 and 11973.1 and 73834.1 and 66335.2 and	Mouse metabolic/ transport/ demand reaction
MMATPtn	MMatp[c] <=> MMatp[n]	-1000	1000	11739.1 or 433923.1 or 11740.1	Mouse metabolic/ transport/ demand reaction
MMATPtx	MMatp[c] <=> MMatp[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMAVITE1t	MMavite1[e] -> MMavite1[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMAVITE2t	MMavite2[e] -> MMavite2[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMA_MANASE	2 MMh2o[c] + MMm2mn[c] -> 2 MMman[c] + MMmn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMA_MANASEly	2 MMh2o[l] + MMm2mn[l] -> 2 MMman[l] + MMmn[l]	0	1000	73744.1	Mouse metabolic/ transport/ demand reaction
MMB3GALT3g	MMthcrm_hs[g] + MMudpacgal[g] -> MMh[g] + MMudp[g] + MMgbside_hs[g]	0	1000	17159.1	Mouse metabolic/ transport/ demand reaction
MMB3GALT41g	MMudpgal[g] + MMga2_hs[g] -> MMh[g] + MMudp[g] + MMga1_hs[g]	0	1000	26879.1 or 26879.2 or 26879.3 or 26879.4	Mouse metabolic/ transport/ demand reaction
MMB3GALT42g	MMudpgal[g] + MMgm2_hs[g] -> MMh[g] + MMudp[g] + MMgm1_hs[g]	0	1000	54218.1	Mouse metabolic/ transport/ demand reaction
MMB3GALT43g	MMudpgal[g] + MMgd2_hs[g] -> MMh[g] + MMudp[g] + MMgd1b_hs[g]	0	1000	54218.1	Mouse metabolic/ transport/ demand reaction
MMB3GALT44g	MMudpgal[g] + MMgt2_hs[g] -> MMh[g] + MMudp[g] + MMgt1c_hs[g]	0	1000	54218.1	Mouse metabolic/ transport/ demand reaction
MMB3GALT5g	MMudpgal[g] + MMgbside_hs[g] -> MMh[g] + MMudp[g] + MMgalgbside_hs[g]	0	1000	54218.1	Mouse metabolic/ transport/ demand reaction
MMB3GALTg	MMudpgal[g] + MMacglcgalgluside_hs[g] -> MMh[g] + MMudp[g] + MMgalacglcgalgluside_hs[g]	0	1000	93961.1 or 93961.2 or 93961.3 or 93961.4 or 93961.5	Mouse metabolic/ transport/ demand reaction

MMB3GNT11g	MMuacgam[g] + MMgal14acglcgalgluside_hs[g] -> MMfl[g] + MMudp[g] + MMacglcgal14acglcgalgluside_hs[g]	0	1000		Mouse metabolic/ transport/ demand reaction
MMB3GNT12g	MMuacgam[g] + MMgalacglcgal14acglcgalgluside_hs[g] -> MMfl[g] + MMudp[g] + MMacglc13galacglcgal14acglcgalgluside_hs[g]	0	1000	53625.1	Mouse metabolic/ transport/ demand reaction
MMB3GNT310g	MMudpgal[g] + MMacglcgalgluside_hs[g] -> MMfl[g] + MMudp[g] + MMgal14acglcgalgluside_hs[g]	0	1000	53625.1 or 53625.1	Mouse metabolic/ transport/ demand reaction
MMB3GNT311g	MMudpgal[g] + MMacgalfuc12gal14acglcgalgluside_hs[g] -> MMfl[g] + MMudp[g] + MMgalacgalfuc12gal14acglcgalgluside_hs[g]	0	1000	72297.1	Mouse metabolic/ transport/ demand reaction
MMB3GNT312g	MMudpgal[g] + MMacglcgal14acglcgalgluside_hs[g] -> MMfl[g] + MMudp[g] + MMgalacglcgal14acglcgalgluside_hs[g]	0	1000	72297.1	Mouse metabolic/ transport/ demand reaction
MMB3GNT313g	MMudpgal[g] + MMacgalfucgalacglcgal14acglcgalgluside_hs[g] -> MMfl[g] + MMudp[g] + MMgalacgalfucgalacglcgal14acglcgalgluside_hs[g]	0	1000	72297.1	Mouse metabolic/ transport/ demand reaction
MMB3GNT314g	MMudpgal[g] + MMacglcgalacglcgal14acglcgalgluside_hs[g] -> MMfl[g] + MMudp[g] + MMgalacglcgalacglcgal14acglcgalgluside_hs[g]	0	1000	72297.1	Mouse metabolic/ transport/ demand reaction
MMB3GNT315g	MMudpgal[g] + MMacglc13galacglcgal14acglcgalgluside_hs[g] -> MMfl[g] + MMudp[g] + MMgalacglc13galacglcgal14acglcgalgluside_hs[g]	0	1000	72297.1	Mouse metabolic/ transport/ demand reaction
MMB3GNT31g	MMudpgal[g] + MMthcrm_hs[g] -> MMfl[g] + MMudp[g] + MMgalthcrm_hs[g]	0	1000	72297.1	Mouse metabolic/ transport/ demand reaction
MMB3GNT32g	MMudpgal[g] + MMgalthcrm_hs[g] -> MMfl[g] + MMudp[g] + MMgalgalthcrm_hs[g]	0	1000	72297.1	Mouse metabolic/ transport/ demand reaction
MMB3GNT33g	MMudpgal[g] + MMgalgalthcrm_hs[g] -> MMfl[g] + MMudp[g] + MMgalgalgalthcrm_hs[g]	0	1000	72297.1	Mouse metabolic/ transport/ demand reaction
MMB3GNT34g	MMuacgam[g] + MMgalglcside_hs[g] -> MMfl[g] + MMudp[g] + MMacglcgalglcside_hs[g]	0	1000	72297.1	Mouse metabolic/ transport/ demand reaction
MMB3GNT35g	MMudpgal[g] + MMacglcgalglcside_hs[g] -> MMfl[g] + MMudp[g] + MMgalacglcgalglcside_hs[g]	0	1000	72297.1	Mouse metabolic/ transport/ demand reaction
MMB3GNT36g	MMacgal[g] + MMglcside_hs[g] -> MMacglcglcside_hs[g] + MMh2o[g]	0	1000	72297.1	Mouse metabolic/ transport/ demand reaction
MMB3GNT37g	MMudpgal[g] + MMgm2a_hs[g] -> MMfl[g] + MMudp[g] + MMgm1a_hs[g]	0	1000	72297.1	Mouse metabolic/ transport/ demand reaction
MMB3GNT39g	MMudpgal[g] + MMgluside_hs[g] -> MMgalgluside_hs[g] + MMfl[g] + MMudp[g]	0	1000	72297.1	Mouse metabolic/ transport/ demand reaction
MMB3GNT51g	MMgalgluside_hs[g] + MMuacgam[g] -> MMfl[g] + MMudp[g] + MMacglcgalgluside_hs[g]	0	1000	72297.1	Mouse metabolic/ transport/ demand reaction
MMBAAT1x	MMgly[x] + MMcholcoa[x] -> MMcoa[x] + MMgchola[x]	0	1000	108105.1	Mouse metabolic/ transport/ demand reaction
MMBAAT2x	MMcholcoa[x] + MMtaur[x] -> MMcoa[x] + MMtchola[x]	0	1000	12012.1	Mouse metabolic/ transport/ demand reaction
MMBAAT3x	MMgly[x] + MMdgcholcoa[x] -> MMcoa[x] + MMdgchol[x]	0	1000	12012.1	Mouse metabolic/ transport/ demand reaction
MMBAAT4x	MMgly[x] + MMdcholcoa[x] -> MMcoa[x] + MMgdchola[x]	0	1000	12012.1	Mouse metabolic/ transport/ demand reaction
MMBAAT5x	MMtaur[x] + MMdcholcoa[x] -> MMcoa[x] + MMtdchola[x]	0	1000	12012.1	Mouse metabolic/ transport/ demand reaction
MMBACCL	MMatp[c] + MMh[c] + MMbtn[c] -> MMppi[c] + MMbtamp[c]	0	1000	12012.1	Mouse metabolic/ transport/ demand reaction
MMBACCLm	MMfl[m] + MMatp[m] + MMbtn[m] -> MMppi[m] + MMbtamp[m]	0	1000	110948.1	Mouse metabolic/ transport/ demand reaction
MMBALABETAtc	2 MMma1[u] + MMcl[u] + MMala-B[u] -> 2 MMma1[c] + MMcl[c] + MMala-B[c]	0	1000	110948.1	Mouse metabolic/ transport/ demand reaction
MMBALAPAT1tc	MMfl[u] + MMala-B[u] -> MMfl[c] + MMala-B[c]	0	1000	56774.1	Mouse metabolic/ transport/ demand reaction
MMBALAVECSEC	MMh2o[c] + MMatp[c] + 3 MMala-B[c] -> MMadp[c] + MMfl[c] + MMpi[c] + 3 MMala-B[e]	0	1000	215335.1	Mouse metabolic/ transport/ demand reaction
MMBALAtmr	MMala-B[c] <=> MMala-B[m]	-1000	1000	22348.1	Mouse metabolic/ transport/ demand reaction
MMBAMPPALDOX	MMh2o[c] + MMbamppald[c] + MMnad[c] -> 2 MMfl[c] + MMnadh[c] + MMala-B[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMBAMPPALDOXm	MMh2o[m] + MMnad[m] + MMbamppald[m] -> 2 MMfl[m] + MMnadh[m] + MMala-B[m]	0	1000	19378.1 or 56752.1 or 110695.1 or 11668.1 or 11671.1 or 19378.2 or 19378.3	Mouse metabolic/ transport/ demand reaction
MMBBHOX	MMo2[c] + MMaldg[c] + MM4tmeabutn[c] -> MMco2[c] + MMcrn[c] + MMsuacr[c]	0	1000	11669.1 or 212647.1 or 212647.2 or 72535.1	Mouse metabolic/ transport/ demand reaction
MMBCDO	MMo2[c] + MMcaro[c] -> 2 MMretinal[c]	0	1000	170442.1	Mouse metabolic/ transport/ demand reaction
MMBDHm	MMnad[m] + MMhhb[m] <=> MMfl[m] + MMnadh[m] + MMacac[m]	-1000	1000	63857.1	Mouse metabolic/ transport/ demand reaction
MMBDMT_L	0.1 MMchito2pdol_L[c] + MMgdpmann[c] -> MMfl[c] + MMgdp[c] + 0.1 MMmpdol_L[c]	0	1000	71911.1 or 71911.2 or 71911.3	Mouse metabolic/ transport/ demand reaction
MMBDMT_U	MMgdpmann[c] + 0.1 MMchito2pdol_U[c] -> MMfl[c] + MMgdp[c] + 0.1 MMmpdol_U[c]	0	1000	208211.1	Mouse metabolic/ transport/ demand reaction
MMBETALDHx	MMh2o[c] + MMnad[c] + MMbetald[c] -> 2 MMfl[c] + MMnadh[c] + MMgbb[c]	0	1000	208211.1	Mouse metabolic/ transport/ demand reaction
MMBETALDHxm	MMh2o[m] + MMnad[m] + MMbetald[m] -> 2 MMfl[m] + MMnadh[m] + MMgbb[m]	0	1000	56752.1	Mouse metabolic/ transport/ demand reaction
MMBGLCt	MMfl[e] + MMbglc[e] <=> MMfl[c] + MMbglc[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMBGLUGCHe	MMbglc[u] + MMgchola[u] -> MMglgchb[u]	0	1000		Mouse metabolic/ transport/ demand reaction
MMBGLUGCHt	MMbe[e] + MMglgchlo[e] <=> MMfl[c] + MMglgchlo[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMBGLUTCHLe	MMbgk[u] + MMtchola[u] -> MMgltcho[u]	0	1000		Mouse metabolic/ transport/ demand reaction
MMBGLUTCHLt	MMfl[e] + MMgltcho[e] <=> MMfl[c] + MMgltcho[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMBGLUTDECHOe	MMbgk[u] + MMtdechola[u] -> MMgltdechol[u]	0	1000		Mouse metabolic/ transport/ demand reaction
MMBGLUTDECHOt	MMfl[e] + MMgltdechol[e] <=> MMfl[c] + MMgltdechol[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMBHBt	MMfl[e] + MMhbhb[e] <=> MMfl[c] + MMhbhb[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMBHBtm	MMfl[c] + MMhbhb[c] <=> MMfl[m] + MMhbhb[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMBHMT	MMhcys-L[c] + MMglyb[c] -> MMdmgly[c] + MMmet-L[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMBILDGLCURte	MMh2o[c] + MMatp[c] + MMbildglcur[c] <=> MMadp[c] + MMfl[c] + MMpi[c] + MMbildglcur[e]	0	0	12116.1 or 64918.1	Mouse metabolic/ transport/ demand reaction
MMBILDGLCURtr	MMbildglcur[c] <=> MMbildglcur[r]	-1000	1000	17250.1	Mouse metabolic/ transport/ demand reaction
MMBILGLCURte	MMh2o[c] + MMatp[c] + MMbilglcur[c] <=> MMadp[c] + MMfl[c] + MMpi[c] + MMbilglcur[e]	0	0		Mouse metabolic/ transport/ demand reaction
MMBILGLCURtr	MMbilglcur[c] <=> MMbilglcur[r]	-1000	1000	17250.1	Mouse metabolic/ transport/ demand reaction
MMBILIRED	MMfl[c] + MMnadph[c] + MMbiliverd[c] -> MMnadp[c] + MMbilirub[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMBILIRUBt2	MMhco3[c] + MMbilirub[e] <=> MMhco3[e] + MMbilirub[c]	-1000	1000	233016.1 or 109778.1	Mouse metabolic/ transport/ demand reaction
MMBILIRUBtr	MMbilirub[c] <=> MMbilirub[r]	-1000	1000	18669.1	Mouse metabolic/ transport/ demand reaction
MMBIOCYTtn	MMbiocyt[c] <=> MMbiocyt[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMBMTer_L	0.1 MMdolmanp_L[r] + MMmemgacpail_hs[r] -> 0.1 MMdolp_L[r] + MMfl[r] + MMm2emgacpail_hs[r]	0	1000		Mouse metabolic/ transport/ demand reaction
MMBMTer_U	MMmemgacpail_hs[r] + 0.1 MMdolmanp_U[r] -> MMfl[r] + MMm2emgacpail_hs[r] + 0.1 MMdolp_U[r]	0	1000	55981.1	Mouse metabolic/ transport/ demand reaction
MMBPNT	MMh2o[c] + MMpap[c] -> MMpi[c] + MMamp[c]	0	1000	55981.1	Mouse metabolic/ transport/ demand reaction
MMBPNT2	MMh2o[c] + MMpaps[c] -> MMpi[c] + MMaps[c]	0	1000	23827.1	Mouse metabolic/ transport/ demand reaction
MMBTND1	MMh2o[c] + MMbiocyt[c] -> MMlys-L[c] + MMbtn[c]	0	1000	23827.1	Mouse metabolic/ transport/ demand reaction
MMBTND1n	MMbiocyt[n] + MMh2o[n] -> MMbtn[n] + MMlys-L[n]	0	1000	26363.1	Mouse metabolic/ transport/ demand reaction
MMBTNDe	MMh2o[e] + MMbiocyt[e] -> MMlys-L[e] + MMbtn[e]	0	1000	26363.1	Mouse metabolic/ transport/ demand reaction
MMBTNDm	MMh2o[m] + MMbiocyt[m] -> MMlys-L[m] + MMbtn[m]	0	1000	26363.1	Mouse metabolic/ transport/ demand reaction
MMBTNPL	MMapoC-Lys[c] + MMbtamp[c] -> MMfl[c] + MMamp[c] + MMapoC-Lys_btn[c]	0	1000	26363.1	Mouse metabolic/ transport/ demand reaction
MMBTNPLm	MMapoC-Lys[m] + MMbtamp[m] -> MMfl[m] + MMamp[m] + MMapoC-Lys_btn[m]	0	1000	110948.1	Mouse metabolic/ transport/ demand reaction
MMBTNTe	MMbtn[e] -> MMbtn[e]	0	1000	110948.1	Mouse metabolic/ transport/ demand reaction
MMBTNt2	MMfl[e] + MMbtn[e] <=> MMfl[c] + MMbtn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMBTNt2m	MMfl[c] + MMbtn[c] <=> MMfl[m] + MMbtn[m]	-1000	1000	20501.1	Mouse metabolic/ transport/ demand reaction
MMBTNt3i	MMh2o[c] + MMatp[c] + 2 MMma1[e] + MMbtn[e] -> MMadp[c] + MMfl[c] + MMpi[c] + 2 MMma1[c] + MMbtn[c]	0	1000	20501.1	Mouse metabolic/ transport/ demand reaction
MMBTNt4i	MMfl[c] + MMbtn[e] -> MMfl[e] + MMbtn[c]	0	1000	330064.1	Mouse metabolic/ transport/ demand reaction
MMBTNtn	MMbtn[c] <=> MMbtn[n]	-1000	1000	80721.1	Mouse metabolic/ transport/ demand reaction
MMBUP2	MMh2o[c] + 2 MMfl[c] + MM3sib[c] -> MMmbsl[c] + MMco2[c] + MM3sib-D[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMBUTt2m	MMfl[c] + MMbut[c] <=> MMfl[m] + MMbut[m]	-1000	1000	103149.1	Mouse metabolic/ transport/ demand reaction
MMBUTt2r	MMfl[e] + MMbut[e] <=> MMfl[c] + MMbut[c]	0	1000	20501.1	Mouse metabolic/ transport/ demand reaction
MMBVITEt	MMbvite[e] -> MMbvite[c]	0	1000	20501.1	Mouse metabolic/ transport/ demand reaction
MMBZt	MMbz[e] <=> MMbz[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMBZtr	MMbz[c] <=> MMbz[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMB_MANNASEly	MMh2o[l] + MMmnt[l] -> MMacgam[l] + MMmnn[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MMC110CPT2m	MMcoa[m] + MMdmmoncrn[m] -> MMcrn[m] + MMdmmoncoa[m]	0	1000	110173.1	Mouse metabolic/ transport/ demand reaction

MMC14STRr	MMh[r] + MM44mxtr[r] + MMnadph[r] -> MM44mxym[r] + MMnadp[r]	0	1000		Mouse metabolic/ transport/ demand reaction
MMC160CPT1c	MMcrn[c] + MMpmtcoa[c] <=> MMcoa[c] + MMpmtcrn[c]	-1000	1000	73166.1	Mouse metabolic/ transport/ demand reaction
MMC160CPT2	MMcoa[m] + MMpmtcrn[m] -> MMcrn[m] + MMpmtcoa[m]	0	1000	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	Mouse metabolic/ transport/ demand reaction
MMC160CRNt	MMpmtcrn[c] -> MMpmtcrn[m]	0	1000	12896.1	Mouse metabolic/ transport/ demand reaction
MMC161CPT12	MMcrn[c] + MMhtdd2coa[c] -> MMcoa[c] + MMhtdd2crn[c]	0	1000	57279.1	Mouse metabolic/ transport/ demand reaction
MMC161CPT1c	MMcrn[c] + MMhtdcoa[c] <=> MMcoa[c] + MMhtdcecrn[c]	-1000	1000	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	Mouse metabolic/ transport/ demand reaction
MMC161CPT22	MMcoa[m] + MMhtdd2crn[m] -> MMcrn[m] + MMhtdd2coa[m]	0	1000	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	Mouse metabolic/ transport/ demand reaction
MMC161CPT2m	MMcoa[m] + MMhtdcecrn[m] <=> MMcrn[m] + MMhtdcoa[m]	-1000	1000	12896.1	Mouse metabolic/ transport/ demand reaction
MMC161CRN2t	MMhtdd2crn[c] -> MMhtdd2crn[m]	0	1000	12896.1	Mouse metabolic/ transport/ demand reaction
MMC161CRNt	MMhtdcecrn[c] -> MMhtdcecrn[m]	0	1000	57279.1	Mouse metabolic/ transport/ demand reaction
MMC180CPT1	MMcrn[c] + MMstcoa[c] -> MMcoa[c] + MMstcrn[c]	0	1000	57279.1	Mouse metabolic/ transport/ demand reaction
MMC180CPT2	MMcoa[m] + MMstcrn[m] -> MMcrn[m] + MMstcoa[m]	0	1000	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	Mouse metabolic/ transport/ demand reaction
MMC180CRNt	MMstcrn[c] -> MMstcrn[m]	0	1000	12896.1	Mouse metabolic/ transport/ demand reaction
MMC181CPT1c	MMcrn[c] + MModecoa[c] <=> MMcoa[c] + MModecrn[c]	-1000	1000	57279.1	Mouse metabolic/ transport/ demand reaction
MMC181CPT2m	MMcoa[m] + MModecrn[m] <=> MMcrn[m] + MModecoa[m]	-1000	1000	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	Mouse metabolic/ transport/ demand reaction
MMC181CRNt	MModecrn[c] -> MModecrn[m]	0	1000	12896.1	Mouse metabolic/ transport/ demand reaction
MMC204CPT1	MMcrn[c] + MMarachdcoa[c] -> MMcoa[c] + MMarachdcrn[c]	0	1000	57279.1	Mouse metabolic/ transport/ demand reaction
MMC204CPT2	MMcoa[m] + MMarachdcrn[m] -> MMcrn[m] + MMarachdcoa[m]	0	1000	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	Mouse metabolic/ transport/ demand reaction
MMC204CRNt	MMarachdcrn[c] -> MMarachdcrn[m]	0	1000	12896.1	Mouse metabolic/ transport/ demand reaction
MMC20CPT1	MMaccoa[c] + MMcrn[c] -> MMcoa[c] + MMacrn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMC226COAtx	MMc226coa[c] <=> MMc226coa[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMC226CPT1	MMcrn[c] + MMc226coa[c] -> MMcoa[c] + MMc226crn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMC226CPT2	MMcoa[m] + MMc226crn[m] -> MMcrn[m] + MMc226coa[m]	0	1000	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	Mouse metabolic/ transport/ demand reaction
MMC226CRNt	MMc226crn[c] -> MMc226crn[m]	0	1000	12896.1	Mouse metabolic/ transport/ demand reaction
MMC2M26DCOAHLm	MMh2o[m] + MMc2m26dcoa[m] <=> MM3h26dm5coa[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMC2M26DCOAHLx	MMh2o[x] + MMc2m26dcoa[x] <=> MM3h26dm5coa[x]	-1000	1000	11992.1 or 231086.1 or 97212.1	Mouse metabolic/ transport/ demand reaction
MMC3STDH1Pr	MMnadp[r] + MM44mxym_int1[r] -> MMh[r] + MMnadph[r] + MM44mxym_int2[r] + MMco2[r]	0	1000	74147.1 or 51798.1	Mouse metabolic/ transport/ demand reaction
MMC3STDH1r	MM44mxym_int1[r] + MMnad[r] -> MMh[r] + MM44mxym_int2[r] + MMco2[r] + MMnadh[r]	0	1000	18194.1	Mouse metabolic/ transport/ demand reaction
MMC3STKR2r	MMh[r] + MMnadph[r] + MMzym_int2[r] -> MMnadp[r] + MMzymst[r]	0	1000	18194.1	Mouse metabolic/ transport/ demand reaction
MMC4STMO1r	3 MMo2[r] + 3 MMh[r] + 3 MMnadph[r] + MM44mxym[r] -> 4 MMh2o[r] + 3 MMnadp[r] + MM44mxym_int1[r]	0	1000	15488.1	Mouse metabolic/ transport/ demand reaction
MMC4STMO2Pr	MMo2[r] + MMnadp[r] + MM44mxym_int2[r] -> MMh[r] + MMnadph[r] + MMco2[r] + MMzym_int2[r]	0	1000	66234.1	Mouse metabolic/ transport/ demand reaction
MMC4STMO2r	MMo2[r] + MM44mxym_int2[r] + MMnad[r] -> MMh[r] + MMco2[r] + MMnadh[r] + MMzym_int2[r]	0	1000	18194.1	Mouse metabolic/ transport/ demand reaction
MMCAATPS	MMh2o[c] + MMatp[c] + 2 MMca2[c] -> MMadp[c] + MMpi[c] + MMh[e] + 2 MMca2[e]	0	1000	66234.1 or 18194.1	Mouse metabolic/ transport/ demand reaction
MMCAMPt	MMh2o[c] + MMatp[c] + MMcamp[c] -> MMadp[c] + MMh[c] + MMpi[c] + MMcamp[e]	0	1000	11941.1 or 67972.1 or 381290.1 or 320707.1	Mouse metabolic/ transport/ demand reaction
MMCARNCNc	MMh2o[c] + MMcarn[c] <=> MMala-B[c] + MMbis-L[c]	-1000	1000	27416.1 or 27416.2 or 239273.1	Mouse metabolic/ transport/ demand reaction
MMCARO3r	MMcaro[e] <=> MMcaro[c]	0	1000	(338403.1 or 66054.1)	Mouse metabolic/ transport/ demand reaction
MMCARPEPT1tc	MMh[u] + MMcarn[u] -> MMh[c] + MMcarn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCARVEOLte	MMcarveol[e] <=> MMcarveol[c]	0	1000	215335.1	Mouse metabolic/ transport/ demand reaction
MMCARhPTtc	MMcarn[l] -> MMh[l] + MMcarn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCAT2p	MMh2o2[x] + MMetoh[x] -> MMacald[x] + 2 MMh2o[x]	0	1000	(65221.1 or 100561.1)	Mouse metabolic/ transport/ demand reaction
MMCATm	2 MMh2o2[m] -> MMo2[m] + 2 MMh2o[m]	0	1000	12359.1	Mouse metabolic/ transport/ demand reaction
MMCATp	2 MMh2o2[x] -> MMo2[x] + 2 MMh2o[x]	0	1000	12359.1	Mouse metabolic/ transport/ demand reaction
MMCAt7r	3 MMna1[e] + MMca2[c] <=> 3 MMna1[c] + MMca2[e]	0	1000	12359.1	Mouse metabolic/ transport/ demand reaction
MMCBL2OR	MMh[c] + MMnadh[c] + 2 MMaqcobal[c] -> 2 MMh2o[c] + MMnad[c] + 2 MMcbl2[c]	0	1000	110893.1 or 110893.2 or 110891.1 or 20541.1 or 110893.3 or 110893.4 or 110893.5 or 110893.6	Mouse metabolic/ transport/ demand reaction
MMCBL2tm	MMcbl2[c] -> MMcbl2[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCBLATm	MMh[m] + MMatp[m] + MMcbl1[m] <=> MMadocbl[m] + MMppp[m]	-1000	1000	109136.1	Mouse metabolic/ transport/ demand reaction
MMCBLTDe_r	MMadocbl[c] <=> MMadocbl[e]	-1000	1000	109136.1	Mouse metabolic/ transport/ demand reaction
MMCBLtlu	MMadocbl[u] -> MMadocbl[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCBPPer	MMh[r] + MMctp[r] + MMglc-D[r] -> MMco2[r] + MMg6p[r] + MMeth4[r]	0	1000	(14603.1 or 65969.1 or 93835.1)	Mouse metabolic/ transport/ demand reaction
MMCBPS	MMh2o[c] + 2 MMatp[c] + MMhco3[c] + MMgln-L[c] -> 2 MMadp[c] + 2 MMh[c] + MMpi[c] + MMglu-L[c] + MMcbp[c]	0	1000	14378.1 or 14377.1 or 68401.1	Mouse metabolic/ transport/ demand reaction
MMCBPSam	2 MMatp[m] + MMhco3[m] + MMnsh4[m] -> 2 MMh[m] + 2 MMadp[m] + MMpi[m] + MMcbp[m]	0	1000	69719.1	Mouse metabolic/ transport/ demand reaction
MMCBPter	MMpi[c] + MMppi[c] + MMcbp[c] <=> MMcbp[r] + MMpi[r] + MMppi[r]	-1000	1000	227231.1 or 227231.2	Mouse metabolic/ transport/ demand reaction
MMCBR1	MMh[c] + MMnadph[c] + MMprostg1[c] -> MMnadp[c] + MMprostge1[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCBR2	MMh[c] + MMnadph[c] + MMprostge2[c] -> MMnadp[c] + MMprostgf2[c]	0	1000	12408.1	Mouse metabolic/ transport/ demand reaction
MMCCA_D3t	MMcca_d3[c] -> MMcca_d3[e]	0	1000	12408.1	Mouse metabolic/ transport/ demand reaction
MMCCA_D3tm	MMcca_d3[m] -> MMcca_d3[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCDIPTr	MMcdpdag_hs[c] + MMinost[c] <=> MMh[c] + MMcmp[c] + MMpail_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMCDPDAGtm	MMcdpdag_hs[c] <=> MMcdpdag_hs[m]	-1000	1000	52858.1 or 52858.2	Mouse metabolic/ transport/ demand reaction
MMCDS	MMh[c] + MMpa_hs[c] + MMctp[c] -> MMppi[c] + MMcdpdag_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCDSm	MMh[m] + MMctp[m] + MMpa_hs[m] -> MMppi[m] + MMcdpdag_hs[m]	0	1000	74596.1	Mouse metabolic/ transport/ demand reaction
MMCEPTC	MMcdpcho[c] + MMdag_hs[c] -> MMh[c] + MMcmp[c] + MMpchol_hs[c]	0	1000	110911.1	Mouse metabolic/ transport/ demand reaction
MMCEPTE	MMcdpea[c] + MMdag_hs[c] -> MMh[c] + MMcmp[c] + MMpe_hs[c]	0	1000	212862.1 or 99712.1	Mouse metabolic/ transport/ demand reaction
MMCERK	MMatp[c] + MMcrm_hs[c] -> MMadp[c] + MMh[c] + MMcrmp_hs[c]	0	1000	99712.1	Mouse metabolic/ transport/ demand reaction
MMCERT1gt	MMcrm_hs[c] <=> MMcrm_hs[g]	-1000	1000	223753.1 or 223753.2	Mouse metabolic/ transport/ demand reaction
MMCERT1rt	MMcrm_hs[c] <=> MMcrm_hs[r]	-1000	1000	68018.1	Mouse metabolic/ transport/ demand reaction
MMCERT2gt	MMgluside_hs[c] <=> MMgluside_hs[g]	-1000	1000	68018.1	Mouse metabolic/ transport/ demand reaction
MMCERT2rt	MMgluside_hs[c] <=> MMgluside_hs[r]	-1000	1000	68018.1	Mouse metabolic/ transport/ demand reaction
MMCGLY3_2_	2 MMh[e] + MMcgly[e] -> 2 MMh[c] + MMcgly[c]	0	1000	68018.1	Mouse metabolic/ transport/ demand reaction
MMCGMPt	MMh2o[c] + MMatp[c] + MM35cgmp[c] -> MMadp[c] + MMh[c] + MMpi[c] + MM35cgmp[e]	0	1000	57738.1	Mouse metabolic/ transport/ demand reaction
MMCH25H	MMo2[r] + MMh[r] + MMnadph[r] + MMchsterol[r] -> MMh2o[r] + MMnadp[r] + MMsul25oh[r]	0	1000	27416.1 or 27416.2 or 239273.1	Mouse metabolic/ transport/ demand reaction
MMCHAT	MMaccoa[c] + MMchol[c] <=> MMcoa[c] + MMach[c]	-1000	1000	12642.1	Mouse metabolic/ transport/ demand reaction
MMCHATn	MMaccoa[n] + MMchol[n] <=> MMach[n] + MMcoa[n]	-1000	1000	12647.1 or 12647.2 or 12647.3 or 12647.4	Mouse metabolic/ transport/ demand reaction
MMCHLP	MMh2o[c] + MMcholp[c] -> MMpi[c] + MMchol[c]	0	1000	12647.1 or 12647.2 or 12647.3 or 12647.4	Mouse metabolic/ transport/ demand reaction
MMCHLPCTD	MMh[c] + MMctp[c] + MMcholp[c] -> MMppi[c] + MMcdpcho[c]	0	1000	237928.1	Mouse metabolic/ transport/ demand reaction
MMCHLtm	MMchol[c] <=> MMchol[m]	-1000	1000	13026.1 or 236899.1	Mouse metabolic/ transport/ demand reaction
MMCHOLABCAet	MMh2o[c] + MMatp[c] + MMchsterol[c] -> MMadp[c] + MMh[c] + MMpi[c] + MMchsterol[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCHOLABEtc	MMh2o[c] + MMatp[c] + MMchsterol[c] -> MMadp[c] + MMh[c] + MMpi[c] + MMchsterol[u]	0	1000	11303.1	Mouse metabolic/ transport/ demand reaction
MMCHOLATEt2	2 MMna1[e] + MMcholate[e] -> 2 MMna1[c] + MMcholate[c]	0	1000	(27409.1 and 67470.1)	Mouse metabolic/ transport/ demand reaction
MMCHOLATEt3	MMh2o[c] + MMatp[c] + MMcholate[c] -> MMadp[c] + MMh[c] + MMpi[c] + MMcholate[e]	0	1000	20494.1 or 20493.1	Mouse metabolic/ transport/ demand reaction
MMCHOLD2m	MMfad[m] + MMchol[m] -> MMfadh2[m] + MMbetald[m]	0	1000	27413.1 or 76408.2 or 76408.3 or 76408.1	Mouse metabolic/ transport/ demand reaction
MMCHOLESTTDe	MMchsterol[c] <=> MMchsterol[e]	0	1000	218865.1	Mouse metabolic/ transport/ demand reaction
MMCHOLETDtu	MMchsterol[u] <=> MMchsterol[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMCHOLK	MMatp[c] + MMchol[c] -> MMadp[c] + MMh[c] + MMcholp[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCHOLNPtc	MMchsterol[u] -> MMchsterol[c]	0	1000	12651.1 or 12660.1 or 12651.2 or 12660.2	Mouse metabolic/ transport/ demand reaction

MMCHOLPtg	MMcholp[c] <=> MMcholp[g]	-1000	1000	237636.1	Mouse metabolic/ transport/ demand reaction
MMCHOLPtl	MMcholp[c] <=> MMcholp[l]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMCHOLt4	MMna1[e] + MMchol[e] <=> MMna1[c] + MMchol[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCHOLtg	MMchol[g] <=> MMchol[c]	-1000	1000	63993.1	Mouse metabolic/ transport/ demand reaction
MMCHOLtn	MMchol[c] <=> MMchol[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMCHOLtr	MMchol[r] <=> MMchol[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMCHOLtu	MMchol[e] <=> MMchol[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCHSTEROLSULT	MMpaps[c] + MMchsterol[c] -> MMh[c] + MMpap[c] + MMchsterols[c]	0	1000	20518.1 or 20520.1 or 20518.2	Mouse metabolic/ transport/ demand reaction
MMCHSTEROLt	MMh2o[c] + MMatp[c] + MMchsterol[c] -> MMadp[c] + MMh[c] + MMpi[c] + MMchsterol[e]	0	1000	54200.1	Mouse metabolic/ transport/ demand reaction
MMCHSTEROLt1	MMchsterol[l] <=> MMchsterol[m]	-1000	1000	11303.1	Mouse metabolic/ transport/ demand reaction
MMCHSTEROLt2	MMchsterol[r] <=> MMchsterol[m]	-1000	1000	59045.1	Mouse metabolic/ transport/ demand reaction
MMCHSTEROLt3	MMchsterol[c] <=> MMchsterol[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMCHSTEROLtg	MMh2o[c] + MMatp[c] + MMchsterol[g] -> MMadp[c] + MMh[c] + MMpi[c] + MMchsterol[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCHTNASE	2 MMh2o[c] + MMchtn[c] -> 3 MMacgam[c]	0	1000	11303.1	Mouse metabolic/ transport/ demand reaction
MMCHTNASEe	2 MMh2o[e] + MMchtn[e] -> 3 MMacgam[e]	0	1000	81600.1 or 71884.1 or 67729.1	Mouse metabolic/ transport/ demand reaction
MMCITL	MMcit[c] -> MMac[c] + MMoaa[c]	0	1000	81600.2	Mouse metabolic/ transport/ demand reaction
MMCITMCOAHm	MMh2o[m] + MMitaccoa[m] <=> MMcitmcoa-L[m]	-1000	1000	69634.1 or 69634.2	Mouse metabolic/ transport/ demand reaction
MMCITMCOALm	MMcitmcoa-L[m] -> MMpyr[m] + MMaccoa[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCITRtm	MMcitr-L[m] <=> MMcitr-L[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMCITt4_2	2 MMna1[e] + MMcit[e] <=> 2 MMna1[c] + MMcit[c]	0	1000	18408.1 or 83885.1	Mouse metabolic/ transport/ demand reaction
MMCITt4_4	4 MMna1[e] + MMcit[e] <=> 4 MMna1[c] + MMcit[c]	0	1000	20500.1	Mouse metabolic/ transport/ demand reaction
MMCITtam	MMcit[c] + MMmal-L[m] <=> MMcit[m] + MMmal-L[c]	-1000	1000	237831.1	Mouse metabolic/ transport/ demand reaction
MMCITtbm	MMcit[c] + MMpep[m] <=> MMpep[c] + MMcit[m]	-1000	1000	13358.1	Mouse metabolic/ transport/ demand reaction
MMCK	MMatp[m] + MMcreat[m] <=> MMadp[m] + MMpcreat[m]	0	1000	13358.1	Mouse metabolic/ transport/ demand reaction
MMCKc	MMatp[c] + MMcreat[c] <=> MMadp[c] + MMpcreat[c]	-1000	1000	76722.1	Mouse metabolic/ transport/ demand reaction
MMCLFORtex	2 MMfor[c] + MMcl[e] -> MMcl[c] + 2 MMfor[e]	0	1000	12709.1 or 12715.1	Mouse metabolic/ transport/ demand reaction
MMCLFORtex2	MMfor[c] + 2 MMcl[e] -> 2 MMcl[c] + MMfor[e]	0	1000	23985.1	Mouse metabolic/ transport/ demand reaction
MMCLHCO3tex2	MMhco3[c] + 2 MMcl[e] -> MMhco3[e] + 2 MMcl[c]	0	1000	171429.1 or 171429.2 or 171429.3	Mouse metabolic/ transport/ demand reaction
MMCLHCOtex	2 MMhco3[c] + MMcl[e] -> 2 MMhco3[e] + MMcl[c]	0	1000	171429.1 or 171429.2 or 171429.3	Mouse metabolic/ transport/ demand reaction
MMCLI2tex	MMcl[e] + 2 MMi[c] -> MMcl[c] + 2 MMi[e]	0	1000	13487.1 or 224661.1 or 208890.1 or 224661.2 or 320718.1 or 13521.1 or 23985.1 or 208890.2 or 320718.2	Mouse metabolic/ transport/ demand reaction
MMCLOHtex2	MMoh1[c] + 2 MMcl[e] -> 2 MMcl[c] + MMoh1[e]	0	1000	23985.1	Mouse metabolic/ transport/ demand reaction
MMCLOXAtex2	2 MMcl[e] + MMoxa[c] -> 2 MMcl[c] + MMoxa[e]	0	1000	171429.1 or 171429.2 or 171429.3	Mouse metabolic/ transport/ demand reaction
MMCLPNDCOAtx	MMclpndcoa[c] <=> MMclpndcoa[x]	-1000	1000	171429.1 or 171429.2 or 171429.3	Mouse metabolic/ transport/ demand reaction
MMCLPNDCPT1	MMcrn[c] + MMclpndcoa[c] -> MMcoa[c] + MMclpndcrn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCLPNDCPT2	MMcoa[m] + MMclpndcrn[m] -> MMcrn[m] + MMclpndcoa[m]	0	1000	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	Mouse metabolic/ transport/ demand reaction
MMCLPNDCRNt	MMclpndcrn[c] -> MMclpndcrn[m]	0	1000	12896.1	Mouse metabolic/ transport/ demand reaction
MMCLPNDt	MMclpnd[e] <=> MMclpnd[c]	0	1000	57279.1	Mouse metabolic/ transport/ demand reaction
MMCLS_hs	MMcdpdag_hs[c] + MMpglyc_hs[c] -> MMh[c] + MMcmp[c] + MMclpn_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCMPACNAtg	MMcmpacna[c] + MMcmp[g] <=> MMcmp[c] + MMcmpacna[g]	-1000	1000	66586.1	Mouse metabolic/ transport/ demand reaction
MMCMPACNAtn	MMcmpacna[n] -> MMcmpacna[c]	0	1000	24060.1	Mouse metabolic/ transport/ demand reaction
MMCMPSAS	MMacnam[c] + MMctp[c] -> MMppi[c] + MMcmpacna[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCMPSASn	MMacnam[n] + MMctp[n] -> MMcmpacna[n] + MMppi[n]	0	1000	12764.1	Mouse metabolic/ transport/ demand reaction
MMCO2t	MMco2[e] <=> MMco2[c]	0	1000	12764.1	Mouse metabolic/ transport/ demand reaction
MMCO2ter	MMco2[c] <=> MMco2[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMCO2tg	MMco2[c] <=> MMco2[g]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMCO2tm	MMco2[c] <=> MMco2[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMCO2tn	MMco2[n] <=> MMco2[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMCO2tp	MMco2[c] <=> MMco2[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMCOAtg	MMcoa[c] <=> MMcoa[g]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMCOAtl	MMcoa[c] <=> MMcoa[l]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMCOAtm	MMcoa[c] <=> MMcoa[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMCOAtn	MMcoa[c] <=> MMcoa[n]	-1000	1000	73132.1	Mouse metabolic/ transport/ demand reaction
MMCOAtp	MMcoa[c] <=> MMcoa[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMCOAtr	MMcoa[c] <=> MMcoa[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMCOKECBESr	MMh2o[r] + MMcoke[r] -> MMh[r] + MMbz[r] + MMegme[r]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCOQ3m	MMamet[m] + MM2dpmhobq[m] -> MMh[m] + MMahcys[m] + MMq10[m]	0	1000	436059.1	Mouse metabolic/ transport/ demand reaction
MMCOQ5m	MMamet[m] + MM2dp6mobq[m] -> MMh[m] + MMahcys[m] + MM2dp6mobq_me[m]	0	1000	230027.1	Mouse metabolic/ transport/ demand reaction
MMCOQ6m	MMo2[m] + MM2dp6mep[m] -> MMh2o[m] + MM2dp6mobq[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCOQ7m	MMh[m] + MMnadph[m] + MMo2[m] + MM2dp6mobq_me[m] -> MMh2o[m] + MMnadp[m] + MM2dpmhobq[m]	0	1000	217707.1 or 217707.2	Mouse metabolic/ transport/ demand reaction
MMCORE3GTg	MMuacgam[g] + MMTn_antigen[g] -> MMh[g] + MMudp[g] + MMcore3[g]	0	1000	12850.1	Mouse metabolic/ transport/ demand reaction
MMCORE4GTg	MMuacgam[g] + MMcore3[g] -> MMh[g] + MMudp[g] + MMcore4[g]	0	1000	272411.1	Mouse metabolic/ transport/ demand reaction
MMCORE4t	MMcore4[g] -> MMcore4[e]	0	1000	72077.1	Mouse metabolic/ transport/ demand reaction
MMCORE5GTg	MMudpacgal[g] + MMTn_antigen[g] -> MMh[g] + MMudp[g] + MMcore5[g]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCORE5t	MMcore5[g] -> MMcore5[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCORE6GTg	MMuacgam[g] + MMTn_antigen[g] -> MMh[g] + MMudp[g] + MMcore6[g]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCORE7GTg	MMudpacgal[g] + MMTn_antigen[g] -> MMh[g] + MMudp[g] + MMcore7[g]	0	1000	14537.1	Mouse metabolic/ transport/ demand reaction
MMCORE7t	MMcore7[g] -> MMcore7[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCORE8GTg	MMudpgal[g] + MMTn_antigen[g] -> MMh[g] + MMudp[g] + MMcore8[g]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCORE8t	MMcore8[g] -> MMcore8[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCOUCOAFm	MMcoa[m] + MMatp[m] + MMT4hcinnm[m] -> MMcoucoa[m] + MMamp[m] + MMppi[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCOUMARINte	MMcoumarin[e] <=> MMcoumarin[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCOt	MMco[c] <=> MMco[e]	-1000	0		Mouse metabolic/ transport/ demand reaction
MMCPCTDTX	MMh[c] + MMctp[c] + MMntm2amep[c] -> MMppi[c] + MMcmpntm2amep[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCPPPGO	MMo2[c] + 2 MMh[c] + MMcpppg3[c] -> 2 MMh2o[c] + 2 MMco2[c] + MMpppg9[c]	0	1000	13026.1 or 236899.1	Mouse metabolic/ transport/ demand reaction
MMCREATt4_2_r	2 MMna1[e] + MMcreat[e] <=> 2 MMna1[c] + MMcreat[c]	0	1000	12892.1	Mouse metabolic/ transport/ demand reaction
MMCREATtmdiffir	MMcreat[c] -> MMcreat[m]	0	1000	102857.1	Mouse metabolic/ transport/ demand reaction
MMCRMPte	MMcrmp_hs[c] <=> MMcrmp_hs[e]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMCRNCAR3tp	MMcrn[c] + MMpcrn[x] -> MMpcrn[c] + MMcrn[x]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCRNCARtp	MMcrn[c] + MMacrn[x] -> MMacrn[c] + MMcrn[x]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCRNt	MMcrn[e] <=> MMcrn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCRNtHa	MMh[e] + MMcrn[c] -> MMh[c] + MMcrn[e]	0	1000	20520.1	Mouse metabolic/ transport/ demand reaction
MMCRNtim	MMcrn[m] -> MMcrn[c]	0	1000	30805.1	Mouse metabolic/ transport/ demand reaction
MMCRNtuIR	MMcrn[e] -> MMcrn[c]	0	1000	57279.1	Mouse metabolic/ transport/ demand reaction
MMCRNtuNa	MMna1[e] + MMcrn[e] -> MMna1[c] + MMcrn[c]	0	1000	30805.1	Mouse metabolic/ transport/ demand reaction

MMCRNtx	MMdmnoncm[x] <=> MMdmnoncm[m]	-1000	1000	20520.1	Mouse metabolic/ transport/ demand reaction
MMCRTNsyn	MMpcreat[c] -> MMh[c] + MMpi[c] + MMcrtn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCRTSLt	MMcrtnl[e] <=> MMcrtnl[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCRTSLtm	MMcrtnl[c] <=> MMcrtnl[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMCRTSLtr	MMcrtnl[c] <=> MMcrtnl[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMCRTSTRNt	MMcrtstrn[e] <=> MMcrtstrn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCRTSTRNtm	MMcrtstrn[c] <=> MMcrtstrn[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMCRTSTRNtr	MMcrtstrn[c] <=> MMcrtstrn[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMCRVNCtr	MMcrvnc[e] <=> MMcrvnc[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCSAPASEly	MMh2o[l] + MMcspg_a[l] -> MMSer_Gly_Ala_X_Gly[l] + MMcs_a[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCSBPASEly	MMh2o[l] + MMcspg_b[l] -> MMSer_Gly_Ala_X_Gly[l] + MMcs_b[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCSCPASEly	MMh2o[l] + MMcspg_c[l] -> MMSer_Gly_Ala_X_Gly[l] + MMcs_c[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCSDPASEly	MMh2o[l] + MMcspg_d[l] -> MMSer_Gly_Ala_X_Gly[l] + MMcs_d[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCSEPASEly	MMh2o[l] + MMcspg_e[l] -> MMSer_Gly_Ala_X_Gly[l] + MMcs_e[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCSNAT2m	MMcoa[m] + MMpcrn[m] <=> MMppcoa[m] + MMcrn[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMCSNAT2x	MMcrn[x] + MMdmnoncoa[x] <=> MMcoa[x] + MMdmnoncrn[x]	-1000	1000	12908.1	Mouse metabolic/ transport/ demand reaction
MMCSNAT3x	MMcrn[x] + MMppcoa[x] <=> MMcoa[x] + MMpcrn[x]	-1000	1000	12908.2 or 74114.1	Mouse metabolic/ transport/ demand reaction
MMCSNATer	MMaccoa[r] + MMcrn[r] <=> MMcoa[r] + MMacrn[r]	-1000	1000	12908.2	Mouse metabolic/ transport/ demand reaction
MMCSNATm	MMcoa[m] + MMacrn[m] <=> MMaccoa[m] + MMcrn[m]	-1000	1000	12908.3	Mouse metabolic/ transport/ demand reaction
MMCSNATp	MMaccoa[x] + MMcrn[x] <=> MMcoa[x] + MMacrn[x]	-1000	1000	12908.1	Mouse metabolic/ transport/ demand reaction
MMCSNATr	MMaccoa[c] + MMcrn[c] <=> MMcoa[c] + MMacrn[c]	-1000	1000	12908.2	Mouse metabolic/ transport/ demand reaction
MMCSND	MMh2o[c] + MMh[c] + MMcsn[c] -> MMmbtd[c] + MMura[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCSNt	MMcsn[e] <=> MMcsn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCSPG_At	MMcspg_a[g] -> MMcspg_a[e]	0	1000	13340.1	Mouse metabolic/ transport/ demand reaction
MMCSPG_Atly	MMcspg_a[e] -> MMcspg_a[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCSPG_Bt	MMcspg_b[g] -> MMcspg_b[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCSPG_Btly	MMcspg_b[e] -> MMcspg_b[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCSPG_Ct	MMcspg_c[g] -> MMcspg_c[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCSPG_Ctly	MMcspg_c[e] -> MMcspg_c[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCSPG_Dt	MMcspg_d[g] -> MMcspg_d[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCSPG_Dtly	MMcspg_d[e] -> MMcspg_d[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCSPG_Et	MMcspg_e[g] -> MMcspg_e[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCSPG_Ely	MMcspg_e[e] -> MMcspg_e[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCSm	MMh2o[m] + MMaccoa[m] + MMcoaa[m] -> MMh[m] + MMcoa[m] + MMcit[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCTPS1	MMmbtd[c] + MMatp[c] + MMutp[c] -> MMadp[c] + 2 MMh[c] + MMpi[c] + MMctp[c]	0	1000	12974.1 or 12974.2	Mouse metabolic/ transport/ demand reaction
MMCTPS2	MMh2o[c] + MMatp[c] + MMgln-L[c] + MMutp[c] -> MMadp[c] + 2 MMh[c] + MMpi[c] + MMglu-L[c] + MMctp[c]	0	1000	51797.1	Mouse metabolic/ transport/ demand reaction
MMCTPtn	MMctp[c] <=> MMctp[n]	-1000	1000	55936.1 or 55936.2	Mouse metabolic/ transport/ demand reaction
MMCYANSTm	MMcyan[m] + MMtsul[m] -> MMh[m] + MMso3[m] + MMtcynt[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCYANt	MMcyan[e] <=> MMcyan[c]	0	1000	22117.1	Mouse metabolic/ transport/ demand reaction
MMCYANtm	MMcyan[c] <=> MMcyan[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMCYOOm2	8 MMh[m] + MMo2[m] + 4 MMficytC[m] -> 4 MMh[c] + 2 MMh2o[m] + 4 MMficytC[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCYOOm3	7.92 MMh[m] + MMo2[m] + 4 MMficytC[m] -> 4 MMh[c] + 1.96 MMh2o[m] + 4 MMficytC[m] + 0.02 MMo2s[m]	0	0		Mouse metabolic/ transport/ demand reaction
MMCYOR_u10m	2 MMh[m] + 2 MMficytC[m] + MMq10h2[m] -> 4 MMh[c] + MMq10[m] + 2 MMficytC[m]	0	1000	78174.1 or 12864.1 or 11532.1 or 75483.1 or 629383.1 or 333182.1 or 84682.1 or 12647.1 or 110323.1 or 12857.1 or 12865.1 or 12859.1 or 17708.1 or 12868.1 or 12866.1 or 66142.1 or 12858.1 or 12861.1 or 12862.1	Mouse metabolic/ transport/ demand reaction
MMCYSALANaEx	MMna1[e] + MMala-L[c] + MMcys-L[e] -> MMna1[c] + MMala-L[e] + MMcys-L[c]	0	1000	22273.1 and 100042918.1 and 66152.1 and 66594.1 and 17711.1 and 67003.1 and 66694.1 and 66445.1 and 22272.1 and 67530.1 or 22273.1 and 100042918.1 and 17711.1 and 66594.1 and 66152.2 and 67003.1 and 66445.1 and 66694.1 and 22272.1 and 67530.1	Mouse metabolic/ transport/ demand reaction
MMCYSAMO	MMo2[c] + MMcysam[c] -> 2 MMh[c] + MMhyptaur[c]	0	1000	20514.1 or 55963.1	Mouse metabolic/ transport/ demand reaction
MMCYSASNNaEx	MMna1[e] + MMasn-L[c] + MMcys-L[e] -> MMna1[c] + MMasn-L[e] + MMcys-L[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCYSATB0tc	2 MMna1[u] + MMcl[u] + MMcys-L[u] -> 2 MMna1[c] + MMcl[c] + MMcys-L[c]	0	1000	20514.1	Mouse metabolic/ transport/ demand reaction
MMCYSB0AT1Atc	MMna1[u] + MMcys-L[u] -> MMna1[c] + MMcys-L[c]	0	1000	56774.1	Mouse metabolic/ transport/ demand reaction
MMCYSGLNNaEx	MMna1[e] + MMcys-L[e] + MMgln-L[c] -> MMna1[c] + MMcys-L[c] + MMgln-L[e]	0	1000	(70008.1 or (74338.1 and 57394.1))	Mouse metabolic/ transport/ demand reaction
MMCYSGLTH	MMLcystin[c] + 2 MMgthrd[c] <=> 2 MMcys-L[c] + MMgthox[c]	-1000	1000	20514.1	Mouse metabolic/ transport/ demand reaction
MMCYSGLUexR	MMcys-L[e] + MMgln-L[c] <=> MMcys-L[c] + MMgln-L[e]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMCYSGLYex	MMcys-L[c] + MMgly[e] -> MMcys-L[e] + MMgly[c]	0	1000	53896.1 or 17254.1	Mouse metabolic/ transport/ demand reaction
MMCYSGLYexR	MMcys-L[c] + MMgly[e] <=> MMcys-L[e] + MMgly[c]	-1000	1000	50934.1 or 17254.1 or 50934.2	Mouse metabolic/ transport/ demand reaction
MMCYSILELAT2tc	MMcys-L[e] + MMile-L[c] -> MMcys-L[c] + MMile-L[e]	0	1000	53896.1 or 17254.1	Mouse metabolic/ transport/ demand reaction
MMCYSLYSL	MMh2o[c] + MMLcystin[c] -> MMmbtd[c] + MMpyr[c] + MMthcys[c]	0	1000	(20539.1 and 17254.1)	Mouse metabolic/ transport/ demand reaction
MMCYSO	MMo2[c] + MMcys-L[c] -> 2 MMh[c] + MM3sala[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCYSPHELAT2tc	MMcys-L[e] + MMphe-L[c] -> MMcys-L[c] + MMphe-L[e]	0	1000	12583.1	Mouse metabolic/ transport/ demand reaction
MMCYSSERNaEx	MMna1[e] + MMcys-L[e] + MMser-L[c] -> MMna1[c] + MMcys-L[c] + MMser-L[e]	0	1000	(20539.1 and 17254.1)	Mouse metabolic/ transport/ demand reaction
MMCYSSNAT5tc	MMh[c] + MMna1[u] + MMcys-L[u] <=> MMna1[c] + MMh[u] + MMcys-L[c]	-1000	1000	20514.1 or 55963.1	Mouse metabolic/ transport/ demand reaction
MMCYSTA	MMakg[c] + MMcys-L[c] <=> MMglu-L[c] + MMmercppyr[c]	-1000	1000	209837.1	Mouse metabolic/ transport/ demand reaction
MMCYSTALArBATtc	MMala-L[c] + MMLcystin[u] -> MMala-L[u] + MMLcystin[c]	0	1000	14718.1	Mouse metabolic/ transport/ demand reaction
MMCYSTAm	MMakg[m] + MMcys-L[m] <=> MMglu-L[m] + MMmercppyr[m]	-1000	1000	(30962.1 and 20532.1)	Mouse metabolic/ transport/ demand reaction
MMCYSTGL	MMh2o[c] + MMcyst-L[c] -> MMmbtd[c] + MMcys-L[c] + MM2obut[c]	0	1000	14719.1	Mouse metabolic/ transport/ demand reaction
MMCYSTGLUex	MMglu-L[c] + MMLcystin[e] -> MMLcystin[c] + MMglu-L[e]	0	1000	107869.1 or 107869.2	Mouse metabolic/ transport/ demand reaction
MMCYSTHRNaEx	MMna1[e] + MMcys-L[e] + MMthr-L[c] -> MMna1[c] + MMcys-L[c] + MMthr-L[e]	0	1000	17254.1 and 26570.1	Mouse metabolic/ transport/ demand reaction
MMCYSTLEUrBATtc	MMleu-L[c] + MMLcystin[u] -> MMleu-L[u] + MMLcystin[c]	0	1000	20514.1 or 55963.1	Mouse metabolic/ transport/ demand reaction
MMCYSTS	MMhcys-L[c] + MMser-L[c] -> MMh2o[c] + MMcyst-L[c]	0	1000	(30962.1 and 20532.1)	Mouse metabolic/ transport/ demand reaction
MMCYSTSERex	MMser-L[c] + MMLcystin[e] -> MMser-L[e] + MMLcystin[c]	0	1000	12411.1	Mouse metabolic/ transport/ demand reaction
MMCYSt4	MMna1[e] + MMcys-L[e] -> MMna1[c] + MMcys-L[c]	0	1000	20532.1 and 30962.1	Mouse metabolic/ transport/ demand reaction
MMCYStec	MMcys-L[e] <=> MMcys-L[c]	0	1000	56774.1	Mouse metabolic/ transport/ demand reaction
MMCYTD	MMh2o[c] + MMh[c] + MMcytd[c] -> MMmbtd[c] + MMuri[c]	0	1000	215113.1	Mouse metabolic/ transport/ demand reaction
MMCYTDK1	MMatp[c] + MMcytd[c] -> MMadp[c] + MMh[c] + MMcmp[c]	0	1000	72269.1 or 11628.1	Mouse metabolic/ transport/ demand reaction
MMCYTDK2m	MMatp[m] + MMcytd[m] -> MMh[m] + MMadp[m] + MMcmp[m]	0	1000	22245.1 or 80914.1	Mouse metabolic/ transport/ demand reaction
MMCYTDn	MMh2o[n] + MMcytd[n] + MMh[n] -> MMmbtd[n] + MMuri[n]	0	1000		Mouse metabolic/ transport/ demand reaction
MMCYTDt	MMcytd[e] <=> MMcytd[c]	0	1000	11628.1	Mouse metabolic/ transport/ demand reaction
MMCYTDt4	MMna1[e] + MMcytd[e] -> MMna1[c] + MMcytd[c]	0	1000	13340.1 or 63959.1	Mouse metabolic/ transport/ demand reaction
MMCYTDt5	2 MMna1[e] + MMcytd[e] -> 2 MMna1[c] + MMcytd[c]	0	1000	114304.1 or 434203.1 or 434203.2	Mouse metabolic/ transport/ demand reaction
MMCYTDtl	MMcytd[l] <=> MMcytd[c]	-1000	1000	114304.1	Mouse metabolic/ transport/ demand reaction
MMCYTDtm	MMcytd[c] <=> MMcytd[m]	-1000	1000	71279.1	Mouse metabolic/ transport/ demand reaction
MMCYTDtn	MMcytd[c] <=> MMcytd[n]	-1000	1000	63959.1	Mouse metabolic/ transport/ demand reaction
MMCYTK1	MMatp[c] + MMcmp[c] <=> MMadp[c] + MMcdp[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction

MMCYTK10	MMcmp[c] + MMdgtp[c] <=> MMcdp[c] + MMdgtp[c]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMCYTK10n	MMcmp[n] + MMdgtp[n] <=> MMcdp[n] + MMdgtp[n]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMCYTK11	MMdgtp[c] + MMdcmp[c] <=> MMdgtp[c] + MMdcdp[c]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMCYTK11n	MMdgtp[n] + MMdcmp[n] <=> MMdgtp[n] + MMdcdp[n]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMCYTK12	MMdcmp[c] + MMdctp[c] <=> 2 MMdcdp[c]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMCYTK12n	MMdcmp[n] + MMdctp[n] <=> 2 MMdcdp[n]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMCYTK13	MMdatp[c] + MMdcmp[c] <=> MMdadp[c] + MMdcdp[c]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMCYTK13n	MMdcmp[n] + MMdatp[n] <=> MMdcdp[n] + MMdadp[n]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMCYTK14	MMutp[c] + MMdcmp[c] <=> MMudp[c] + MMdcdp[c]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMCYTK14n	MMdcmp[n] + MMutp[n] <=> MMdcdp[n] + MMudp[n]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMCYTK1m	MMatp[m] + MMcmp[m] <=> MMadp[m] + MMcdp[m]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMCYTK1n	MMatp[n] + MMcmp[n] <=> MMcdp[n] + MMadp[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMCYTK2	MMatp[c] + MMdcmp[c] <=> MMadp[c] + MMdcdp[c]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMCYTK2n	MMatp[n] + MMdcmp[n] <=> MMdcdp[n] + MMadp[n]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMCYTK3	MMgtp[c] + MMcmp[c] <=> MMgdp[c] + MMcdp[c]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMCYTK3n	MMctp[n] + MMdcmp[n] <=> MMcdp[n] + MMdcdp[n]	-1000	1000	229949.1 or 229949.2	Mouse metabolic/ transport/ demand reaction
MMCYTK4	MMgtp[c] + MMdcmp[c] <=> MMgdp[c] + MMdcdp[c]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMCYTK4n	MMdcmp[n] + MMgtp[n] <=> MMdcdp[n] + MMgdp[n]	-1000	1000	229949.1 or 229949.2	Mouse metabolic/ transport/ demand reaction
MMCYTK5	MMctp[c] + MMdcmp[c] <=> MMcdp[c] + MMdcdp[c]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMCYTK5n	MMcmp[n] + MMgtp[n] <=> MMcdp[n] + MMgdp[n]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMCYTK6	MMcmp[c] + MMctp[c] <=> 2 MMcdp[c]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMCYTK6n	MMctp[n] + MMcmp[n] <=> 2 MMcdp[n]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMCYTK7	MMcmp[c] + MMutp[c] <=> MMudp[c] + MMcdp[c]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMCYTK7n	MMcmp[n] + MMutp[n] <=> MMcdp[n] + MMudp[n]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMCYTK8	MMdatp[c] + MMcmp[c] <=> MMdadp[c] + MMcdp[c]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMCYTK8n	MMcmp[n] + MMdatp[n] <=> MMcdp[n] + MMdadp[n]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMCYTK9	MMcmp[c] + MMdctp[c] <=> MMcdp[c] + MMdcdp[c]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMCYTK9n	MMcmp[n] + MMdctp[n] <=> MMcdp[n] + MMdcdp[n]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMCytOxe-	MMfocytC[m] -> MMfcytC[m] + MMe-[m]	0	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMD3AIBTm	MMpyr[m] + MM3aib-D[m] <=> MM2mop[m] + MMala-L[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDADA	MMh2o[c] + MMh[c] + MMdad-2[c] -> MMnh4[c] + MMdin[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDADAe	MMh[e] + MMh2o[e] + MMdad-2[e] -> MMnh4[e] + MMdin[e]	0	1000	11486.1	Mouse metabolic/ transport/ demand reaction
MMDADNK	MMatp[c] + MMdad-2[c] -> MMadp[c] + MMh[c] + MMdamp[c]	0	1000	11486.1	Mouse metabolic/ transport/ demand reaction
MMDADNt4	MMdad-2[e] <=> MMdad-2[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDAGHSTDhi	MMdag_hs[u] <=> MMdag_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDAGKn_hs	MMatp[n] + MMdag_hs[n] <=> MMh[n] + MMadp[n] + MMpa_hs[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDAG_HSter	MMdag_hs[r] -> MMdag_hs[c]	0	1000	104418.1 or 320127.1	Mouse metabolic/ transport/ demand reaction
MMDAGt	MMdag_hs[e] <=> MMdag_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDALAOXx	MMo2[x] + MMh2o[x] + MMala-D[x] -> MMh2o2[x] + MMpyr[x] + MMnh4[x]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDALAt2r	MMh[e] + MMala-D[e] <=> MMh[c] + MMala-D[c]	0	1000	13142.1	Mouse metabolic/ transport/ demand reaction
MMDALAt2rL	MMh[l] + MMala-D[l] <=> MMh[c] + MMala-D[c]	-1000	1000	215335.1	Mouse metabolic/ transport/ demand reaction
MMDALAxt	MMala-D[c] -> MMala-D[x]	0	1000	215335.1	Mouse metabolic/ transport/ demand reaction
MMDARGOp	MMo2[x] + MMh2o[x] + MMarg-D[x] -> MMh2o2[x] + MMnh4[x] + MM5g2oxpt[x]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDASCBH	MMh2o[c] + MMdhdascb[c] -> MMh[c] + MM23dogulnt[c]	0	1000	13142.1	Mouse metabolic/ transport/ demand reaction
MMDASCBR	MMh[c] + MMnadph[c] + MMdhdascb[c] -> MMnadp[c] + MMascb-L[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDASPO1p	MMo2[x] + MMh2o[x] + MMasp-D[x] -> MMh2o2[x] + MMnh4[x] + MMoaa[x]	0	1000	93692.1 or 69367.1 or 69367.2	Mouse metabolic/ transport/ demand reaction
MMDATPtn	MMdatp[c] <=> MMdatp[n]	-1000	1000	70503.1 or 70503.2	Mouse metabolic/ transport/ demand reaction
MMDC1m	MMdd2coa[m] <=> MMdd3coa[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDCK1m	MMatp[m] + MMdcyt[m] <=> MMh[m] + MMadp[m] + MMdcmp[m]	-1000	1000	13177.1	Mouse metabolic/ transport/ demand reaction
MMDCK1n	MMatp[n] + MMdcyt[n] <=> MMh[n] + MMdcmp[n] + MMadp[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDCK2n	MMutp[n] + MMdcyt[n] <=> MMh[n] + MMdcmp[n] + MMudp[n]	-1000	1000	13178.1	Mouse metabolic/ transport/ demand reaction
MMDCMPDA	MMh2o[c] + MMh[c] + MMdcmp[c] <=> MMnh4[c] + MMdump[c]	-1000	1000	13178.1	Mouse metabolic/ transport/ demand reaction
MMDCSPTN1COAtx	MMdcsptn1coa[c] <=> MMdcsptn1coa[x]	-1000	1000	320685.1	Mouse metabolic/ transport/ demand reaction
MMDCSPTN1CPT1	MMcm[c] + MMdcsptn1coa[c] -> MMcoa[c] + MMdcsptn1crn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDCSPTN1CPT2	MMcoa[m] + MMdcsptn1crn[m] -> MMcm[m] + MMdcsptn1coa[m]	0	1000	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	Mouse metabolic/ transport/ demand reaction
MMDCSPTN1CRNt	MMdcsptn1crn[c] -> MMdcsptn1crn[m]	0	1000	12896.1	Mouse metabolic/ transport/ demand reaction
MMDCSPTN1t	MMdcsptn1[e] <=> MMdcsptn1[c]	0	1000	57279.1	Mouse metabolic/ transport/ demand reaction
MMDCT	MML-dpchrm[c] <=> MM56dihindlcrbxd[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDCTPtn	MMdctp[c] <=> MMdctp[n]	-1000	1000	13190.1	Mouse metabolic/ transport/ demand reaction
MMDCYTD	MMh2o[c] + MMh[c] + MMdcyt[c] -> MMnh4[c] + MMdurd[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDCYTDn	MMh2o[n] + MMh[n] + MMdcyt[n] -> MMnh4[n] + MMdurd[n]	0	1000	72269.1 or 11628.1	Mouse metabolic/ transport/ demand reaction
MMDCYTt	MMdcyt[e] <=> MMdcyt[c]	0	1000	11628.1	Mouse metabolic/ transport/ demand reaction
MMDDPGAm	MM4h2ogh[m] <=> MMpyr[m] + MMgh[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDEBRISOQUINEt	MMdebrisoquine[e] <=> MMdebrisoquine[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDECDPtm	MMdecdp[c] <=> MMdecdp[m]	-1000	1000	20518.1 or 20518.2	Mouse metabolic/ transport/ demand reaction
MMDEDOLP1_L	MMh2o[c] + 0.1 MMdedoldp_L[c] -> MMh[c] + MMpi[c] + 0.1 MMdedolp_L[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDEDOLP1_U	MMh2o[c] + 0.1 MMdedoldp_U[c] -> MMh[c] + MMpi[c] + 0.1 MMdedolp_U[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDEDOLP2_L	MMh2o[c] + 0.1 MMdedolp_L[c] -> MMpi[c] + 0.1 MMdedol_L[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDEDOLP2_U	MMh2o[c] + 0.1 MMdedolp_U[c] -> MMpi[c] + 0.1 MMdedol_U[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDEDOLR_L	MMh[c] + MMnadph[c] + 0.1 MMdedol_L[c] -> MMnadp[c] + 0.1 MMdolichol_L[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDEDOLR_U	MMh[c] + MMnadph[c] + 0.1 MMdedol_U[c] -> MMnadp[c] + 0.1 MMdolichol_U[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDESAT16_2	MMo2[c] + MMh[c] + MMnadh[c] + MMpmtcoa[c] -> 2 MMh2o[c] + MMnad[c] + MMhtcoa[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDESAT18_10	MMo2[c] + MMh[c] + MMnadh[c] + MMhtdcacoa[c] -> 2 MMh2o[c] + MMnad[c] + MMstrdtccoa[c]	0	1000	20249.1	Mouse metabolic/ transport/ demand reaction
MMDESAT18_3	MMo2[c] + MMh[c] + MMnadh[c] + MMstcoa[c] -> 2 MMh2o[c] + MMnad[c] + MModecoa[c]	0	1000	56473.1	Mouse metabolic/ transport/ demand reaction
MMDESAT18_4	MMo2[c] + MMh[c] + MMnadh[c] + MMstcoa[c] -> 2 MMh2o[c] + MMnad[c] + MMvaccoa[c]	0	1000	20249.1	Mouse metabolic/ transport/ demand reaction
MMDESAT18_5	MMo2[c] + MMh[c] + MMnadh[c] + MMstcoa[c] -> 2 MMh2o[c] + MMnad[c] + MMod2coa[c]	0	1000	20249.1	Mouse metabolic/ transport/ demand reaction
MMDESAT18_6	MMo2[c] + MMh[c] + MMnadh[c] + MModecoa[c] -> 2 MMh2o[c] + MMnad[c] + MMhtedtccoa[c]	0	1000	20249.1	Mouse metabolic/ transport/ demand reaction
MMDESAT18_7	MMo2[c] + MMh[c] + MMnadh[c] + MMvaccoa[c] -> 2 MMh2o[c] + MMnad[c] + MMhtetdccoa[c]	0	1000	56473.1	Mouse metabolic/ transport/ demand reaction
MMDESAT18_8	MMo2[c] + MMh[c] + MMnadh[c] + MMod2coa[c] -> 2 MMh2o[c] + MMnad[c] + MMhtetdccoa[c]	0	1000	56473.1	Mouse metabolic/ transport/ demand reaction
MMDESAT18_9	MMo2[c] + MMh[c] + MMnadh[c] + MMhtdcacoa[c] -> 2 MMh2o[c] + MMnad[c] + MMhtdcgcoa[c]	0	1000	56473.1	Mouse metabolic/ transport/ demand reaction
MMDESAT20_1	MMo2[c] + MMh[c] + MMnadh[c] + MMdhtdcgcoa[c] -> 2 MMh2o[c] + MMnad[c] + MMarachdcoa[c]	0	1000	56473.1	Mouse metabolic/ transport/ demand reaction
MMDESAT20_2	MMo2[c] + MMh[c] + MMnadh[c] + MMeicosetcoa[c] -> 2 MMh2o[c] + MMnad[c] + MMtrndncoa[c]	0	1000	76267.1	Mouse metabolic/ transport/ demand reaction
MMDESAT22_1p	MMh[x] + MMnadh[x] + MMo2[x] + MMadrncoa[x] -> MMnad[x] + 2 MMh2o[x] + MMdcsptn1coa[x]	0	1000	76267.1	Mouse metabolic/ transport/ demand reaction
MMDESAT22_2p	MMh[x] + MMnadh[x] + MMo2[x] + MMclpnelcoa[x] -> MMnad[x] + 2 MMh2o[x] + MMc226coa[x]	0	1000		Mouse metabolic/ transport/ demand reaction

MMDESAT24_1	MMo2[c] + MMh[c] + MMnadh[c] + MMtetpent3coa[c] -> 2 MMh2o[c] + MMnad[c] + MMtethex3coa[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDGAT	MMRtotal3coa[c] + MMdag_hs[c] -> MMcoa[c] + MMtag_hs[c]	0	1000	56473.1	Mouse metabolic/ transport/ demand reaction
MMDGCHOLte	MMdgchol[e] <=> MMdgchol[c]	-1000	1000	13350.1 or 67800.1	Mouse metabolic/ transport/ demand reaction
MMDGCHOLtx	MMdgchol[x] <=> MMdgchol[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDGK1	MMatp[c] + MMdgmp[c] <=> MMadp[c] + MMdgdp[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDGK2m	MMdatp[m] + MMdgmp[m] <=> MMdadp[m] + MMdgdp[m]	-1000	1000	14923.1	Mouse metabolic/ transport/ demand reaction
MMDGNSKm	MMatp[m] + MMdgua[m] -> MMh[m] + MMadp[m] + MMdgmp[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDGSNt	MMdgsn[e] <=> MMdgsn[c]	0	1000	27369.1 or 27369.2 or 27369.3 or 27369.4 or 27369.5	Mouse metabolic/ transport/ demand reaction
MMDGSNtm	MMdgsn[c] <=> MMdgsn[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDGTPtn	MMdgtp[c] <=> MMdgtp[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDGULND	MMh[c] + MM3dhguln[c] <=> MMco2[c] + MMxylu-L[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDHAAt1r	MMdhdascb[e] <=> MMdhdascb[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDHAPA	MMdhap[c] + MMRtotalcoa[c] -> MMcoa[c] + MMadhap_hs[c]	0	1000	20528.1 or 20527.1 or 20525.1	Mouse metabolic/ transport/ demand reaction
MMDHAPAx	MMRtotalcoa[x] + MMdhap[x] -> MMcoa[x] + MMadhap_hs[x]	0	1000	14712.1	Mouse metabolic/ transport/ demand reaction
MMDHCHOLESTANATEtm	MMdhcholestanate[m] <=> MMdhcholestanate[x]	-1000	1000	14712.1	Mouse metabolic/ transport/ demand reaction
MMDHCR241r	MMzymst[r] + MMfadh2[r] -> MMfad[r] + MMzymstn[r]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDHCR242r	MMfadh2[r] + MMchlstol[r] -> MMfad[r] + MMlthstr[r]	0	1000	74754.1	Mouse metabolic/ transport/ demand reaction
MMDHCR243r	MMfadh2[r] + MMdsmstero[r] -> MMchstero[r] + MMfad[r]	0	1000	74754.1	Mouse metabolic/ transport/ demand reaction
MMDHCR71r	MMh[r] + MMnadph[r] + MMddsmstero[r] -> MMnadp[r] + MMdsmstero[r]	0	1000	74754.1	Mouse metabolic/ transport/ demand reaction
MMDHCR72r	MM7dhchstero[r] + MMh[r] + MMnadph[r] -> MMnadp[r] + MMchstero[r]	0	1000	13360.1	Mouse metabolic/ transport/ demand reaction
MMDHCRD1	MMnadp[c] + MMdhcrm_hs[c] -> MMh[c] + MMnadph[c] + MMcrm_hs[c]	0	1000	13360.1	Mouse metabolic/ transport/ demand reaction
MMDHCRD2	MMdhcrm_hs[c] + MMfad[c] -> MMcrm_hs[c] + MMfadh2[c]	0	1000	13244.2 or 13244.1	Mouse metabolic/ transport/ demand reaction
MMDHDPBMTm	MM3dpdhh[m] + MMamet[m] -> MMh[m] + MMahcys[m] + MM3dpdhh_me[m]	0	1000	13244.2 or 13244.1	Mouse metabolic/ transport/ demand reaction
MMDHEASULT	MMpaps[c] + MMdhea[c] -> MMh[c] + MMpap[c] + MMdheas[c]	0	1000	230027.1	Mouse metabolic/ transport/ demand reaction
MMDHEASir	MMdheas[r] <=> MMdheas[c]	-1000	1000	20859.1 or 20860.1	Mouse metabolic/ transport/ demand reaction
MMDHEAtr	MMdhea[r] <=> MMdhea[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDHFR	MMh[c] + MMnadph[c] + MMdhf[c] <=> MMnadp[c] + MMthf[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDHFtl	MMdhf[c] <=> MMdhf[l]	-1000	1000	13361.1	Mouse metabolic/ transport/ demand reaction
MMDHFtm	MMdhf[c] <=> MMdhf[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDHORD9	MMq10[m] + MMdhor-S[c] -> MMq10h2[m] + MMorot[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDHORTS	MMh2o[c] + MMdhor-S[c] <=> MMh[c] + MMcbasp[c]	-1000	1000	56749.1	Mouse metabolic/ transport/ demand reaction
MMDHPM1	MMh2o[c] + MM56dura[c] -> MMh[c] + MMcala[c]	0	1000	69719.1	Mouse metabolic/ transport/ demand reaction
MMDHPM2	MMh2o[c] + MM56dthtm[c] -> MMh[c] + MM3sulb[c]	0	1000	22240.1 or 64705.1 or 12934.1	Mouse metabolic/ transport/ demand reaction
MMDHPR	MMh[c] + MMnadh[c] + MMdhbpt[c] -> MMnad[c] + MMthbpt[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDHPR2	MM5mthf[c] + MMdhbpt[c] -> MMh[c] + MMthbpt[c] + MMmthf[c]	0	1000	110391.1	Mouse metabolic/ transport/ demand reaction
MMDIDPtn	MMdidp[c] <=> MMdidp[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDIGALSGALSIDEte	MMdigalsgalside_hs[c] <=> MMdigalsgalside_hs[e]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDIGALSGALSIDEtg	MMdigalsgalside_hs[c] <=> MMdigalsgalside_hs[g]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDIGALSIDEtg	MMdigalside_hs[c] <=> MMdigalside_hs[g]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDIGALSIDEtl	MMdigalside_hs[c] <=> MMdigalside_hs[l]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDINt	MMdin[e] <=> MMdin[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDITPtn	MMditp[c] <=> MMditp[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDKMPPD	MMh2o[c] + MMo2[c] + MMdkmpp[c] -> 2 MMh[c] + MMpi[c] + MM4mb[c] + MM2kmb[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDLNLCGCPT1	MMcrn[c] + MMdlnlcgcoa[c] -> MMcoa[c] + MMdlnlcgcrn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDLNLCGCPT2	MMcoa[m] + MMdlnlcgcrn[m] -> MMcrn[m] + MMdlnlcgcoa[m]	0	1000	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	Mouse metabolic/ transport/ demand reaction
MMDLNLCGCRNt	MMdlnlcgcrn[c] -> MMdlnlcgcrn[m]	0	1000	12896.1	Mouse metabolic/ transport/ demand reaction
MMDLNLCGt	MMdlnlcg[e] <=> MMdlnlcg[c]	0	1000	57279.1	Mouse metabolic/ transport/ demand reaction
MMDMANTIPYRINEte	MMdmantipyrine[e] <=> MMdmantipyrine[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDMATT	MMdmpp[c] + MMgpdp[c] -> MMppi[c] + MMgrdp[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDMATTx	MMdmpp[x] + MMgpdp[x] -> MMgrdp[x] + MMppi[x]	0	1000	14593.1	Mouse metabolic/ transport/ demand reaction
MMDMGDHm	MMh2o[m] + MMfad[m] + MMdmgly[m] -> MMfadh2[m] + MMfald[m] + MMsarcs[m]	0	1000	110196.1	Mouse metabolic/ transport/ demand reaction
MMDMGtm	MMdmgly[c] <=> MMdmgly[m]	-1000	1000	74129.1	Mouse metabolic/ transport/ demand reaction
MMDMHPTCRNCPT1	MMcrn[c] + MMdmhptcoa[c] <=> MMcoa[c] + MMdmhptcrn[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDMHPTCRNCPT2	MMcoa[m] + MMdmhptcrn[m] <=> MMcrn[m] + MMdmhptcoa[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDMHPTCRNt	MMdmhptcrn[c] <=> MMdmhptcrn[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDMHPTCRNte	MMdmhptcrn[c] <=> MMdmhptcrn[e]	-1000	0		Mouse metabolic/ transport/ demand reaction
MMDMNONCOACRNCPT1	MMcrn[c] + MMdmnoncoa[c] <=> MMcoa[c] + MMdmnoncrn[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDMNONCRNCPT2	MMcoa[m] + MMdmnoncrn[m] <=> MMcrn[m] + MMdmnoncoa[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDMNONCRNt	MMdmnoncrn[c] <=> MMdmnoncrn[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDM_13_cis_oretn_n_	MM13-cis-oretn[n] ->	0	0		Mouse metabolic/ transport/ demand reaction
MMDM_13_cis_retn_n_	MM13-cis-retn[n] ->	0	0		Mouse metabolic/ transport/ demand reaction
MMDM_Asn_X_Ser_Thr_ly_	MMAsn_X_Ser_Thr[l] ->	0	1000		Mouse metabolic/ transport/ demand reaction
MMDM_Ser_Gly_Ala_X_Gly_ly_	MMSer_Gly_Ala_X_Gly[l] ->	0	1000		Mouse metabolic/ transport/ demand reaction
MMDM_Ser_Thr_ly_	MMSer_Thr[l] ->	0	1000		Mouse metabolic/ transport/ demand reaction
MMDM_T_antigen(g)	MMT_antigen[g] <=>	-1	1000		Mouse metabolic/ transport/ demand reaction
MMDM_avite1_c_	MMavite1[c] ->	0	1000		Mouse metabolic/ transport/ demand reaction
MMDM_avite2_c_	MMavite2[c] ->	0	1000		Mouse metabolic/ transport/ demand reaction
MMDM_bvite_c_	MMbvite[c] ->	0	1000		Mouse metabolic/ transport/ demand reaction
MMDM_core5_g_	MMcore5[g] ->	0	1000		Mouse metabolic/ transport/ demand reaction
MMDM_core7_g_	MMcore7[g] ->	0	1000		Mouse metabolic/ transport/ demand reaction
MMDM_core8_g_	MMcore8[g] ->	0	1000		Mouse metabolic/ transport/ demand reaction
MMDM_datp_m_	MMdatp[m] ->	0	1000		Mouse metabolic/ transport/ demand reaction
MMDM_datp_n_	MMdatp[n] ->	0	1000		Mouse metabolic/ transport/ demand reaction
MMDM_dctp(m)	MMdctp[m] ->	0	1000		Mouse metabolic/ transport/ demand reaction
MMDM_dctp(n)	MMdctp[n] ->	0	1000		Mouse metabolic/ transport/ demand reaction
MMDM_dem2emgacpail_prot_hs(r)	MMdem2emgacpail_prot_hs[r] ->	0	1000		Mouse metabolic/ transport/ demand reaction
MMDM_dgpi_prot_hs(r)	MMdgpi_prot_hs[r] ->	0	1000		Mouse metabolic/ transport/ demand reaction
MMDM_dgtp(m)	MMdgtp[m] ->	0	1000		Mouse metabolic/ transport/ demand reaction
MMDM_dgtp(n)	MMdgtp[n] ->	0	1000		Mouse metabolic/ transport/ demand reaction
MMDM_dsT_antigen(g)	MMdsT_antigen[g] ->	0	1000		Mouse metabolic/ transport/ demand reaction
MMDM_dttp(m)	MMdttp[m] ->	0	1000		Mouse metabolic/ transport/ demand reaction
MMDM_dttp(n)	MMdttp[n] ->	0	1000		Mouse metabolic/ transport/ demand reaction
MMDM_ethamp(r)	MMethamp[r] ->	0	1000		Mouse metabolic/ transport/ demand reaction
MMDM_gncore2(g)	MMgncore2[g] ->	0	1000		Mouse metabolic/ transport/ demand reaction

MMDM_gpi_sig(er)	MMgpi_sig[r] ->	0	1000		Mouse metabolic/ transport/ demand reaction
MMDM_hretn(n)	MMhretn[n] ->	0	1000		Mouse metabolic/ transport/ demand reaction
MMDM_kdn(c)	MMkdn[c] ->	0	1000		Mouse metabolic/ transport/ demand reaction
MMDM_m(em)3gacpail_prot_hs(r)	MMm[em]3gacpail_prot_hs[r] ->	0	1000		Mouse metabolic/ transport/ demand reaction
MMDM_melanin(c)	MMmelanin[c] ->	0	1000		Mouse metabolic/ transport/ demand reaction
MMDM_mem2emgacpail_prot_hs(r)	MMmem2emgacpail_prot_hs[r] ->	0	1000		Mouse metabolic/ transport/ demand reaction
MMDM_n5m2masn(g)	MMn5m2masn[g] ->	0	1000		Mouse metabolic/ transport/ demand reaction
MMDM_oretn(n)	MMoretn[n] ->	0	1000		Mouse metabolic/ transport/ demand reaction
MMDM_sTn_antigen(g)	MMsTn_antigen[g] ->	0	1000		Mouse metabolic/ transport/ demand reaction
MMDM_sprm(c)	MMsprm[c] ->	0	1000		Mouse metabolic/ transport/ demand reaction
MMDM_yvite(c)	MMyvite[c] ->	0	1000		Mouse metabolic/ transport/ demand reaction
MMDNADDP	MMh2o[c] + MMdnad[c] -> 2 MMh[c] + MMamp[c] + MMnicrnt[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDNADtn	MMdnad[c] <=> MMdnad[n]	-1000	1000	18605.1 or 18606.1 or 209558.1	Mouse metabolic/ transport/ demand reaction
MMDNAMTSEn	MMdna[n] + MMseasmet[n] -> MMh[n] + MMdna5mtc[n] + MMseahcys[n]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDNAMTn	MMamet[n] + MMdna[n] -> MMahcys[n] + MMh[n] + MMdna5mtc[n]	0	1000	13434.1 or 13434.2 or 13434.3 or 13434.4 or 13433.1 or 13434.5 or 13436.1 or 13435.1 or 13435.2 or 13436.2 or 13436.4 or 13434.6 or 13435.3 or 13436.3 or 13435.4	Mouse metabolic/ transport/ demand reaction
MMDNDPt10m	MMdadp[c] + MMdcdp[m] -> MMdcdp[c] + MMdadp[m]	0	1000	13434.1 or 13434.2 or 13434.3 or 13434.4 or 13433.1 or 13434.5 or 13436.1 or 13435.1 or 13435.2 or 13436.2 or 13436.4 or 13434.6 or 13435.3 or 13436.3 or 13435.4	Mouse metabolic/ transport/ demand reaction
MMDNDPt11m	MMdadp[c] + MMdgdp[m] -> MMdgdp[c] + MMdadp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt12m	MMadp[m] + MMdadp[c] -> MMadp[c] + MMdadp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt13m	MMatp[m] + MMdadp[c] -> MMatp[c] + MMdadp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt14m	MMdudp[c] + MMdtdp[m] -> MMdtdp[c] + MMdudp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt15m	MMdgdp[m] + MMdudp[c] -> MMdgdp[c] + MMdudp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt16m	MMdadp[m] + MMdudp[c] -> MMdadp[c] + MMdudp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt17m	MMdcdp[m] + MMdudp[c] -> MMdcdp[c] + MMdudp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt18m	MMadp[m] + MMdudp[c] -> MMadp[c] + MMdudp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt19m	MMatp[m] + MMdudp[c] -> MMatp[c] + MMdudp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt1m	MMadp[m] + MMdatp[c] -> MMadp[c] + MMdatp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt20m	MMatp[m] + MMdtdp[c] -> MMatp[c] + MMdtdp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt21m	MMadp[m] + MMdtdp[c] -> MMadp[c] + MMdtdp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt22m	MMdtdp[c] + MMdudp[m] -> MMdudp[c] + MMdtdp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt23m	MMdgdp[m] + MMdtdp[c] -> MMdgdp[c] + MMdtdp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt24m	MMdadp[m] + MMdtdp[c] -> MMdadp[c] + MMdtdp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt25m	MMdcdp[m] + MMdtdp[c] -> MMdcdp[c] + MMdtdp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt26m	MMdcdp[c] + MMdudp[m] -> MMdcdp[m] + MMdudp[c]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt27m	MMdcdp[c] + MMdtdp[m] -> MMdcdp[m] + MMdtdp[c]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt28m	MMdcdp[c] + MMdgdp[m] -> MMdgdp[c] + MMdcdp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt29m	MMdcdp[c] + MMdadp[m] -> MMdadp[c] + MMdcdp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt2m	MMatp[m] + MMdatp[c] -> MMatp[c] + MMdatp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt30m	MMadp[m] + MMdcdp[c] -> MMadp[c] + MMdcdp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt31m	MMatp[m] + MMdcdp[c] -> MMatp[c] + MMdcdp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt32m	MMatp[m] + MMdgdp[c] -> MMatp[c] + MMdgdp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt33m	MMdgdp[c] + MMdudp[m] -> MMdgdp[m] + MMdudp[c]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt34m	MMdgdp[c] + MMdtdp[m] -> MMdgdp[m] + MMdtdp[c]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt35m	MMdgdp[c] + MMdadp[m] -> MMdadp[c] + MMdgdp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt36m	MMdgdp[c] + MMdcdp[m] -> MMdcdp[c] + MMdgdp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt37m	MMdtdp[m] + MMdutp[c] -> MMdtdp[c] + MMdutp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt38m	MMdudp[m] + MMdutp[c] -> MMdudp[c] + MMdutp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt39m	MMdgdp[m] + MMdutp[c] -> MMdgdp[c] + MMdutp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt3m	MMdatp[c] + MMdcdp[m] -> MMdcdp[c] + MMdatp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt40m	MMdadp[m] + MMdutp[c] -> MMdadp[c] + MMdutp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt41m	MMdcdp[m] + MMdutp[c] -> MMdcdp[c] + MMdutp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt42m	MMadp[m] + MMdutp[c] -> MMadp[c] + MMdutp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt43m	MMatp[m] + MMdutp[c] -> MMatp[c] + MMdutp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt44m	MMatp[m] + MMdtp[c] -> MMatp[c] + MMdtp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt45m	MMadp[m] + MMdtp[c] -> MMadp[c] + MMdtp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt46m	MMdudp[m] + MMdtp[c] -> MMdtp[m] + MMdudp[c]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt47m	MMdtdp[m] + MMdtp[c] -> MMdtp[m] + MMdtdp[c]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt48m	MMdgdp[m] + MMdtp[c] -> MMdgdp[c] + MMdtp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt49m	MMdadp[m] + MMdtp[c] -> MMdadp[c] + MMdtp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt4m	MMdatp[c] + MMdudp[m] -> MMdatp[m] + MMdudp[c]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt50m	MMdcdp[m] + MMdtp[c] -> MMdcdp[c] + MMdtp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt51m	MMdctp[c] + MMdcdp[m] -> MMdcdp[c] + MMdctp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt52m	MMdctp[c] + MMdudp[m] -> MMdctp[m] + MMdudp[c]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt53m	MMdctp[c] + MMdgdp[m] -> MMdgdp[c] + MMdctp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt54m	MMdctp[c] + MMdadp[m] -> MMdadp[c] + MMdctp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt55m	MMadp[m] + MMdctp[c] -> MMadp[c] + MMdctp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt56m	MMatp[m] + MMdctp[c] -> MMatp[c] + MMdctp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt57m	MMatp[m] + MMdgtp[c] -> MMatp[c] + MMdgtp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt58m	MMadp[m] + MMdgtp[c] -> MMadp[c] + MMdgtp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt59m	MMdgtp[c] + MMdadp[m] -> MMdadp[c] + MMdgtp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt5m	MMdatp[c] + MMdtdp[m] -> MMdatp[m] + MMdtdp[c]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt60m	MMdgtp[c] + MMdudp[m] -> MMdgtp[m] + MMdudp[c]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt61m	MMdgtp[c] + MMdtdp[m] -> MMdgtp[m] + MMdtdp[c]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt62m	MMdgtp[c] + MMdgdp[m] -> MMdgdp[c] + MMdgtp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt63m	MMdgtp[c] + MMdcdp[m] -> MMdcdp[c] + MMdgtp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt6m	MMdatp[c] + MMdgdp[m] -> MMdgdp[c] + MMdatp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt7m	MMdatp[c] + MMdadp[m] -> MMdadp[c] + MMdatp[m]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt8m	MMdadp[c] + MMdudp[m] -> MMdadp[m] + MMdudp[c]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDNDPt9m	MMdadp[c] + MMdtdp[m] -> MMdadp[m] + MMdtdp[c]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDOGULND1	MMh2o[c] + MM23dogulnt[c] -> MMco2[c] + MMlyxnt[c]	0	1000	67283.1	Mouse metabolic/ transport/ demand reaction
MMDOGULND2	MMh2o[c] + MM23dogulnt[c] -> MMco2[c] + MMxylnt[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDOGULNO1	MMh2o2[c] + MM23dogulnt[c] -> 2 MMh[c] + MMoxa[c] + MMthrnt[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDOGULNO2	MMh2o[c] + MM23dogulnt[c] -> MMh[c] + MMoxa[c] + MMeryrbt[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDOLASNT_Ler	MMAsn_X_Ser_Thr[r] + 0.1 MMg3mHmpdol_L[r] -> MMh[r] + 0.1 MMdoldp_L[r] + MMg3mHmasn[r]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDOLASNT_Uer	MMAsn_X_Ser_Thr[r] + 0.1 MMg3mHmpdol_U[r] -> MMh[r] + MMg3mHmasn[r] + 0.1 MMdoldp_U[r]	0	1000	20014.1 and 13200.1 and 103963.1 and 13135.1	Mouse metabolic/ transport/ demand reaction

MMDOLDPP_Ler	MMh2o[r] + 0.1 MMdoldp_L[r] -> 0.1 MMdolp_L[r] + MMh[r] + MMpi[r]	0	1000	20014.1 and 13200.1 and 103963.1 and 13135.1	Mouse metabolic/ transport/ demand reaction
MMDOLDPP_Uer	MMh2o[r] + 0.1 MMdoldp_U[r] -> MMh[r] + 0.1 MMdolp_U[r] + MMpi[r]	0	1000	57170.1	Mouse metabolic/ transport/ demand reaction
MMDOLGLCP_Lter	0.1 MMdolglcp_L[c] -> 0.1 MMdolglcp_L[r]	0	1000	57170.1	Mouse metabolic/ transport/ demand reaction
MMDOLGLCP_Uter	0.1 MMdolglcp_U[c] -> 0.1 MMdolglcp_U[r]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDOLGPP_Ler	MMh2o[r] + 0.1 MMdolglcp_L[r] -> 0.1 MMdolp_L[r] + MMh[r] + MMglc-D[r]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDOLGPP_Uer	MMh2o[r] + 0.1 MMdolglcp_U[r] -> MMh[r] + 0.1 MMdolp_U[r] + MMglc-D[r]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDOLICHOL_Lter	0.1 MMdolichol_L[r] <=> 0.1 MMdolichol_L[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDOLICHOL_Uter	0.1 MMdolichol_U[r] <=> 0.1 MMdolichol_U[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDOLK_L	MMctp[c] + 0.1 MMdolichol_L[c] -> MMh[c] + MMcdp[c] + 0.1 MMdolp_L[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDOLK_U	MMctp[c] + 0.1 MMdolichol_U[c] -> MMh[c] + MMcdp[c] + 0.1 MMdolp_U[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDOLMANP_Lter	0.1 MMdolmanp_L[c] -> 0.1 MMdolmanp_L[r]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDOLMANP_Uter	0.1 MMdolmanp_U[c] -> 0.1 MMdolmanp_U[r]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDOLPGT1_Ler	0.1 MMdolglcp_L[r] + 0.1 MMm8mpdol_L[r] -> 0.1 MMdolp_L[r] + MMh[r] + 0.1 MMg1m8mpdol_L[r]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDOLPGT1_Uer	0.1 MMdolglcp_U[r] + 0.1 MMm8mpdol_U[r] -> MMh[r] + 0.1 MMdolp_U[r] + 0.1 MMg1m8mpdol_U[r]	0	1000	320438.1	Mouse metabolic/ transport/ demand reaction
MMDOLPGT2_Ler	0.1 MMdolglcp_L[r] + 0.1 MMg1m8mpdol_L[r] -> 0.1 MMdolp_L[r] + MMh[r] + 0.1 MMg2m8mpdol_L[r]	0	1000	320438.1	Mouse metabolic/ transport/ demand reaction
MMDOLPGT2_Uer	0.1 MMdolglcp_U[r] + 0.1 MMg1m8mpdol_U[r] -> MMh[r] + 0.1 MMdolp_U[r] + 0.1 MMg2m8mpdol_U[r]	0	1000	381903.1 or 381903.2 or 381903.3	Mouse metabolic/ transport/ demand reaction
MMDOLPGT3_Ler	0.1 MMdolglcp_L[r] + 0.1 MMg2m8mpdol_L[r] -> 0.1 MMdolp_L[r] + MMh[r] + 0.1 MMg3m8mpdol_L[r]	0	1000	381903.1 or 381903.2 or 381903.3	Mouse metabolic/ transport/ demand reaction
MMDOLPGT3_Uer	0.1 MMdolglcp_U[r] + 0.1 MMg2m8mpdol_U[r] -> MMh[r] + 0.1 MMdolp_U[r] + 0.1 MMg3m8mpdol_U[r]	0	1000	380959.1	Mouse metabolic/ transport/ demand reaction
MMDOLPH_Ler	MMh2o[r] + 0.1 MMdolp_L[r] -> MMpi[r] + 0.1 MMdolichol_L[r]	0	1000	380959.1	Mouse metabolic/ transport/ demand reaction
MMDOLPH_Uer	MMh2o[r] + 0.1 MMdolp_U[r] -> MMpi[r] + 0.1 MMdolichol_U[r]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDOLPMT1_Ler	0.1 MMdolmanp_L[r] + 0.1 MMm4mpdol_L[r] -> 0.1 MMdolp_L[r] + MMh[r] + 0.1 MMm5mpdol_L[r]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDOLPMT1_Uer	0.1 MMdolmanp_U[r] + 0.1 MMm4mpdol_U[r] -> MMh[r] + 0.1 MMdolp_U[r] + 0.1 MMm5mpdol_U[r]	0	1000	208624.1 or 208624.2 or 208624.3 or 208624.4	Mouse metabolic/ transport/ demand reaction
MMDOLPMT2_Ler	0.1 MMdolmanp_L[r] + 0.1 MMm5mpdol_L[r] -> 0.1 MMdolp_L[r] + MMh[r] + 0.1 MMm6mpdol_L[r]	0	1000	208624.1 or 208624.2 or 208624.3 or 208624.4	Mouse metabolic/ transport/ demand reaction
MMDOLPMT2_Uer	0.1 MMdolmanp_U[r] + 0.1 MMm5mpdol_U[r] -> MMh[r] + 0.1 MMdolp_U[r] + 0.1 MMm6mpdol_U[r]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDOLPMT3_Ler	0.1 MMdolmanp_L[r] + 0.1 MMm6mpdol_L[r] -> 0.1 MMdolp_L[r] + MMh[r] + 0.1 MMm7mpdol_L[r]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDOLPMT3_Uer	0.1 MMdolmanp_U[r] + 0.1 MMm6mpdol_U[r] -> MMh[r] + 0.1 MMdolp_U[r] + 0.1 MMm7mpdol_U[r]	0	1000	223774.1	Mouse metabolic/ transport/ demand reaction
MMDOLPMT4_Ler	0.1 MMdolmanp_L[r] + 0.1 MMm7mpdol_L[r] -> 0.1 MMdolp_L[r] + MMh[r] + 0.1 MMm8mpdol_L[r]	0	1000	223774.1	Mouse metabolic/ transport/ demand reaction
MMDOLPMT4_Uer	0.1 MMdolmanp_U[r] + 0.1 MMm7mpdol_U[r] -> MMh[r] + 0.1 MMdolp_U[r] + 0.1 MMm8mpdol_U[r]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDOLPMT_L	MMgdpmann[c] + 0.1 MMdolp_L[c] -> MMgdp[c] + 0.1 MMdolmanp_L[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDOLPMT_U	MMgdpmann[c] + 0.1 MMdolp_U[c] -> MMgdp[c] + 0.1 MMdolmanp_U[c]	0	1000	68563.1 and 13481.1 and 13480.1 or 68563.2 and 13481.1 and 13480.1 or 13481.2 and 68563.1 and 13480.1 or 13481.2 and 68563.2 and 13480.1	Mouse metabolic/ transport/ demand reaction
MMDOLP_Lter	0.1 MMdolp_L[r] -> 0.1 MMdolp_L[c]	0	1000	68563.1 and 13481.1 and 13480.1 or 68563.2 and 13481.1 and 13480.1 or 13481.2 and 68563.1 and 13480.1 or 13481.2 and 68563.2 and 13480.1	Mouse metabolic/ transport/ demand reaction
MMDOLP_Uter	0.1 MMdolp_U[r] -> 0.1 MMdolp_U[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDOPABMO	MMo2[c] + MMdopa[c] + MMascb-L[c] -> MMh2o[c] + MMnrpphr[c] + MMdhdascb[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDOPACHRMISO	MMo2[c] + 2 MM2c23dh56dhoxin[c] -> 2 MMh2o[c] + 2 MML-dpchrm[c]	0	1000	59012.1 or 13166.1	Mouse metabolic/ transport/ demand reaction
MMDOPAMT	MMamet[c] + MMdopa[c] -> MMh[c] + MMahcys[c] + MM3moxtyr[c]	0	1000	22173.1	Mouse metabolic/ transport/ demand reaction
MMDOPAQNISO1	MMdopaqn[c] <=> MMh[c] + MM2c23dh56dhoxin[c]	-1000	1000	12846.1 or 12846.2	Mouse metabolic/ transport/ demand reaction
MMDOPASFt	MMdopasf[c] -> MMdopasf[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDOPAVESSEC	2 MMh2o[c] + 2 MMatp[c] + 3 MMdopa[c] -> 2 MMadp[c] + 2 MMh[c] + 2 MMpi[c] + 3 MMdopa[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDOPAt4_2_r	2 MMna1[e] + MMdopa[e] <=> 2 MMna1[c] + MMdopa[c]	0	1000	214084.1 or 110877.1	Mouse metabolic/ transport/ demand reaction
MMDOPAtu	MMdopa[e] <=> MMdopa[c]	0	1000	20538.1 or 13162.1	Mouse metabolic/ transport/ demand reaction
MMDORNOp	MMo2[x] + MMh2o[x] + MMorn-D[x] -> MMh2o2[x] + MMnh4[x] + MM5a2opntn[x]	0	1000	20518.1 or 20519.1 or 20518.2	Mouse metabolic/ transport/ demand reaction
MMDPCOAK	MMatp[c] + MMdpcoa[c] -> MMadp[c] + MMh[c] + MMcoa[c]	0	1000	13142.1	Mouse metabolic/ transport/ demand reaction
MMDPCOAPP	MMh2o[c] + MMdpcoa[c] -> 2 MMh[c] + MMamp[c] + MMpan4p[c]	0	1000	71743.1	Mouse metabolic/ transport/ demand reaction
MMDPCOAtl	MMdpcoa[l] <=> MMdpcoa[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDPGM	MM13dpg[c] <=> MMh[c] + MM23dpg[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDPGase	MMh2o[c] + MM23dpg[c] -> MMpi[c] + MM3pg[c]	0	1000	12183.1 or 56012.1 or 18648.1 or 12183.2 or 56012.2	Mouse metabolic/ transport/ demand reaction
MMDPHMBDCm	MMh[m] + MM3dpdhb_me[m] -> MMco2[m] + MM2dp6mep[m]	0	1000	12183.1 or 56012.1 or 18648.1 or 12183.2 or 56012.2	Mouse metabolic/ transport/ demand reaction
MMDPMVDx	MMatp[x] + MM5dpmev[x] -> MMadp[x] + MMco2[x] + MMipdp[x] + MMpi[x]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDPPS	7 MMipdp[c] + MMfrdp[c] -> 7 MMppi[c] + MMdecdp[c]	0	1000	192156.1	Mouse metabolic/ transport/ demand reaction
MMDPROOp	MMo2[x] + MMpro-D[x] -> MMh[x] + MMh2o2[x] + MM1p2cbxl[x]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDRBK	MMatp[c] + MMdrib[c] -> MMadp[c] + MMh[c] + MM2dr5p[c]	0	1000	13142.1	Mouse metabolic/ transport/ demand reaction
MMDRIBt	MMdrib[e] <=> MMdrib[c]	-1000	1000	71336.1	Mouse metabolic/ transport/ demand reaction
MMDRPA	MM2dr5p[c] -> MMacald[c] + MMg3p[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDSAT	MMsphgn[c] + MMRtotalcoa[c] -> MMh[c] + MMcoa[c] + MMdhcrm_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDST_ANTIGENt	MMdsT_antigen[g] -> MMdsT_antigen[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDTDPtn	MMdtdp[c] <=> MMdtdp[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDTMPK	MMatp[c] + MMdtmp[c] <=> MMadp[c] + MMdtdp[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDTTPtn	MMdttp[c] <=> MMdttp[n]	-1000	1000	21915.1	Mouse metabolic/ transport/ demand reaction
MMDUDPtn	MMdudp[c] <=> MMdudp[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDUMPtn	MMdump[c] <=> MMdump[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDURAD	MMnadp[c] + MM56dura[c] <=> MMh[c] + MMnadph[c] + MMura[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDURAD2	MMnadp[c] + MM56dthm[c] <=> MMh[c] + MMnadph[c] + MMthym[c]	-1000	1000	99586.1	Mouse metabolic/ transport/ demand reaction
MMDURIK1	MMatp[c] + MMduri[c] -> MMadp[c] + MMh[c] + MMdump[c]	0	1000	99586.1	Mouse metabolic/ transport/ demand reaction
MMDURIK1m	MMatp[m] + MMduri[m] -> MMh[m] + MMadp[m] + MMdump[m]	0	1000	57813.1 or 619653.1	Mouse metabolic/ transport/ demand reaction
MMDURIPP	MMpi[c] + MMduri[c] <=> MM2dr1p[c] + MMura[c]	-1000	1000	57813.1	Mouse metabolic/ transport/ demand reaction
MMDURIt	MMduri[e] <=> MMduri[c]	0	1000	667034.1 or 76654.1	Mouse metabolic/ transport/ demand reaction
MMDURItn	MMduri[c] <=> MMduri[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMDUTPDPm	MMh2o[m] + MMdutp[m] -> MMh[m] + MMppi[m] + MMdump[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMDUTPDPn	MMh2o[n] + MMdutp[n] -> MMppi[n] + MMh[n] + MMdump[n]	0	1000	110074.1	Mouse metabolic/ transport/ demand reaction
MMD_3AIBt	MM3aib-D[c] -> MM3aib-D[e]	0	1000	110074.1	Mouse metabolic/ transport/ demand reaction
MMD_LACt2	MMh[e] + MMlac-D[e] <=> MMh[c] + MMlac-D[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMD_LACtm	MMh[c] + MMlac-D[c] <=> MMh[m] + MMlac-D[m]	-1000	1000	20503.1 or 80879.1 or 20501.1 or 57274.1	Mouse metabolic/ transport/ demand reaction
MMEAFLATOXINte	MMeaflatoxin[e] <=> MMeaflatoxin[c]	0	1000	20501.1	Mouse metabolic/ transport/ demand reaction
MMEBASTINEOHte	MMebastineoh[e] <=> MMebastineoh[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMEBASTINEOHtr	MMebastineoh[r] <=> MMebastineoh[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMEBASTINEte	MMebastine[e] <=> MMebastine[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMEBASTINEtr	MMebastine[r] <=> MMebastine[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMEBP1r	MMzymst[r] -> MMchlstol[r]	0	1000		Mouse metabolic/ transport/ demand reaction
MMEBP2r	MMzymstnl[r] -> MMlthstrl[r]	0	1000	13595.1	Mouse metabolic/ transport/ demand reaction
MMECGISOr	MMecgon[r] <=> MMpecgon[r]	-1000	1000	13595.1	Mouse metabolic/ transport/ demand reaction
MMECOAH12m	MMh2o[m] + MM2mp2coa[m] <=> MM3hibutcoa[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMECOAH1m	MM3hbcoa[m] <=> MMh2o[m] + MMb2coa[m]	-1000	1000	231086.1 or 97212.1 or 93747.1	Mouse metabolic/ transport/ demand reaction

MMECOAH1x	MM3hbcoa[x] <=> MMh2o[x] + MMb2coa[x]	-1000	1000	11992.1 or 231086.1 or 97212.1 or 93747.1	Mouse metabolic/ transport/ demand reaction
MMECOAH9m	MMh2o[m] + MM2mb2coa[m] <=> MM3hmbcoa[m]	-1000	1000	74147.1 or 51798.1	Mouse metabolic/ transport/ demand reaction
MMEGMESTr	MMh2o[r] + MMegme[r] -> MMh[r] + MMecgotr[r] + MMmeoh[r]	0	1000	231086.1 or 97212.1 or 93747.1	Mouse metabolic/ transport/ demand reaction
MMEHGLAT	MMakg[c] + MMe4hglu[c] -> MMglu-L[c] + MM4h2ogl[c]	0	1000	67758.1	Mouse metabolic/ transport/ demand reaction
MMEHGLAT2m	MMe4hglu[m] + MMoaa[m] -> MMasp-L[m] + MM4h2ogl[m]	0	1000	14718.1	Mouse metabolic/ transport/ demand reaction
MMEHGLATm	MMakg[m] + MMe4hglu[m] -> MMglu-L[m] + MM4h2ogl[m]	0	1000	14719.1	Mouse metabolic/ transport/ demand reaction
MMEICOSTETCPT1	MMcrn[c] + MMeicostetcoa[c] -> MMcoa[c] + MMeicostetcrn[c]	0	1000	14719.1	Mouse metabolic/ transport/ demand reaction
MMEICOSTETCPT2	MMcoa[m] + MMeicostetcrn[m] -> MMcrn[m] + MMeicostetcoa[m]	0	1000	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	Mouse metabolic/ transport/ demand reaction
MMEICOSTETCRNt	MMeicostetcrn[c] -> MMeicostetcrn[m]	0	1000	12896.1	Mouse metabolic/ transport/ demand reaction
MMEICOSTETr	MMeicoste[e] <=> MMeicoste[c]	0	1000	57279.1	Mouse metabolic/ transport/ demand reaction
MMELAIDCPT1c	MMcrn[c] + MMod2coa[c] <=> MMcoa[c] + MMelaidcrn[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMELAIDCPT2	MMcoa[m] + MMelaidcrn[m] -> MMcrn[m] + MMod2coa[m]	0	1000	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	Mouse metabolic/ transport/ demand reaction
MMELAIDCRNt	MMelaidcrn[c] -> MMelaidcrn[m]	0	1000	12896.1	Mouse metabolic/ transport/ demand reaction
MMELAIDt	MMelaid[e] <=> MMelaid[c]	0	1000	57279.1	Mouse metabolic/ transport/ demand reaction
MMENGASE	MMh2o[c] + MMs2f2n2m2m[c] -> MMacgam[c] + MMs2f2n2m2m[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMENGASE2	MMh2o[c] + MMn2m2mm[c] -> MMacgam[c] + MMn2m2mm[c]	0	1000	217364.1	Mouse metabolic/ transport/ demand reaction
MMENGASE2ly	MMh2o[l] + MMn2m2mm[l] -> MMacgam[l] + MMn2m2mm[l]	0	1000	217364.1	Mouse metabolic/ transport/ demand reaction
MMENGASE3ly	MMh2o[l] + MMksi_deg2[l] -> MMacgam[l] + MMksi_deg3[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MMENGASEly	MMh2o[l] + MMs2f2n2m2m[l] -> MMacgam[l] + MMs2f2n2m2m[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MMENMAN1g	MMh2o[g] + MMg1m8mass[g] -> MMglc1man[g] + MMm7massA[g]	0	1000		Mouse metabolic/ transport/ demand reaction
MMENMAN2g	MMh2o[g] + MMg2m8mass[g] -> MMm7massA[g] + MMglc2man[g]	0	1000		Mouse metabolic/ transport/ demand reaction
MMENMAN3g	MMh2o[g] + MMg3m8mass[g] -> MMm7massA[g] + MMglc3man[g]	0	1000		Mouse metabolic/ transport/ demand reaction
MMENMAN4g	MMh2o[g] + MMg1m7massC[g] -> MMglc1man[g] + MMm6massC[g]	0	1000		Mouse metabolic/ transport/ demand reaction
MMENMAN5g	MMh2o[g] + MMg1m7massB[g] -> MMglc1man[g] + MMm6massB2[g]	0	1000		Mouse metabolic/ transport/ demand reaction
MMENMAN6g	MMh2o[g] + MMg1m6massB1[g] -> MMglc1man[g] + MMm5massB1[g]	0	1000		Mouse metabolic/ transport/ demand reaction
MMENO	MM2pg[c] <=> MMh2o[c] + MMpep[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMEPAFABPpmtc	MMtmmdnc[u] -> MMtmmdnc[c]	0	1000	13807.1 or 13808.1 or 13808.2 or 13806.1	Mouse metabolic/ transport/ demand reaction
MMEPCTX	MMh[c] + MMctp[c] + MM2amep[c] -> MMppi[c] + MMcrnp2amep[c]	0	1000	(14719.1 or 12491.1)	Mouse metabolic/ transport/ demand reaction
MMESTRADIOLGLCt2	MMh2o[c] + MMatp[c] + MMestradiolglk[c] -> MMadp[c] + MMh[c] + MMpi[c] + MMestradiolglc[e]	0	1000	68671.1	Mouse metabolic/ transport/ demand reaction
MMESTRADIOLGLCtr	MMestradiolglk[c] <=> MMestradiolglc[r]	-1000	1000	239273.1	Mouse metabolic/ transport/ demand reaction
MMESTRADIOLt	MMestradiol[e] <=> MMestradiol[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMESTRADIOLtr	MMestradiol[r] <=> MMestradiol[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMESTRIOLGLCte	MMh2o[c] + MMatp[c] + MMestriolglc[c] -> MMadp[c] + MMh[c] + MMpi[c] + MMestriolglc[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMESTRIOLGLCtr	MMestriolglc[c] <=> MMestriolglc[r]	-1000	1000	17250.1	Mouse metabolic/ transport/ demand reaction
MMESTRIOLt	MMestriol[e] <=> MMestriol[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMESTRONEGLCt	MMh2o[c] + MMatp[c] + MMestronesglc[c] -> MMadp[c] + MMh[c] + MMpi[c] + MMestronesglc[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMESTRONEGLCtr	MMestronesglc[c] <=> MMestronesglc[r]	-1000	1000	76408.1 or 76408.2 or 76408.3	Mouse metabolic/ transport/ demand reaction
MMESTRONESt2	2 MMna1[e] + MMestrones[e] -> 2 MMna1[c] + MMestrones[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMESTRONEtr	MMestrone[r] <=> MMestrone[c]	-1000	1000	20493.1	Mouse metabolic/ transport/ demand reaction
MMESTSULT	MMpaps[c] + MMestrone[c] -> MMh[c] + MMpap[c] + MMestrones[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMETF	MMfadh2[m] + MMetfox[m] -> MMfad[m] + MMetfrd[m]	0	1000	20887.1 or 20887.2 or 20887.3 or 20887.4 or 20860.1 or 20887.5	Mouse metabolic/ transport/ demand reaction
MMETFQO	MMq10[m] + MMetfrd[m] -> MMq10h2[m] + MMetfox[m]	0	1000	110826.1 or 110826.2 or 110842.1	Mouse metabolic/ transport/ demand reaction
MMETHAK	MMatp[c] + MMetha[c] -> MMadp[c] + MMh[c] + MMethamp[c]	0	1000	66841.1	Mouse metabolic/ transport/ demand reaction
MMETHAtr	MMetha[c] -> MMetha[e]	0	1000	214253.1 or 12660.1 or 75320.1 or 12660.2	Mouse metabolic/ transport/ demand reaction
MMETHP	MMh2o[c] + MMethamp[c] -> MMpi[c] + MMetha[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMETOHMO	MMo2[c] + MMh[c] + MMnadph[c] + MMetoh[c] -> 2 MMh2o[c] + MMnadp[c] + MMacald[c]	0	1000	237928.1	Mouse metabolic/ transport/ demand reaction
MMETOHt	MMetoh[e] <=> MMetoh[c]	0	1000	13106.1	Mouse metabolic/ transport/ demand reaction
MMETOHtx	MMetoh[c] <=> MMetoh[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMF1At	MMf1a[g] -> MMf1a[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMF1Atg	MMf1a[g] <=> MMf1a[l]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMF1PGT	MMf[c] + MMgip[c] + MMfuc1p-L[c] <=> MMppi[c] + MMgdpfuc[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMF6Tg	MMgdpfuc[g] + MMn2m2mass[g] -> MMh[g] + MMfn2m2mass[g] + MMgdp[g]	0	1000	75540.1	Mouse metabolic/ transport/ demand reaction
MMFA120ACPH	MMh2o[c] + MMddcaACP[c] <=> MMh[c] + MMACP[c] + MMddca[c]	-1000	1000	53618.1 or 53618.2 or 53618.3 or 53618.4 or 53618.5	Mouse metabolic/ transport/ demand reaction
MMFA140ACPH	MMh2o[c] + MMmyrsACP[c] <=> MMh[c] + MMACP[c] + MMtrdec4a[c]	-1000	1000	99035.1	Mouse metabolic/ transport/ demand reaction
MMFA141ACPH	MMh2o[c] + MMtrdeACP[c] <=> MMh[c] + MMACP[c] + MMtrdtrdec4a[c]	-1000	1000	99035.1	Mouse metabolic/ transport/ demand reaction
MMFA160ACPH	MMh2o[c] + MMpalmACP[c] <=> MMh[c] + MMACP[c] + MMhdd4a[c]	-1000	1000	99035.1	Mouse metabolic/ transport/ demand reaction
MMFA161ACPH	MMh2o[c] + MMhdeACP[c] <=> MMh[c] + MMACP[c] + MMhdcea[c]	-1000	1000	99035.1	Mouse metabolic/ transport/ demand reaction
MMFA180ACPH	MMh2o[c] + MMoctdcaACP[c] <=> MMh[c] + MMACP[c] + MMoctdca[c]	-1000	1000	99035.1	Mouse metabolic/ transport/ demand reaction
MMFA181ACPH	MMh2o[c] + MMoctACP[c] <=> MMh[c] + MMACP[c] + MMoctdcea[c]	-1000	1000	99035.1	Mouse metabolic/ transport/ demand reaction
MMFA1821ACPH	MMh2o[c] + MMlnlcACP[c] <=> MMh[c] + MMACP[c] + MMlnlc[c]	-1000	1000	99035.1	Mouse metabolic/ transport/ demand reaction
MMFA1822ACPH	MMh2o[c] + MMlnleidcACP[c] <=> MMh[c] + MMACP[c] + MMlnleidc[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMFA182ACPH	MMh2o[c] + MMoctdcyaACP[c] <=> MMh[c] + MMACP[c] + MMoctdcya[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMFACOAL140i	MMatp[c] + MMcoa[c] + MMtrdca[c] -> MMamp[c] + MMppi[c] + MMtdcoa[c]	0	1000	99035.1	Mouse metabolic/ transport/ demand reaction
MMFACOAL150	MMatp[c] + MMcoa[c] + MMptdca[c] <=> MMamp[c] + MMppi[c] + MMptdcacoa[c]	-1000	1000	74205.1	Mouse metabolic/ transport/ demand reaction
MMFACOAL160i	MMatp[c] + MMcoa[c] + MMhdca[c] -> MMamp[c] + MMppi[c] + MMpmtcoa[c]	0	1000	(74205.1 or 50790.1 or 14081.1 or 22305.2 or 22305.1 or 74205.2)	Mouse metabolic/ transport/ demand reaction
MMFACOAL161	MMatp[c] + MMcoa[c] + MMhdcea[c] <=> MMamp[c] + MMppi[c] + MMhdcoa[c]	-1000	1000	(433256.1 or 74205.1 or 14081.1 or 22305.2 or 22305.1 or 74205.2)	Mouse metabolic/ transport/ demand reaction
MMFACOAL170	MMatp[c] + MMcoa[c] + MMtpdca[c] <=> MMamp[c] + MMppi[c] + MMtpdcacoa[c]	-1000	1000	14081.1	Mouse metabolic/ transport/ demand reaction
MMFACOAL180i	MMatp[c] + MMcoa[c] + MMocdca[c] -> MMamp[c] + MMppi[c] + MMstcoa[c]	0	1000	(74205.1 or 50790.1 or 14081.1 or 22305.2 or 22305.1 or 74205.2)	Mouse metabolic/ transport/ demand reaction
MMFACOAL1812	MMatp[c] + MMcoa[c] + MMvacc[c] <=> MMamp[c] + MMppi[c] + MMvaccoa[c]	-1000	1000	(433256.1 or 74205.1 or 14081.1 or 22305.2 or 22305.1 or 74205.2)	Mouse metabolic/ transport/ demand reaction
MMFACOAL1813	MMatp[c] + MMcoa[c] + MMdtad[c] <=> MMamp[c] + MMppi[c] + MMtrd2coa[c]	-1000	1000	14081.1	Mouse metabolic/ transport/ demand reaction
MMFACOAL181i	MMatp[c] + MMcoa[c] + MMocdcea[c] -> MMamp[c] + MMppi[c] + MModecoa[c]	0	1000	14081.1	Mouse metabolic/ transport/ demand reaction
MMFACOAL1821	MMatp[c] + MMcoa[c] + MMlnlc[c] <=> MMamp[c] + MMppi[c] + MMlnlcoa[c]	-1000	1000	74205.1 or 14081.1 or 74205.2	Mouse metabolic/ transport/ demand reaction
MMFACOAL1822	MMatp[c] + MMcoa[c] + MMlnleidc[c] <=> MMamp[c] + MMppi[c] + MMlnleidcoa[c]	-1000	1000	14081.1	Mouse metabolic/ transport/ demand reaction
MMFACOAL1831	MMatp[c] + MMcoa[c] + MMlnlncg[c] <=> MMamp[c] + MMppi[c] + MMlnlncgcoa[c]	-1000	1000	14081.1	Mouse metabolic/ transport/ demand reaction
MMFACOAL1832	MMatp[c] + MMcoa[c] + MMlnlnca[c] <=> MMamp[c] + MMppi[c] + MMlnlncacoa[c]	-1000	1000	14081.1	Mouse metabolic/ transport/ demand reaction
MMFACOAL184	MMatp[c] + MMcoa[c] + MMstrdnc[c] <=> MMamp[c] + MMppi[c] + MMstrdncoa[c]	-1000	1000	14081.1	Mouse metabolic/ transport/ demand reaction
MMFACOAL191	MMatp[c] + MMcoa[c] + MMprist[c] -> MMamp[c] + MMppi[c] + MMpristcoa[c]	0	1000	14081.1	Mouse metabolic/ transport/ demand reaction
MMFACOAL200	MMatp[c] + MMcoa[c] + MMarach[c] <=> MMamp[c] + MMppi[c] + MMarachcoa[c]	-1000	1000	26458.1	Mouse metabolic/ transport/ demand reaction
MMFACOAL203	MMatp[c] + MMcoa[c] + MMdhlcg[c] <=> MMamp[c] + MMppi[c] + MMdhlcgcoa[c]	-1000	1000	14081.1	Mouse metabolic/ transport/ demand reaction
MMFACOAL204	MMatp[c] + MMcoa[c] + MMarachd[c] <=> MMamp[c] + MMppi[c] + MMarachdcoa[c]	-1000	1000	14081.1	Mouse metabolic/ transport/ demand reaction
MMFACOAL2042	MMatp[c] + MMcoa[c] + MMeicostet[c] <=> MMamp[c] + MMppi[c] + MMeicostetcoa[c]	-1000	1000	14081.1	Mouse metabolic/ transport/ demand reaction
MMFACOAL204i	MMatp[c] + MMcoa[c] + MMarachd[c] -> MMamp[c] + MMppi[c] + MMarachdcoa[c]	0	1000	14081.1	Mouse metabolic/ transport/ demand reaction
MMFACOAL205	MMatp[c] + MMcoa[c] + MMtmmdnc[c] <=> MMamp[c] + MMppi[c] + MMtmmdncoa[c]	-1000	1000	(50790.1 or 74205.1 or 50790.2 or 14081.1 or 22305.2 or 22305.1 or 74205.2)	Mouse metabolic/ transport/ demand reaction
MMFACOAL206	MMatp[c] + MMcoa[c] + MMphytd[c] <=> MMamp[c] + MMppi[c] + MMphytcoa[c]	-1000	1000	14081.1	Mouse metabolic/ transport/ demand reaction
MMFACOAL224	MMatp[c] + MMcoa[c] + MMadm[c] <=> MMamp[c] + MMppi[c] + MMadmcoa[c]	-1000	1000	26458.1	Mouse metabolic/ transport/ demand reaction

MMFACOAL2251	MMatp[c] + MMcoa[c] + MMdcsptn1[c] <=> MMamp[c] + MMppi[c] + MMdcsptn1coa[c]	-1000	1000	14081.1	Mouse metabolic/ transport/ demand reaction
MMFACOAL2252	MMatp[c] + MMcoa[c] + MMclpnd[c] <=> MMamp[c] + MMppi[c] + MMclpndcoa[c]	-1000	1000	14081.1	Mouse metabolic/ transport/ demand reaction
MMFACOAL226	MMatp[c] + MMcoa[c] + MMcrvnc[c] <=> MMamp[c] + MMppi[c] + MMc226coa[c]	-1000	1000	14081.1	Mouse metabolic/ transport/ demand reaction
MMFACOAL226i	MMatp[c] + MMcoa[c] + MMcrvnc[c] -> MMamp[c] + MMppi[c] + MMc226coa[c]	0	1000	14081.1	Mouse metabolic/ transport/ demand reaction
MMFACOAL240	MMatp[c] + MMcoa[c] + MMlgnc[c] <=> MMamp[c] + MMppi[c] + MMlgnccoa[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMFACOAL241	MMatp[c] + MMcoa[c] + MMnrvnc[c] <=> MMamp[c] + MMppi[c] + MMnrvnccoa[c]	-1000	1000	14081.1	Mouse metabolic/ transport/ demand reaction
MMFACOAL244_1	MMatp[c] + MMcoa[c] + MMtetrtet6[c] <=> MMamp[c] + MMppi[c] + MMtetrtet6coa[c]	-1000	1000	14081.1	Mouse metabolic/ transport/ demand reaction
MMFACOAL245_1	MMatp[c] + MMcoa[c] + MMteipent6[c] <=> MMamp[c] + MMppi[c] + MMteipent6coa[c]	-1000	1000	14081.1	Mouse metabolic/ transport/ demand reaction
MMFACOAL245_2	MMatp[c] + MMcoa[c] + MMteipent3[c] <=> MMamp[c] + MMppi[c] + MMteipent3coa[c]	-1000	1000	14081.1	Mouse metabolic/ transport/ demand reaction
MMFACOAL246_1	MMatp[c] + MMcoa[c] + MMtethex3[c] <=> MMamp[c] + MMppi[c] + MMtethex3coa[c]	-1000	1000	14081.1	Mouse metabolic/ transport/ demand reaction
MMFACOAL260	MMatp[c] + MMcoa[c] + MMhexc[c] <=> MMamp[c] + MMppi[c] + MMhexccoa[c]	-1000	1000	14081.1	Mouse metabolic/ transport/ demand reaction
MMFACOAL40im	MMcoa[m] + MMatp[m] + MMbut[m] -> MMamp[m] + MMppi[m] + MMbtcoa[m]	0	1000	14081.1	Mouse metabolic/ transport/ demand reaction
MMFACOAL80i	MMatp[c] + MMcoa[c] + MMocta[c] -> MMamp[c] + MMppi[c] + MMoccoa[c]	0	1000	117147.1	Mouse metabolic/ transport/ demand reaction
MMFADDP	MMth2o[c] + MMfadf[c] -> 2 MMth[c] + MMamp[c] + MMfmn[c]	0	1000	74205.1 or 74205.2	Mouse metabolic/ transport/ demand reaction
MMFADH2tru	MMfadh2[c] -> MMfadh2[r]	0	1000	18605.1	Mouse metabolic/ transport/ demand reaction
MMFADH2tx	MMfadh2[c] <=> MMfadh2[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMFADtru	MMfad[r] -> MMfad[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMFADtx	MMfad[c] <=> MMfad[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMFAEL183	MMo2[c] + 5 MMh[c] + 4 MMnadph[c] + MMmalcoa[c] + MMhlnlcgcoa[c] -> 3 MMh2o[c] + 4 MMnadp[c] + MMco2[c] + MMcoa[c] + MMdhlnlcgcoa[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMFAEL184	MMo2[c] + 5 MMh[c] + 4 MMnadph[c] + MMmalcoa[c] + MMstrdncoa[c] -> 3 MMh2o[c] + 4 MMnadp[c] + MMco2[c] + MMcoa[c] + MMeicostetcoa[c]	0	1000	83603.1	Mouse metabolic/ transport/ demand reaction
MMFAEL204	MMo2[c] + 5 MMh[c] + 4 MMnadph[c] + MMmalcoa[c] + MMarachdcoa[c] -> 3 MMh2o[c] + 4 MMnadp[c] + MMco2[c] + MMcoa[c] + MMadrncoa[c]	0	1000	83603.1	Mouse metabolic/ transport/ demand reaction
MMFAEL205	MMo2[c] + 5 MMh[c] + 4 MMnadph[c] + MMmalcoa[c] + MMtmndncoa[c] -> 3 MMh2o[c] + 4 MMnadp[c] + MMco2[c] + MMcoa[c] + MMclpndcoa[c]	0	1000	83603.1	Mouse metabolic/ transport/ demand reaction
MMFAH1	MMo2[c] + MMh[c] + MMnadph[c] + MMddca[c] -> MMh2o[c] + MMnadp[c] + MMwhddca[c]	0	1000	83603.1	Mouse metabolic/ transport/ demand reaction
MMFAH2	MMo2[c] + MMh[c] + MMnadph[c] + MMtdca[c] -> MMh2o[c] + MMnadp[c] + MMwhtdca[c]	0	1000	13117.1	Mouse metabolic/ transport/ demand reaction
MMFAH3	MMo2[c] + MMh[c] + MMnadph[c] + MMhdca[c] -> MMh2o[c] + MMnadp[c] + MMwhhdca[c]	0	1000	13117.1	Mouse metabolic/ transport/ demand reaction
MMFALDH	MMnad[c] + MMghmd[c] + MMfald[c] <=> MMh[c] + MMnadh[c] + MMSfdunh[c]	-1000	1000	13117.1	Mouse metabolic/ transport/ demand reaction
MMFALDhly	MMfald[l] <=> MMfald[c]	-1000	1000	11532.1	Mouse metabolic/ transport/ demand reaction
MMFALDtm	MMfald[m] <=> MMfald[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMFAOXC11	MMth2o[m] + MMcoa[m] + MMnad[m] + MMdmnoncoa[m] -> MMh[m] + MMnadh[m] + MMaccoa[m] + MMdmhptcoa[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMFAOXC140	6 MMth2o[m] + 6 MMcoa[m] + 6 MMnad[m] + 6 MMfad[m] + MMtdcoa[m] -> 6 MMh[m] + 6 MMnadh[m] + 7 MMaccoa[m] + 6 MMfadh2[m]	0	1000	11364.1	Mouse metabolic/ transport/ demand reaction
MMFAOXC150m	6 MMth2o[m] + 6 MMcoa[m] + 6 MMnad[m] + 6 MMfad[m] + MMptdcacoa[m] -> 6 MMh[m] + 6 MMnadh[m] + 6 MMaccoa[m] + MMppcoa[m] + 6 MMfadh2[m]	0	1000	11364.1 or 11409.1	Mouse metabolic/ transport/ demand reaction
MMFAOXC160	7 MMth2o[m] + 7 MMcoa[m] + 7 MMnad[m] + 7 MMfad[m] + MMpmtcoa[m] -> 7 MMh[m] + 7 MMnadh[m] + 8 MMaccoa[m] + 7 MMfadh2[m]	0	1000	11364.1 or 11409.1	Mouse metabolic/ transport/ demand reaction
MMFAOXC16080m	4 MMth2o[m] + 4 MMcoa[m] + 4 MMnad[m] + 4 MMfad[m] + MMpmtcoa[m] -> 4 MMh[m] + 4 MMnadh[m] + 4 MMaccoa[m] + 4 MMfadh2[m] + MMoccoa[m]	0	1000	11364.1 or 11409.1	Mouse metabolic/ transport/ demand reaction
MMFAOXC16080x	4 MMnad[x] + 4 MMcoa[x] + MMpmtcoa[x] + 4 MMo2[x] + 4 MMth2o[x] -> 4 MMh[x] + 4 MMnadh[x] + 4 MMaccoa[x] + MMoccoa[x] + 4 MMth2o2[x]	0	1000	11364.1 or 11409.1	Mouse metabolic/ transport/ demand reaction
MMFAOXC161802m	4 MMth2o[m] + 4 MMcoa[m] + 4 MMnad[m] + 3 MMfad[m] + MMhtdd2coa[m] -> 4 MMh[m] + 4 MMnadh[m] + 4 MMaccoa[m] + 3 MMfadh2[m] + MMoccoa[m]	0	1000	74147.1 and 113868.1 and 11430.1 or 113868.1 and 11430.1 and 15488.1 or 74147.1 and 113868.1 and 11430.2 or 113868.1 and 15488.1 and 11430.2	Mouse metabolic/ transport/ demand reaction
MMFAOXC16180m	4 MMth2o[m] + 4 MMcoa[m] + 4 MMnad[m] + 3 MMfad[m] + MMhtdcoa[m] -> 4 MMh[m] + 4 MMnadh[m] + 4 MMaccoa[m] + 3 MMfadh2[m] + MMoccoa[m]	0	1000	11364.1 or 11409.1	Mouse metabolic/ transport/ demand reaction
MMFAOXC170m	7 MMth2o[m] + 7 MMcoa[m] + 7 MMnad[m] + 7 MMfad[m] + MMhpdcacoa[m] -> 7 MMh[m] + 7 MMnadh[m] + 7 MMaccoa[m] + MMppcoa[m] + 7 MMfadh2[m]	0	1000	11364.1 or 11409.1	Mouse metabolic/ transport/ demand reaction
MMFAOXC180	MMth2o[m] + MMcoa[m] + MMnad[m] + MMfad[m] + MMstcoa[m] -> MMh[m] + MMnadh[m] + MMaccoa[m] + MMfadh2[m] + MMpmtcoa[m]	0	1000	11364.1	Mouse metabolic/ transport/ demand reaction
MMFAOXC180x	MMnad[x] + MMcoa[x] + MMo2[x] + MMth2o[x] + MMstcoa[x] -> MMh[x] + MMnadh[x] + MMaccoa[x] + MMpmtcoa[x] + MMth2o2[x]	0	1000	11364.1 or 11409.1	Mouse metabolic/ transport/ demand reaction
MMFAOXC1811601m	5 MMth2o[m] + 5 MMcoa[m] + 5 MMnad[m] + 4 MMfad[m] + MMotd2coa[m] -> 5 MMh[m] + 5 MMnadh[m] + 5 MMaccoa[m] + 4 MMfadh2[m] + MMoccoa[m]	0	1000	74147.1 and 113868.1 and 11430.1 or 113868.1 and 11430.1 and 15488.1 or 74147.1 and 113868.1 and 11430.2 or 113868.1 and 15488.1 and 11430.2	Mouse metabolic/ transport/ demand reaction
MMFAOXC1811602m	5 MMth2o[m] + 5 MMcoa[m] + 5 MMnad[m] + 4 MMfad[m] + MMvaccoa[m] -> 5 MMh[m] + 5 MMnadh[m] + 5 MMaccoa[m] + 4 MMfadh2[m] + MMoccoa[m]	0	1000	11364.1 or 11409.1	Mouse metabolic/ transport/ demand reaction
MMFAOXC1811603m	5 MMth2o[m] + 5 MMcoa[m] + 5 MMnad[m] + 4 MMfad[m] + MModecoa[m] -> 5 MMh[m] + 5 MMnadh[m] + 5 MMaccoa[m] + 4 MMfadh2[m] + MMoccoa[m]	0	1000	11364.1 or 11409.1	Mouse metabolic/ transport/ demand reaction
MMFAOXC182806m	5 MMth2o[m] + 5 MMcoa[m] + 5 MMnad[m] + 3 MMfad[m] + MMhlnlccoa[m] -> 5 MMh[m] + 5 MMnadh[m] + 5 MMaccoa[m] + 3 MMfadh2[m] + MMoccoa[m]	0	1000	11364.1 or 11409.1	Mouse metabolic/ transport/ demand reaction
MMFAOXC18280m	5 MMth2o[m] + 5 MMcoa[m] + 5 MMnad[m] + 3 MMfad[m] + MMhneldccoa[m] -> 5 MMh[m] + 5 MMnadh[m] + 5 MMaccoa[m] + 3 MMfadh2[m] + MMoccoa[m]	0	1000	11364.1 or 11409.1	Mouse metabolic/ transport/ demand reaction
MMFAOXC183803m	5 MMth2o[m] + 5 MMcoa[m] + 5 MMnad[m] + 2 MMfad[m] + MMhlnlncacoa[m] -> 5 MMh[m] + 5 MMnadh[m] + 5 MMaccoa[m] + 2 MMfadh2[m] + MMoccoa[m]	0	1000	11364.1 or 11409.1	Mouse metabolic/ transport/ demand reaction
MMFAOXC183806m	2 MMo2[m] + 5 MMth2o[m] + 5 MMcoa[m] + 5 MMnad[m] + MMhlnlncgcoa[m] -> 5 MMh[m] + 5 MMnadh[m] + 5 MMaccoa[m] + 2 MMth2o2[m] + MMoccoa[m]	0	1000	11364.1 or 11409.1	Mouse metabolic/ transport/ demand reaction
MMFAOXC183806x	5 MMnad[x] + 5 MMcoa[x] + 2 MMo2[x] + 5 MMth2o[x] + MMhlnlncgcoa[x] -> 5 MMh[x] + 5 MMnadh[x] + 5 MMaccoa[x] + MMoccoa[x] + 2 MMth2o2[x]	0	1000	11364.1 or 11409.1	Mouse metabolic/ transport/ demand reaction
MMFAOXC18480m	5 MMth2o[m] + 5 MMcoa[m] + 5 MMnad[m] + MMfad[m] + MMstrdncoa[m] -> 5 MMh[m] + 5 MMnadh[m] + 5 MMaccoa[m] + MMfadh2[m] + MMoccoa[m]	0	1000	74147.1 and 113868.1 and 11430.1 or 113868.1 and 11430.1 and 15488.1 or 74147.1 and 113868.1 and 11430.2 or 113868.1 and 15488.1 and 11430.2	Mouse metabolic/ transport/ demand reaction
MMFAOXC18480x	5 MMnad[x] + 5 MMcoa[x] + MMo2[x] + 5 MMth2o[x] + MMstrdncoa[x] -> 5 MMh[x] + 5 MMnadh[x] + 5 MMaccoa[x] + MMoccoa[x] + MMth2o2[x]	0	1000	11364.1 or 11409.1	Mouse metabolic/ transport/ demand reaction
MMFAOXC200180m	MMth2o[m] + MMcoa[m] + MMnad[m] + MMfad[m] + MMarachcoa[m] -> MMh[m] + MMnadh[m] + MMaccoa[m] + MMfadh2[m] + MMstcoa[m]	0	1000	74147.1 and 113868.1 and 11430.1 or 113868.1 and 11430.1 and 15488.1 or 74147.1 and 113868.1 and 11430.2 or 113868.1 and 15488.1 and 11430.2	Mouse metabolic/ transport/ demand reaction
MMFAOXC200180x	MMnad[x] + MMcoa[x] + MMo2[x] + MMth2o[x] + MMarachcoa[x] -> MMh[x] + MMnadh[x] + MMaccoa[x] + MMth2o2[x] + MMstcoa[x]	0	1000	11364.1 or 11409.1	Mouse metabolic/ transport/ demand reaction
MMFAOXC2031836m	MMth2o[m] + MMcoa[m] + MMnad[m] + MMfad[m] + MMdhlnlcgcoa[m] -> MMh[m] + MMnadh[m] + MMaccoa[m] + MMfadh2[m] + MMhlnlcgcoa[m]	0	1000	74147.1 and 113868.1 and 11430.1 or 113868.1 and 11430.1 and 15488.1 or 74147.1 and 113868.1 and 11430.2 or 113868.1 and 15488.1 and 11430.2	Mouse metabolic/ transport/ demand reaction
MMFAOXC204	9 MMth2o[m] + 9 MMcoa[m] + 9 MMnad[m] + 5 MMfad[m] + MMarachdcoa[m] -> 9 MMh[m] + 9 MMnadh[m] + 10 MMaccoa[m] + 5 MMfadh2[m]	0	1000	11364.1 or 11409.1	Mouse metabolic/ transport/ demand reaction
MMFAOXC204184m	MMth2o[m] + MMcoa[m] + MMnad[m] + MMfad[m] + MMeicostetcoa[m] -> MMh[m] + MMnadh[m] + MMaccoa[m] + MMfadh2[m] + MMstrdncoa[m]	0	1000	11364.1 or 11409.1	Mouse metabolic/ transport/ demand reaction
MMFAOXC2051843m	MMth2o[m] + MMcoa[m] + MMnad[m] + MMtmndncoa[m] -> MMh[m] + MMnadh[m] + MMaccoa[m] + MMstrdncoa[m]	0	1000	11364.1 or 11409.1	Mouse metabolic/ transport/ demand reaction
MMFAOXC2051843x	MMnad[x] + MMcoa[x] + MMth2o[x] + MMtmndncoa[x] -> MMh[x] + MMnadh[x] + MMaccoa[x] + MMstrdncoa[x]	0	1000	11364.1 or 11409.1	Mouse metabolic/ transport/ demand reaction
MMFAOXC2242046m	MMth2o[m] + MMcoa[m] + MMnad[m] + MMfad[m] + MMadrncoa[m] -> MMh[m] + MMnadh[m] + MMaccoa[m] + MMfadh2[m] + MMarachdcoa[m]	0	1000	74147.1 and 113868.1 and 11430.1 or 113868.1 and 11430.1 and 15488.1 or 74147.1 and 113868.1 and 11430.2 or 113868.1 and 15488.1 and 11430.2	Mouse metabolic/ transport/ demand reaction
MMFAOXC2242046x	MMnad[x] + MMcoa[x] + MMo2[x] + MMth2o[x] + MMadrncoa[x] > MMh[x] + MMnadh[x] + MMaccoa[x] + MMth2o2[x] + MMarachdcoa[x]	0	1000	11364.1 or 11409.1	Mouse metabolic/ transport/ demand reaction

MMFAOXC2251836m	2 MMh2o[m] + 2 MMcoa[m] + 2 MMnad[m] + MMdcspin1coa[m] -> 2 MMh[m] + 2 MMnadh[m] + 2 MMaccoa[m] + MMmlncgcoa[m]	0	1000	74147.1 and 113868.1 and 11430.1 or 113868.1 and 11430.1 and 15488.1 or 74147.1 and 113868.1 and 11430.2 or 113868.1 and 15488.1 and 11430.2	Mouse metabolic/ transport/ demand reaction
MMFAOXC2251836x	2 MMnad[x] + 2 MMcoa[x] + 2 MMh2o[x] + MMdcspin1coa[x] -> 2 MMh[x] + 2 MMnadh[x] + 2 MMaccoa[x] + MMmlncgcoa[x]	0	1000	11364.1 or 11409.1	Mouse metabolic/ transport/ demand reaction
MMFAOXC2252053m	MMco2[m] + MMh2o[m] + MMcoa[m] + MMnad[m] + MMdcspin1coa[m] -> MMh[m] + MMnadh[m] + MMaccoa[m] + MMh2o2[m] + MMmmdncoaa[m]	0	1000	74147.1 and 113868.1 and 11430.1 or 113868.1 and 11430.1 and 15488.1 or 74147.1 and 113868.1 and 11430.2 or 113868.1 and 15488.1 and 11430.2	Mouse metabolic/ transport/ demand reaction
MMFAOXC2252053x	MMnad[x] + MMcoa[x] + MMco2[x] + MMh2o[x] + MMdcspin1coa[x] -> MMh[x] + MMnadh[x] + MMaccoa[x] + MMh2o2[x] + MMmmdncoaa[x]	0	1000	11364.1 or 11409.1	Mouse metabolic/ transport/ demand reaction
MMFAOXC226	10 MMh2o[m] + 10 MMcoa[m] + 10 MMnad[m] + 4 MMfad[m] + MMc226coa[m] -> 10 MMh[m] + 10 MMnadh[m] + 11 MMaccoa[m] + 4 MMfadh2[m]	0	1000	74147.1 and 113868.1 and 11430.1 or 113868.1 and 11430.1 and 15488.1 or 74147.1 and 113868.1 and 11430.2 or 113868.1 and 15488.1 and 11430.2	Mouse metabolic/ transport/ demand reaction
MMFAOXC226205m	MMh2o[m] + MMcoa[m] + MMnad[m] + MMc226coa[m] -> MMh[m] + MMnadh[m] + MMaccoa[m] + MMmmdncoaa[m]	0	1000	11364.1 or 11409.1	Mouse metabolic/ transport/ demand reaction
MMFAOXC226205x	MMnad[x] + MMcoa[x] + MMh2o[x] + MMc226coa[x] -> MMh[x] + MMnadh[x] + MMaccoa[x] + MMmmdncoaa[x]	0	1000	11364.1 or 11409.1	Mouse metabolic/ transport/ demand reaction
MMFAOXC240200x	2 MMnad[x] + 2 MMcoa[x] + 2 MMo2[x] + 2 MMh2o[x] + MMlgncoa[x] -> 2 MMh[x] + 2 MMnadh[x] + 2 MMaccoa[x] + 2 MMh2o2[x] + MMarachcoa[x]	0	1000	74147.1 and 113868.1 and 11430.1 or 113868.1 and 11430.1 and 15488.1 or 74147.1 and 113868.1 and 11430.2 or 113868.1 and 15488.1 and 11430.2	Mouse metabolic/ transport/ demand reaction
MMFAOXC241181x	3 MMnad[x] + 3 MMcoa[x] + 3 MMo2[x] + 3 MMh2o[x] + MMnrvncoa[x] -> 3 MMh[x] + 3 MMnadh[x] + 3 MMaccoa[x] + 3 MMh2o2[x] + MModecoa[x]	0	1000	74147.1 and 113868.1 and 11430.1 or 113868.1 and 11430.1 and 15488.1 or 74147.1 and 113868.1 and 11430.2 or 113868.1 and 15488.1 and 11430.2	Mouse metabolic/ transport/ demand reaction
MMFAOXC2442246x	MMnad[x] + MMcoa[x] + MMco2[x] + MMh2o[x] + MMtetrte6coa[x] -> MMh[x] + MMnadh[x] + MMaccoa[x] + MMh2o2[x] + MMadmcoa[x]	0	1000	74147.1 and 113868.1 and 11430.1 or 113868.1 and 11430.1 and 15488.1 or 74147.1 and 113868.1 and 11430.2 or 113868.1 and 15488.1 and 11430.2	Mouse metabolic/ transport/ demand reaction
MMFAOXC2452253x	MMnad[x] + MMcoa[x] + MMo2[x] + MMh2o[x] + MMtetpent3coa[x] -> MMh[x] + MMnadh[x] + MMaccoa[x] + MMh2o2[x] + MMdcspndcoa[x]	0	1000	74147.1 and 113868.1 and 11430.1 or 113868.1 and 11430.1 and 15488.1 or 74147.1 and 113868.1 and 11430.2 or 113868.1 and 15488.1 and 11430.2	Mouse metabolic/ transport/ demand reaction
MMFAOXC2452256x	MMnad[x] + MMcoa[x] + MMo2[x] + MMh2o[x] + MMtetpent6coa[x] -> MMh[x] + MMnadh[x] + MMaccoa[x] + MMh2o2[x] + MMdcspin1coa[x]	0	1000	74147.1 and 113868.1 and 11430.1 or 113868.1 and 11430.1 and 15488.1 or 74147.1 and 113868.1 and 11430.2 or 113868.1 and 15488.1 and 11430.2	Mouse metabolic/ transport/ demand reaction
MMFAOXC246226x	MMnad[x] + MMcoa[x] + MMo2[x] + MMh2o[x] + MMtethex3coa[x] -> MMh[x] + MMnadh[x] + MMaccoa[x] + MMh2o2[x] + MMc226coa[x]	0	1000	74147.1 and 113868.1 and 11430.1 or 113868.1 and 11430.1 and 15488.1 or 74147.1 and 113868.1 and 11430.2 or 113868.1 and 15488.1 and 11430.2	Mouse metabolic/ transport/ demand reaction
MMFAOXC260240x	MMnad[x] + MMcoa[x] + MMo2[x] + MMh2o[x] + MMhexccoa[x] -> MMh[x] + MMnadh[x] + MMaccoa[x] + MMh2o2[x] + MMlgncoa[x]	0	1000	74147.1 and 113868.1 and 11430.1 or 113868.1 and 11430.1 and 15488.1 or 74147.1 and 113868.1 and 11430.2 or 113868.1 and 15488.1 and 11430.2	Mouse metabolic/ transport/ demand reaction
MMFAOXC80	3 MMh2o[m] + 3 MMcoa[m] + 3 MMnad[m] + 3 MMfad[m] + MMoccoa[m] -> 3 MMh[m] + 3 MMnadh[m] + 4 MMaccoa[m] + 3 MMfadh2[m]	0	1000	74147.1 and 113868.1 and 11430.1 or 113868.1 and 11430.1 and 15488.1 or 74147.1 and 113868.1 and 11430.2 or 113868.1 and 15488.1 and 11430.2	Mouse metabolic/ transport/ demand reaction
MMFAS100COA	3 MMf[c] + 2 MMnadph[c] + MMmalcoa[c] + MMoccoa[c] -> MMh2o[c] + 2 MMnadp[c] + MMco2[c] + MMcoa[c] + MMdcacoa[c]	0	1000	11364.1 or 11409.1	Mouse metabolic/ transport/ demand reaction
MMFAS120COA	3 MMf[c] + 2 MMnadph[c] + MMmalcoa[c] + MMdcacoa[c] -> MMh2o[c] + 2 MMnadp[c] + MMco2[c] + MMcoa[c] + MMddcacoa[c]	0	1000	14104.1	Mouse metabolic/ transport/ demand reaction
MMFAS140COA	3 MMf[c] + 2 MMnadph[c] + MMmalcoa[c] + MMddcacoa[c] -> MMh2o[c] + 2 MMnadp[c] + MMco2[c] + MMcoa[c] + MMtdcoa[c]	0	1000	14104.1	Mouse metabolic/ transport/ demand reaction
MMFAS160COA	3 MMf[c] + 2 MMnadph[c] + MMmalcoa[c] + MMtdcoa[c] -> MMh2o[c] + 2 MMnadp[c] + MMco2[c] + MMcoa[c] + MMpmtcoa[c]	0	1000	14104.1	Mouse metabolic/ transport/ demand reaction
MMFAS180COA	3 MMf[c] + 2 MMnadph[c] + MMmalcoa[c] + MMpmtcoa[c] -> MMh2o[c] + 2 MMnadp[c] + MMco2[c] + MMcoa[c] + MMstcoa[c]	0	1000	14104.1	Mouse metabolic/ transport/ demand reaction
MMFAS80COA_L	9 MMh[c] + 6 MMnadph[c] + MMaccoa[c] + 3 MMmalcoa[c] -> 3 MMh2o[c] + 6 MMnadp[c] + 3 MMco2[c] + 3 MMcoa[c] + MMoccoa[c]	0	1000	14104.1	Mouse metabolic/ transport/ demand reaction
MMFATP1t	MMna1[c] + MMhdca[c] <=> MMna1[e] + MMhdca[e]	-1000	0	14104.1	Mouse metabolic/ transport/ demand reaction
MMFATP2t	MMna1[c] + MMocdceaa[c] <=> MMna1[e] + MMocdcea[e]	-1000	0	26457.1 or 26569.1 or 26568.1 or 26457.2	Mouse metabolic/ transport/ demand reaction
MMFATP3t	MMna1[c] + MMocdca[c] <=> MMna1[e] + MMocdca[e]	-1000	0	26457.1 or 26457.2	Mouse metabolic/ transport/ demand reaction
MMFATP4t	MMna1[c] + MMarach[c] <=> MMna1[e] + MMarach[e]	-1000	0	26457.1 or 26457.2	Mouse metabolic/ transport/ demand reaction
MMFATP5t	MMna1[c] + MMarachd[c] <=> MMna1[e] + MMarachd[e]	-1000	0	26459.1	Mouse metabolic/ transport/ demand reaction
MMFATP6t	MMna1[c] + MMadrn[c] <=> MMna1[e] + MMadrn[e]	-1000	0	26459.1	Mouse metabolic/ transport/ demand reaction
MMFATP7t	MMna1[c] + MMcrvnc[c] <=> MMna1[e] + MMcrvnc[e]	-1000	0	26458.1 or 26459.1	Mouse metabolic/ transport/ demand reaction
MMFATP8t	MMna1[c] + MMlgnc[c] <=> MMna1[e] + MMlgnc[e]	-1000	0	26458.1 or 26459.1	Mouse metabolic/ transport/ demand reaction
MMFATP9t	MMna1[c] + MMnrvnc[c] <=> MMna1[e] + MMnrvnc[e]	-1000	0	26458.1 or 26459.1	Mouse metabolic/ transport/ demand reaction
MMFBA	MMf4p[c] <=> MMdhap[c] + MMg3p[c]	-1000	1000	26458.1 or 26459.1	Mouse metabolic/ transport/ demand reaction
MMFBA2	MMf1p[c] <=> MMdhap[c] + MMglyald[c]	-1000	1000	230163.1 or 11674.1 or 11674.3 or 11674.2 or 11676.1	Mouse metabolic/ transport/ demand reaction
MMFBA4	MMxu1p-D[c] <=> MMdhap[c] + MMgcald[c]	-1000	1000	230163.1 or 11674.1 or 11674.3 or 11674.2 or 11676.1	Mouse metabolic/ transport/ demand reaction
MMFBA5	MMxg1p-D[c] <=> MMdhap[c] + MMglyald[c]	-1000	1000	230163.1 or 11674.1 or 11674.3 or 11674.2 or 11676.1	Mouse metabolic/ transport/ demand reaction
MMFBP	MMh2o[c] + MMf6p[c] -> MMpi[c] + MMf6p[c]	0	1000	230163.1	Mouse metabolic/ transport/ demand reaction
MMFBP26	MMh2o[c] + MMf26bp[c] -> MMpi[c] + MMf6p[c]	0	1000	14120.1 or 14121.1	Mouse metabolic/ transport/ demand reaction
MMFCLTm	MMfe2[m] + MMppp9[m] -> 2 MMh[m] + MMpheme[m]	0	1000	14120.1 or 18639.1 or 18640.1 or 14121.1 or 270198.1 or 170768.1	Mouse metabolic/ transport/ demand reaction
MMFCOAH	MMh2o[c] + MMformcoa(c) -> 5 MMh[c] + MMcoa[c] + MMfor[c]	0	1000	14151.1 or 14151.2	Mouse metabolic/ transport/ demand reaction
MMFDH	MMnad[c] + MMfor[c] -> MMnadh[c] + MMco2[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMFE2t	MMfe2[e] -> MMfe2[c]	0	1000	107747.1	Mouse metabolic/ transport/ demand reaction
MMFE2tm	MMh[c] + MMfe2[c] -> MMh[m] + MMfe2[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMFE3R2e	MMascb-L[e] + 2 MMfe3[e] -> 2 MMh[e] + MMdhdiascb[e] + 2 MMfe2[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMFK	MMatp[c] + MMfuc-L[c] -> MMadp[c] + MMh[c] + MMfuc1p-L[c]	0	1000	73649.1	Mouse metabolic/ transport/ demand reaction
MMFKYNH	MMh2o[c] + MMLfmkynr[c] -> MMf[c] + MMfor[c] + MMLkynr[c]	0	1000	234730.1	Mouse metabolic/ transport/ demand reaction
MMFMNAT	MMatp[c] + MMh[c] + MMfmn[c] -> MMppi[c] + MMfad[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMFOLR2	MMnadph[c] + MMfol[c] -> MMnadp[c] + MMdhf[c]	0	1000	319945.1 or 319945.2	Mouse metabolic/ transport/ demand reaction
MMFOLTDhu	MMfol[u] -> MMfol[c]	0	1000	13361.1	Mouse metabolic/ transport/ demand reaction
MMFOLThu	MMh[u] + MMfol[u] -> MMh[c] + MMfol[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMFOLt2	MMoh1[c] + MMfol[e] <=> MMoh1[e] + MMfol[c]	-1000	1000	52466.1	Mouse metabolic/ transport/ demand reaction
MMFORMCOAtx	MMformcoa[x] <=> MMformcoa[c]	-1000	1000	20509.1 or 20509.2	Mouse metabolic/ transport/ demand reaction
MMFORt2m	MMfor[m] <=> MMfor[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMFORtr	MMfor[c] <=> MMfor[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMFORtrn	MMfor[c] <=> MMfor[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMFPGS	4 MMatp[c] + 4 MMglu-L[c] + MMdhf[c] -> 4 MMadp[c] + 4 MMh[c] + 4 MMpi[c] + MM5dhf[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMFPGS2	MMatp[c] + MMglu-L[c] + MM5dhf[c] -> MMadp[c] + MMh[c] + MMpi[c] + MM6dhf[c]	0	1000	14287.1	Mouse metabolic/ transport/ demand reaction
MMFPGS2m	MMglu-L[m] + MM5dhf[m] + MMatp[m] -> MMh[m] + MM6dhf[m] + MMadp[m] + MMpi[m]	0	1000	14287.1	Mouse metabolic/ transport/ demand reaction
MMFPGS3	MMatp[c] + MMglu-L[c] + MM6dhf[c] -> MMadp[c] + MMh[c] + MMpi[c] + MM7dhf[c]	0	1000	14287.1	Mouse metabolic/ transport/ demand reaction
MMFPGS3m	MMglu-L[m] + MM6dhf[m] + MMatp[m] -> MMh[m] + MM7dhf[m] + MMadp[m] + MMpi[m]	0	1000	14287.1	Mouse metabolic/ transport/ demand reaction
MMFPGS4	4 MMatp[c] + 4 MMglu-L[c] + MMdhf[c] -> 4 MMadp[c] + 4 MMh[c] + 4 MMpi[c] + MM5dhf[c]	0	1000	14287.1	Mouse metabolic/ transport/ demand reaction
MMFPGS4m	4 MMglu-L[m] + 4 MMatp[m] + MMdhf[m] -> 4 MMh[m] + 4 MMadp[m] + 4 MMpi[m] + MM5dhf[m]	0	1000	14287.1	Mouse metabolic/ transport/ demand reaction
MMFPGS5	MMatp[c] + MMglu-L[c] + MM5dhf[c] -> MMadp[c] + MMh[c] + MMpi[c] + MM6dhf[c]	0	1000	14287.1	Mouse metabolic/ transport/ demand reaction
MMFPGS5m	MMglu-L[m] + MMatp[m] + MM5dhf[m] -> MMh[m] + MM6dhf[m] + MMadp[m] + MMpi[m]	0	1000	14287.1	Mouse metabolic/ transport/ demand reaction
MMFPGS6	MMatp[c] + MMglu-L[c] + MM6dhf[c] -> MMadp[c] + MMh[c] + MMpi[c] + MM7dhf[c]	0	1000	14287.1	Mouse metabolic/ transport/ demand reaction
MMFPGS6m	MMglu-L[m] + MM6dhf[m] + MMatp[m] -> MMh[m] + MM7dhf[m] + MMadp[m] + MMpi[m]	0	1000	14287.1	Mouse metabolic/ transport/ demand reaction
MMFPGS7	MM10fhf[c] + 4 MMatp[c] + 4 MMglu-L[c] -> MM10fhf5glu[c] + 4 MMadp[c] + 4 MMh[c] + 4 MMpi[c]	0	1000	14287.1	Mouse metabolic/ transport/ demand reaction
MMFPGS7m	MM10fhf[m] + 4 MMglu-L[m] + 4 MMatp[m] -> MM10fhf5glu[m] + 4 MMh[m] + 4 MMadp[m] + 4 MMpi[m]	0	1000	14287.1	Mouse metabolic/ transport/ demand reaction
MMFPGS8	MM10fhf5glu[c] + MMatp[c] + MMglu-L[c] -> MM10fhf6glu[c] + MMadp[c] + MMh[c] + MMpi[c]	0	1000	14287.1	Mouse metabolic/ transport/ demand reaction
MMFPGS8m	MM10fhf5glu[m] + MMglu-L[m] + MMatp[m] -> MM10fhf6glu[m] + MMh[m] + MMadp[m] + MMpi[m]	0	1000	14287.1	Mouse metabolic/ transport/ demand reaction
MMFPGS9	MM10fhf6glu[c] + MMatp[c] + MMglu-L[c] -> MM10fhf7glu[c] + MMadp[c] + MMh[c] + MMpi[c]	0	1000	14287.1	Mouse metabolic/ transport/ demand reaction
MMFPGS9m	MM10fhf6glu[m] + MMglu-L[m] + MMatp[m] -> MM10fhf7glu[m] + MMh[m] + MMadp[m] + MMpi[m]	0	1000	14287.1	Mouse metabolic/ transport/ demand reaction
MMFPGSm	4 MMglu-L[m] + 4 MMatp[m] + MMdhf[m] -> 4 MMh[m] + MM5dhf[m] + 4 MMadp[m] + 4 MMpi[m]	0	1000	14287.1	Mouse metabolic/ transport/ demand reaction

MMFRDPtc	MMfrdp[x] <=> MMfrdp[c]	-1000	1000	14287.1	Mouse metabolic/ transport/ demand reaction
MMFRDPtr	MMfrdp[x] <=> MMfrdp[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMFRTT	MMipdp[c] + MMfrdp[c] -> MMppi[c] + MMggdp[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMFRUt4	MMnai1[e] + MMfru[e] <=> MMnai1[c] + MMfru[c]	0	1000	14593.1	Mouse metabolic/ transport/ demand reaction
MMFT	MMipdp[c] + MMfrdp[c] -> MMppi[c] + MMttc-ggdp[c]	0	1000	230612.1	Mouse metabolic/ transport/ demand reaction
MMFTCD	2 MMth[c] + MM5forthf[c] -> MMmlnh4[c] + MMmmthf[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMFTHFCL	MMatp[c] + MM5thf[c] -> MMadp[c] + MMpi[c] + MMmmthf[c]	0	1000	14317.1 or 14317.2	Mouse metabolic/ transport/ demand reaction
MMFTHFDH	MM10thf[c] + MMh2o2[c] + MMnadp[c] -> MMthf[c] + MMnadph[c] + MMco2[c] + MMthf[c]	0	1000	107885.1	Mouse metabolic/ transport/ demand reaction
MMFTHFL	MMatp[c] + MMthf[c] + MMfor[c] <=> MM10thf[c] + MMadp[c] + MMpi[c]	0	1000	107747.1	Mouse metabolic/ transport/ demand reaction
MMFTHFLm	MMatp[m] + MMfor[m] + MMthf[m] <=> MM10thf[m] + MMadp[m] + MMpi[m]	0	1000	108156.1	Mouse metabolic/ transport/ demand reaction
MMFUC13GALACGLCGAL14ACGLCGALGLUSIDEte	MMfuc13galacglcgal14acglcgalgluside_hs[e] <=> MMfuc13galacglcgal14acglcgalgluside_hs[c]	-1000	1000	270685.1	Mouse metabolic/ transport/ demand reaction
MMFUC13GALACGLCGAL14ACGLCGALGLUSIDEtg	MMfuc13galacglcgal14acglcgalgluside_hs[g] <=> MMfuc13galacglcgal14acglcgalgluside_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMFUC14GALACGLCGALGLUSIDEte	MMfuc14galacglcgalgluside_hs[e] <=> MMfuc14galacglcgalgluside_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMFUC14GALACGLCGALGLUSIDEtg	MMfuc14galacglcgalgluside_hs[g] <=> MMfuc14galacglcgalgluside_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMFUCACGALFUCGALACGLCGALGLUSIDEte	MMfucacgalfucgalacglcgalgluside_hs[e] <=> MMfucacgalfucgalacglcgalgluside_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMFUCACGALFUCGALACGLCGALGLUSIDEtg	MMfucacgalfucgalacglcgalgluside_hs[g] <=> MMfucacgalfucgalacglcgalgluside_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMFUCACNGAL14ACGLCGALGLUSIDEte	MMfucacngal14acglcgalgluside_hs[e] <=> MMfucacngal14acglcgalgluside_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMFUCACNGAL14ACGLCGALGLUSIDEtg	MMfucacngal14acglcgalgluside_hs[g] <=> MMfucacngal14acglcgalgluside_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMFUCACNGALACGLCGALGLUSIDEte	MMfucacngalacglcgalgluside_hs[e] <=> MMfucacngalacglcgalgluside_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMFUCACNGALACGLCGALGLUSIDEtg	MMfucacngalacglcgalgluside_hs[g] <=> MMfucacngalacglcgalgluside_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMFUCASE2e	MMh2o[e] + MMksi[e] -> MMfuc-L[e] + MMksi_deg1[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMFUCASE2ly	MMh2o[l] + MMksi[l] -> MMfuc-L[l] + MMksi_deg1[l]	0	1000	66848.1	Mouse metabolic/ transport/ demand reaction
MMFUCASEe	MMh2o[e] + MMs2f2fn2m2mnss[e] -> MMfuc-L[e] + MMs2f2n2m2mnss[e]	0	1000	71665.1	Mouse metabolic/ transport/ demand reaction
MMFUCASEly	MMh2o[l] + MMs2f2fn2m2mnss[l] -> MMfuc-L[l] + MMs2f2n2m2mnss[l]	0	1000	66848.1	Mouse metabolic/ transport/ demand reaction
MMFUCFUC12GAL14ACGLCGALGLUSIDEte	MMfucfuc12gal14acglcgalgluside_hs[e] <=> MMfucfuc12gal14acglcgalgluside_hs[c]	-1000	1000	71665.1	Mouse metabolic/ transport/ demand reaction
MMFUCFUC12GAL14ACGLCGALGLUSIDEtg	MMfucfuc12gal14acglcgalgluside_hs[g] <=> MMfucfuc12gal14acglcgalgluside_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMFUCFUC132GALACGLCGAL14ACGLCGALGLUSIDEte	MMfucfuc132galacglcgal14acglcgalgluside_hs[e] <=> MMfucfuc132galacglcgal14acglcgalgluside_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMFUCFUC132GALACGLCGAL14ACGLCGALGLUSIDEtg	MMfucfuc132galacglcgal14acglcgalgluside_hs[g] <=> MMfucfuc132galacglcgal14acglcgalgluside_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMFUCFUCFUCGALACGLC13GALACGLCGAL14ACGLCGALGLUSIDEte	MMfucfucfucgalacglc13galacglcgal14acglcgalgluside_hs[e] <=> MMfucfucfucgalacglc13galacglcgal14acglcgalgluside_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMFUCFUCFUCGALACGLC13GALACGLCGAL14ACGLCGALGLUSIDEtg	MMfucfucfucgalacglc13galacglcgal14acglcgalgluside_hs[g] <=> MMfucfucfucgalacglc13galacglcgal14acglcgalgluside_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMFUCFUCFUCGALACGLCGAL14ACGLCGALGLUSIDEte	MMfucfucfucgalacglcgal14acglcgalgluside_hs[e] <=> MMfucfucfucgalacglcgal14acglcgalgluside_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMFUCFUCFUCGALACGLCGAL14ACGLCGALGLUSIDEtg	MMfucfucfucgalacglcgal14acglcgalgluside_hs[g] <=> MMfucfucfucgalacglcgal14acglcgalgluside_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMFUCFUCFUCGALACGLCGALGLUSIDEte	MMfucfucfucgalacglcgalgluside_hs[e] <=> MMfucfucfucgalacglcgalgluside_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMFUCFUCFUCGALACGLCGALGLUSIDEtg	MMfucfucfucgalacglcgalgluside_hs[g] <=> MMfucfucfucgalacglcgalgluside_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMFUCGAL14ACGLCGALGLUSIDEte	MMfucgal14acglcgalgluside_hs[e] <=> MMfucgal14acglcgalgluside_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMFUCGAL14ACGLCGALGLUSIDEtg	MMfucgal14acglcgalgluside_hs[g] <=> MMfucgal14acglcgalgluside_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMFUCGALFUCGALACGLCGALGLUSIDEte	MMfucgalfucgalacglcgalgluside_hs[e] <=> MMfucgalfucgalacglcgalgluside_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMFUCGALFUCGALACGLCGALGLUSIDEtg	MMfucgalfucgalacglcgalgluside_hs[g] <=> MMfucgalfucgalacglcgalgluside_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMFUCGALGBSIDEte	MMfucgalgbside_hs[c] <=> MMfucgalgbside_hs[e]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMFUCGALGBSIDEtg	MMfucgalgbside_hs[c] <=> MMfucgalgbside_hs[g]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMFUCly	MMfuc-L[l] -> MMfuc-L[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMFUM	MMh2o[c] + MMfum[c] <=> MMmal-L[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMFUMAC	MMh2o[c] + MM4fumacac[c] -> MMh[c] + MMacac[c] + MMfum[c]	0	1000	14194.1	Mouse metabolic/ transport/ demand reaction
MMFUMSO3tm	MMso3[m] + MMfum[c] <=> MMso3[c] + MMfum[m]	-1000	1000	14085.1	Mouse metabolic/ transport/ demand reaction
MMFUMSO4tm	MMfum[c] + MMso4[m] <=> MMfum[m] + MMso4[c]	-1000	1000	27376.1	Mouse metabolic/ transport/ demand reaction
MMFUMTSULtm	MMfum[c] + MMtsul[m] <=> MMfum[m] + MMtsul[c]	-1000	1000	27376.1	Mouse metabolic/ transport/ demand reaction
MMFUMtm	MMh2o[m] + MMfum[m] <=> MMmal-L[m]	-1000	1000	27376.1	Mouse metabolic/ transport/ demand reaction
MMFUMtm	MMpi[m] + MMfum[c] <=> MMpi[c] + MMfum[m]	-1000	1000	14194.1	Mouse metabolic/ transport/ demand reaction
MMFUT11g	MMgalgbside_hs[g] + MMgdpfuc[g] -> MMh[g] + MMgdp[g] + MMfucgalgbside_hs[g]	0	1000	27376.1	Mouse metabolic/ transport/ demand reaction
MMFUT12g	MMgalacglcgalgluside_hs[g] + MMgdpfuc[g] -> MMh[g] + MMgdp[g] + MMfucgalacglcgalgluside_hs[g]	0	1000	14343.1	Mouse metabolic/ transport/ demand reaction
MMFUT14g	MMgal14acglcgalgluside_hs[g] + MMgdpfuc[g] -> MMh[g] + MMgdp[g] + MMfuc12gal14acglcgalgluside_hs[g]	0	1000	14343.1	Mouse metabolic/ transport/ demand reaction
MMFUT15g	MMgalacgalfuc12gal14acglcgalgluside_hs[g] + MMgdpfuc[g] -> MMh[g] + MMgdp[g] + MMfucgalacgalfuc12gal14acglcgalgluside_hs[g]	0	1000	14343.1	Mouse metabolic/ transport/ demand reaction
MMFUT16g	MMgalacglcgal14acglcgalgluside_hs[g] + MMgdpfuc[g] -> MMh[g] + MMgdp[g] + MMfucgalacglcgal14acglcgalgluside_hs[g]	0	1000	14343.1	Mouse metabolic/ transport/ demand reaction
MMFUT17g	MMgalacgalfucgalacglcgal14acglcgalgluside_hs[g] + MMgdpfuc[g] -> MMh[g] + MMgdp[g] + MMfucgalacgalfucgalacglcgal14acglcgalgluside_hs[g]	0	1000	14343.1	Mouse metabolic/ transport/ demand reaction
MMFUT18g	MMgalacglcgalacglcgal14acglcgalgluside_hs[g] + 2 MMgdpfuc[g] -> 2 MMh[g] + 2 MMgdp[g] + MMfucfucgalacglcgalacglcgal14acglcgalgluside_hs[g]	0	1000	14343.1	Mouse metabolic/ transport/ demand reaction
MMFUT910g	MMgdpfuc[g] + MMfucgalacglc13galacglcgal14acglcgalgluside_hs[g] -> MMh[g] + MMgdp[g] + MMfucfucgalacglc13galacglcgal14acglcgalgluside_hs[g]	0	1000	14343.1	Mouse metabolic/ transport/ demand reaction
MMFUT911g	MMgdpfuc[g] + MMfucfucgalacglc13galacglcgal14acglcgalgluside_hs[g] -> MMh[g] + MMgdp[g] + MMfucfucfucgalacglc13galacglcgal14acglcgalgluside_hs[g]	0	1000	14348.1	Mouse metabolic/ transport/ demand reaction
MMFUT91g	MMgal14acglcgalgluside_hs[g] + MMgdpfuc[g] -> MMh[g] + MMgdp[g] + MMfucgal14acglcgalgluside_hs[g]	0	1000	14348.1	Mouse metabolic/ transport/ demand reaction
MMFUT92g	MMgdpfuc[g] + MMacngal14acglcgalgluside_hs[g] -> MMh[g] + MMgdp[g] + MMfucacngal14acglcgalgluside_hs[g]	0	1000	14348.1	Mouse metabolic/ transport/ demand reaction
MMFUT93g	MMgdpfuc[g] + MMfuc12gal14acglcgalgluside_hs[g] -> MMh[g] + MMgdp[g] + MMfuc12gal14acglcgalgluside_hs[g]	0	1000	14348.1	Mouse metabolic/ transport/ demand reaction
MMFUT94g	MMgdpfuc[g] + MMfucgalacglcgal14acglcgalgluside_hs[g] -> MMh[g] + MMgdp[g] + MMfucfucgalacglcgal14acglcgalgluside_hs[g]	0	1000	14348.1	Mouse metabolic/ transport/ demand reaction
MMFUT95g	MMgdpfuc[g] + MMfucfucgalacglcgal14acglcgalgluside_hs[g] -> MMh[g] + MMgdp[g] + MMfucfucfucgalacglcgal14acglcgalgluside_hs[g]	0	1000	14348.1	Mouse metabolic/ transport/ demand reaction
MMFUT96g	MMgalacglcgal14acglcgalgluside_hs[g] + MMgdpfuc[g] -> MMh[g] + MMgdp[g] + MMfuc132galacglcgal14acglcgalgluside_hs[g]	0	1000	14348.1	Mouse metabolic/ transport/ demand reaction
MMFUT97g	MMgdpfuc[g] + MMfuc132galacglcgal14acglcgalgluside_hs[g] -> MMh[g] + MMgdp[g] + MMfucfuc132galacglcgal14acglcgalgluside_hs[g]	0	1000	14348.1	Mouse metabolic/ transport/ demand reaction
MMFUT98g	MMgalacglcgal14acglcgalgluside_hs[g] + MMgdpfuc[g] -> MMh[g] + MMgdp[g] + MMfuc13galacglcgal14acglcgalgluside_hs[g]	0	1000	14348.1	Mouse metabolic/ transport/ demand reaction
MMFUT99g	MMgalacglc13galacglcgal14acglcgalgluside_hs[g] + MMgdpfuc[g] -> MMh[g] + MMgdp[g] + MMfucgalacglc13galacglcgal14acglcgalgluside_hs[g]	0	1000	14348.1	Mouse metabolic/ transport/ demand reaction
MMG12MT1_L	MMgdpmnm[c] + 0.1 MMm2mpdol_L[c] -> MMh[c] + MMgdp[c] + 0.1 MMm3mpdol_L[c]	0	1000	14348.1	Mouse metabolic/ transport/ demand reaction
MMG12MT1_U	MMgdpmnm[c] + 0.1 MMm2mpdol_U[c] -> MMh[c] + MMgdp[c] + 0.1 MMm3mpdol_U[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMG12MT2_L	MMgdpmnm[c] + 0.1 MMm3mpdol_L[c] -> MMh[c] + MMgdp[c] + 0.1 MMm4mpdol_L[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMG12MT2_U	MMgdpmnm[c] + 0.1 MMm3mpdol_U[c] -> MMh[c] + MMgdp[c] + 0.1 MMm4mpdol_U[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMG13MT_L	MMgdpmnm[c] + 0.1 MMmpdol_L[c] -> MMh[c] + MMgdp[c] + 0.1 MMm1mpdol_L[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMG13MT_U	MMgdpmnm[c] + 0.1 MMmpdol_U[c] -> MMh[c] + MMgdp[c] + 0.1 MMm1mpdol_U[c]	0	1000	56737.1 or 56737.2	Mouse metabolic/ transport/ demand reaction

MMG14T10g	MMudpgal[g] + MMksi_pre14[g] -> MMh[g] + MMudp[g] + MMksi_pre15[g]	0	1000	56737.1 or 56737.2	Mouse metabolic/ transport/ demand reaction
MMG14T11g	MMudpgal[g] + MMksi_pre17[g] -> MMh[g] + MMudp[g] + MMksi_pre18[g]	0	1000	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	Mouse metabolic/ transport/ demand reaction
MMG14T12g	MMudpgal[g] + MMksi_pre20[g] -> MMh[g] + MMudp[g] + MMksi_pre21[g]	0	1000	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	Mouse metabolic/ transport/ demand reaction
MMG14T13g	MMudpgal[g] + MMksi_pre23[g] -> MMh[g] + MMudp[g] + MMksi_pre24[g]	0	1000	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	Mouse metabolic/ transport/ demand reaction
MMG14T14g	MMudpgal[g] + MMksi_pre26[g] -> MMh[g] + MMudp[g] + MMksi_pre27[g]	0	1000	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	Mouse metabolic/ transport/ demand reaction
MMG14T15g	MMudpgal[g] + MMksi_pre29[g] -> MMh[g] + MMudp[g] + MMksi_pre30[g]	0	1000	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	Mouse metabolic/ transport/ demand reaction
MMG14T16g	MMudpgal[g] + MMksi_pre32[g] -> MMh[g] + MMudp[g] + MMksi_pre33[g]	0	1000	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	Mouse metabolic/ transport/ demand reaction
MMG14T17g	MMudpgal[g] + MMksi_pre35[g] -> MMh[g] + MMudp[g] + MMksi_pre36[g]	0	1000	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	Mouse metabolic/ transport/ demand reaction
MMG14T18g	2 MMudpgal[g] + MMcore4[g] -> 2 MMh[g] + 2 MMudp[g] + MMksii_core4_pre1[g]	0	1000	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	Mouse metabolic/ transport/ demand reaction
MMG14T19g	MMudpgal[g] + MMksii_core4_pre3[g] -> MMh[g] + MMudp[g] + MMksii_core4_pre4[g]	0	1000	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	Mouse metabolic/ transport/ demand reaction
MMG14T20g	MMudpgal[g] + MMksii_core4_pre6[g] -> MMh[g] + MMudp[g] + MMksii_core4_pre7[g]	0	1000	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	Mouse metabolic/ transport/ demand reaction
MMG14T21g	MMudpgal[g] + MMksii_core4_pre9[g] -> MMh[g] + MMudp[g] + MMksii_core4_pre10[g]	0	1000	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	Mouse metabolic/ transport/ demand reaction
MMG14T2g	MMudpgal[g] + MMksii_core2_pre1[g] -> MMh[g] + MMudp[g] + MMksii_core2_pre2[g]	0	1000	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	Mouse metabolic/ transport/ demand reaction
MMG14T3g	MMudpgal[g] + MMksii_core2_pre3[g] -> MMh[g] + MMudp[g] + MMksii_core2_pre4[g]	0	1000	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	Mouse metabolic/ transport/ demand reaction
MMG14T4g	MMudpgal[g] + MMksii_core2_pre6[g] -> MMh[g] + MMudp[g] + MMksii_core2_pre7[g]	0	1000	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	Mouse metabolic/ transport/ demand reaction
MMG14T5g	MMudpgal[g] + MMksii_core2_pre9[g] -> MMh[g] + MMudp[g] + MMksii_core2_pre10[g]	0	1000	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	Mouse metabolic/ transport/ demand reaction
MMG14T6g	MMudpgal[g] + MMksi_pre2[g] -> MMh[g] + MMudp[g] + MMksi_pre3[g]	0	1000	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	Mouse metabolic/ transport/ demand reaction
MMG14T7g	MMudpgal[g] + MMksi_pre5[g] -> MMh[g] + MMudp[g] + MMksi_pre6[g]	0	1000	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	Mouse metabolic/ transport/ demand reaction
MMG14T8g	MMudpgal[g] + MMksi_pre8[g] -> MMh[g] + MMudp[g] + MMksi_pre9[g]	0	1000	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	Mouse metabolic/ transport/ demand reaction
MMG14T9g	MMudpgal[g] + MMksi_pre11[g] -> MMh[g] + MMudp[g] + MMksi_pre12[g]	0	1000	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	Mouse metabolic/ transport/ demand reaction
MMG14Tg	2 MMudpgal[g] + MMfn2m2masn[g] -> 2 MMh[g] + 2 MMudp[g] + MMl2fn2m2masn[g]	0	1000	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	Mouse metabolic/ transport/ demand reaction
MMG16MT_L	MMgdpmann[c] + 0.1 MMm1mpdol_L[c] -> MMh[c] + MMgdp[c] + 0.1 MMm2mpdol_L[c]	0	1000	56336.1 or 14595.1 or 53418.1 or 53418.2 or 57370.1	Mouse metabolic/ transport/ demand reaction
MMG16MT_U	MMgdpmann[c] + 0.1 MMm1mpdol_U[c] -> MMh[c] + MMgdp[c] + 0.1 MMm2mpdol_U[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMG1M6MASNB1terg	MMg1m6masnB1[r] -> MMg1m6masnB1[g]	0	1000		Mouse metabolic/ transport/ demand reaction
MMG1M7MASNBterg	MMg1m7masnB[r] -> MMg1m7masnB[g]	0	1000		Mouse metabolic/ transport/ demand reaction
MMG1M7MASNCterg	MMg1m7masnC[r] -> MMg1m7masnC[g]	0	1000		Mouse metabolic/ transport/ demand reaction
MMG1M8MASNterg	MMg1m8masn[r] -> MMg1m8masn[g]	0	1000		Mouse metabolic/ transport/ demand reaction
MMG1PTT	MMh[c] + MMg1p[c] + MMdttp[c] -> MMppi[c] + MMdtdpglu[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMG2M8MASNterg	MMg2m8masn[r] -> MMg2m8masn[g]	0	1000		Mouse metabolic/ transport/ demand reaction
MMG3M8MASNterg	MMg3m8masn[r] -> MMg3m8masn[g]	0	1000		Mouse metabolic/ transport/ demand reaction
MMG3PD1	MMnad[c] + MMglyc3p[c] <=> MMh[c] + MMnadh[c] + MMdhap[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMG3PD2m	MMfad[m] + MMglyc3p[c] -> MMfadh2[m] + MMdhap[c]	0	1000	14555.1	Mouse metabolic/ transport/ demand reaction
MMG5SADrm	MMglu5sa[m] <=> MMh[m] + MMh2o[m] + MM1pyr5c[m]	-1000	1000	14571.1	Mouse metabolic/ transport/ demand reaction
MMG5SADs	MMglu5sa[c] -> MMh2o[c] + MMh[c] + MM1pyr5c[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMG5SDym	MMh[m] + MMnadph[m] + MMglu5p[m] -> MMnadp[m] + MMpi[m] + MMglu5sa[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMG6PDA	MMh2o[c] + MMgam6p[c] -> MMnh4[c] + MMf6p[c]	0	1000	56454.1	Mouse metabolic/ transport/ demand reaction
MMG6PDH1er	MMnad[r] + MMg6p[r] -> MMh[r] + MMnadh[r] + MM6pgl[r]	0	1000	67980.1 or 26384.1	Mouse metabolic/ transport/ demand reaction
MMG6PDH1rer	MMnad[r] + MMg6p[r] <=> MMh[r] + MMnadh[r] + MM6pgl[r]	-1000	1000	100198.1	Mouse metabolic/ transport/ demand reaction
MMG6PDH2r	MMnadp[c] + MMg6p[c] <=> MMh[c] + MMnadph[c] + MM6pgl[c]	-1000	1000	100198.1	Mouse metabolic/ transport/ demand reaction
MMG6PDH2rer	MMnadp[r] + MMg6p[r] <=> MMh[r] + MMnadph[r] + MM6pgl[r]	-1000	1000	14381.1	Mouse metabolic/ transport/ demand reaction
MMG6PPer	MMh2o[r] + MMg6p[r] -> MMglc-D[r] + MMpi[r]	0	1000	100198.1	Mouse metabolic/ transport/ demand reaction
MMG6Pter	MMg6p[c] <=> MMg6p[r]	-1000	1000	14378.1 or 14377.1 or 68401.1	Mouse metabolic/ transport/ demand reaction
MMGABAPAT1tc	MMh[u] + MM4abut[u] -> MMh[c] + MM4abut[c]	0	1000	14385.1	Mouse metabolic/ transport/ demand reaction
MMGABAVESSEC	MMh2o[c] + MMatp[c] + 3 MM4abut[c] -> MMadp[c] + MMh[c] + MMpi[c] + 3 MM4abut[e]	0	1000	215335.1	Mouse metabolic/ transport/ demand reaction
MMGACMTRc	MMamet[c] + MMgudac[c] <=> MMh[c] + MMahcys[c] + MMcreat[c]	-1000	1000	22348.1	Mouse metabolic/ transport/ demand reaction
MMGACPAILter	MMgacpail_hs[c] -> MMgacpail_hs[r]	0	1000	14431.1 or 14431.2	Mouse metabolic/ transport/ demand reaction
MMGAL3ST11	MMgalside_hs[g] + MMpaps[g] -> MMh[g] + MMpap[g] + MMsgalside_hs[g]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGAL3ST12	MMdigalside_hs[g] + MMpaps[g] -> MMh[g] + MMdigalsgalside_hs[g] + MMpap[g]	0	1000	53897.1	Mouse metabolic/ transport/ demand reaction
MMGALACGLCGALGBSIDEte	MMgalacglcgalgbside_hs[c] <=> MMgalacglcgalgbside_hs[e]	-1000	1000	53897.1	Mouse metabolic/ transport/ demand reaction
MMGALACGLCGALGBSIDEtg	MMgalacglcgalgbside_hs[c] <=> MMgalacglcgalgbside_hs[g]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGALAMtr	MMgalam[e] <=> MMgalam[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGALASE10ly	MMh2o[l] + MMksi_deg26[l] -> MMgal[l] + MMksi_deg27[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGALASE11ly	MMh2o[l] + MMksi_deg29[l] -> MMgal[l] + MMksi_deg30[l]	0	1000	50917.1 or 19025.1 or 12091.1 or 18010.1	Mouse metabolic/ transport/ demand reaction
MMGALASE12ly	MMh2o[l] + MMksi_deg32[l] -> MMgal[l] + MMksi_deg33[l]	0	1000	50917.1 or 19025.1 or 12091.1 or 18010.1	Mouse metabolic/ transport/ demand reaction
MMGALASE13ly	MMh2o[l] + MMksi_deg35[l] -> MMgal[l] + MMksi_deg36[l]	0	1000	50917.1 or 19025.1 or 12091.1 or 18010.1	Mouse metabolic/ transport/ demand reaction
MMGALASE14ly	MMh2o[l] + MMksi_deg38[l] -> MMgal[l] + MMksi_deg39[l]	0	1000	50917.1 or 19025.1 or 12091.1 or 18010.1	Mouse metabolic/ transport/ demand reaction
MMGALASE15ly	MMh2o[l] + MMksi_deg40[l] -> MMgal[l] + MMksi_deg41[l]	0	1000	50917.1 or 19025.1 or 12091.1 or 18010.1	Mouse metabolic/ transport/ demand reaction
MMGALASE16ly	2 MMh2o[l] + MMksii_core2_deg2[l] -> 2 MMgal[l] + MMksii_core2_deg3[l]	0	1000	50917.1 or 19025.1 or 12091.1 or 18010.1	Mouse metabolic/ transport/ demand reaction
MMGALASE17ly	MMh2o[l] + MMksii_core2_deg5[l] -> MMgal[l] + MMksii_core2_deg6[l]	0	1000	50917.1 or 19025.1 or 12091.1 or 18010.1	Mouse metabolic/ transport/ demand reaction
MMGALASE18ly	MMh2o[l] + MMksii_core2_deg8[l] -> MMgal[l] + MMksii_core2_deg9[l]	0	1000	50917.1 or 19025.1 or 12091.1 or 18010.1	Mouse metabolic/ transport/ demand reaction
MMGALASE19ly	MMh2o[l] + MMf1a[l] -> MMgal[l] + MMcore6[l]	0	1000	50917.1 or 19025.1 or 12091.1 or 18010.1	Mouse metabolic/ transport/ demand reaction
MMGALASE1ly	2 MMh2o[l] + MMl2n2m2mn[l] -> MMn2m2mn[l] + 2 MMgal[l]	0	1000	50917.1 or 19025.1 or 12091.1 or 18010.1	Mouse metabolic/ transport/ demand reaction
MMGALASE20ly	2 MMh2o[l] + MMksii_core4_deg2[l] -> 2 MMgal[l] + MMksii_core4_deg3[l]	0	1000	50917.1 or 19025.1 or 12091.1 or 18010.1	Mouse metabolic/ transport/ demand reaction
MMGALASE3ly	2 MMh2o[l] + MMksi_deg5[l] -> 2 MMgal[l] + MMksi_deg6[l]	0	1000	50917.1 or 19025.1 or 12091.1 or 18010.1	Mouse metabolic/ transport/ demand reaction
MMGALASE4ly	MMh2o[l] + MMksi_deg8[l] -> MMgal[l] + MMksi_deg9[l]	0	1000	50917.1 or 19025.1 or 12091.1 or 18010.1	Mouse metabolic/ transport/ demand reaction
MMGALASE5ly	MMh2o[l] + MMksi_deg11[l] -> MMgal[l] + MMksi_deg12[l]	0	1000	50917.1 or 19025.1 or 12091.1 or 18010.1	Mouse metabolic/ transport/ demand reaction
MMGALASE6ly	MMh2o[l] + MMksi_deg14[l] -> MMgal[l] + MMksi_deg15[l]	0	1000	50917.1 or 19025.1 or 12091.1 or 18010.1	Mouse metabolic/ transport/ demand reaction
MMGALASE7ly	MMh2o[l] + MMksi_deg17[l] -> MMgal[l] + MMksi_deg18[l]	0	1000	50917.1 or 19025.1 or 12091.1 or 18010.1	Mouse metabolic/ transport/ demand reaction
MMGALASE8ly	MMh2o[l] + MMksi_deg20[l] -> MMgal[l] + MMksi_deg21[l]	0	1000	50917.1 or 19025.1 or 12091.1 or 18010.1	Mouse metabolic/ transport/ demand reaction
MMGALASE9ly	MMh2o[l] + MMksi_deg23[l] -> MMgal[l] + MMksi_deg24[l]	0	1000	50917.1 or 19025.1 or 12091.1 or 18010.1	Mouse metabolic/ transport/ demand reaction
MMGALC	MMh2o[l] + MMgalside_hs[l] -> MMcrm_hs[l] + MMgal[l]	0	1000	50917.1 or 19025.1 or 12091.1 or 18010.1	Mouse metabolic/ transport/ demand reaction
MMGALFUC12GAL14ACGLCGALGLUSIDEte	MMgalfuc12gal14acglcgalgluside_hs[e] <=> MMgalfuc12gal14acglcgalgluside_hs[c]	-1000	1000	14420.1	Mouse metabolic/ transport/ demand reaction
MMGALFUC12GAL14ACGLCGALGLUSIDEtg	MMgalfuc12gal14acglcgalgluside_hs[g] <=> MMgalfuc12gal14acglcgalgluside_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGALFUCGALACGLCGAL14ACGLCGALGLUSIDEte	MMgalfucgalacglcgal14acglcgalgluside_hs[e] <=> MMgalfucgalacglcgal14acglcgalgluside_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGALFUCGALACGLCGAL14ACGLCGALGLUSIDEtg	MMgalfucgalacglcgal14acglcgalgluside_hs[g] <=> MMgalfucgalacglcgal14acglcgalgluside_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGALGALFUCFUCGALACGLCGALACGLCGAL14ACGLCGALGLUSIDEte	MMgalgalfucfucgalacglcgalacglcgal14acglcgalgluside_hs[e] <=> MMgalgalfucfucgalacglcgalacglcgal14acglcgalgluside_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGALGALFUCFUCGALACGLCGALACGLCGAL14ACGLCGALGLUSIDEtg	MMgalgalfucfucgalacglcgalacglcgal14acglcgalgluside_hs[g] <=> MMgalgalfucfucgalacglcgalacglcgal14acglcgalgluside_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGALGALGALTHCRMte	MMgalgalgalthcrm_hs[c] <=> MMgalgalgalthcrm_hs[e]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGALGALGALTHCRMtg	MMgalgalgalthcrm_hs[c] <=> MMgalgalgalthcrm_hs[g]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGALGLUSIDEtg	MMgalgluside_hs[c] <=> MMgalgluside_hs[g]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGALGLUSIDEtl	MMgalgluside_hs[c] <=> MMgalgluside_hs[l]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGALGT1	MMgalgluside_hs[g] + MMudpacgal[g] -> MMh[g] + MMudp[g] + MMga2_hs[g]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGALGT2	MMudpacgal[g] + MMgm3_hs[g] -> MMh[g] + MMudp[g] + MMgm2_hs[g]	0	1000	14421.1	Mouse metabolic/ transport/ demand reaction

MMGALGT3	MMudpacgal[g] + MMgt3_hs[g] -> MMtf[g] + MMudp[g] + MMgt2_hs[g]	0	1000	14421.1	Mouse metabolic/ transport/ demand reaction
MMGALGT4	MMudpacgal[g] + MMgt3_hs[g] -> MMtf[g] + MMudp[g] + MMgt2_hs[g]	0	1000	14421.1	Mouse metabolic/ transport/ demand reaction
MMGALK	MMatp[c] + MMgal[c] -> MMadp[c] + MMtf[c] + MMgal1p[c]	0	1000	14421.1	Mouse metabolic/ transport/ demand reaction
MMGALNACT1g	MMudpacgal[g] + MMcs_bs_linkage[g] -> MMtf[g] + MMudp[g] + MMcs_pre[g]	0	1000	69976.1 or 69976.2 or 14635.1	Mouse metabolic/ transport/ demand reaction
MMGALNACT2g	MMuacgam[g] + MMcs_a_b_pre2[g] -> MMtf[g] + MMudp[g] + MMcs_a_b_pre3[g]	0	1000	78752.1 or 234356.1	Mouse metabolic/ transport/ demand reaction
MMGALNACT3g	MMuacgam[g] + MMcs_c_pre2[g] -> MMtf[g] + MMudp[g] + MMcs_c_pre3[g]	0	1000	78752.1 or 78923.1 or 74241.1 or 269941.1 or 234356.1	Mouse metabolic/ transport/ demand reaction
MMGALNACT4g	MMuacgam[g] + MMcs_d_pre3[g] -> MMtf[g] + MMudp[g] + MMcs_d_pre4[g]	0	1000	78752.1 or 78923.1 or 74241.1 or 269941.1 or 234356.1	Mouse metabolic/ transport/ demand reaction
MMGALNACT5g	MMuacgam[g] + MMcs_e_pre3[g] -> MMtf[g] + MMudp[g] + MMcs_e_pre4[g]	0	1000	78752.1 or 78923.1 or 74241.1 or 269941.1 or 234356.1	Mouse metabolic/ transport/ demand reaction
MMGALOR	MMtf[c] + MMnadph[c] + MMgal[c] <=> MMnadp[c] + MMgal[c]	-1000	1000	78752.1 or 78923.1 or 74241.1 or 269941.1 or 234356.1	Mouse metabolic/ transport/ demand reaction
MMGALSGLT1hi	MMh2o[c] + MMatp[c] + 2 MMna1[u] + MMgal[u] -> MMadp[c] + MMtf[c] + MMpi[c] + 2 MMna1[c] + MMgal[c]	0	1000	58810.1 or 11677.1 or 58810.2	Mouse metabolic/ transport/ demand reaction
MMGALSIDEig	MMgalside_hs[c] <=> MMgalside_hs[g]	-1000	1000	20537.1	Mouse metabolic/ transport/ demand reaction
MMGALSIDEil	MMgalside_hs[c] <=> MMgalside_hs[l]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGALT	MMtf[c] + MMutp[c] + MMgal1p[c] <=> MMudpgal[c] + MMppi[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGALT2g	MMudpgal[g] + MMhser[g] -> MMtf[g] + MMudp[g] + MMO2ser[g]	0	1000	14430.1 or 14430.2 or 14430.3	Mouse metabolic/ transport/ demand reaction
MMGALTg	MMudpgal[g] + MMxser[g] -> MMtf[g] + MMudp[g] + MMhser[g]	0	1000	117592.1	Mouse metabolic/ transport/ demand reaction
MMGALU	MMtf[c] + MMg1p[c] + MMutp[c] <=> MMppi[c] + MMudpg[c]	-1000	1000	218271.1	Mouse metabolic/ transport/ demand reaction
MMGALt1r	MMgal[e] <=> MMgal[c]	0	1000	216558.1 or 216558.2	Mouse metabolic/ transport/ demand reaction
MMGALt2_2	2 MMtf[e] + MMgal[e] <=> 2 MMtf[c] + MMgal[c]	-1000	1000	20527.1 or 20525.1 or 56017.1 or 170441.1 or 20526.1	Mouse metabolic/ transport/ demand reaction
MMGALt4	MMna1[e] + MMgal[e] <=> MMna1[c] + MMgal[c]	0	1000	20537.1	Mouse metabolic/ transport/ demand reaction
MMGALt4_2	2 MMna1[e] + MMgal[e] <=> 2 MMna1[c] + MMgal[c]	0	1000	230612.1	Mouse metabolic/ transport/ demand reaction
MMGALtly	MMgal[l] -> MMgal[c]	0	1000	20537.1	Mouse metabolic/ transport/ demand reaction
MMGAMYe	MMh2o[e] + MMglygn5[e] -> MMTyr-ggn[e] + MMmalt[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGAMt1r	MMgam[e] <=> MMgam[c]	0	1000	232714.1	Mouse metabolic/ transport/ demand reaction
MMGAO1	MMaccoa[c] + MMgt3_hs[c] -> MMcoa[c] + MMoagt3_hs[c]	0	1000	20528.1 or 20525.1 or 20526.1	Mouse metabolic/ transport/ demand reaction
MMGAO1g	MMaccoa[g] + MMgt3_hs[g] -> MMcoa[g] + MMoagt3_hs[g]	0	1000	11416.1	Mouse metabolic/ transport/ demand reaction
MMGAO2	MMaccoa[c] + MMgt3_hs[c] -> MMcoa[c] + MMoagt3_hs[c]	0	1000	11416.1	Mouse metabolic/ transport/ demand reaction
MMGAO2g	MMaccoa[g] + MMgt3_hs[g] -> MMcoa[g] + MMoagt3_hs[g]	0	1000	11416.1	Mouse metabolic/ transport/ demand reaction
MMGAPD	MMp[c] + MMnad[c] + MMg3p[c] <=> MMh[c] + MMnadh[c] + MM13dpg[c]	-1000	1000	11416.1	Mouse metabolic/ transport/ demand reaction
MMGARFT	MM10thf[c] + MMgar[c] <=> MMh[c] + MMthf[c] + MMfgam[c]	-1000	1000	100043349.1 or 14447.1	Mouse metabolic/ transport/ demand reaction
MMGASNASE2ly	MMh2o[l] + MMn2m2mnasn[l] -> MMAsn_X_Ser_Thr[l] + MMn2m2nm[l]	0	1000	14450.1 or 14450.2	Mouse metabolic/ transport/ demand reaction
MMGASNASE3ly	MMh2o[l] + MMksi_deg1[l] -> MMAsn_X_Ser_Thr[l] + MMksi_deg2[l]	0	1000	11593.1	Mouse metabolic/ transport/ demand reaction
MMGASNASEly	MMh2o[l] + MMs2f2n2m2masn[l] -> MMAsn_X_Ser_Thr[l] + MMs2f2n2m2nf[l]	0	1000	11593.1	Mouse metabolic/ transport/ demand reaction
MMGBA	MMh2o[c] + MMgbside_hs[c] -> MMcrm_hs[c] + MMglc-D[c]	0	1000	11593.1	Mouse metabolic/ transport/ demand reaction
MMGBAl	MMh2o[l] + MMgbside_hs[l] -> MMcrm_hs[l] + MMglc-D[l]	0	1000	14466.1 or 14466.2 or 14466.3 or 14466.4 or 14466.5	Mouse metabolic/ transport/ demand reaction
MMGBGT1	MMudpacgal[g] + MMgbside_hs[g] -> MMtf[g] + MMudp[g] + MMacgagbside_hs[g]	0	1000	14466.1 or 14466.2 or 14466.3 or 14466.4 or 14466.5	Mouse metabolic/ transport/ demand reaction
MMGBSIDEte	MMgbside_hs[c] <=> MMgbside_hs[e]	-1000	1000	227671.1	Mouse metabolic/ transport/ demand reaction
MMGBSIDEtl	MMgbside_hs[c] <=> MMgbside_hs[l]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGCALDD	MMh2o[c] + MMnad[c] + MMgcald[c] -> 2 MMh[c] + MMnadh[c] + MMglycl[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGCALDDm	MMh2o[m] + MMnad[m] + MMgcald[m] -> 2 MMh[m] + MMnadh[m] + MMglycl[m]	0	1000	19378.1 or 56752.1 or 11670.1 or 110695.1 or 67689.1 or 56847.1 or 11668.1 or 11671.1 or 19378.2 or 19378.3	Mouse metabolic/ transport/ demand reaction
MMGCC2am	MMh[m] + MMglyc[m] + MMpam[m] <=> MMco2[m] + MMalpam[m]	-1000	1000	104776.1 or 212647.1 or 11669.1 or 214579.1 or 56454.1 or 214579.2 or 212647.2 or 72535.1	Mouse metabolic/ transport/ demand reaction
MMGCC2bim	MMthf[m] + MMalpam[m] -> MMnh4[m] + MMdhbim[m] + MMmthf[m]	0	1000	68133.1 or 434437.1 or 13382.1 or 104174.1	Mouse metabolic/ transport/ demand reaction
MMGCC2cm	MMnad[m] + MMdhbar[m] <=> MMh[m] + MMnadh[m] + MMpam[m]	-1000	1000	68133.1 or 434437.1 or 13382.1 or 104174.1	Mouse metabolic/ transport/ demand reaction
MMGCCam	MMh[m] + MMglyb[m] + MMlpro[m] <=> MMco2[m] + MMalpro[m]	-1000	1000	68133.1 or 434437.1 or 13382.1 or 104174.1	Mouse metabolic/ transport/ demand reaction
MMGCCbim	MMthf[m] + MMalpro[m] -> MMnh4[m] + MMmthf[m] + MMdhlpro[m]	0	1000	68133.1 or 434437.1 or 13382.1 or 104174.1	Mouse metabolic/ transport/ demand reaction
MMGCCcm	MMnad[m] + MMdhlpro[m] <=> MMh[m] + MMnadh[m] + MMlpro[m]	-1000	1000	68133.1 or 434437.1 or 13382.1 or 104174.1	Mouse metabolic/ transport/ demand reaction
MMGCHOLAt2	2 MMna1[e] + MMgchola[e] -> 2 MMna1[c] + MMgchola[c]	0	1000	68133.1 or 434437.1 or 13382.1 or 104174.1	Mouse metabolic/ transport/ demand reaction
MMGCHOLAt3	MMh2o[c] + MMatp[c] + MMgchola[c] -> MMadp[c] + MMtf[c] + MMpi[c] + MMgchola[e]	0	1000	20494.1 or 20493.1	Mouse metabolic/ transport/ demand reaction
MMGCHOLAte	MMgchola[e] <=> MMgchola[c]	-1000	1000	27413.1 or 76408.2 or 76408.3 or 76408.1	Mouse metabolic/ transport/ demand reaction
MMGCHOLAtx	MMgchola[x] <=> MMgchola[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGCNTg	MMuacgam[g] + MMgalacglcgal1-4acglcgalglside_hs[g] -> MMtf[g] + MMudp[g] + MMacglcgalacglcgal1-4acglcgalglside_hs[g]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGD1B2te	MMgd1b2_hs[c] <=> MMgd1b2_hs[e]	-1000	1000	14538.1	Mouse metabolic/ transport/ demand reaction
MMGD1B2tg	MMgd1b2_hs[c] <=> MMgd1b2_hs[g]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGD1Cte	MMgd1c_hs[c] <=> MMgd1c_hs[e]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGD1Ctg	MMgd1c_hs[c] <=> MMgd1c_hs[g]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGDCHOLAte	MMgglchola[e] <=> MMgglchola[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGDCHOLAtx	MMgglchola[x] <=> MMgglchola[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGDPFUCtg	MMgglpfuc[c] + MMgmp[g] <=> MMggdpfuc[g] + MMgmp[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGDPtg	MMgdp[c] <=> MMgdp[g]	-1000	1000	228368.1	Mouse metabolic/ transport/ demand reaction
MMGF6PTA	MMglu-L[c] + MMf6p[c] -> MMglu-L[c] + MMgam6p[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGFUCS	MMh[c] + MMnadph[c] + MMgdpddman[c] -> MMnadp[c] + MMgdpfuc[c]	0	1000	14584.1 or 14583.1	Mouse metabolic/ transport/ demand reaction
MMGGH_10FTHF5GLUe	4 MMh2o[e] + MM10thf5glu6[e] -> 4 MMglu-L[e] + MM10thf6[e]	0	1000	22122.1	Mouse metabolic/ transport/ demand reaction
MMGGH_10FTHF5GLUl	MM10thf5glu6[l] + 4 MMh2o[l] -> MM10thf[l] + 4 MMglu-L[l]	0	1000	667301.1	Mouse metabolic/ transport/ demand reaction
MMGGH_10FTHF6GLUe	MMh2o[e] + MM10thf6glu6[e] -> MMglu-L[e] + MM10thf5glu6[e]	0	1000	667301.1	Mouse metabolic/ transport/ demand reaction
MMGGH_10FTHF6GLUl	MM10thf6glu6[l] + MMh2o[l] -> MM10thf5glu6[l] + MMglu-L[l]	0	1000	667301.1	Mouse metabolic/ transport/ demand reaction
MMGGH_10FTHF7GLUe	MMh2o[e] + MM10thf7glu6[e] -> MMglu-L[e] + MM10thf6glu6[e]	0	1000	667301.1	Mouse metabolic/ transport/ demand reaction
MMGGH_10FTHF7GLUl	MM10thf7glu6[l] + MMh2o[l] -> MM10thf6glu6[l] + MMglu-L[l]	0	1000	667301.1	Mouse metabolic/ transport/ demand reaction
MMGGH_5DHFe	4 MMh2o[e] + MM5dhf[e] -> 4 MMglu-L[e] + MMdhf[e]	0	1000	667301.1	Mouse metabolic/ transport/ demand reaction
MMGGH_5DHFl	4 MMh2o[l] + MM5dhf[l] -> MMdhf[l] + 4 MMglu-L[l]	0	1000	667301.1	Mouse metabolic/ transport/ demand reaction
MMGGH_5THFe	4 MMh2o[e] + MM5thf[e] -> 4 MMglu-L[e] + MMthf[e]	0	1000	667301.1	Mouse metabolic/ transport/ demand reaction
MMGGH_5THFl	4 MMh2o[l] + MM5thf[l] -> 4 MMglu-L[l] + MMthf[l]	0	1000	667301.1	Mouse metabolic/ transport/ demand reaction
MMGGH_6DHFe	MMh2o[e] + MM6dhf[e] -> MMglu-L[e] + MM5dhf[e]	0	1000	667301.1	Mouse metabolic/ transport/ demand reaction
MMGGH_6DHFl	MMh2o[l] + MM6dhf[l] -> MM5dhf[l] + MMglu-L[l]	0	1000	667301.1	Mouse metabolic/ transport/ demand reaction
MMGGH_6THFe	MMh2o[e] + MM6thf[e] -> MMglu-L[e] + MM5thf[e]	0	1000	667301.1	Mouse metabolic/ transport/ demand reaction
MMGGH_6THFl	MMh2o[l] + MM6thf[l] -> MM5thf[l] + MMglu-L[l]	0	1000	667301.1	Mouse metabolic/ transport/ demand reaction
MMGGH_7DHFe	MMh2o[e] + MM7dhf[e] -> MMglu-L[e] + MM6dhf[e]	0	1000	667301.1	Mouse metabolic/ transport/ demand reaction
MMGGH_7DHFl	MMh2o[l] + MM7dhf[l] -> MM6dhf[l] + MMglu-L[l]	0	1000	667301.1	Mouse metabolic/ transport/ demand reaction
MMGGH_7THFe	MMh2o[e] + MM7thf[e] -> MMglu-L[e] + MM6thf[e]	0	1000	667301.1	Mouse metabolic/ transport/ demand reaction
MMGGH_7THFl	MMh2o[l] + MM7thf[l] -> MM6thf[l] + MMglu-L[l]	0	1000	667301.1	Mouse metabolic/ transport/ demand reaction
MMGGLUCT	MMgluala[e] -> MMala-L[c] + MM5oxpro[c]	0	1000	667301.1	Mouse metabolic/ transport/ demand reaction
MMGGNG	8 MMudpg[c] + MMTyr-ggn[c] -> 8 MMh[c] + 8 MMudp[c] + MMggn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGGTSr	MMh2o[r] + MMleuktrC4[r] <=> MMglu-L[r] + MMleuktrD4[r]	-1000	1000	14936.1 or 232493.1 or 27357.1	Mouse metabolic/ transport/ demand reaction
MMGGT6	MMglu-L[c] + MMleuktrE4[c] <=> MMh2o[c] + MMleuktrF4[c]	-1000	1000	23887.1	Mouse metabolic/ transport/ demand reaction
MMGGT_L	17.6 MMgdp[c] + MMtic- ggp[c] -> 17.6 MMppi[c] + 0.1 MMdedoldp_L[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGGT_U	16.5 MMgdp[c] + MMtic- ggp[c] -> 16.5 MMppi[c] + 0.1 MMdedoldp_U[c]	0	1000		Mouse metabolic/ transport/ demand reaction

MMGHMT2r	MMthf[c] + MMser-L[c] <=> MMth2o[c] + MMgly[c] + MMmlthf[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGHMT2rm	MMthf[m] + MMser-L[m] <=> MMth2o[m] + MMgly[m] + MMmlthf[m]	-1000	1000	20425.1 or 20425.2	Mouse metabolic/ transport/ demand reaction
MMGHMT3	MMth[c] + MM3htrmelys[c] -> MMgly[c] + MM4tmeabut[c]	0	1000	108037.1	Mouse metabolic/ transport/ demand reaction
MMGHMT3m	MMth[m] + MM3htrmelys[m] -> MMgly[m] + MM4tmeabut[m]	0	1000	20425.1 or 20425.2	Mouse metabolic/ transport/ demand reaction
MMGK1	MMatp[c] + MMgmp[c] <=> MMadp[c] + MMgdp[c]	-1000	1000	108037.1	Mouse metabolic/ transport/ demand reaction
MMGK1m	MMatp[m] + MMgmp[m] <=> MMadp[m] + MMgdp[m]	-1000	1000	14923.1	Mouse metabolic/ transport/ demand reaction
MMGLACO	2 MMh2o[c] + MMnad[c] + MMglac[c] -> 3 MMh[c] + MMnadh[c] + MMglcr[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGLACOm	2 MMh2o[m] + MMnad[m] + MMglac[m] -> 3 MMh[m] + MMnadh[m] + MMglcr[m]	0	1000	19378.1 or 56752.1 or 11670.1 or 67689.1 or 56847.1 or 11668.1 or 11671.1 or 19378.2 or 19378.3	Mouse metabolic/ transport/ demand reaction
MMGLACter	MMglac[c] <=> MMglac[r]	-1000	1000	212647.1 or 11669.1 or 212647.2 or 72535.1	Mouse metabolic/ transport/ demand reaction
MMGLAl	MMh2o[l] + MMdigsktide_hs[l] -> MMgsktide_hs[l] + MMgsa[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGLB1	MMh2o[l] + MMgalgluside_hs[l] -> MMgal[l] + MMgluside_hs[l]	0	1000	11605.1	Mouse metabolic/ transport/ demand reaction
MMGLBRAN	MMglygn1[c] -> MMglygn2[c]	0	1000	50917.1 or 19025.1 or 12091.1 or 18010.1	Mouse metabolic/ transport/ demand reaction
MMGLCAASE1ly	MMh2o[l] + MMhs_deg0[l] -> MMglcur[l] + MMhs_deg10[l]	0	1000	74185.1	Mouse metabolic/ transport/ demand reaction
MMGLCAASE4ly	MMh2o[l] + MMcs_a_deg2[l] -> MMglcur[l] + MMcs_a_deg3[l]	0	1000	110006.1	Mouse metabolic/ transport/ demand reaction
MMGLCAASE5ly	MMh2o[l] + MMcs_c_deg2[l] -> MMglcur[l] + MMcs_c_deg3[l]	0	1000	110006.1	Mouse metabolic/ transport/ demand reaction
MMGLCAASE6ly	MMh2o[l] + MMcs_d_deg3[l] -> MMglcur[l] + MMcs_d_deg4[l]	0	1000	110006.1	Mouse metabolic/ transport/ demand reaction
MMGLCAASE7ly	MMh2o[l] + MMcs_e_deg3[l] -> MMglcur[l] + MMcs_e_deg4[l]	0	1000	110006.1	Mouse metabolic/ transport/ demand reaction
MMGLCAASE8ly	MMth2o[l] + MMha[l] -> MMglcur[l] + MMha_deg1[l]	0	1000	110006.1	Mouse metabolic/ transport/ demand reaction
MMGLCAASE9ly	2 MMh2o[l] + MMha_pre1[l] -> MMacgam[l] + MMglcur[l]	0	1000	110006.1	Mouse metabolic/ transport/ demand reaction
MMGLCAE1g	MMcs_a_b_pre3[g] -> MMcs_b_pre4[g]	0	1000	110006.1	Mouse metabolic/ transport/ demand reaction
MMGLCAE2g	MMhs_pre10[g] -> MMhs_pre11[g]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGLCAT2g	MMcs_a_b_e_pre1[g] + MMudpglcur[g] -> MMh[g] + MMudp[g] + MMcs_a_b_pre2[g]	0	1000	93683.1	Mouse metabolic/ transport/ demand reaction
MMGLCAT3g	MMudpglcur[g] + MMcs_c_d_e_pre1[g] -> MMh[g] + MMudp[g] + MMcs_c_pre2[g]	0	1000	78923.1 or 74241.1 and 269941.1 or 100910.1	Mouse metabolic/ transport/ demand reaction
MMGLCAT4g	MMudpglcur[g] + MMcs_d_pre2[g] -> MMh[g] + MMudp[g] + MMcs_d_pre3[g]	0	1000	78923.1 or 74241.1 and 269941.1 or 100910.1	Mouse metabolic/ transport/ demand reaction
MMGLCAT5g	MMudpglcur[g] + MMcs_e_pre2[g] -> MMh[g] + MMudp[g] + MMcs_e_pre3[g]	0	1000	78923.1 or 74241.1 and 269941.1 or 100910.1	Mouse metabolic/ transport/ demand reaction
MMGLCAT6g	MMudpglcur[g] + MMhs_pre1[g] -> MMh[g] + MMudp[g] + MMhs_pre2[g]	0	1000	78923.1 or 74241.1 and 269941.1 or 100910.1	Mouse metabolic/ transport/ demand reaction
MMGLCAT7g	MMudpglcur[g] + MMhs_pre3[g] -> MMh[g] + MMudp[g] + MMhs_pre4[g]	0	1000	14043.1 and 14042.1 or 14042.1 and 14043.2	Mouse metabolic/ transport/ demand reaction
MMGLCAT8g	MMudpglcur[g] + MMhs_pre5[g] -> MMh[g] + MMudp[g] + MMhs_pre6[g]	0	1000	14043.1 and 14042.1 or 14042.1 and 14043.2	Mouse metabolic/ transport/ demand reaction
MMGLCAT9g	MMudpglcur[g] + MMhs_pre7[g] -> MMh[g] + MMudp[g] + MMhs_pre8[g]	0	1000	14043.1 and 14042.1 or 14042.1 and 14043.2	Mouse metabolic/ transport/ demand reaction
MMGLCATg	MMf2xser[g] + MMudpglcur[g] -> MMh[g] + MMudp[g] + MMcs_hs_linkage[g]	0	1000	14043.1 and 14042.1 or 14042.1 and 14043.2	Mouse metabolic/ transport/ demand reaction
MMGLCMter	MMglc-D[r] -> MMglc-D[e]	0	0	76898.1 or 72727.1 or 280645.1 or 76898.2	Mouse metabolic/ transport/ demand reaction
MMGLCNACASE1ly	MMh2o[l] + MMhs_deg3[l] -> MMacgam[l] + MMhs_deg4[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGLCNACASE2ly	MMh2o[l] + MMhs_deg8[l] -> MMacgam[l] + MMhs_deg9[l]	0	1000	27419.1	Mouse metabolic/ transport/ demand reaction
MMGLCNACASE3ly	MMh2o[l] + MMhs_deg14[l] -> MMacgam[l] + MMhs_deg15[l]	0	1000	27419.1	Mouse metabolic/ transport/ demand reaction
MMGLCNACASE4ly	MMh2o[l] + MMhs_deg20[l] -> MMacgam[l] + MMhs_deg21[l]	0	1000	27419.1	Mouse metabolic/ transport/ demand reaction
MMGLCNACASE5ly	MMh2o[l] + MMhs_deg24[l] -> MMacgam[l] + MMhs_deg25[l]	0	1000	27419.1	Mouse metabolic/ transport/ demand reaction
MMGLCNACDASg	4 MMh2o[g] + 4 MMpaps[g] + MMhs_pre9[g] -> 4 MMh[g] + 4 MMac[g] + 4 MMpap[g] + MMhs_pre10[g]	0	1000	27419.1	Mouse metabolic/ transport/ demand reaction
MMGLCNACPT_L	0.1 MMdolp_L[c] + MMuacgam[c] -> 0.1 MMnagk2p_L[c] + MMump[c]	0	1000	17423.1 or 83398.1 or 64580.1 or 15531.1	Mouse metabolic/ transport/ demand reaction
MMGLCNACPT_U	0.1 MMdolp_U[c] + MMuacgam[c] -> MMump[c] + 0.1 MMnagk2p_U[c]	0	1000	13478.1 or 13478.2	Mouse metabolic/ transport/ demand reaction
MMGLCNACT1g	MMuacgam[g] + MMcs_hs_linkage[g] -> MMh[g] + MMudp[g] + MMhs_pre1[g]	0	1000	13478.1 or 13478.2	Mouse metabolic/ transport/ demand reaction
MMGLCNACT2g	MMuacgam[g] + MMhs_pre2[g] -> MMh[g] + MMudp[g] + MMhs_pre3[g]	0	1000	54616.1 or 58193.1	Mouse metabolic/ transport/ demand reaction
MMGLCNACT3g	MMuacgam[g] + MMhs_pre4[g] -> MMh[g] + MMudp[g] + MMhs_pre5[g]	0	1000	14043.1 and 14042.1 or 54616.1 or 56219.1 or 14042.1 and 14043.2	Mouse metabolic/ transport/ demand reaction
MMGLCNACT4g	MMuacgam[g] + MMhs_pre6[g] -> MMh[g] + MMudp[g] + MMhs_pre7[g]	0	1000	14043.1 and 14042.1 or 54616.1 or 56219.1 or 14042.1 and 14043.2	Mouse metabolic/ transport/ demand reaction
MMGLCNACT5g	MMuacgam[g] + MMhs_pre8[g] -> MMh[g] + MMudp[g] + MMhs_pre9[g]	0	1000	14043.1 and 14042.1 or 54616.1 or 56219.1 or 14042.1 and 14043.2	Mouse metabolic/ transport/ demand reaction
MMGLCNACT_L	MMuacgam[c] + 0.1 MMnagk2p_L[c] -> MMh[c] + MMudp[c] + 0.1 MMchito2pdol_L[c]	0	1000	14043.1 and 14042.1 or 54616.1 or 56219.1 or 14042.1 and 14043.2	Mouse metabolic/ transport/ demand reaction
MMGLCNACT_U	MMuacgam[c] + 0.1 MMnagk2p_U[c] -> MMh[c] + MMudp[c] + 0.1 MMchito2pdol_U[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGLCSGLT1lu	MMh2o[c] + MMatp[c] + 2 MMna1[u] + MMglc-D[u] -> MMadp[c] + MMh[c] + MMpi[c] + 2 MMna1[c] + MMglc-D[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGLCURter	MMglcur[c] -> MMglcur[r]	0	1000	20537.1	Mouse metabolic/ transport/ demand reaction
MMGLCURtly	MMh[c] + MMglcur[c] <=> MMh[l] + MMglcur[l]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGLCURtr	MMglcur[c] -> MMglcur[e]	0	1000	235504.1	Mouse metabolic/ transport/ demand reaction
MMGLCt2_2	2 MMh[e] + MMglc-D[e] <=> 2 MMh[c] + MMglc-D[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGLCt2r	MMh[e] + MMglc-D[e] <=> MMh[c] + MMglc-D[c]	0	1000	20537.1	Mouse metabolic/ transport/ demand reaction
MMGLCt4	MMna1[e] + MMglc-D[e] <=> MMna1[c] + MMglc-D[c]	0	1000	246787.1	Mouse metabolic/ transport/ demand reaction
MMGLCt4_2	2 MMna1[e] + MMglc-D[e] <=> 2 MMna1[c] + MMglc-D[c]	0	1000	53881.1 or 109342.1 or 241612.1 or 230612.1 or 246787.1	Mouse metabolic/ transport/ demand reaction
MMGLCter	MMglc-D[c] <=> MMglc-D[r]	-1000	1000	20537.1	Mouse metabolic/ transport/ demand reaction
MMGLCtg	MMglc-D[c] <=> MMglc-D[g]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGLCtly	MMglc-D[l] -> MMglc-D[c]	0	1000	20525.1	Mouse metabolic/ transport/ demand reaction
MMGLDBRAN	MMh2o[c] + MMdxtrm[c] -> MMglc-D[c] + MMglygn3[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGLGNS1	3 MMudpg[c] + MMggn[c] -> 3 MMh[c] + 3 MMudp[c] + MMglygn1[c]	0	1000	77559.1 or 77559.2 or 77559.3 or 77559.4 or 77559.5 or 77559.6	Mouse metabolic/ transport/ demand reaction
MMGLINOFABPpmtc	MMlnlncg[u] -> MMlnlncg[c]	0	1000	14936.1 or 232493.1 or 27357.1	Mouse metabolic/ transport/ demand reaction
MMGLNALANaEx	MMna1[e] + MMala-L[c] + MMglp-L[e] -> MMna1[c] + MMala-L[e] + MMglp-L[c]	0	1000	(14719.1 or 12491.1)	Mouse metabolic/ transport/ demand reaction
MMGLNASNNaEx	MMna1[e] + MMasn-L[c] + MMglp-L[e] -> MMna1[c] + MMasn-L[e] + MMglp-L[c]	0	1000	20514.1	Mouse metabolic/ transport/ demand reaction
MMGLNATB0tc	2 MMna1[u] + MMcit[u] + MMgln-L[u] -> 2 MMna1[c] + MMcit[c] + MMgln-L[c]	0	1000	20514.1	Mouse metabolic/ transport/ demand reaction
MMGLNB0AT1tc	MMna1[u] + MMgln-L[u] -> MMna1[c] + MMgln-L[c]	0	1000	56774.1	Mouse metabolic/ transport/ demand reaction
MMGLNCYSNaEx	MMna1[e] + MMcys-L[c] + MMglp-L[e] -> MMna1[c] + MMcys-L[e] + MMglp-L[c]	0	1000	(70008.1 or (74338.1 and 57394.1))	Mouse metabolic/ transport/ demand reaction
MMGLNILELAT2tc	MMgln-L[e] + MMile-L[c] -> MMgln-L[c] + MMile-L[e]	0	1000	20514.1	Mouse metabolic/ transport/ demand reaction
MMGLNLASEer	MMh[r] + MMgln[r] <=> MMh2o[r] + MMgullac[r]	-1000	1000	(20539.1 and 17254.1)	Mouse metabolic/ transport/ demand reaction
MMGLNLAT1tc	MMleu-L[c] + MMgln-L[u] -> MMleu-L[u] + MMgln-L[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGLNPHELAT2tc	MMgln-L[e] + MMphe-L[c] -> MMgln-L[c] + MMphe-L[e]	0	1000	(20539.1 and 17254.1)	Mouse metabolic/ transport/ demand reaction
MMGLNS	MMmlnl4[c] + MMatp[c] + MMglu-L[c] -> MMadp[c] + MMh[c] + MMpi[c] + MMgln-L[c]	0	1000	(20539.1 and 17254.1)	Mouse metabolic/ transport/ demand reaction
MMGLNSERNaEx	MMna1[e] + MMgln-L[e] + MMser-L[c] -> MMna1[c] + MMgln-L[c] + MMser-L[e]	0	1000	266744.1 or 14645.1	Mouse metabolic/ transport/ demand reaction
MMGLNTHRNaEx	MMna1[e] + MMgln-L[e] + MMthr-L[c] -> MMna1[c] + MMgln-L[c] + MMthr-L[e]	0	1000	20514.1	Mouse metabolic/ transport/ demand reaction
MMGLNt4	MMna1[e] + MMgln-L[e] -> MMna1[c] + MMgln-L[c]	0	1000	20514.1	Mouse metabolic/ transport/ demand reaction
MMGLNtN1	MMh[c] + 2 MMna1[e] + MMgln-L[e] <=> MMh[e] + 2 MMna1[c] + MMgln-L[c]	0	1000	105727.1 or 67760.1 or 69354.1 or 56774.1	Mouse metabolic/ transport/ demand reaction
MMGLNtm	MMgln-L[c] -> MMgln-L[m]	0	1000	209837.1 or 76257.1	Mouse metabolic/ transport/ demand reaction
MMGLNyLATtc	MMna1[e] + MMgln-L[e] + MMarg-L[c] -> MMna1[c] + MMgln-L[c] + MMarg-L[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGLNyLATthc	MMh[e] + MMgln-L[e] + MMarg-L[c] -> MMh[c] + MMgln-L[c] + MMarg-L[e]	0	1000	(20540.1 or (330836.1 and 17254.1))	Mouse metabolic/ transport/ demand reaction
MMGLPASE1	3 MMpi[c] + MMglygn2[c] -> 3 MMg1p[c] + MMdxtrm[c]	0	1000	(20540.1 or (330836.1 and 17254.1))	Mouse metabolic/ transport/ demand reaction
MMGLPASE2	7 MMh2o[c] + MMglygn3[c] -> 7 MMglc-D[c] + MMTyr-ggn[c]	0	1000	19309.1 or 110078.1 or 110095.1	Mouse metabolic/ transport/ demand reaction
MMGLRASE	MMnadp[c] + MMgallac[c] <=> MMh[c] + MMnadph[c] + MMglac[c]	-1000	1000	19309.1 or 110078.1 or 110095.1	Mouse metabolic/ transport/ demand reaction
MMGLU5Km	MMglu-L[m] + MMatp[m] -> MMadp[m] + MMglu5p[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGLUCYS	MMatp[c] + MMglu-L[c] + MMcys-L[c] -> MMadp[c] + MMh[c] + MMpi[c] + MMglucys[c]	0	1000	56454.1	Mouse metabolic/ transport/ demand reaction
MMGLUDC	MMh[c] + MMglu-L[c] -> MMco2[c] + MM4abut[c]	0	1000	14630.1 or 14629.1	Mouse metabolic/ transport/ demand reaction
MMGLUNm	MMh2o[m] + MMgln-L[m] -> MMglu-L[m] + MMnh4[m]	0	1000	14415.1 or 14417.1 or 14415.2	Mouse metabolic/ transport/ demand reaction

MMGLUPRT	MMh2o[c] + MMprpp[c] + MMglu-L[c] -> MMglu-L[c] + MMppi[c] + MMpram[c]	0	1000	216456.1 or 14660.1 or 216456.2	Mouse metabolic/ transport/ demand reaction
MMGLUTCOADHim	MMh[m] + MMglutcoa[m] + MM4ad[m] -> MMco2[m] + MMb2coa[m] + MM4adh[m]	0	1000	231327.1	Mouse metabolic/ transport/ demand reaction
MMGLUt2m	MMh[c] + MMglu-L[c] <=> MMh[m] + MMglu-L[m]	-1000	1000	270076.1 or 270076.2	Mouse metabolic/ transport/ demand reaction
MMGLUt6	MMh[e] + 3 MMna1[e] + MMk[c] + MMglu-L[e] -> MMh[c] + 3 MMna1[c] + MMglu-L[c] + MMk[e]	0	1000	71803.1 or 68267.1 or 78830.1 or 50799.1	Mouse metabolic/ transport/ demand reaction
MMGLUt7l	MMglu-L[l] -> MMglu-L[c]	0	1000	242607.1 or 20511.1 or 20513.1 or 20510.1 or 20512.1	Mouse metabolic/ transport/ demand reaction
MMGLUtr	MMglu-L[c] <=> MMglu-L[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGLXO2p	MMo2[x] + MMh2o[x] + MMglx[x] -> MMf[x] + MMh2o2[x] + MMoxa[x]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGLXtm	MMglx[c] <=> MMglx[m]	-1000	1000	15112.1 or 56185.1 or 56185.2	Mouse metabolic/ transport/ demand reaction
MMGLXtp	MMglx[c] <=> MMglx[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGLYAMDTRc	MMgly[c] + MMarg-L[c] <=> MMorn[c] + MMgudac[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGLYATB0tc	2 MMna1[u] + MMcl[u] + MMgly[u] -> 2 MMna1[c] + MMcl[c] + MMgly[c]	0	1000	67092.1	Mouse metabolic/ transport/ demand reaction
MMGLYATm	MMaccoa[m] + MMgly[m] <=> MMcoa[m] + MM2aobut[m]	-1000	1000	56774.1	Mouse metabolic/ transport/ demand reaction
MMGLYB0AT1tc	MMna1[u] + MMgly[u] -> MMna1[c] + MMgly[c]	0	1000	26912.1	Mouse metabolic/ transport/ demand reaction
MMGLYBt4_2_r	2 MMna1[e] + MMglybt[e] <=> 2 MMna1[c] + MMglybt[c]	0	1000	(70008.1 or (74338.1 and 57394.1))	Mouse metabolic/ transport/ demand reaction
MMGLYBtm	MMglybt[m] <=> MMglybt[c]	-1000	1000	14411.1	Mouse metabolic/ transport/ demand reaction
MMGLYC3Ptm	MMglyc3p[c] -> MMglyc3p[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGLYCK2	MMatp[c] + MMglyc-R[c] -> MMadp[c] + MMf[c] + MM2pg[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGLYCLTDy	MMh[c] + MMnadph[c] + MMglx[c] -> MMnadp[c] + MMglycl[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGLYCLTDym	MMh[m] + MMnadph[m] + MMglx[m] -> MMnadp[m] + MMglycl[m]	0	1000	76238.1	Mouse metabolic/ transport/ demand reaction
MMGLYCLTip	MMglycl[c] -> MMglycl[x]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGLYCTO1p	MMo2[x] + MMglycl[x] -> MMh2o2[x] + MMglx[x]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGLYC_St	MMglyc-S[c] -> MMglyc-S[e]	0	1000	15112.1 or 56185.1 or 56185.2	Mouse metabolic/ transport/ demand reaction
MMGLYCt	MMglyc[c] <=> MMglyc[e]	-1000	0		Mouse metabolic/ transport/ demand reaction
MMGLYCtm	MMglyc[c] <=> MMglyc[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGLYGLYCNc	MMh2o[c] + MMglygly[c] <=> 2 MMgly[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGLYGLYPEPT1tc	MMglygly[u] -> MMh[u] + MMglygly[c]	0	1000	(338403.1 or 66054.1)	Mouse metabolic/ transport/ demand reaction
MMGLYGLYt	MMf[e] + MMglygly[e] <=> MMf[c] + MMglygly[c]	-1000	1000	215335.1	Mouse metabolic/ transport/ demand reaction
MMGLYK	MMatp[c] + MMglyc[c] -> MMadp[c] + MMh[c] + MMglyc3p[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGLYKm	MMatp[m] + MMglyc[m] -> MMh[m] + MMadp[m] + MMglyc3p[m]	0	1000	14933.1 or 14933.2 or 14626.1	Mouse metabolic/ transport/ demand reaction
MMGLYLEUHYDROc	MMh2o[c] + MMglyleu[c] <=> MMleu-L[c] + MMgly[c]	-1000	1000	14933.1 or 14933.2 or 14626.1	Mouse metabolic/ transport/ demand reaction
MMGLYLEUPEPT1tc	MMh[u] + MMglyleu[u] -> MMh[c] + MMglyleu[c]	0	1000	(13479.1 or 66054.1)	Mouse metabolic/ transport/ demand reaction
MMGLYOX	MMh2o[c] + MMglz-S[c] -> MMh[c] + MMglxbrd[c] + MMlac-D[c]	0	1000	215335.1	Mouse metabolic/ transport/ demand reaction
MMGLYOXm	MMh2o[m] + MMglz-S[m] -> MMh[m] + MMlac-D[m] + MMglxbrd[m]	0	1000	14651.1 or 68977.2 or 68977.1	Mouse metabolic/ transport/ demand reaction
MMGLYOp	MMo2[x] + MMh2o[x] + MMgly[x] -> MMh2o2[x] + MMglx[x] + MMmhd[x]	0	1000	14651.1	Mouse metabolic/ transport/ demand reaction
MMGLYPAT1c	MMf[u] + MMgly[u] -> MMf[c] + MMgly[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGLYPHEPEPT1tc	MMf[u] + MMglyphe[u] -> MMf[c] + MMglyphe[c]	0	1000	215335.1	Mouse metabolic/ transport/ demand reaction
MMGLYPHEt	MMf[e] + MMglyphe[e] <=> MMf[c] + MMglyphe[c]	-1000	1000	215335.1	Mouse metabolic/ transport/ demand reaction
MMGLYPROPEPT1tc	MMf[u] + MMglypro[u] -> MMf[c] + MMglypro[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGLYPROPRO1c	MMh2o[c] + MMglypro[c] <=> MMgly[c] + MMpro-L[c]	-1000	1000	215335.1	Mouse metabolic/ transport/ demand reaction
MMGLYSARCNc	MMh2o[c] + MMglysar[c] <=> MMgly[c] + MMsarcs[c]	-1000	1000	18624.1	Mouse metabolic/ transport/ demand reaction
MMGLYSARPEPT1tc	MMf[u] + MMglysar[u] -> MMf[c] + MMglysar[c]	0	1000	12751.1	Mouse metabolic/ transport/ demand reaction
MMGLYSARt	MMf[e] + MMglysar[e] <=> MMf[c] + MMglysar[c]	-1000	1000	215335.1	Mouse metabolic/ transport/ demand reaction
MMGLYSNAT5tc	MMf[c] + MMna1[u] + MMgly[u] <=> MMna1[c] + MMf[u] + MMgly[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGLYVESSEC	MMh2o[c] + MMatp[c] + 3 MMgly[c] -> MMadp[c] + MMf[c] + MMpi[c] + 3 MMgly[e]	0	1000	209837.1	Mouse metabolic/ transport/ demand reaction
MMGLYt2r	MMh[e] + MMgly[e] <=> MMf[c] + MMgly[c]	0	1000	22348.1	Mouse metabolic/ transport/ demand reaction
MMGLYt2rL	MMh[l] + MMgly[l] <=> MMf[c] + MMgly[c]	-1000	1000	215335.1	Mouse metabolic/ transport/ demand reaction
MMGLYt4	MMna1[e] + MMgly[e] -> MMna1[c] + MMgly[c]	0	1000	215335.1	Mouse metabolic/ transport/ demand reaction
MMGLYt7_211_r	2 MMna1[e] + MMgly[e] + MMcl[e] <=> 2 MMna1[c] + MMcl[c] + MMgly[c]	0	1000	105727.1 or 67760.1 or 69354.1 or 56774.1	Mouse metabolic/ transport/ demand reaction
MMGLYt7_311_r	3 MMna1[e] + MMgly[e] + MMcl[e] <=> 3 MMna1[c] + MMcl[c] + MMgly[c]	0	1000	14664.1 or 14664.2	Mouse metabolic/ transport/ demand reaction
MMGLYtm	MMgly[c] <=> MMgly[m]	-1000	1000	104245.1	Mouse metabolic/ transport/ demand reaction
MMGLYtp	MMgly[c] <=> MMgly[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGMAND	MMgdpmann[c] -> MMh2o[c] + MMgdpddman[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGMPR	2 MMf[c] + MMnadph[c] + MMgmp[c] -> MMnbtd[c] + MMnadp[c] + MMimp[c]	0	1000	218138.1	Mouse metabolic/ transport/ demand reaction
MMGMPS2	MMh2o[c] + MMatp[c] + MMgln-L[c] + MMxmp[c] -> 2 MMf[c] + MMglu-L[c] + MMamp[c] + MMppi[c] + MMgmp[c]	0	1000	105446.1 or 105446.2 or 105446.3 or 66355.1	Mouse metabolic/ transport/ demand reaction
MMGMPtg	MMgmp[c] <=> MMgmp[g]	-1000	1000	229363.1	Mouse metabolic/ transport/ demand reaction
MMGMPtn	MMgmp[c] <=> MMgmp[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGNCORE1t	MMgncore1[g] -> MMgncore1[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGNCORE2t	MMgncore2[g] -> MMgncore2[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGND	MMnadp[c] + MM6pgc[c] -> MMnadph[c] + MMco2[c] + MMru5p-D[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGNDer	MMnadp[r] + MM6pgc[r] -> MMnadph[r] + MMco2[r] + MMru5p-D[r]	0	1000	110208.1	Mouse metabolic/ transport/ demand reaction
MMGNMT	MMamet[c] + MMgly[c] -> MMh[c] + MMahcys[c] + MMsarcs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGP1CALPHAte	MMgp1calpha_hs[c] <=> MMgp1calpha_hs[e]	-1000	1000	14711.1	Mouse metabolic/ transport/ demand reaction
MMGP1CALPHAtg	MMgp1calpha_hs[c] <=> MMgp1calpha_hs[g]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGP1Cte	MMgp1c_hs[c] <=> MMgp1c_hs[e]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGP1Ctg	MMgp1c_hs[c] <=> MMgp1c_hs[g]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGPAM_hs	MMRtotalcoa[c] + MMglyc3p[c] -> MMcoa[c] + MMalpa_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGPAMm_hs	MMRtotalcoa[m] + MMglyc3p[m] -> MMcoa[m] + MMalpa_hs[m]	0	1000	14732.1	Mouse metabolic/ transport/ demand reaction
MMGPDDA1	MMh2o[c] + MMg3pc[c] -> MMh[c] + MMchol[c] + MMglyc3p[c]	0	1000	14732.1	Mouse metabolic/ transport/ demand reaction
MMGPIAT	MMgpail_hs[c] + MMpmtcoa[c] -> MMcoa[c] + MMgtcpail_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGPIDA2er	MMh2o[r] + MMem2emgacpail_prot_hs[r] -> MMh[r] + MMdem2emgacpail_prot_hs[r] + MMhlcla[r]	0	1000	70325.1	Mouse metabolic/ transport/ demand reaction
MMGPIDAer	MMh2o[r] + MMgpi_prot_hs[r] -> MMh[r] + MMdgpi_prot_hs[r] + MMhlcla[r]	0	1000	241062.1	Mouse metabolic/ transport/ demand reaction
MMGPIMTer_L	0.1 MMdolmanp_L[r] + MMgacpail_hs[r] -> 0.1 MMdolp_L[r] + MMf[r] + MMmgacpail_hs[r]	0	1000	241062.1	Mouse metabolic/ transport/ demand reaction
MMGPIMTer_U	0.1 MMdolmanp_U[r] + MMgacpail_hs[r] -> MMf[r] + 0.1 MMdolp_U[r] + MMmgacpail_hs[r]	0	1000	67556.1 or 72084.1	Mouse metabolic/ transport/ demand reaction
MMGQ1BALPHAte	MMgq1balpha_hs[c] <=> MMgq1balpha_hs[e]	-1000	1000	67556.1 or 72084.1	Mouse metabolic/ transport/ demand reaction
MMGQ1BALPHAtg	MMgq1balpha_hs[c] <=> MMgq1balpha_hs[g]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGQ1Bte	MMgq1b_hs[c] <=> MMgq1b_hs[e]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGQ1Btg	MMgq1b_hs[c] <=> MMgq1b_hs[g]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGRTT	MMpidp[c] + MMgrdp[c] -> MMppi[c] + MMfrdp[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGRTTx	MMpidp[x] + MMgrdp[x] -> MMppi[x] + MMfrdp[x]	0	1000	14593.1	Mouse metabolic/ transport/ demand reaction
MMGSNKm	MMatp[m] + MMgsn[m] -> MMh[m] + MMadp[m] + MMgmp[m]	0	1000	110196.1	Mouse metabolic/ transport/ demand reaction
MMGSNt	MMgsn[e] <=> MMgsn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGSNt4	MMna1[e] + MMgsn[e] -> MMna1[c] + MMgsn[c]	0	1000	13340.1 or 63959.1	Mouse metabolic/ transport/ demand reaction
MMGSNt5	2 MMna1[e] + MMgsn[e] -> 2 MMna1[c] + MMgsn[c]	0	1000	114304.1 or 269346.1	Mouse metabolic/ transport/ demand reaction
MMGSNtl	MMgsn[l] <=> MMgsn[c]	-1000	1000	114304.1	Mouse metabolic/ transport/ demand reaction

MMGSNtm	MMgsn[c] <=> MMgsn[m]	-1000	1000	71279.1	Mouse metabolic/ transport/ demand reaction
MMGT1Ate	MMgt1a_hs[c] <=> MMgt1a_hs[e]	-1000	1000	63959.1	Mouse metabolic/ transport/ demand reaction
MMGT1Atg	MMgt1a_hs[c] <=> MMgt1a_hs[g]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGTHDH	MMdhdascb[c] + 2 MMgthrd[c] -> MMascb-L[c] + MMgthox[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGTHO	MMh[c] + MMnadph[c] + MMgthox[c] -> MMnadp[c] + 2 MMgthrd[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGTHOm	MMh[m] + MMnadph[m] + MMgthox[m] -> MMnadp[m] + 2 MMgthrd[m]	0	1000	14782.1	Mouse metabolic/ transport/ demand reaction
MMGTHP	MMh2o2[c] + 2 MMgthrd[c] <=> 2 MMh2o[c] + MMgthox[c]	-1000	1000	14782.1	Mouse metabolic/ transport/ demand reaction
MMGTHPe	2 MMgthrd[e] + MMh2o2[e] <=> 2 MMh2o[e] + MMgthox[e]	-1000	1000	14776.1 or 14775.1 or 18477.1 or 21672.1 or 21672.2 or 18477.2 or 625249.1 or 18477.3 or 14775.2 or 21672.3	Mouse metabolic/ transport/ demand reaction
MMGTHPm	MMh2o2[m] + 2 MMgthrd[m] <=> 2 MMh2o[m] + MMgthox[m]	-1000	1000	75512.1 or 14778.1	Mouse metabolic/ transport/ demand reaction
MMGTHRDr	MMh2o[c] + MMnadp[c] + MMgthrd[c] <=> MMnadph[c] + MMh[c] + MMp[c] + MMgthrd[m]	-1000	1000	625249.1 or 11757.1 or 11757.2	Mouse metabolic/ transport/ demand reaction
MMGTHRDtr	MMgthrd[c] <=> MMgthrd[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGTHS	MMatp[c] + MMgly[c] + MMglucys[c] -> MMadp[c] + MMh[c] + MMp[c] + MMgthrd[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGTMLTe	MMala-L[c] + MMgthrd[c] -> MMcgly[e] + MMgluala[e]	0	1000	14854.1	Mouse metabolic/ transport/ demand reaction
MMGTPCI	MMh2o[c] + MMgtp[c] -> MMH[c] + MMfor[c] + MMahdt[c]	0	1000	14598.1 or 14598.2 or 14598.3	Mouse metabolic/ transport/ demand reaction
MMGTPCIn	MMh2o[n] + MMgtp[n] -> MMH[n] + MMfor[n] + MMahdt[n]	0	1000	14528.1	Mouse metabolic/ transport/ demand reaction
MMGTPtn	MMgtp[c] <=> MMgtp[n]	-1000	1000	14528.1	Mouse metabolic/ transport/ demand reaction
MMGUACYC	MMgtp[c] -> MM35cgmp[c] + MMppi[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGUAD	MMh2o[c] + MMH[c] + MMgua[c] -> MMnh4[c] + MMxan[c]	0	1000	(230103.1 or (60596.1 and 239134.1) or 234889.1 and 239134.1 or 14917.1 or (54195.1 and 234889.1) or 14919.1 or 230103.2 or 245650.1 or 18160.1 or (54195.1 and 60596.1))	Mouse metabolic/ transport/ demand reaction
MMGUAPRT	MMprpp[c] + MMgua[c] -> MMppi[c] + MMgmp[c]	0	1000	14544.1	Mouse metabolic/ transport/ demand reaction
MMGUAt	MMgua[e] <=> MMgua[c]	0	1000	15452.1	Mouse metabolic/ transport/ demand reaction
MMGULLACter	MMgullac[c] -> MMgullac[r]	0	1000	13340.1	Mouse metabolic/ transport/ demand reaction
MMGULN3D	MMnad[c] + MMgulnl[c] <=> MMh[c] + MMnadh[c] + MM3dhgulnl[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGULNDer	MMh[r] + MMnadph[r] + MMglcur[r] <=> MMnadp[r] + MMgulnl[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGULNter	MMgulnl[r] -> MMgulnl[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGUMDCHAe	MMgum[u] + MMdchac[u] -> MMgumdchac[u]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGUMDCHAt	MMh[e] + MMgumdchac[e] <=> MMh[c] + MMgumdchac[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGUMGCHLe	MMgchola[u] + MMgum[u] -> MMgumgchol[u]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGUMGCHLt	MMh[e] + MMgumgchol[e] <=> MMh[c] + MMgumgchol[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGUMTCHOLe	MMichola[u] + MMgum[u] -> MMgumtchol[u]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGUMTCHOLt	MMh[e] + MMgumtchol[e] <=> MMh[c] + MMgumtchol[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGUMt	MMH[e] + MMgum[e] <=> MMh[c] + MMgum[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMGUR1PP	MMh2o[c] + MMglcur1p[c] -> MMp4[c] + MMglcur[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMGluForTx	MMh[c] + MMthf[c] + MMforglu[c] -> MMglu-L[c] + MM5forthf[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMH2CO3D	MMh2o[c] + MMco2[c] <=> MMh2co3[c]	-1000	1000	14317.1 or 14317.2	Mouse metabolic/ transport/ demand reaction
MMH2CO3D2	MMH[c] + MMhco3[c] <=> MMh2co3[c]	-1000	1000	12354.1 or 76459.2 or 76459.1 or 12349.1 or 12351.1 or 12350.1 or 12346.1 or 71934.1 or 12354.2 or 23831.1 or 230099.1	Mouse metabolic/ transport/ demand reaction
MMH2CO3D2m	MMh[m] + MMhco3[m] <=> MMh2co3[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMH2CO3Dm	MMh2o[m] + MMco2[m] <=> MMh2co3[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMH2ETer	MMmgacpail_hs[r] + MMpe_hs[c] -> MMdag_hs[r] + MMemgacpail_hs[r]	0	1000	12352.1 or 56078.1	Mouse metabolic/ transport/ demand reaction
MMH2MTer_L	0.1 MMdolmanp_L[r] + MMmgacpail_hs[r] -> 0.1 MMdolp_L[r] + MMh[r] + MMm2gacpail_hs[r]	0	1000	27392.1 or 27392.2	Mouse metabolic/ transport/ demand reaction
MMH2MTer_U	0.1 MMdolmanp_U[r] + MMmgacpail_hs[r] -> MMh[r] + 0.1 MMdolp_U[r] + MMm2gacpail_hs[r]	0	1000	230801.1	Mouse metabolic/ transport/ demand reaction
MMH2O2syn	MMo2[c] + MMH[c] + MMnadph[c] -> MMh2o2[c] + MMnadp[c]	0	1000	230801.1	Mouse metabolic/ transport/ demand reaction
MMH2O2t	MMh2o2[e] <=> MMh2o2[c]	0	1000	99439.1 or 99439.2 or 214593.1	Mouse metabolic/ transport/ demand reaction
MMH2O2tly	MMh2o2[c] <=> MMh2o2[l]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMH2O2tm	MMh2o2[c] <=> MMh2o2[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMH2O2tn	MMh2o2[c] <=> MMh2o2[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMH2O2tp	MMh2o2[c] <=> MMh2o2[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMH2Ot	MMh2o[e] <=> MMh2o[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMH2Oter	MMh2o[c] <=> MMh2o[r]	-1000	1000	20537.1	Mouse metabolic/ transport/ demand reaction
MMH2Otg	MMh2o[c] <=> MMh2o[g]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMH2Otly	MMh2o[c] <=> MMh2o[l]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMH2Otm	MMh2o[c] <=> MMh2o[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMH2Otn	MMh2o[n] <=> MMh2o[c]	-1000	1000	11833.1	Mouse metabolic/ transport/ demand reaction
MMH2Otp	MMh2o[c] <=> MMh2o[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMH3ETer	MMpe_hs[r] + MMm2gacpail_hs[r] -> MMmemgacpail_hs[r] + MMdag_hs[r]	0	1000		Mouse metabolic/ transport/ demand reaction
MMH3MTer_L	0.1 MMdolmanp_L[r] + MMm2gacpail_hs[r] -> 0.1 MMdolp_L[r] + MMh[r] + MMm3gacpail_hs[r]	0	1000	27392.1 or 27392.2	Mouse metabolic/ transport/ demand reaction
MMH3MTer_U	0.1 MMdolmanp_U[r] + MMm2gacpail_hs[r] -> MMh[r] + 0.1 MMdolp_U[r] + MMm3gacpail_hs[r]	0	1000	55981.1	Mouse metabolic/ transport/ demand reaction
MMH4ET3er	MMpe_hs[r] + MMm3gacpail_hs[r] -> MMdag_hs[r] + MMem3gacpail_hs[r]	0	1000	55981.1	Mouse metabolic/ transport/ demand reaction
MMH4ETer	MMpe_hs[r] + MMm3gacpail_hs[r] -> MMm2emgacpail_hs[r] + MMdag_hs[r]	0	1000	56703.1 or 18701.1 or 18701.2 or 56703.2	Mouse metabolic/ transport/ demand reaction
MMH5MTer_L	0.1 MMdolmanp_L[r] + MMemgacpail_hs[r] -> MMmemgacpail_hs[r] + 0.1 MMdolp_L[r] + MMh[r]	0	1000	27392.1 or 27392.2	Mouse metabolic/ transport/ demand reaction
MMH5MTer_U	MMdolmanp_U[r] + MMemgacpail_hs[r] -> MMmemgacpail_hs[r] + 2 MMh[r] + MMdolp_U[r]	0	1000	230801.1	Mouse metabolic/ transport/ demand reaction
MMH6ET3er	MMm2emgacpail_hs[r] + MMpe_hs[r] -> MMdag_hs[r] + MMem2emgacpail_hs[r]	0	1000	230801.1	Mouse metabolic/ transport/ demand reaction
MMH6MTer_L	0.1 MMdolmanp_L[r] + MMm2emgacpail_hs[r] -> 0.1 MMdolp_L[r] + MMh[r] + MMm1emgacpail_hs[r]	0	1000	56703.1 or 18701.1 or 18701.2 or 56703.2	Mouse metabolic/ transport/ demand reaction
MMH6MTer_U	MMm2emgacpail_hs[r] + 0.1 MMdolmanp_U[r] -> MMh[r] + 0.1 MMdolp_U[r] + MMm1emgacpail_hs[r]	0	1000	239827.1	Mouse metabolic/ transport/ demand reaction
MMH6_ET2er	MMpe_hs[r] + MMem3gacpail_hs[r] -> MMdag_hs[r] + MMemem2gacpail_hs[r]	0	1000	239827.1	Mouse metabolic/ transport/ demand reaction
MMH6_ETer	MMpe_hs[r] + MMem3gacpail_hs[r] -> MMdag_hs[r] + MMem2emgacpail_hs[r]	0	1000	18701.1 or 433931.1 or 18701.2	Mouse metabolic/ transport/ demand reaction
MMH7ET2er	MMpe_hs[r] + MMem2emgacpail_hs[r] -> MMdag_hs[r] + MMgpi_hs[r]	0	1000	27392.1 or 27392.2	Mouse metabolic/ transport/ demand reaction
MMH7MTer_L	0.1 MMdolmanp_L[r] + MMem2emgacpail_hs[r] -> 0.1 MMdolp_L[r] + MMh[r] + MMemem2emgacpail_hs[r]	0	1000	18701.1 or 433931.1 or 18701.2	Mouse metabolic/ transport/ demand reaction
MMH7MTer_U	MMdolmanp_U[r] + MMem2emgacpail_hs[r] -> 2 MMh[r] + MMdolp_U[r] + MMmem2emgacpail_hs[r]	0	1000	239827.1	Mouse metabolic/ transport/ demand reaction
MMH7_ETer	MMpe_hs[r] + MMemem2gacpail_hs[r] -> MMdag_hs[r] + MMgpi_hs[r]	0	1000	239827.1	Mouse metabolic/ transport/ demand reaction
MMH7_TAer	MMem2emgacpail_hs[r] + MMpre_prot[r] -> MMgpi_sig[r] + MMem2emgacpail_prot_hs[r]	0	1000	27392.1 or 27392.2	Mouse metabolic/ transport/ demand reaction
MMH8MTer_L	0.1 MMdolmanp_L[r] + MMgpi_hs[r] -> 0.1 MMdolp_L[r] + MMh[r] + MMm[em]3gacpail_hs[r]	0	1000	276846.1 or 78928.1 or 228812.1 or 14731.1 or 329777.1	Mouse metabolic/ transport/ demand reaction
MMH8MTer_U	0.1 MMdolmanp_U[r] + MMgpi_hs[r] -> MMh[r] + 0.1 MMdolp_U[r] + MMm[em]3gacpail_hs[r]	0	1000	239827.1	Mouse metabolic/ transport/ demand reaction
MMH8TAer	MMgpi_hs[r] + MMpre_prot[r] -> MMgpi_sig[r] + MMgpi_prot_hs[r]	0	1000	239827.1	Mouse metabolic/ transport/ demand reaction
MMHACD1m	MMh[m] + MMnadh[m] + MMaacoa[m] <=> MMnad[m] + MM3hbcoa[m]	-1000	1000	276846.1 or 78928.1 or 228812.1 or 14731.1 or 329777.1	Mouse metabolic/ transport/ demand reaction
MMHACD1x	MMh[x] + MMnadh[x] + MMaacoa[x] <=> MMnad[x] + MM3hbcoa[x]	-1000	1000	15107.1 or 231086.1 or 97212.1 or 15108.1	Mouse metabolic/ transport/ demand reaction
MMHACD9m	MMnad[m] + MM3hmbcoa[m] <=> MMh[m] + MMnadh[m] + MM2maacoa[m]	-1000	1000	74147.1 or 15488.1	Mouse metabolic/ transport/ demand reaction
MMHAS1	MMaacgam[c] + MMudpglcur[c] -> 2 MMh[c] + 2 MMudp[c] + MMha_pre1[e]	0	1000	15108.1	Mouse metabolic/ transport/ demand reaction
MMHAS2	MMha_pre1[e] + MMaacgam[c] + MMudpglcur[c] -> 2 MMh[c] + 2 MMudp[c] + MMha[e]	0	1000	15118.1 or 15116.1 or 15117.1 or 15118.2	Mouse metabolic/ transport/ demand reaction
MMHAtly	MMha[e] -> MMha[l]	0	1000	15118.1 or 15116.1 or 15117.1 or 15118.2	Mouse metabolic/ transport/ demand reaction
MMHBZOPT10m	MM4hbz[m] + MMdecdp[m] -> MM3dphb[m] + MMppi[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMHCO3_CLt	MMhco3[e] + MMcl[c] <=> MMhco3[c] + MMcl[e]	-1000	1000	71883.1	Mouse metabolic/ transport/ demand reaction
MMHCO3_NAt	MMhco3[e] + MMna1[e] <=> MMhco3[c] + MMna1[c]	-1000	1000	20533.1 or 20535.1 or 20536.1 or 240215.1 or 20536.2	Mouse metabolic/ transport/ demand reaction
MMHCOUMARINte	MMhcoumarin[e] <=> MMhcoumarin[c]	0	1000	218756.1	Mouse metabolic/ transport/ demand reaction

MMHDCAter	MMhdca[r] -> MMhdca[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMHDCAtr	MMhdca[e] <=> MMhdca[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMHDCEAtr	MMhdcea[e] <=> MMhdcea[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMHDD2COAtx	MMhdd2coa[c] <=> MMhdd2coa[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMHESTRATRIOLte	MMhestratriol[c] <=> MMhestratriol[e]	-1000	0		Mouse metabolic/ transport/ demand reaction
MMHESTRATRIOLtr	MMhestratriol[c] <=> MMhestratriol[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMHEX1	MMatp[c] + MMglc-D[c] -> MMadp[c] + MMh[c] + MMg6p[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMHEX10	MMatp[c] + MMgam[c] -> MMadp[c] + MMh[c] + MMgam6p[c]	0	1000	15275.1 or 212032.1 or 103988.1 or 15275.2 or 15277.1 or 15275.3 or 103988.2 or 103988.3 or 15275.4 or 216019.1 or 15275.5	Mouse metabolic/ transport/ demand reaction
MMHEX4	MMatp[c] + MMman[c] -> MMadp[c] + MMh[c] + MMman6p[c]	0	1000	15275.1 or 212032.1 or 103988.1 or 15275.2 or 15277.1 or 15275.3 or 103988.2 or 103988.3 or 15275.4 or 216019.1 or 15275.5	Mouse metabolic/ transport/ demand reaction
MMHEX7	MMatp[c] + MMfru[c] -> MMadp[c] + MMh[c] + MMf6p[c]	0	1000	15275.1 or 212032.1 or 103988.1 or 15275.2 or 15277.1 or 15275.3 or 103988.2 or 103988.3 or 15275.4 or 216019.1 or 15275.5	Mouse metabolic/ transport/ demand reaction
MMHEXCCOAtx	MMhexccoa[c] <=> MMhexccoa[x]	-1000	1000	15275.1 or 212032.1 or 103988.1 or 15275.2 or 15277.1 or 15275.3 or 103988.2 or 103988.3 or 15275.4 or 216019.1 or 15275.5	Mouse metabolic/ transport/ demand reaction
MMHEXCCPT1	MMcrn[c] + MMhexccoa[c] -> MMcoa[c] + MMhexccrn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMHEXCCPT2	MMcoa[m] + MMhexccrn[m] -> MMcrn[m] + MMhexccoa[m]	0	1000	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	Mouse metabolic/ transport/ demand reaction
MMHEXCCRNt	MMhexccrn[c] -> MMhexccrn[m]	0	1000	12896.1	Mouse metabolic/ transport/ demand reaction
MMHEXCt	MMhexc[e] <=> MMhexc[c]	0	1000	57279.1	Mouse metabolic/ transport/ demand reaction
MMHGNTOR	MMo2[c] + MMhgentis[c] -> MMh[c] + MM4mlacac[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMHIBDm	MMnad[m] + MM3hmp[m] <=> MMh[m] + MMnadh[m] + MM2mop[m]	-1000	1000	15233.1	Mouse metabolic/ transport/ demand reaction
MMHISCAT1	MMhis-L[c] <=> MMhis-L[e]	-1000	1000	58875.1	Mouse metabolic/ transport/ demand reaction
MMHISD	MMhis-L[c] -> MMnh4[c] + MMurcan[c]	0	1000	11987.1	Mouse metabolic/ transport/ demand reaction
MMHISDC	MMh[c] + MMhis-L[c] -> MMco2[c] + MMhista[c]	0	1000	15109.1	Mouse metabolic/ transport/ demand reaction
MMHISILELAT2tc	MMile-L[c] + MMhis-L[e] -> MMile-L[e] + MMhis-L[c]	0	1000	15186.1 or 13195.1	Mouse metabolic/ transport/ demand reaction
MMHISLAT1tc	MMleu-L[c] + MMhis-L[u] -> MMleu-L[u] + MMhis-L[c]	0	1000	(20539.1 and 17254.1)	Mouse metabolic/ transport/ demand reaction
MMHISPHELAT2tc	MMphe-L[c] + MMhis-L[e] -> MMphe-L[e] + MMhis-L[c]	0	1000	(20539.1 and 17254.1)	Mouse metabolic/ transport/ demand reaction
MMHISSNAT5tc	MMh[c] + MMna1[u] + MMhis-L[u] <=> MMna1[c] + MMh[u] + MMhis-L[c]	-1000	1000	(20539.1 and 17254.1)	Mouse metabolic/ transport/ demand reaction
MMHISTASE	MMh2o[c] + MMo2[c] + MMhista[c] -> MMh2o2[c] + MMnh4[c] + MMam4acl[c]	0	1000	209837.1	Mouse metabolic/ transport/ demand reaction
MMHISTAVESSEC	2 MMh2o[c] + 2 MMatp[c] + 3 MMhista[c] -> 2 MMadp[c] + 2 MMh[c] + 2 MMpi[c] + 3 MMhista[e]	0	1000	237940.1 or 237940.2 or 76507.1	Mouse metabolic/ transport/ demand reaction
MMHISTAtu	MMhista[e] <=> MMhista[c]	0	1000	214084.1 or 110877.1	Mouse metabolic/ transport/ demand reaction
MMHISTbPTtc	MMh[l] + MMhis-L[l] -> MMh[c] + MMhis-L[c]	0	1000	20518.1 or 20519.1 or 20518.2	Mouse metabolic/ transport/ demand reaction
MMHITs4	MMna1[e] + MMhis-L[e] -> MMna1[c] + MMhis-L[c]	0	1000	(65221.1 or 100561.1)	Mouse metabolic/ transport/ demand reaction
MMHITsN1	MMh[c] + 2 MMna1[e] + MMhis-L[e] <=> MMh[e] + 2 MMna1[c] + MMhis-L[c]	0	1000	67760.1 or 56774.1	Mouse metabolic/ transport/ demand reaction
MMHITstDF	MMhis-L[e] -> MMhis-L[c]	0	1000	76257.1	Mouse metabolic/ transport/ demand reaction
MMHISyLATltc	MMna1[e] + MMarg-L[c] + MMhis-L[e] -> MMna1[c] + MMarg-L[e] + MMhis-L[c]	0	1000	69354.1	Mouse metabolic/ transport/ demand reaction
MMHISyLATthc	MMh[e] + MMarg-L[c] + MMhis-L[e] -> MMh[c] + MMarg-L[e] + MMhis-L[c]	0	1000	(20540.1 or (330836.1 and 17254.1))	Mouse metabolic/ transport/ demand reaction
MMHKYNH	MMh2o[c] + MMhLkynr[c] -> MM3hanthrn[c] + MMala-L[c]	0	1000	(20540.1 or (330836.1 and 17254.1))	Mouse metabolic/ transport/ demand reaction
MMHKt	MMh2o[c] + MMatp[c] + MMk[e] -> MMadp[c] + MMpi[c] + MMh[e] + MMk[c]	0	1000	70789.1	Mouse metabolic/ transport/ demand reaction
MMHMBS	MMh2o[c] + 4 MMppbng[c] -> 4 MMnh4[c] + MMhmbil[c]	0	1000	11945.1 and 11944.1	Mouse metabolic/ transport/ demand reaction
MMHMGCOARr	2 MMh[r] + 2 MMnadph[r] + MMhmgcoa[r] -> 2 MMnadp[r] + MMcoa[r] + MMmev-R[r]	0	1000	15288.1	Mouse metabolic/ transport/ demand reaction
MMHMGCOARx	2 MMh[x] + MMhmgcoa[x] + 2 MMnadph[x] -> MMcoa[x] + MMmev-R[x] + 2 MMnadp[x]	0	1000	15357.1	Mouse metabolic/ transport/ demand reaction
MMHMGCOASi	MMh2o[c] + MMaacoa[c] + MMaccoa[c] -> MMh[c] + MMcoa[c] + MMhmgcoa[c]	0	1000	15357.1	Mouse metabolic/ transport/ demand reaction
MMHMGCOASim	MMh2o[m] + MMaccoa[m] + MMaacoa[m] -> MMh[m] + MMcoa[m] + MMhmgcoa[m]	0	1000	208715.1 or 208715.2	Mouse metabolic/ transport/ demand reaction
MMHMGCOAtm	MMhmgcoa[c] <=> MMhmgcoa[m]	-1000	1000	15360.1	Mouse metabolic/ transport/ demand reaction
MMHMGCOAtx	MMhmgcoa[c] <=> MMhmgcoa[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMHMGLm	MMhmgcoa[m] -> MMaccoa[m] + MMacac[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMHMGLx	MMhmgcoa[x] -> MMaccoa[x] + MMacac[x]	0	1000	208982.1 or 15356.1	Mouse metabolic/ transport/ demand reaction
MMHOMt4	MMna1[e] + MMhom-L[e] -> MMna1[c] + MMhom-L[c]	0	1000	15356.1	Mouse metabolic/ transport/ demand reaction
MMHOXG	3 MMo2[c] + 5 MMh[c] + 3 MMnadph[c] + MMpheme[c] -> 3 MMh2o[c] + 3 MMnadp[c] + MMbiliverd[c] + MMco[c] + MMfe2[c]	0	1000	11989.1 or 11988.1 or 11987.1	Mouse metabolic/ transport/ demand reaction
MMHPACtr	MM4hphac[c] <=> MM4hphac[e]	-1000	0	15368.1 or 15369.1	Mouse metabolic/ transport/ demand reaction
MMHPCLx	4 MMh[x] + MMphyt2ohcoa[x] -> MMformcoa[x] + MMpristana[x]	0	1000		Mouse metabolic/ transport/ demand reaction
MMHPDCACRNCPT1	MMcrn[c] + MMhpdcacoa[c] -> MMcoa[c] + MMhpdcacrn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMHPDCACRNCPT2	MMcoa[m] + MMhpdcacrn[m] -> MMcrn[m] + MMhpdcacoa[m]	0	1000	12894.1 or 78070.1 or 12895.1 or 12895.2 or 12895.3	Mouse metabolic/ transport/ demand reaction
MMHPDCACRNt	MMhpdcacrn[c] -> MMhpdcacrn[m]	0	1000	12896.1	Mouse metabolic/ transport/ demand reaction
MMHPDCAt	MMhpdca[e] <=> MMhpdca[c]	0	1000	57279.1	Mouse metabolic/ transport/ demand reaction
MMHPETFABP1tc	2 MM5HPET[c] <=> 2 MM5HPET[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMHPROxm	MMnad[m] + MM4hpro-LT[m] -> 2 MMh[m] + MMnadh[m] + MM1p3h5c[m]	0	1000	14080.1	Mouse metabolic/ transport/ demand reaction
MMHPYRDC	MMh[c] + MMhpyr[c] -> MMco2[c] + MMgcald[c]	0	1000	212647.1 or 212647.2	Mouse metabolic/ transport/ demand reaction
MMHPYRDCm	MMh[m] + MMhpyr[m] -> MMco2[m] + MMgcald[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMHPYRR2x	MMh[c] + MMnadh[c] + MMhpyr[c] -> MMnad[c] + MMglyc-S[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMHPYRRy	MMh[c] + MMnadph[c] + MMhpyr[c] -> MMnadp[c] + MMglyc-R[c]	0	1000	16833.1 or 16832.1 or 106557.1 or 16833.2 or 16832.1 and 16828.1 or 52815.1 or 16828.1 or 52815.2	Mouse metabolic/ transport/ demand reaction
MMHPYRtp	MMhpyr[c] <=> MMhpyr[x]	-1000	1000	76238.1	Mouse metabolic/ transport/ demand reaction
MMHRETNtn	MMhretn[c] <=> MMhretn[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMHS1ly	MMh2o[l] + MMhs_deg1[l] -> MMh[l] + MMso4[l] + MMhs_deg2[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MMHS2ly	MMh2o[l] + MMhs_deg6[l] -> MMh[l] + MMso4[l] + MMhs_deg7[l]	0	1000	27029.1	Mouse metabolic/ transport/ demand reaction
MMHS3ly	MMh2o[l] + MMhs_deg12[l] -> MMh[l] + MMso4[l] + MMhs_deg13[l]	0	1000	27029.1	Mouse metabolic/ transport/ demand reaction
MMHS4ly	MMh2o[l] + MMhs_deg18[l] -> MMh[l] + MMso4[l] + MMhs_deg19[l]	0	1000	27029.1	Mouse metabolic/ transport/ demand reaction
MMHSAT1ly	MMaccoa[c] + MMhs_deg2[l] -> MMcoa[c] + MMh[l] + MMhs_deg5[l]	0	1000	27029.1	Mouse metabolic/ transport/ demand reaction
MMHSAT2ly	MMaccoa[c] + MMhs_deg7[l] -> MMcoa[c] + MMh[l] + MMhs_deg8[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MMHSAT3ly	MMaccoa[c] + MMhs_deg13[l] -> MMcoa[c] + MMh[l] + MMhs_deg14[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MMHSAT4ly	MMaccoa[c] + MMhs_deg19[l] -> MMcoa[c] + MMh[l] + MMhs_deg20[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MMHSD11B1r	MMh[r] + MMnadph[r] + MMcortsn[r] <=> MMnadp[r] + MMcrtsl[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMHSD11B2r	MMh[r] + MMnadh[r] + MMcortsn[r] <=> MMnad[r] + MMcrtsl[r]	-1000	1000	15483.1 or 15483.2	Mouse metabolic/ transport/ demand reaction
MMHSD17B1	MMh[c] + MMnadph[c] + MMestrone[c] <=> MMnadp[c] + MMestradiol[c]	-1000	1000	15484.1	Mouse metabolic/ transport/ demand reaction
MMHSD17B2r	MMh[r] + MMnadh[r] + MMandrstndn[r] -> MMnad[r] + MMtestterone[r]	0	1000	14979.1 or 15485.1	Mouse metabolic/ transport/ demand reaction
MMHSD17B3r	MMh[r] + MMnadph[r] + MMandrstndn[r] -> MMnadp[r] + MMtestterone[r]	0	1000	15486.1	Mouse metabolic/ transport/ demand reaction
MMHSD17B42x	MMh[x] + MMo2[x] + MMthcholoylcoa[x] + MMnadph[x] -> 2 MMh2o[x] + MMnadp[x] + MMdhocholoylcsa[x]	0	1000	15487.1	Mouse metabolic/ transport/ demand reaction
MMHSD17B4x	MMh[x] + MMo2[x] + MMcholcoads[x] + MMnadph[x] -> MMh2o[x] + MMnadp[x] + MMcholcoaone[x]	0	1000	15488.1	Mouse metabolic/ transport/ demand reaction
MMHSD17B7r	MMh[r] + MMnadph[r] + MMestrone[r] -> MMnadp[r] + MMestradiol[r]	0	1000	15488.1	Mouse metabolic/ transport/ demand reaction
MMHSD17B8r	MMh[r] + MMnadh[r] + MMestrone[r] -> MMnad[r] + MMestradiol[r]	0	1000	15490.1	Mouse metabolic/ transport/ demand reaction
MMHSD17B9r	1.5 MMo2[r] + MMandrstnr[r] + MMh[r] + MMnadph[r] -> 2 MMh2o[r] + MMnadp[r] + MMeandrstnr[r]	0	1000	15486.1	Mouse metabolic/ transport/ demand reaction
MMHSD3A1r	MMh[r] + MMnadh[r] + MMandrstandn[r] <=> MMandrstnr[r] + MMnad[r]	-1000	1000	15490.1	Mouse metabolic/ transport/ demand reaction
MMHSD3A2r	MMh[r] + MMnadph[r] + MMandrstandn[r] <=> MMandrstnr[r] + MMnadp[r]	-1000	1000	83702.1	Mouse metabolic/ transport/ demand reaction
MMHSD3B11	MMnad[c] + MMprgnlone[c] -> MMh[c] + MMnadh[c] + MMprgstrn[c]	0	1000	83702.1	Mouse metabolic/ transport/ demand reaction

MMHSD3B11r	MMnad[r] + MMprgnlone[r] -> MMh[r] + MMnadh[r] + MMprgstrn[r]	0	1000	15493.1	Mouse metabolic/ transport/ demand reaction
MMHSD3B12r	MMnad[r] + MMdhea[r] -> MMh[r] + MMnadh[r] + MMandrstndn[r]	0	1000	15492.1	Mouse metabolic/ transport/ demand reaction
MMHSD3B13	MMnad[c] + MM17ahprgnlone[c] -> MMh[c] + MMnadh[c] + MM17ahprgstrn[c]	0	1000	15492.1	Mouse metabolic/ transport/ demand reaction
MMHSD3B13r	MMnad[r] + MM17ahprgnlone[r] -> MMh[r] + MMnadh[r] + MM17ahprgstrn[r]	0	1000	15493.1	Mouse metabolic/ transport/ demand reaction
MMHSD3B2r	MMh[r] + MMnadh[r] + MMeandrstrn[r] -> MMh2o[r] + MMnad[r] + MMandrstandn[r]	0	1000	15492.1	Mouse metabolic/ transport/ demand reaction
MMHSD3B3r	MMh[r] + MMnadph[r] + MMeandrstrn[r] -> MMh2o[r] + MMnadp[r] + MMandrstandn[r]	0	1000	15492.1	Mouse metabolic/ transport/ demand reaction
MMHSD3B7	MMnad[r] + MMxol7a[r] -> MMh[r] + MMnadh[r] + MMxol7aone[r]	0	1000	15492.1	Mouse metabolic/ transport/ demand reaction
MMHSD3B7P	MMnadp[r] + MMxol7a[r] -> MMh[r] + MMnadph[r] + MMxol7aone[r]	0	1000	101502.1	Mouse metabolic/ transport/ demand reaction
MMHSPASEly	MMh2o[l] + MMhspg[l] -> MMSer_Gly_Ala_X_Gly[l] + MMhs[l]	0	1000	101502.1	Mouse metabolic/ transport/ demand reaction
MMHSPGt	MMhspg[g] -> MMhspg[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMHSPGtly	MMhspg[e] -> MMhspg[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MMHTAXOLte	MMhtaxol[e] <=> MMhtaxol[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMHXANtl	MMhxan[l] <=> MMhxan[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMHXANtx	MMhxan[c] -> MMhxan[x]	0	1000	71279.1	Mouse metabolic/ transport/ demand reaction
MMHXPRT	MMprpp[c] + MMhxan[c] -> MMppi[c] + MMimp[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMHYPOE	MMh2o[c] + MMpyam5p[c] -> MMpi[c] + MMpydam[c]	0	1000	15452.1	Mouse metabolic/ transport/ demand reaction
MMHYPTROX	MMo2[c] + 2 MMh[c] + 2 MMhyptaur[c] -> 2 MMtaur[c]	0	1000	57028.1	Mouse metabolic/ transport/ demand reaction
MMHYXNt	MMhxan[e] <=> MMhxan[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMHtg	MMh[g] <=> MMh[c]	-1000	1000	13340.1	Mouse metabolic/ transport/ demand reaction
MMHtm	MMh[c] -> MMh[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMHtr	MMh[c] <=> MMh[r]	-1000	1000	22229.1 or 74011.1 or 22229.2 or 22228.1 or 22227.1 or 20523.1 or 20523.2	Mouse metabolic/ transport/ demand reaction
MMHtx	MMh[c] <=> MMh[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMICDHxm	MMnad[m] + MMicit[m] -> MMakg[m] + MMco2[m] + MMnadh[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMICDHy	MMnadp[c] + MMicit[c] -> MMnadph[c] + MMakg[c] + MMco2[c]	0	1000	15929.1 and 67834.1 and 170718.1 or 15929.1 and 67834.1 and 170718.2 or 15929.1 and 67834.1 and 170718.3 or 67834.1 and 170718.1 and 15929.2 or 67834.1 and 15929.2 and 170718.2 or 15929.2 and 67834.1 and 170718.3	Mouse metabolic/ transport/ demand reaction
MMICDHyp	MMnadp[x] + MMicit[x] -> MMakg[x] + MMco2[x] + MMnadph[x]	0	1000	15926.1	Mouse metabolic/ transport/ demand reaction
MMICDHyrm	MMnadp[m] + MMicit[m] <=> MMnadph[m] + MMakg[m] + MMco2[m]	-1000	1000	15926.1	Mouse metabolic/ transport/ demand reaction
MMIDHPOXOX2b	MM3ityr-L[c] + MMiodine[c] -> MMh[c] + MMi[c] + MM35diotyr[c]	0	1000	269951.1	Mouse metabolic/ transport/ demand reaction
MMIDHPOXOX3	MMh2o2[c] + MM3ityr-L[c] + MM35diotyr[c] -> 2 MMh2o[c] + MM2amac[c] + MMtriodthy[c]	0	1000	22018.1 or 22018.2 or 22018.3 or 22018.4 or 22018.5	Mouse metabolic/ transport/ demand reaction
MMIDHPOXOX4	MMh2o2[c] + 2 MM35diotyr[c] -> 2 MMh2o[c] + MM2amac[c] + MMthyox-L[c]	0	1000	22018.1 or 22018.2 or 22018.3 or 22018.4 or 22018.5	Mouse metabolic/ transport/ demand reaction
MMIDHPOXOXb	MMiodine[c] + MMtyr-L[c] -> MMh[c] + MMi[c] + MM3ityr-L[c]	0	1000	22018.1 or 22018.2 or 22018.3 or 22018.4 or 22018.5	Mouse metabolic/ transport/ demand reaction
MMIDOAASE1ly	MMh2o[l] + MMhs_deg4[l] -> MMhs_deg5[l] + MMidour[l]	0	1000	22018.1 or 22018.2 or 22018.3 or 22018.4 or 22018.5	Mouse metabolic/ transport/ demand reaction
MMIDOAASE2ly	MMh2o[l] + MMhs_deg16[l] -> MMidour[l] + MMhs_deg17[l]	0	1000	15932.1	Mouse metabolic/ transport/ demand reaction
MMIDOAASE3ly	MMh2o[l] + MMhs_deg22[l] -> MMidour[l] + MMhs_deg23[l]	0	1000	15932.1	Mouse metabolic/ transport/ demand reaction
MMIDOAASE4ly	MMh2o[l] + MMcs_b_deg3[l] -> MMcs_a_deg3[l] + MMidour[l]	0	1000	15932.1	Mouse metabolic/ transport/ demand reaction
MMIDOURtly	MMh[c] + MMidour[c] <=> MMh[l] + MMidour[l]	-1000	1000	15932.1	Mouse metabolic/ transport/ demand reaction
MMIDPtn	MMidp[c] <=> MMidp[n]	-1000	1000	235504.1	Mouse metabolic/ transport/ demand reaction
MMILEATB0tc	2 MMna1[u] + MMcl[u] + MMile-L[e] -> 2 MMna1[c] + MMcl[c] + MMile-L[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMILEB0ATtc	MMna1[u] + MMile-L[u] -> MMna1[c] + MMile-L[c]	0	1000	56774.1	Mouse metabolic/ transport/ demand reaction
MMILELAT1tc	MMleu-L[c] + MMile-L[u] -> MMleu-L[u] + MMile-L[c]	0	1000	(70008.1 or (74338.1 and 57394.1))	Mouse metabolic/ transport/ demand reaction
MMILEPHELAT2tc	MMile-L[e] + MMphe-L[c] -> MMile-L[c] + MMphe-L[e]	0	1000	(20539.1 and 17254.1)	Mouse metabolic/ transport/ demand reaction
MMILETA	MMakg[c] + MMile-L[c] <=> MMglu-L[c] + MM3mop[c]	-1000	1000	(20539.1 and 17254.1)	Mouse metabolic/ transport/ demand reaction
MMILETAm	MMakg[m] + MMile-L[m] <=> MMglu-L[m] + MM3mop[m]	-1000	1000	12035.1	Mouse metabolic/ transport/ demand reaction
MMILEt4	MMna1[e] + MMile-L[e] -> MMna1[c] + MMile-L[c]	0	1000	12036.1	Mouse metabolic/ transport/ demand reaction
MMILEt5m	MMile-L[c] <=> MMile-L[m]	-1000	1000	56774.1	Mouse metabolic/ transport/ demand reaction
MMILEtec	MMile-L[e] <=> MMile-L[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMIMACTD	MMh2o[c] + MMnad[c] + MMim4act[c] -> 2 MMh[c] + MMnadh[c] + MMim4ac[c]	0	1000	215113.1 or 72401.1	Mouse metabolic/ transport/ demand reaction
MMIMACTD_m	MMh2o[m] + MMnad[m] + MMim4act[m] -> 2 MMh[m] + MMnadh[m] + MMim4ac[m]	0	1000	19378.1 or 56752.1 or 110695.1 or 11668.1 or 11671.1 or 19378.2 or 19378.3	Mouse metabolic/ transport/ demand reaction
MMIMPC	MMh2o[c] + MMimp[c] <=> MMfprica[c]	-1000	1000	11669.1 or 212647.1 or 212647.2 or 72535.1	Mouse metabolic/ transport/ demand reaction
MMIMPD	MMh2o[c] + MMnad[c] + MMimp[c] -> MMh[c] + MMnadh[c] + MMxmp[c]	0	1000	108147.1	Mouse metabolic/ transport/ demand reaction
MMINOSTO	MMo2[c] + MMinost[c] -> MMh2o[c] + MMh[c] + MMglcur[c]	0	1000	23917.1 or 23918.1 or 23917.2	Mouse metabolic/ transport/ demand reaction
MMINSKm	MMatp[m] + MMins[m] -> MMh[m] + MMadp[m] + MMimp[m]	0	1000	56727.1	Mouse metabolic/ transport/ demand reaction
MMINSTt2r	MMh[e] + MMinost[e] <=> MMh[c] + MMinost[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMINSTt4	MMna1[e] + MMinost[e] <=> MMna1[c] + MMinost[c]	0	1000	239606.1	Mouse metabolic/ transport/ demand reaction
MMINSTt4_2	2 MMna1[e] + MMinost[e] <=> 2 MMna1[c] + MMinost[c]	0	1000	53881.1	Mouse metabolic/ transport/ demand reaction
MMINSt	MMins[e] <=> MMins[c]	0	1000	233836.1	Mouse metabolic/ transport/ demand reaction
MMINSt4	MMna1[e] + MMins[e] -> MMna1[c] + MMins[c]	0	1000	13340.1 or 63959.1	Mouse metabolic/ transport/ demand reaction
MMINSt5	2 MMna1[e] + MMins[e] -> 2 MMna1[c] + MMins[c]	0	1000	114304.1 or 269346.1	Mouse metabolic/ transport/ demand reaction
MMINStl	MMins[l] <=> MMins[c]	-1000	1000	114304.1	Mouse metabolic/ transport/ demand reaction
MMINStm	MMins[c] <=> MMins[m]	-1000	1000	71279.1	Mouse metabolic/ transport/ demand reaction
MMIPDDIx	MMipdp[x] <=> MMdmpp[x]	-1000	1000	63959.1	Mouse metabolic/ transport/ demand reaction
MMIPDPtr	MMipdp[r] <=> MMipdp[c]	-1000	1000	319554.1 or 320581.1	Mouse metabolic/ transport/ demand reaction
MMIPDPtx	MMipdp[x] <=> MMipdp[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMITCOAL1m	MMcoa[m] + MMgtp[m] + MMitacon[m] <=> MMpi[m] + MMgdp[m] + MMitaccoa[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMITCOALm	MMcoa[m] + MMatp[m] + MMitacon[m] <=> MMadp[m] + MMpi[m] + MMitaccoa[m]	-1000	1000	20917.1 and 56451.1	Mouse metabolic/ transport/ demand reaction
MMITPtn	MMitp[c] <=> MMitp[n]	-1000	1000	56451.1 and 20916.1	Mouse metabolic/ transport/ demand reaction
MMIZPN	MMh2o[c] + MM4izp[c] -> MMh[c] + MMforglu[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMIt	MMi[e] <=> MMi[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMKAS8	20 MMh[c] + 14 MMnadph[c] + MMaccoa[c] + 7 MMmalcoa[c] -> 6 MMh2o[c] + 14 MMnadp[c] + 7 MMco2[c] + 8 MMcoa[c] + MMhdca[c]	0	1000	216225.1	Mouse metabolic/ transport/ demand reaction
MMKCC2t	MMnh4[e] + MMcl[e] <=> MMnh4[c] + MMcl[c]	-1000	1000	14104.1	Mouse metabolic/ transport/ demand reaction
MMKCCt	MMk[e] + MMcl[e] <=> MMcl[c] + MMk[c]	-1000	1000	107723.1 or 20499.1 or 20498.1	Mouse metabolic/ transport/ demand reaction
MMKDNH	MMh2o[c] + MMkdnp[c] -> MMpi[c] + MMkdn[c]	0	1000	107723.1 or 20499.1 or 57138.1 or 20498.1	Mouse metabolic/ transport/ demand reaction
MMKHK	MMatp[c] + MMfru[c] -> MMadp[c] + MMh[c] + MMf1p[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMKHK2	MMatp[c] + MMxylu-D[c] -> MMadp[c] + MMh[c] + MMxu1p-D[c]	0	1000	16548.1 or 16548.2	Mouse metabolic/ transport/ demand reaction
MMKHK3	MMatp[c] + MMtagat-D[c] -> MMadp[c] + MMh[c] + MMtag1p-D[c]	0	1000	16548.1 or 16548.2	Mouse metabolic/ transport/ demand reaction
MMKSII_CORE2t	MMksii_core2[g] -> MMksii_core2[e]	0	1000	16548.1 or 16548.2	Mouse metabolic/ transport/ demand reaction
MMKSII_CORE2tly	MMksii_core2[e] -> MMksii_core2[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MMKSII_CORE4t	MMksii_core4[g] -> MMksii_core4[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMKSII_CORE4tly	MMksii_core4[e] -> MMksii_core4[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MMKSIt	MMksi[g] -> MMksi[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMKSItly	MMksi[e] -> MMksi[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MMKYN	MMh2o[c] + MMLkynr[c] -> MMh[c] + MMala-L[c] + MManth[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMKYN3OX	MMo2[c] + MMh[c] + MMnadph[c] + MMLkynr[c] -> MMh2o[c] + MMnadp[c] + MMhLkynr[c]	0	1000	70789.1	Mouse metabolic/ transport/ demand reaction
MMKYNAKGAT	MMakg[c] + MMLkynr[c] -> MMglu-L[c] + MM4aphdob[c]	0	1000	98256.1	Mouse metabolic/ transport/ demand reaction

MMKYNATESYN	MM4aphdiob[c] -> MMth2o[c] + MMkynate[c]	0	1000	23923.1 or 70266.1 or 23923.2	Mouse metabolic/ transport/ demand reaction
MMKt2lg	MMf[g] + MMfk[c] <=> MMf[c] + MMk[g]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMLACZe	MMth2o[e] + MMlcts[e] -> MMglc-D[e] + MMgal[e]	0	1000	236727.1 or 77031.1	Mouse metabolic/ transport/ demand reaction
MMLACZly	MMth2o[l] + MMlcts[l] -> MMgal[l] + MMglc-D[l]	0	1000	226413.1	Mouse metabolic/ transport/ demand reaction
MMLALDD	MMnadp[c] + MMlald-D[c] <=> MMh[c] + MMnadph[c] + MMmthgx[c]	-1000	1000	50917.1 or 19025.1 or 12091.1 or 18010.1	Mouse metabolic/ transport/ demand reaction
MMLALDO	MMnad[c] + MMglthrd[c] + MMlald-D[c] <=> MMh[c] + MMnadh[c] + MMglc-S[c]	-1000	1000	76238.1	Mouse metabolic/ transport/ demand reaction
MMLALDO2	MMh[c] + MMnadph[c] + MMmthgx[c] -> MMnadp[c] + MMlald-D[c]	0	1000	11532.1	Mouse metabolic/ transport/ demand reaction
MMLALDO2x	MMh[c] + MMnadh[c] + MMmthgx[c] -> MMnad[c] + MMlald-D[c]	0	1000	110198.1 or 58810.2 or 11677.1 or 58810.1	Mouse metabolic/ transport/ demand reaction
MMLAPCOAl	MMth2o[l] + MMccoa[l] -> MMpi[l] + MMdpcoa[l]	0	1000	110198.1	Mouse metabolic/ transport/ demand reaction
MMLCADi	MMth2o[c] + MMnad[c] + MMlald-L[c] -> 2 MMh[c] + MMnadh[c] + MMlac-L[c]	0	1000	11432.1	Mouse metabolic/ transport/ demand reaction
MMLCADi_D	MMth2o[c] + MMnad[c] + MMlald-D[c] -> 2 MMh[c] + MMnadh[c] + MMlac-D[c]	0	1000	19378.1 or 56752.1 or 11670.1 or 110695.1 or 67689.1 or 56847.1 or 11668.1 or 11671.1 or 19378.2 or 19378.3	Mouse metabolic/ transport/ demand reaction
MMLCADi_Dm	MMth2o[m] + MMnad[m] + MMlald-D[m] -> 2 MMh[m] + MMnadh[m] + MMlac-D[m]	0	1000	19378.1 or 56752.1 or 11670.1 or 110695.1 or 67689.1 or 56847.1 or 11668.1 or 11671.1 or 19378.2 or 19378.3	Mouse metabolic/ transport/ demand reaction
MMLCADim	MMth2o[m] + MMnad[m] + MMlald-L[m] -> 2 MMh[m] + MMnadh[m] + MMlac-L[m]	0	1000	(104776.1 or 11669.1 or 212647.1 or 214579.1 or 56454.1 or 214579.2 or 212647.2 or 72535.1)	Mouse metabolic/ transport/ demand reaction
MMLCAT1e	MMchsterol[e] + MMpchol_hs[e] -> MMpchol_hs[e] + MMxolest2_hs[e]	0	1000	(104776.1 or 11669.1 or 212647.1 or 214579.1 or 56454.1 or 214579.2 or 212647.2 or 72535.1)	Mouse metabolic/ transport/ demand reaction
MMLCTStg	MMlcts[g] -> MMlcts[e]	0	1000	16816.1	Mouse metabolic/ transport/ demand reaction
MMLCTStl	MMlcts[c] -> MMlcts[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MMLCYSTAT	MMLcyst[c] + MMakg[c] <=> MMglu-L[c] + MM3spyr[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMLCYSTATm	MMakg[m] + MMLcyst[m] <=> MMglu-L[m] + MM3spyr[m]	-1000	1000	14718.1	Mouse metabolic/ transport/ demand reaction
MMLCYSTCBOXL	MMh[c] + MMLcys[c] -> MMco2[c] + MMtaur[c]	0	1000	14719.1	Mouse metabolic/ transport/ demand reaction
MMLDH_D	MMnad[c] + MMlac-D[c] <=> MMh[c] + MMpyr[c] + MMnadh[c]	-1000	1000	246277.1 or 14415.1 or 14417.1 or 14415.2	Mouse metabolic/ transport/ demand reaction
MMLDH_Lm	MMnad[m] + MMlac-L[m] <=> MMh[m] + MMnadh[m] + MMpyr[m]	-1000	1000	52815.1 or 52815.2	Mouse metabolic/ transport/ demand reaction
MMLEUATB0tc	MMleu-L[u] + 2 MMna1[u] + MMc3[u] -> 2 MMna1[c] + MMleu-L[c] + MMc3[c]	0	1000	16828.1	Mouse metabolic/ transport/ demand reaction
MMLEUB0ATtc	MMleu-L[u] + MMna1[u] -> MMna1[c] + MMleu-L[c]	0	1000	56774.1	Mouse metabolic/ transport/ demand reaction
MMLEUGLYHYc	MMh2o[c] + MMleugly[c] <=> MMleu-L[c] + MMgly[c]	-1000	1000	(70008.1 or (74338.1 and 57394.1))	Mouse metabolic/ transport/ demand reaction
MMLEUGLYPEPT1tc	MMh[u] + MMleugly[u] -> MMh[c] + MMleugly[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMLEUGLYt	MMh[e] + MMleugly[e] -> MMh[c] + MMleugly[c]	0	1000	215335.1	Mouse metabolic/ transport/ demand reaction
MMLEUILELAT2tc	MMile-L[c] + MMleu-L[e] <=> MMleu-L[c] + MMile-L[e]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMLEUKTRA4t	MMleuktrA4[e] <=> MMleuktrA4[c]	0	1000	(20539.1 and 17254.1)	Mouse metabolic/ transport/ demand reaction
MMLEUKTRA4tr	MMleuktrA4[c] <=> MMleuktrA4[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMLEUKTRB4t	MMleuktrB4[e] <=> MMleuktrB4[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMLEUKTRB4tr	MMleuktrB4[c] <=> MMleuktrB4[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMLEUKTRD4t	MMleuktrD4[e] <=> MMleuktrD4[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMLEUKTRD4tr	MMleuktrD4[c] <=> MMleuktrD4[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMLEUKTRE4t	MMleuktrE4[e] <=> MMleuktrE4[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMLEUKTRF4t	MMleuktrF4[e] <=> MMleuktrF4[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMLEULEULAPc	MMth2o[c] + MMleuleu[c] <=> 2 MMleu-L[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMLEULEUPEPT1tc	MMh[u] + MMleuleu[u] -> MMh[c] + MMleuleu[c]	0	1000	66988.1	Mouse metabolic/ transport/ demand reaction
MMLEULEUt	MMh[e] + MMleuleu[e] -> MMh[c] + MMleuleu[c]	0	1000	215335.1	Mouse metabolic/ transport/ demand reaction
MMLEUPHELAT2tc	MMphe-L[c] + MMleu-L[e] <=> MMleu-L[c] + MMphe-L[e]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMLEUTA	MMakg[c] + MMleu-L[c] <=> MMglu-L[c] + MM4mop[c]	-1000	1000	(20539.1 and 17254.1)	Mouse metabolic/ transport/ demand reaction
MMLEUTAm	MMakg[m] + MMleu-L[m] <=> MMglu-L[m] + MM4mop[m]	-1000	1000	12035.1	Mouse metabolic/ transport/ demand reaction
MMLEUt4	MMna1[e] + MMleu-L[e] -> MMna1[c] + MMleu-L[c]	0	1000	12036.1	Mouse metabolic/ transport/ demand reaction
MMLEUt5m	MMleu-L[c] <=> MMleu-L[m]	-1000	1000	105727.1 or 67760.1 or 69354.1 or 56774.1 or 11989.1 or 11988.1 or 11987.1	Mouse metabolic/ transport/ demand reaction
MMLEUtec	MMleu-L[e] <=> MMleu-L[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMLEUyLATbtc	MMh[e] + MMarg-L[c] + MMleu-L[e] -> MMh[c] + MMleu-L[c] + MMarg-L[e]	0	1000	215113.1 or 72401.1	Mouse metabolic/ transport/ demand reaction
MMLEUyLATtc	MMna1[e] + MMarg-L[c] + MMleu-L[e] -> MMna1[c] + MMleu-L[c] + MMarg-L[e]	0	1000	(20540.1 or (330836.1 and 17254.1))	Mouse metabolic/ transport/ demand reaction
MMLFORKYNHYD	MMh2o[c] + MMLfmkynr[c] -> MMh[c] + MMala-L[c] + MMinformanth[c]	0	1000	(20540.1 or (330836.1 and 17254.1))	Mouse metabolic/ transport/ demand reaction
MMLGNCCOAtx	MMlgnccoa[c] <=> MMlgnccoa[x]	-1000	1000	70789.1	Mouse metabolic/ transport/ demand reaction
MMLGNCCPT1	MMccm[c] + MMlgnccoa[c] -> MMcoa[c] + MMlgnccm[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMLGNCCPT2	MMcoa[m] + MMlgnccm[m] -> MMccm[m] + MMlgnccoa[m]	0	1000	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	Mouse metabolic/ transport/ demand reaction
MMLGNCCRNt	MMlgnccm[c] -> MMlgnccm[m]	0	1000	12896.1	Mouse metabolic/ transport/ demand reaction
MMLGNCt	MMlgnc[e] <=> MMlgnc[c]	0	1000	57279.1	Mouse metabolic/ transport/ demand reaction
MMLGTHL	MMmthgx[c] + MMglthrd[c] -> MMlgt-S[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMLIMNENte	MMlimnen[e] <=> MMlimnen[c]	0	1000	109801.1	Mouse metabolic/ transport/ demand reaction
MMLINKDEG1ly	3 MMth2o[l] + MMlts_deg25[l] -> 2 MMgal[l] + MMglcur[l] + MMxyl-D[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MMLINKDEG2ly	4 MMth2o[l] + MMcs_a_deg5[l] -> MMh[l] + MMso4[l] + 2 MMgal[l] + MMglcur[l] + MMxyl-D[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MMLINKDEG3ly	4 MMth2o[l] + MMcs_c_deg5[l] -> MMh[l] + MMso4[l] + 2 MMgal[l] + MMglcur[l] + MMxyl-D[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MMLINKDEG4ly	5 MMh2o[l] + MMcs_e_deg7[l] -> 2 MMh[l] + 2 MMso4[l] + 2 MMgal[l] + MMglcur[l] + MMxyl-D[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MMLINOFABPpmtc	MMlnlc[u] -> MMlnlc[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMLINOFATPtc	MMatp[c] + MMccoa[c] + MMlnlc[u] -> MMamp[c] + MMppi[c] + MMlnlccoa[c]	0	1000	(14719.1 or 12491.1)	Mouse metabolic/ transport/ demand reaction
MMLIPOti	MMh2o[c] + MMatp[c] + 2 MMna1[e] + MMlipoate[e] -> MMadp[c] + MMh[c] + MMpi[c] + 2 MMna1[c] + MMlipoate[c]	0	1000	26569.1	Mouse metabolic/ transport/ demand reaction
MMLNELDCCPT1c	MMccm[c] + MMlneldccoa[c] <=> MMccoa[c] + MMlneldccm[c]	-1000	1000	330064.1	Mouse metabolic/ transport/ demand reaction
MMLNELDCCPT2	MMccoa[m] + MMlneldccm[m] -> MMccm[m] + MMlneldccoa[m]	0	1000	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	Mouse metabolic/ transport/ demand reaction
MMLNELDCCRNt	MMlneldccm[c] -> MMlneldccm[m]	0	1000	12896.1	Mouse metabolic/ transport/ demand reaction
MMLNELDCt	MMlneldc[e] <=> MMlneldc[c]	0	1000	57279.1	Mouse metabolic/ transport/ demand reaction
MMLNLCCPT1	MMccm[c] + MMlnlccoa[c] -> MMcoa[c] + MMlnlccm[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMLNLCCPT2	MMcoa[m] + MMlnlccm[m] -> MMccm[m] + MMlnlccoa[m]	0	1000	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	Mouse metabolic/ transport/ demand reaction
MMLNLCCRNt	MMlnlccm[c] -> MMlnlccm[m]	0	1000	12896.1	Mouse metabolic/ transport/ demand reaction
MMLNLCt	MMlnlc[e] <=> MMlnlc[c]	0	1000	57279.1	Mouse metabolic/ transport/ demand reaction
MMLNLNCACPT1	MMccm[c] + MMlnlncacoa[c] -> MMcoa[c] + MMlnlncacm[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMLNLNCACPT2	MMcoa[m] + MMlnlncacm[m] -> MMccm[m] + MMlnlncacoa[m]	0	1000	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	Mouse metabolic/ transport/ demand reaction
MMLNLNCACRNt	MMlnlncacm[c] -> MMlnlncacm[m]	0	1000	12896.1	Mouse metabolic/ transport/ demand reaction
MMLNLNCAt	MMlnlnca[e] <=> MMlnlnca[c]	0	1000	57279.1	Mouse metabolic/ transport/ demand reaction
MMLNLNCGCPT1	MMccm[c] + MMlnlncgcoa[c] -> MMcoa[c] + MMlnlncgcm[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMLNLNCGCPT2	MMcoa[m] + MMlnlncgcm[m] -> MMccm[m] + MMlnlncgcoa[m]	0	1000	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	Mouse metabolic/ transport/ demand reaction
MMLNLNCGCRNt	MMlnlncgcm[c] -> MMlnlncgcm[m]	0	1000	12896.1	Mouse metabolic/ transport/ demand reaction
MMLNLNCGt	MMlnlncg[e] <=> MMlnlncg[c]	0	1000	57279.1	Mouse metabolic/ transport/ demand reaction
MMLNS14DM	3 MMo2[c] + 2 MMh[c] + 3 MMnadph[c] + MMlanost[c] -> 4 MMh2o[c] + 3 MMnadp[c] + MMlofr[c] + MM44mctr[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMLNS14DMr	3 MMo2[r] + 2 MMh[r] + 3 MMnadph[r] + MMlanost[r] -> 4 MMh2o[r] + MM44mctr[r] + 3 MMnadp[r] + MMlofr[r]	0	1000	208285.1	Mouse metabolic/ transport/ demand reaction
MMLNSTLSr	MMSsq23epx[r] -> MMlanost[r]	0	1000	13121.1	Mouse metabolic/ transport/ demand reaction
MMLPCHOLTDlu	MMlpchol_hs[u] <=> MMlpchol_hs[c]	-1000	1000	16987.1	Mouse metabolic/ transport/ demand reaction
MMLPCHOLt	MMlpchol_hs[e] <=> MMlpchol_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMLPCOXp	MMLpipecol[x] + MMo2[x] -> MMh[x] + MMh2o2[x] + MMthp2c[x]	0	1000		Mouse metabolic/ transport/ demand reaction

MMLPS	MMh2o[c] + MMtag_hs[c] -> MMh[c] + MMRtotal3[c] + MMdag_hs[c]	0	1000	19193.1	Mouse metabolic/ transport/ demand reaction
MMLPS2	MMh2o[e] + MMdag_hs[e] -> MMh[e] + MMRtotal[e] + MMmag_hs[e]	0	1000	16956.1	Mouse metabolic/ transport/ demand reaction
MMLPS2e	MMh2o[e] + MMdag_hs[e] -> MMh[e] + MMRtotal[e] + MMmag_hs[e]	0	1000	16956.1	Mouse metabolic/ transport/ demand reaction
MMLPS3	MMh2o[c] + MMmag_hs[c] -> MMh[c] + MMRtotal2[c] + MMglyc[c]	0	1000	15450.1	Mouse metabolic/ transport/ demand reaction
MMLPS3e	MMh2o[e] + MMmag_hs[e] -> MMh[e] + MMRtotal2[e] + MMglyc[e]	0	1000	23945.1 or 23945.2	Mouse metabolic/ transport/ demand reaction
MMLPS4e	MMh2o[e] + MMpglyc_hs[e] -> MMh[e] + MM1glyc_hs[e] + MMRtotal2[e]	0	1000	15450.1	Mouse metabolic/ transport/ demand reaction
MMLPSe	MMh2o[e] + MMtag_hs[e] -> MMh[e] + MMdag_hs[e] + MMRtotal3[e]	0	1000	237625.1	Mouse metabolic/ transport/ demand reaction
MMLRAT	MMpchol_hs[c] + MMretinol[c] -> MMpchol_hs[c] + MMretfa[c]	0	1000	16891.1 or 67717.1 or 69060.1 or 18946.1 or 15450.1 or 18947.1	Mouse metabolic/ transport/ demand reaction
MMLRAT1	MMpchol_hs[c] + MMretinol-cis-11[c] -> MMlpchol_hs[c] + MM11-cis-retfa[c]	0	1000	79235.1	Mouse metabolic/ transport/ demand reaction
MMLRAT2	MMpchol_hs[c] + MMretinol-9-cis[c] -> MMlpchol_hs[c] + MM9-cis-retfa[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMLS3	MMpd3[c] <=> MMkmt3[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMLSTO1r	MMo2[r] + MMh[r] + MMnadph[r] + MMchlsto[r] -> 2 MMh2o[r] + MMnadp[r] + MMddsmsterol[r]	0	1000		Mouse metabolic/ transport/ demand reaction
MMLSTO2r	MMo2[r] + MMh[r] + MMnadph[r] + MMlhstrl[r] -> MM7dhcholesterol[r] + 2 MMh2o[r] + MMnadp[r]	0	1000	235293.1	Mouse metabolic/ transport/ demand reaction
MMLTA4H	MMh2o[c] + MMleuktrA4[c] -> MMleuktrB4[c]	0	1000	235293.1	Mouse metabolic/ transport/ demand reaction
MMLTC4CP	MMh2o[c] + MMleuktrC4[c] <=> MMglyc[c] + MMleuktrF4[c]	-1000	1000	16993.1	Mouse metabolic/ transport/ demand reaction
MMLTC4Sr	MMgthrd[r] + MMleuktrA4[r] -> MMleuktrC4[r]	0	1000		Mouse metabolic/ transport/ demand reaction
MMLTD4DP	MMh2o[c] + MMleuktrD4[c] <=> MMglyc[c] + MMleuktrE4[c]	-1000	1000	17001.1 or 17001.2 or 211666.1 or 66447.1	Mouse metabolic/ transport/ demand reaction
MMLTDCL	MMh[c] + MMtrp-L[c] -> MMco2[c] + MMtrypta[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMLYSALAtBATic	MMala-L[c] + MMlys-L[u] -> MMala-L[u] + MMlys-L[c]	0	1000	13195.1	Mouse metabolic/ transport/ demand reaction
MMLYSATB0tc	2 MMna1[u] + MMcl[u] + MMlys-L[u] -> 2 MMna1[c] + MMcl[c] + MMlys-L[c]	0	1000	(30962.1 and 20532.1)	Mouse metabolic/ transport/ demand reaction
MMLYSLEUrBATic	MMleu-L[c] + MMlys-L[u] -> MMleu-L[u] + MMlys-L[c]	0	1000	56774.1	Mouse metabolic/ transport/ demand reaction
MMLYSMTF1n	MMamet[n] + MMpeplys[n] -> MMahcys[n] + MMNmelys[n]	0	1000	(30962.1 and 20532.1)	Mouse metabolic/ transport/ demand reaction
MMLYSMTF2n	MMamet[n] + MMNmelys[n] -> MMahcys[n] + MMNdmelys[n]	0	1000	239122.1 or 77683.1 or 110147.1 or 231051.1 or 67956.1 or 73251.1 or 64707.1 or 110147.2 or 208266.1 or 84505.1 or 231051.2 or 20937.1	Mouse metabolic/ transport/ demand reaction
MMLYSMTF3n	MMamet[n] + MMNdmelys[n] -> MMahcys[n] + MMNtmelys[n]	0	1000	239122.1 or 77683.1 or 110147.1 or 231051.1 or 67956.1 or 73251.1 or 64707.1 or 110147.2 or 208266.1 or 84505.1 or 231051.2 or 20937.1	Mouse metabolic/ transport/ demand reaction
MMLYSOXp	MMo2[x] + MMh2o[x] + MMlys-L[x] -> MMh2o2[x] + MMnh4[x] + MM6a2ohxn[x]	0	1000	239122.1 or 77683.1 or 110147.1 or 231051.1 or 67956.1 or 73251.1 or 64707.1 or 110147.2 or 208266.1 or 84505.1 or 231051.2 or 20937.1	Mouse metabolic/ transport/ demand reaction
MMLYSt4	MMna1[e] + MMlys-L[e] -> MMna1[c] + MMlys-L[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMLYSt5r	MMlys-L[e] <=> MMlys-L[c]	-1000	1000	56774.1 or 20520.1	Mouse metabolic/ transport/ demand reaction
MMLYStl0F	MMlys-L[e] -> MMlys-L[c]	0	1000	11987.1	Mouse metabolic/ transport/ demand reaction
MMLYStlp	MMlys-L[c] -> MMlys-L[x]	0	1000	69354.1 or 11989.1 or 11988.1 or 11987.1	Mouse metabolic/ transport/ demand reaction
MMLYStm	MMh[m] + MMlys-L[c] <=> MMh[c] + MMlys-L[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMLYStn	MMlys-L[c] <=> MMlys-L[n]	-1000	1000	18408.1 or 83885.1	Mouse metabolic/ transport/ demand reaction
MML_LACDcm	2 MMficytC[m] + MMlac-L[c] -> 2 MMh[c] + MMpyr[c] + 2 MMfocytC[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MML_LACi2r	MMh[e] + MMlac-L[e] <=> MMh[c] + MMlac-L[c]	0	1000	626571.1	Mouse metabolic/ transport/ demand reaction
MML_LACi4r	MMna1[e] + MMlac-L[e] <=> MMna1[c] + MMlac-L[c]	0	1000	20503.1 or 80879.1 or 20501.1 or 57274.1	Mouse metabolic/ transport/ demand reaction
MML_LACtcm	MMlac-L[c] -> MMlac-L[m]	0	0		Mouse metabolic/ transport/ demand reaction
MML_LACtm	MMh[c] + MMlac-L[c] <=> MMh[m] + MMlac-L[m]	0	0	64008.1	Mouse metabolic/ transport/ demand reaction
MMM1316Mg	2 MMh2o[g] + MMnm4masn[g] -> 2 MMnan[g] + MMnn2masn[g]	0	1000	20501.1	Mouse metabolic/ transport/ demand reaction
MMM13N2Tg	MMuacgam[g] + MMnm4mns[g] -> MMh[g] + MMudp[g] + MMnm4masn[g]	0	1000	17158.1 or 140481.1	Mouse metabolic/ transport/ demand reaction
MMM13N4Tg	MMuacgam[g] + MMn2m2masn[g] -> MMh[g] + MMudp[g] + MMn3m2masn[g]	0	1000	17308.1	Mouse metabolic/ transport/ demand reaction
MMM14NTg	MMuacgam[g] + MMn2m2masn[g] -> MMh[g] + MMudp[g] + MMn2m2mnasn[g]	0	1000	103534.1 or 269181.1 or 103534.2	Mouse metabolic/ transport/ demand reaction
MMM16N4Tg	MMuacgam[g] + MMn4n2masn[g] -> MMh[g] + MMudp[g] + MMn5m2masn[g]	0	1000	17309.1	Mouse metabolic/ transport/ demand reaction
MMM16N6Tg	MMuacgam[g] + MMn3m2masn[g] -> MMh[g] + MMudp[g] + MMn4m2masn[g]	0	1000		Mouse metabolic/ transport/ demand reaction
MMM16NTg	MMuacgam[g] + MMnm2masn[g] -> MMh[g] + MMudp[g] + MMn2m2masn[g]	0	1000	107895.1	Mouse metabolic/ transport/ demand reaction
MMM4ATAer	MMpre_pro[r] + MMmh[em]3gacpail_hs[r] -> MMgpi_sig[r] + MMmf[em]3gacpail_prot_hs[r]	0	1000	217664.1	Mouse metabolic/ transport/ demand reaction
MMM4BET2er	MMpe_hs[r] + MMmem2emgacpail_hs[r] -> MMdag_hs[r] + MMmf[em]3gacpail_hs[r]	0	1000	276846.1 or 228812.1 or 14731.1 or 329777.1	Mouse metabolic/ transport/ demand reaction
MMM4BTAer	MMmem2emgacpail_hs[r] + MMpre_pro[r] -> MMgpi_sig[r] + MMmem2emgacpail_prot_hs[r]	0	1000	18701.1 or 433931.1 or 18701.2	Mouse metabolic/ transport/ demand reaction
MMM4CET3er	MMpe_hs[r] + MMm2emgacpail_hs[r] -> MMdag_hs[r] + MMmem2emgacpail_hs[r]	0	1000	276846.1 or 78928.1 or 228812.1 or 14731.1 or 329777.1	Mouse metabolic/ transport/ demand reaction
MMM4MPDOL_Ler	MMm4mpdol_L[c] -> MMm4mpdol_L[r]	0	1000	56703.1 or 18701.1 or 18701.2 or 56703.2	Mouse metabolic/ transport/ demand reaction
MMM4MPDOL_Uter	MMm4mpdol_U[c] -> MMm4mpdol_U[r]	0	1000		Mouse metabolic/ transport/ demand reaction
MMM7MASNBterg	MMm7massnB[r] -> MMm7massnB[g]	0	1000		Mouse metabolic/ transport/ demand reaction
MMM8MASNterg	MMm8massn[r] -> MMm8massn[g]	0	1000		Mouse metabolic/ transport/ demand reaction
MMMACACI	MM4mlacac[c] -> MM4fumacac[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMMACOXO	MMh2o[c] + MMnadl[c] + MM3mkkd[c] -> 2 MMh[c] + MMnadh[c] + MM3mkla[c]	0	1000	14874.2 or 14874.3 or 14874.1	Mouse metabolic/ transport/ demand reaction
MMMAGHSTDHu	MMmag_hs[u] <=> MMmag_hs[c]	-1000	1000	109731.1 or 11670.1 or 67689.1 or 56847.1	Mouse metabolic/ transport/ demand reaction
MMMAGt	MMmag_hs[e] <=> MMmag_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMMALSO3tm	MMso3[m] + MMmal-L[c] <=> MMso3[c] + MMmal-L[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMMALSO4tm	MMmal-L[c] + MMso4[m] <=> MMmal-L[m] + MMso4[c]	-1000	1000	27376.1	Mouse metabolic/ transport/ demand reaction
MMMALT	MMh2o[c] + MMmalt[c] -> 2 MMglc-D[c]	0	1000	27376.1	Mouse metabolic/ transport/ demand reaction
MMMALTSULtm	MMmal-L[c] + MMtsul[m] <=> MMmal-L[m] + MMtsul[c]	-1000	1000	76051.1	Mouse metabolic/ transport/ demand reaction
MMMALTe	MMh2o[e] + MMmalt[e] -> 2 MMglc-D[e]	0	1000	27376.1	Mouse metabolic/ transport/ demand reaction
MMMALTly	MMh2o[l] + MMmalt[l] -> 2 MMglc-D[l]	0	1000	23271.4.1	Mouse metabolic/ transport/ demand reaction
MMMALTt1r	MMmalt[e] <=> MMmalt[c]	0	1000	14387.1	Mouse metabolic/ transport/ demand reaction
MMMALtm	MMp[m] + MMmal-L[c] <=> MMp[c] + MMmal-L[m]	-1000	1000	20527.1	Mouse metabolic/ transport/ demand reaction
MMMAN1PT2	MMh[c] + MMglp[c] + MMmanp1p[c] -> MMp[c] + MMgdpmanr[c]	0	1000	27376.1	Mouse metabolic/ transport/ demand reaction
MMMAN1_6B1er	MMh2o[r] + MMg1m7masnC[r] -> MMg1m6masnB1[r] + MMman[r]	0	1000	331026.1 or 331026.2 or 69080.1 or 69080.2	Mouse metabolic/ transport/ demand reaction
MMMAN1_7Ber	MMh2o[r] + MMg1m8masn[r] -> MMg1m7masnB[r] + MMman[r]	0	1000	227619.1	Mouse metabolic/ transport/ demand reaction
MMMAN2_6B1er	MMh2o[r] + MMg1m7masnB[r] -> MMg1m6masnB1[r] + MMman[r]	0	1000	227619.1	Mouse metabolic/ transport/ demand reaction
MMMAN2_7Cer	MMh2o[r] + MMg1m8masn[r] -> MMg1m7masnC[r] + MMman[r]	0	1000		Mouse metabolic/ transport/ demand reaction
MMMAN6PI	MMmanl6p[c] <=> MMl6p[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMMANt1r	MMman[e] <=> MMman[c]	0	1000	110119.1	Mouse metabolic/ transport/ demand reaction
MMMANt4	MMna1[e] + MMman[e] <=> MMna1[c] + MMman[c]	-1000	1000	20527.1 or 20525.1 or 20526.1	Mouse metabolic/ transport/ demand reaction
MMMANter	MMman[r] -> MMman[c]	0	1000	230612.1	Mouse metabolic/ transport/ demand reaction
MMMANtg	MMman[g] -> MMman[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMMANtly	MMman[l] -> MMman[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMMAOLNOR	MMh2o[c] + MMo2[c] + MMnormete-L[c] -> MMh2o2[c] + MMnh4[c] + MM3mt4hpg[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMMAOX	MMh2o[c] + MMo2[c] + MMmma[c] -> MMh2o2[c] + MMnh4[c] + MMfrlt[c]	0	1000	109731.1 or 17161.1	Mouse metabolic/ transport/ demand reaction
MMMCCCrm	MMatp[m] + MMhco3[m] + MM3mh2coa[m] <=> MMf[m] + MMadp[m] + MMp[m] + MM3mgcoa[m]	-1000	1000	237940.1 or 237940.2 or 11754.1 or 76507.1	Mouse metabolic/ transport/ demand reaction
MMMCD	MMh[c] + MMmalcoa[c] -> MMco2[c] + MMaccoa[c]	0	1000	72039.1 and 78038.1	Mouse metabolic/ transport/ demand reaction
MMMCDm	MMh[m] + MMmalcoa[m] -> MMco2[m] + MMaccoa[m]	0	1000	56690.1	Mouse metabolic/ transport/ demand reaction
MMMCDp	MMh[x] + MMmalcoa[x] -> MMaccoa[x] + MMco2[x]	0	1000	56690.1	Mouse metabolic/ transport/ demand reaction
MMMCITS	MMh2o[c] + MMppcoa[c] + MMoaa[c] -> MMh[c] + MM2mcit[c] + MMcoa[c]	0	1000	56690.1	Mouse metabolic/ transport/ demand reaction
MMMCLACCYSR	MMnad[c] + MMcys-L[c] + MMmercplac[c] -> MMh[c] + MMnadh[c] + MMmercplaccys[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMMCOATA	MMmalcoa[c] + MMACP[c] <=> MMcoa[c] + MMmalACP[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction

MMMCOATAm	MMmalcoa[m] + MMACP[m] <=> MMcoa[m] + MMmalACP[m]	-1000	1000	14104.1	Mouse metabolic/ transport/ demand reaction
MMMCPST	MMcyan[c] + MMmercppyr[c] -> MMh[c] + MMpyr[c] + MMtcynt[c]	0	1000	223722.1 or 223722.2	Mouse metabolic/ transport/ demand reaction
MMMDH	MMnad[c] + MMmal-L[c] <=> MMh[c] + MMnadh[c] + MMoaa[c]	-1000	1000	246221.1	Mouse metabolic/ transport/ demand reaction
MMMDHm	MMnad[m] + MMmal-L[m] <=> MMh[m] + MMnadh[m] + MMoaa[m]	-1000	1000	76668.1 or 17449.1	Mouse metabolic/ transport/ demand reaction
MMMDRPD	MM5mdru1p[c] -> MMh2o[c] + MMdkmpp[c]	0	1000	17448.1	Mouse metabolic/ transport/ demand reaction
MMME1m	MMnad[m] + MMmal-L[m] -> MMco2[m] + MMnadh[m] + MMpyr[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMME2	MMnadp[c] + MMmal-L[c] -> MMpyr[c] + MMnadph[c] + MMco2[c]	0	1000	107029.1	Mouse metabolic/ transport/ demand reaction
MMME2m	MMnadp[m] + MMmal-L[m] -> MMnadph[m] + MMco2[m] + MMpyr[m]	0	1000	17436.1	Mouse metabolic/ transport/ demand reaction
MMMECOALm	MMcoa[m] + MMatp[m] + MMmescon[m] <=> MMadp[m] + MMpi[m] + MMmescoa[m]	-1000	1000	107029.1 or 109264.1	Mouse metabolic/ transport/ demand reaction
MMMECOAS1m	MMcoa[m] + MMgtp[m] + MMmescon[m] <=> MMpi[m] + MMgdp[m] + MMmescoa[m]	-1000	1000	56451.1 and 20916.1	Mouse metabolic/ transport/ demand reaction
MMMELATN23DOX	MMo2[c] + MMmelatn[c] -> MMfna5moxam[c]	0	1000	20917.1 and 56451.1	Mouse metabolic/ transport/ demand reaction
MMMELATNOX	MMo2[c] + MMh[c] + MMnadph[c] + MMmelatn[c] -> MMh2o[c] + MMnadp[c] + MM6hoxmelatn[c]	0	1000	15930.1	Mouse metabolic/ transport/ demand reaction
MMMEOHt2	MMmeoh[e] <=> MMmeoh[c]	0	1000	404195.1 or 13078.1 or 13077.1 or 13076.1	Mouse metabolic/ transport/ demand reaction
MMMEOHtly	MMmeoh[c] <=> MMmeoh[l]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMMEOHtr	MMmeoh[c] <=> MMmeoh[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMMEPIVESSte	2 MMh2o[c] + 2 MMatp[c] + 3 MMmepi[c] -> 2 MMadp[c] + 2 MMh[c] + 2 MMpi[c] + 3 MMmepi[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMMERCPLACCYSt	MMmercplaccys[c] -> MMmercplaccys[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMMESCOALm	MMh2o[m] + MMmescoa[m] -> MMpyr[m] + MMaccoa[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMMETAT	MMh2o[c] + MMatp[c] + MMmet-L[c] -> MMpi[c] + MMamet[c] + MMppi[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMMETATB0tc	2 MMna1[u] + MMcl[u] + MMmet-L[u] -> 2 MMna1[c] + MMcl[c] + MMmet-L[c]	0	1000	((232087.1 and 108645.1) or (108645.2 and 232087.1) or 11720.1)	Mouse metabolic/ transport/ demand reaction
MMMETB0ATAtc	MMna1[u] + MMmet-L[u] -> MMna1[c] + MMmet-L[c]	0	1000	56774.1	Mouse metabolic/ transport/ demand reaction
MMMETILELAT2tc	MMile-L[c] + MMmet-L[e] -> MMile-L[e] + MMmet-L[c]	0	1000	(70008.1 or (74338.1 and 57394.1))	Mouse metabolic/ transport/ demand reaction
MMMETLAT1tc	MMleu-L[c] + MMmet-L[u] -> MMleu-L[u] + MMmet-L[c]	0	1000	(20539.1 and 17254.1)	Mouse metabolic/ transport/ demand reaction
MMMETLEUex	MMleu-L[c] + MMmet-L[e] -> MMmet-L[c] + MMleu-L[e]	0	1000	(20539.1 and 17254.1)	Mouse metabolic/ transport/ demand reaction
MMMETPHELAT2tc	MMphe-L[c] + MMmet-L[e] -> MMphe-L[e] + MMmet-L[c]	0	1000	17254.1 and 20539.1	Mouse metabolic/ transport/ demand reaction
MMMETS	MM5mthf[c] + MMhcys-L[c] -> MMh[c] + MMthf[c] + MMmet-L[c]	0	1000	(20539.1 and 17254.1)	Mouse metabolic/ transport/ demand reaction
MMMETt4	MMna1[e] + MMmet-L[e] -> MMna1[c] + MMmet-L[c]	0	1000	238505.1	Mouse metabolic/ transport/ demand reaction
MMMETtec	MMmet-L[e] <=> MMmet-L[c]	0	1000	105727.1 or 67760.1 or 56774.1 or 20520.1	Mouse metabolic/ transport/ demand reaction
MMMETyLATtc	MMna1[e] + MMarg-L[c] + MMmet-L[e] -> MMna1[c] + MMarg-L[e] + MMmet-L[c]	0	1000	215113.1 or 72401.1	Mouse metabolic/ transport/ demand reaction
MMMETyLATthc	MMh[e] + MMarg-L[c] + MMmet-L[e] -> MMh[c] + MMarg-L[e] + MMmet-L[c]	0	1000	(20540.1 or (330836.1 and 17254.1))	Mouse metabolic/ transport/ demand reaction
MMMEVK1x	MMatp[x] + MMmev-R[x] -> MMh[x] + MMadp[x] + MM5pmev[x]	0	1000	(20540.1 or (330836.1 and 17254.1))	Mouse metabolic/ transport/ demand reaction
MMMG1er	MMh2o[r] + MMg3m8masn[r] -> MMglc-D[r] + MMg2m8masn[r]	0	1000	17855.1	Mouse metabolic/ transport/ demand reaction
MMMG2er	MMh2o[r] + MMg2m8masn[r] -> MMglc-D[r] + MMg1m8masn[r]	0	1000	57377.1	Mouse metabolic/ transport/ demand reaction
MMMG3er	MMh2o[r] + MMg1m8masn[r] -> MMglc-D[r] + MMm8masn[r]	0	1000		Mouse metabolic/ transport/ demand reaction
MMMGACONm	MMcitmcoa-L[m] <=> MMh2o[m] + MMmescoa[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMMGCHrm	MMh2o[m] + MM3mgcoa[m] <=> MMhmgcoa[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMMGSA	MMdhap[c] -> MMpi[c] + MMmthgxl[c]	0	1000	11992.1	Mouse metabolic/ transport/ demand reaction
MMMGSA2	MMg3p[c] -> MMpi[c] + MMmthgxl[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMMHISOR	MMh2o[c] + MMo2[c] + MMmhista[c] -> MMh2o2[c] + MMnh4[c] + MM3mldz[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMMI13456PK	MMatp[c] + MMmi13456p[c] -> MMadp[c] + MMh[c] + MMminohp[c]	0	1000	237940.1 or 237940.2 or 11754.1 or 76507.1	Mouse metabolic/ transport/ demand reaction
MMMI13456Ptn	MMmi13456p[c] <=> MMmi13456p[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMMI1345PKn	MMatp[n] + MMmi1345p[n] -> MMh[n] + MMadp[n] + MMmi13456p[n]	0	1000		Mouse metabolic/ transport/ demand reaction
MMMI1345PP	MMh2o[c] + MMmi1345p[c] -> MMpi[c] + MMmi134p[c]	0	1000	69718.1	Mouse metabolic/ transport/ demand reaction
MMMI1346PKn	MMatp[n] + MMmi1346p[n] -> MMh[n] + MMadp[n] + MMmi13456p[n]	0	1000	104015.1 or 170835.1 or 170835.1 or 16331.1 or 212111.1 or 64436.1 or 16330.1 or 16332.1 or 104015.2	Mouse metabolic/ transport/ demand reaction
MMMI1346Ptn	MMmi1346p[c] <=> MMmi1346p[n]	-1000	1000	69718.1	Mouse metabolic/ transport/ demand reaction
MMMI134P4P	MMh2o[c] + MMmi134p[c] -> MMpi[c] + MMmi13p[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMMI134PK	MMatp[c] + MMmi134p[c] -> MMadp[c] + MMh[c] + MMmi1346p[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMMI134PP	MMh2o[c] + MMmi134p[c] -> MMpi[c] + MMmi34p[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMMI13PP	MMh2o[c] + MMmi13p[c] -> MMpi[c] + MMmi1p-D[c]	0	1000	16329.1	Mouse metabolic/ transport/ demand reaction
MMMI1456PKn	MMatp[n] + MMmi1456p[n] -> MMh[n] + MMadp[n] + MMmi13456p[n]	0	1000		Mouse metabolic/ transport/ demand reaction
MMMI145P6Kn	MMatp[n] + MMmi145p[n] -> MMh[n] + MMadp[n] + MMmi1456p[n]	0	1000	69718.1	Mouse metabolic/ transport/ demand reaction
MMMI145PK	MMatp[c] + MMmi145p[c] -> MMadp[c] + MMh[c] + MMmi1345p[c]	0	1000	69718.1	Mouse metabolic/ transport/ demand reaction
MMMI145PKn	MMatp[n] + MMmi145p[n] -> MMh[n] + MMadp[n] + MMmi1345p[n]	0	1000	228550.1 or 233011.1 or 320404.1	Mouse metabolic/ transport/ demand reaction
MMMI145PP	MMh2o[c] + MMmi145p[c] -> MMpi[c] + MMmi14p[c]	0	1000	69718.1	Mouse metabolic/ transport/ demand reaction
MMMI14P4P	MMh2o[c] + MMmi14p[c] -> MMpi[c] + MMmi1p-D[c]	0	1000	104015.1 or 170835.1 or 170835.1 or 16331.1 or 212111.1 or 64436.1 or 16330.1 or 16332.1 or 104015.2	Mouse metabolic/ transport/ demand reaction
MMMI14PP	MMh2o[c] + MMmi14p[c] -> MMpi[c] + MMmi4p-D[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMMI14Ptn	MMmi14p[c] <=> MMmi14p[n]	-1000	1000	16329.1	Mouse metabolic/ transport/ demand reaction
MMMI1PP	MMh2o[c] + MMmi1p-D[c] -> MMpi[c] + MMinost[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMMI1PS	MMg6p[c] -> MMmi1p-D[c]	0	1000	114663.1 or 55980.1	Mouse metabolic/ transport/ demand reaction
MMMI1P_Dtn	MMmi1p-D[c] <=> MMmi1p-D[n]	-1000	1000	71780.1	Mouse metabolic/ transport/ demand reaction
MMMI3456PK	MMatp[c] + MMmi3456p[c] -> MMadp[c] + MMh[c] + MMmi13456p[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMMI34PP	MMh2o[c] + MMmi34p[c] -> MMpi[c] + MMmi3p-D[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMMI3PP	MMh2o[c] + MMmi3p-D[c] -> MMpi[c] + MMinost[c]	0	1000	234515.1 or 269180.1 or 269180.2	Mouse metabolic/ transport/ demand reaction
MMMI4PP	MMh2o[c] + MMmi4p-D[c] -> MMpi[c] + MMinost[c]	0	1000	114663.1 or 55980.1	Mouse metabolic/ transport/ demand reaction
MMMICITDr	MMh2o[c] + MM2mcacn[c] <=> MMmicit[c]	-1000	1000	114663.1 or 55980.1	Mouse metabolic/ transport/ demand reaction
MMMINOHPtn	MMminohp[c] <=> MMminohp[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMMK10t	MMmqn10[c] <=> MMmqn10[e]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMMK11t	MMmqn11[c] <=> MMmqn11[e]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMMK7t	MMmqn7[c] <=> MMmqn7[e]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMMK8t	MMmqn8[c] <=> MMmqn8[e]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMMK9t	MMmqn9[c] <=> MMmqn9[e]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMMLTG1	MMh2o[c] + MMmalttr[c] -> MMglc-D[c] + MMmalt[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMMLTG1e	MMh2o[e] + MMmalttr[e] -> MMglc-D[e] + MMmalt[e]	0	1000	76051.1	Mouse metabolic/ transport/ demand reaction
MMMLTG1ly	MMh2o[l] + MMmalttr[l] -> MMglc-D[l] + MMmalt[l]	0	1000	232714.1	Mouse metabolic/ transport/ demand reaction
MMMM5ag	MMh2o[g] + MMm5masnC[g] -> MMman[g] + MMm4masn[g]	0	1000	14387.1	Mouse metabolic/ transport/ demand reaction
MMMM5bg	MMh2o[g] + MMm5masnB1[g] -> MMman[g] + MMm4masn[g]	0	1000	17156.1 or 230815.1 or 17155.1	Mouse metabolic/ transport/ demand reaction
MMMM5cg	MMh2o[g] + MMm5masnB2[g] -> MMman[g] + MMm4masn[g]	0	1000	17156.1 or 230815.1 or 17155.1	Mouse metabolic/ transport/ demand reaction
MMMM6B1ag	MMh2o[g] + MMm6masnB1[g] -> MMm5masnB1[g] + MMman[g]	0	1000	17156.1 or 230815.1 or 17155.1	Mouse metabolic/ transport/ demand reaction
MMMM6B1bg	MMh2o[g] + MMm6masnB2[g] -> MMm5masnB1[g] + MMman[g]	0	1000	17156.1 or 230815.1 or 17155.1	Mouse metabolic/ transport/ demand reaction
MMMM6B2g	MMh2o[g] + MMm6masnB2[g] -> MMman[g] + MMm5masnB2[g]	0	1000	17156.1 or 230815.1 or 17155.1	Mouse metabolic/ transport/ demand reaction
MMMM6ag	MMh2o[g] + MMm6masnA[g] -> MMman[g] + MMm5masnC[g]	0	1000	17156.1 or 230815.1 or 17155.1	Mouse metabolic/ transport/ demand reaction
MMMM6bg	MMh2o[g] + MMm6masnC[g] -> MMman[g] + MMm5masnC[g]	0	1000	230815.1	Mouse metabolic/ transport/ demand reaction
MMMM7Ag	MMh2o[g] + MMm7masnA[g] -> MMman[g] + MMm6masnA[g]	0	1000	17156.1 or 230815.1 or 17155.1	Mouse metabolic/ transport/ demand reaction
MMMM7B1g	MMh2o[g] + MMm7masnB[g] -> MMman[g] + MMm6masnB1[g]	0	1000	230815.1	Mouse metabolic/ transport/ demand reaction
MMMM7B2g	MMh2o[g] + MMm7masnB[g] -> MMm6masnB2[g] + MMman[g]	0	1000	17156.1 or 230815.1 or 17155.1	Mouse metabolic/ transport/ demand reaction

MMMM7Cag	MMh2o[g] + MMm7masnA[g] -> MMm6masnC[g] + MMman[g]	0	1000	17156.1 or 230815.1 or 17155.1	Mouse metabolic/ transport/ demand reaction
MMMM7Chg	MMh2o[g] + MMm7masnC[g] -> MMm6masnC[g] + MMman[g]	0	1000	17156.1 or 230815.1 or 17155.1	Mouse metabolic/ transport/ demand reaction
MMMM8Ag	MMh2o[g] + MMm8masn[g] -> MMm7masnA[g] + MMman[g]	0	1000	17156.1 or 230815.1 or 17155.1	Mouse metabolic/ transport/ demand reaction
MMMM8Ber	MMh2o[r] + MMm8masn[r] -> MMm7masn8[r] + MMman[r]	0	1000	17156.1 or 230815.1 or 17155.1	Mouse metabolic/ transport/ demand reaction
MMMM8Cg	MMh2o[g] + MMm8masn[g] -> MMman[g] + MMm7masnC[g]	0	1000	227619.1	Mouse metabolic/ transport/ demand reaction
MMMMCD	MMh[c] + MMmmcoa-S[c] -> MMco2[c] + MMppcoa[c]	0	1000	17156.1 or 230815.1 or 17155.1	Mouse metabolic/ transport/ demand reaction
MMMMCDm	MMh[m] + MMmmcoa-S[m] -> MMco2[m] + MMppcoa[m]	0	1000	56690.1	Mouse metabolic/ transport/ demand reaction
MMMMCDp	MMh[x] + MMmmcoa-S[x] -> MMco2[x] + MMppcoa[x]	0	1000	56690.1	Mouse metabolic/ transport/ demand reaction
MMMMEm	MMmmcoa-R[m] <=> MMmmcoa-S[m]	-1000	1000	56690.1	Mouse metabolic/ transport/ demand reaction
MMMMMm	MMmmcoa-R[m] <=> MMsuccoa[m]	-1000	1000	73724.1	Mouse metabolic/ transport/ demand reaction
MMMMSAD1m	MMcoa[m] + MMnad[m] + MM2mop[m] -> MMco2[m] + MMnadh[m] + MMppcoa[m]	0	1000	17850.1	Mouse metabolic/ transport/ demand reaction
MMMMSAD3m	MMcoa[m] + MMnad[m] + MMmsa[m] -> MMco2[m] + MMnadh[m] + MMaccoa[m]	0	1000	104776.1	Mouse metabolic/ transport/ demand reaction
MMMMTSADm	MMcoa[m] + MMnad[m] + MM2mop[m] -> MMh[m] + MMnadh[m] + MMmmcoa-R[m]	0	1000	104776.1	Mouse metabolic/ transport/ demand reaction
MMMOGAT	MMRtotalcoa[c] + MMmag_hs[c] -> MMcoa[c] + MMdag_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMMTAP	MMpi[c] + MM5mta[c] -> MMade[c] + MM5mdr1p[c]	0	1000	233549.1 or 68393.1	Mouse metabolic/ transport/ demand reaction
MMMTHFC	MMh2o[c] + MMmeth[c] <=> MM10fthf[c] + MMh[c]	-1000	1000	66902.1	Mouse metabolic/ transport/ demand reaction
MMMTHFCm	MMh2o[m] + MMmeth[m] <=> MM10fthf[m] + MMh[m]	-1000	1000	108156.1	Mouse metabolic/ transport/ demand reaction
MMMTHFD	MMnadp[c] + MMmthf[c] <=> MMnadph[c] + MMmeth[c]	-1000	1000	17768.1 or 270685.1	Mouse metabolic/ transport/ demand reaction
MMMTHFD2	MMnad[c] + MMmthf[c] <=> MMnadh[c] + MMmeth[c]	-1000	1000	108156.1	Mouse metabolic/ transport/ demand reaction
MMMTHFD2m	MMnad[m] + MMmthf[m] <=> MMnadh[m] + MMmeth[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMMTHFDm	MMnadp[m] + MMmthf[m] <=> MMnadph[m] + MMmeth[m]	-1000	1000	17768.1	Mouse metabolic/ transport/ demand reaction
MMMTHFR3	2 MMh[c] + MMnadph[c] + MMmthf[c] -> MMnadp[c] + MM5mthf[c]	0	1000	17768.1 or 270685.1	Mouse metabolic/ transport/ demand reaction
MMMTHFTe	MM5mthf[c] -> MM5mthf[e]	0	1000	17769.1	Mouse metabolic/ transport/ demand reaction
MMMTHGXLt	MMmthgx[c] -> MMmthgx[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMMTRI	MM5mdr1p[c] <=> MM5mdru1p[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMN2M2NMASNt	MMn2m2nmasn[g] -> MMn2m2nmasn[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMN2M2NMASNtly	MMn2m2nmasn[e] -> MMn2m2nmasn[]	0	1000		Mouse metabolic/ transport/ demand reaction
MMN3Tg	MMudpga[g] + MMTn_antigen[g] -> MMh[g] + MMudp[g] + MMT_antigen[g]	0	1000		Mouse metabolic/ transport/ demand reaction
MMN4Tg	MMudpga[g] + MMcore6[g] -> MMh[g] + MMudp[g] + MMf1a[g]	0	1000	94192.1	Mouse metabolic/ transport/ demand reaction
MMNABTNO	MMh2o[c] + MMnad[c] + MMn4aburn[c] -> 2 MMh[c] + MMnadh[c] + MM4aaburn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMNABTNOm	MMh2o[m] + MMnad[m] + MMn4aburn[m] -> 2 MMh[m] + MMnadh[m] + MM4aaburn[m]	0	1000	19378.1 or 56752.1 or 110695.1 or 11668.1 or 11671.1 or 19378.2 or 19378.3	Mouse metabolic/ transport/ demand reaction
MMNACASPAH	MMh2o[c] + MMNacasp[c] -> MMasp-L[c] + MMac[c]	0	1000	212647.1 or 11669.1 or 72535.1	Mouse metabolic/ transport/ demand reaction
MMNACASPtm	MMNacasp[m] -> MMNacasp[c]	0	1000	11484.1 or 71670.1	Mouse metabolic/ transport/ demand reaction
MMNACDe	MMnac[c] -> MMnac[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMNACHEX10ly	2 MMh2o[l] + MMksi_deg7[l] -> 2 MMacgam[l] + MMksi_deg8[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MMNACHEX11ly	MMh2o[l] + MMksi_deg10[l] -> MMacgam[l] + MMksi_deg11[l]	0	1000	(15211.1 or 15212.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEX12ly	MMh2o[l] + MMksi_deg13[l] -> MMacgam[l] + MMksi_deg14[l]	0	1000	(15211.1 or 15212.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEX13ly	MMh2o[l] + MMksi_deg16[l] -> MMacgam[l] + MMksi_deg17[l]	0	1000	(15211.1 or 15212.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEX14ly	MMh2o[l] + MMksi_deg19[l] -> MMacgam[l] + MMksi_deg20[l]	0	1000	(15211.1 or 15212.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEX15ly	MMh2o[l] + MMksi_deg22[l] -> MMacgam[l] + MMksi_deg23[l]	0	1000	(15211.1 or 15212.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEX16ly	MMh2o[l] + MMksi_deg25[l] -> MMacgam[l] + MMksi_deg26[l]	0	1000	(15211.1 or 15212.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEX17ly	MMh2o[l] + MMksi_deg28[l] -> MMacgam[l] + MMksi_deg29[l]	0	1000	(15211.1 or 15212.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEX18ly	MMh2o[l] + MMksi_deg31[l] -> MMacgam[l] + MMksi_deg32[l]	0	1000	(15211.1 or 15212.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEX19ly	MMh2o[l] + MMksi_deg34[l] -> MMacgam[l] + MMksi_deg35[l]	0	1000	(15211.1 or 15212.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEX1ly	MMh2o[l] + MMcs_a_deg1[l] -> MMacgal[l] + MMcs_a_deg2[l]	0	1000	(15211.1 or 15212.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEX20ly	MMh2o[l] + MMksi_deg37[l] -> MMacgam[l] + MMksi_deg38[l]	0	1000	(15211.1 or 15212.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEX21ly	MMh2o[l] + MMksi_deg39[l] -> MMacgam[l] + MMksi_deg40[l]	0	1000	(15211.1 or 15212.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEX22ly	MMh2o[l] + MMksi_deg41[l] -> MMacgam[l] + MMm2mn[l]	0	1000	(15211.1 or 15212.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEX23ly	MMh2o[l] + MMksii_core2_deg4[l] -> MMacgam[l] + MMksii_core2_deg5[l]	0	1000	(15211.1 or 15212.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEX24ly	MMh2o[l] + MMksii_core2_deg7[l] -> MMacgam[l] + MMksii_core2_deg8[l]	0	1000	(15211.1 or 15212.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEX25ly	MMh2o[l] + MMksii_core2_deg9[l] -> MMacgam[l] + MMf1a[l]	0	1000	(15211.1 or 15212.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEX26ly	2 MMh2o[l] + MMksii_core4_deg4[l] -> 2 MMacgam[l] + MMksii_core2_deg5[l]	0	1000	(15211.1 or 15212.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEX27ly	MMh2o[l] + MMhs_deg1[l] -> MMacgam[l] + MMhs_pre1[l]	0	1000	(15211.1 or 15212.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEX2ly	MMh2o[l] + MMcs_a_deg4[l] -> MMacgal[l] + MMcs_a_deg5[l]	0	1000	(15211.1 or 15212.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEX3ly	MMh2o[l] + MMcs_b_deg1[l] -> MMacgal[l] + MMcs_b_deg2[l]	0	1000	(15211.1 or 15212.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEX4ly	MMh2o[l] + MMcs_c_deg1[l] -> MMacgal[l] + MMcs_c_deg2[l]	0	1000	(15211.1 or 15212.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEX5ly	MMh2o[l] + MMcs_c_deg4[l] -> MMacgal[l] + MMcs_c_deg5[l]	0	1000	(15211.1 or 15212.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEX6ly	MMh2o[l] + MMcs_d_deg1[l] -> MMacgal[l] + MMcs_d_deg2[l]	0	1000	(15211.1 or 15212.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEX7ly	MMh2o[l] + MMcs_d_deg5[l] -> MMacgal[l] + MMcs_d_deg6[l]	0	1000	(15211.1 or 15212.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEX8ly	MMh2o[l] + MMcs_e_deg2[l] -> MMacgal[l] + MMcs_e_deg3[l]	0	1000	(15211.1 or 15212.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEX9ly	MMh2o[l] + MMcs_e_deg6[l] -> MMacgal[l] + MMcs_e_deg7[l]	0	1000	(15211.1 or 15212.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEXA10ly	2 MMh2o[l] + MMksi_deg8[l] -> MMh[l] + MMacgam[l] + MMso4[l] + MMksi_deg11[l]	0	1000	(15211.1 or 15212.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEXA11ly	2 MMh2o[l] + MMksi_deg12[l] -> MMh[l] + MMacgam[l] + MMso4[l] + MMksi_deg14[l]	0	1000	(15211.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEXA12ly	2 MMh2o[l] + MMksi_deg15[l] -> MMh[l] + MMacgam[l] + MMso4[l] + MMksi_deg17[l]	0	1000	(15211.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEXA13ly	2 MMh2o[l] + MMksi_deg18[l] -> MMh[l] + MMacgam[l] + MMso4[l] + MMksi_deg20[l]	0	1000	(15211.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEXA14ly	2 MMh2o[l] + MMksi_deg21[l] -> MMh[l] + MMacgam[l] + MMso4[l] + MMksi_deg23[l]	0	1000	(15211.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEXA15ly	2 MMh2o[l] + MMksi_deg24[l] -> MMh[l] + MMacgam[l] + MMso4[l] + MMksi_deg26[l]	0	1000	(15211.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEXA16ly	2 MMh2o[l] + MMksi_deg27[l] -> MMh[l] + MMacgam[l] + MMso4[l] + MMksi_deg29[l]	0	1000	(15211.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEXA17ly	2 MMh2o[l] + MMksi_deg30[l] -> MMh[l] + MMacgam[l] + MMso4[l] + MMksi_deg32[l]	0	1000	(15211.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEXA18ly	2 MMh2o[l] + MMksi_deg33[l] -> MMh[l] + MMacgam[l] + MMso4[l] + MMksi_deg35[l]	0	1000	(15211.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEXA19ly	2 MMh2o[l] + MMksi_deg36[l] -> MMh[l] + MMacgam[l] + MMso4[l] + MMksi_deg38[l]	0	1000	(15211.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEXA1ly	2 MMh2o[l] + MMcs_a[l] -> MMh[l] + MMacgal[l] + MMso4[l] + MMcs_a_deg2[l]	0	1000	(15211.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEXA20ly	2 MMh2o[l] + MMksii_core2_deg3[l] -> MMh[l] + MMacgam[l] + MMso4[l] + MMksii_core2_deg5[l]	0	1000	(15211.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEXA21ly	2 MMh2o[l] + MMksii_core2_deg6[l] -> MMh[l] + MMacgam[l] + MMso4[l] + MMksii_core2_deg8[l]	0	1000	(15211.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEXA22ly	3 MMh2o[l] + MMksii_core4_deg3[l] -> MMh[l] + 2 MMacgam[l] + MMso4[l] + MMksii_core2_deg5[l]	0	1000	(15211.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEXA2ly	2 MMh2o[l] + MMcs_b[l] -> MMh[l] + MMacgal[l] + MMso4[l] + MMcs_b_deg2[l]	0	1000	(15211.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEXA3ly	2 MMh2o[l] + MMcs_c[l] -> MMh[l] + MMacgal[l] + MMso4[l] + MMcs_c_deg2[l]	0	1000	(15211.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEXA4ly	2 MMh2o[l] + MMcs_c_deg3[l] -> MMh[l] + MMacgal[l] + MMso4[l] + MMcs_c_deg5[l]	0	1000	(15211.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEXA5ly	2 MMh2o[l] + MMcs_d[l] -> MMh[l] + MMacgal[l] + MMso4[l] + MMcs_d_deg2[l]	0	1000	(15211.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEXA6ly	2 MMh2o[l] + MMcs_d_deg4[l] -> MMh[l] + MMacgal[l] + MMso4[l] + MMcs_d_deg5[l]	0	1000	(15211.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEXA7ly	3 MMh2o[l] + MMcs_e[l] -> 2 MMh[l] + MMacgal[l] + 2 MMso4[l] + MMcs_e_deg3[l]	0	1000	(15211.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEXA8ly	3 MMh2o[l] + MMcs_e_deg4[l] -> 2 MMh[l] + MMacgal[l] + 2 MMso4[l] + MMcs_e_deg7[l]	0	1000	(15211.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHEXA9ly	3 MMh2o[l] + MMksi_deg6[l] -> MMh[l] + 2 MMacgam[l] + MMso4[l] + MMksi_deg8[l]	0	1000	(15211.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACHORCTL3ku	MMh[u] + MMnac[u] -> MMh[c] + MMnac[c]	0	1000	(15211.1 or (15212.1 and 15211.1))	Mouse metabolic/ transport/ demand reaction
MMNACUP	MMnac[e] -> MMnac[c]	0	1000	102570.1	Mouse metabolic/ transport/ demand reaction

MMNADH2_u10m	5 MMh[m] + MMnadh[m] + MMq10[m] -> 4 MMh[c] + MMnad[m] + MMq10h2[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMNADHtpu	MMnadh[c] -> MMnadh[x]	0	1000	17992.1 or 66495.1 or 66218.1 or 17993.1 or 68342.1 or 78330.1 or 66377.1 or 67184.1 or 17991.1 or 72900.1 or 66108.1 or 69875.1 or 100043472.1 or 54405.1 or 230075.2 or 66091.1 or 75406.1 or 67273.1 or 80286.2 or 66046.1 or 78330.2 or 66916.1 or 68198.1 or 225887.1 or 227197.1 or 68349.1 or 230075.1 or 227197.1 or 66416.1 or 68375.1 or 226646.1 or 80286.1 or 407785.1 or 17995.1 or 68197.1 or 595136.1 or 66414.1 or 67130.1 or 67264.1 or 68202.1 or 68194.1	Mouse metabolic/ transport/ demand reaction
MMNADHtru	MMnadh[c] -> MMnadh[r]	0	1000		Mouse metabolic/ transport/ demand reaction
MMNADK	MMatp[c] + MMnad[c] -> MMadp[c] + MMh[c] + MMnadp[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMNADN	MMh2o[c] + MMnad[c] -> MMh[c] + MMadprib[c] + MMncam[c]	0	1000	192185.1	Mouse metabolic/ transport/ demand reaction
MMNADNe	MMh2o[e] + MMnad[e] -> MMh[e] + MMadprib[e] + MMncam[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMNADPHtru	MMnadph[c] -> MMnadph[r]	0	1000	12494.1	Mouse metabolic/ transport/ demand reaction
MMNADPHtxu	MMnadph[c] -> MMnadph[x]	0	1000		Mouse metabolic/ transport/ demand reaction
MMNADPN	MMh2o[c] + MMnadp[c] -> MMh[c] + MMncam[c] + MMadprhp[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMNADPNe	MMh2o[e] + MMnadp[e] -> MMh[e] + MMadprhp[e] + MMncam[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMNADPtru	MMnadp[r] -> MMnadp[c]	0	1000	12494.1	Mouse metabolic/ transport/ demand reaction
MMNADPtxu	MMnadp[x] -> MMnadp[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMNADS2	MMh2o[c] + MMatp[c] + MMgln-L[c] + MMdnnad[c] -> MMh[c] + MMnad[c] + MMglu-L[c] + MMamp[c] + MMppi[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMNADtn	MMnad[n] <=> MMnad[c]	-1000	1000	78914.1	Mouse metabolic/ transport/ demand reaction
MMNADtpu	MMnadh[x] -> MMnadh[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMNADtru	MMnad[r] -> MMnad[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMNAGA2ly	MMh[l] + MMTn_antigen[l] + MMudp[l] -> MMSer_Thr[l] + MMudpacga[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MMNAGAlby	MMh[l] + MMacgbgbside_hs[l] + MMudp[l] -> MMgbside_hs[l] + MMudpacga[l]	0	1000	17939.1	Mouse metabolic/ transport/ demand reaction
MMNAGAly	MMh[l] + MMacgagbside_hs[l] + MMudp[l] -> MMgbside_hs[l] + MMudpacga[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MMNAGLCAly	MMh2o[l] + MMcore6[l] -> MMacgam[l] + MMTn_antigen[l]	0	1000	17939.1	Mouse metabolic/ transport/ demand reaction
MMNAHCO3_HCLt	MMh[c] + MMhco3[e] + MMna1[e] + MMcl[c] <=> MMh[e] + MMhco3[c] + MMna1[c] + MMcl[e]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMNAlt	2 MMna1[e] + MM[e] <=> 2 MMna1[c] + MM[c]	0	1000	94229.1 or 59033.1	Mouse metabolic/ transport/ demand reaction
MMNAt	MMna1[e] <=> MMna1[c]	0	1000	114479.1	Mouse metabolic/ transport/ demand reaction
MMNAt3_1	MMh[e] + MMna1[c] <=> MMh[c] + MMna1[e]	-1000	0	53881.1 or 20537.1 or 114479.1	Mouse metabolic/ transport/ demand reaction
MMNAt3_1g	MMna1[c] + MMh[g] <=> MMh[c] + MMna1[g]	-1000	1000	277973.1 or 105243.1 or 226999.1 or 20544.1 or 110895.1	Mouse metabolic/ transport/ demand reaction
MMNAt5	MMna1[c] + MMnbt4[e] <=> MMnbt4[c] + MMna1[e]	0	1000	236727.1 or 77031.1	Mouse metabolic/ transport/ demand reaction
MMNAtx	MMna1[c] <=> MMna1[x]	-1000	1000	105243.1 or 226999.1 or 20544.1	Mouse metabolic/ transport/ demand reaction
MMNBAHH_ir	MMh2o[c] + MMcarn[c] -> MMala-B[c] + MMhis-L[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMNCAMDe	MMncam[c] -> MMncam[e]	0	1000	338403.1	Mouse metabolic/ transport/ demand reaction
MMNCAMUP	MMncam[e] -> MMncam[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMNCCt	MMna1[e] + MMcl[e] -> MMna1[c] + MMcl[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMNCKt	4 MMna1[c] + MMk[e] + MMca2[e] <=> 4 MMna1[e] + MMk[c] + MMca2[c]	-1000	1000	20497.1	Mouse metabolic/ transport/ demand reaction
MMNCNt	4 MMna1[c] + MMnbt4[e] + MMca2[e] <=> MMnbt4[c] + 4 MMna1[e] + MMca2[c]	-1000	1000	238384.1 or 214111.1 or 238384.2 or 238384.3 or 76376.1 or 94249.1	Mouse metabolic/ transport/ demand reaction
MMNDP10ex	MMh2o[e] + MMdp[e] -> MMh[e] + MMpi[e] + MMimp[e]	0	1000	214111.1 or 76376.1	Mouse metabolic/ transport/ demand reaction
MMNDP3ex	MMh2o[e] + MMgdp[e] -> MMh[e] + MMpi[e] + MMgmp[e]	0	1000	76025.1	Mouse metabolic/ transport/ demand reaction
MMNDP6	MMh2o[c] + MMdcdp[c] -> MMh[c] + MMpi[c] + MMdcmp[c]	0	1000	76025.1	Mouse metabolic/ transport/ demand reaction
MMNDP7er	MMh2o[r] + MMudp[r] -> MMh[r] + MMpi[r] + MMump[r]	0	1000		Mouse metabolic/ transport/ demand reaction
MMNDP7ex	MMh2o[e] + MMudp[e] -> MMh[e] + MMpi[e] + MMump[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMNDP7g	MMudp[g] + MMh2o[g] -> MMh[g] + MMpi[g] + MMump[g]	0	1000	76025.1	Mouse metabolic/ transport/ demand reaction
MMNDP8	MMh2o[c] + MMdudp[c] -> MMh[c] + MMpi[c] + MMdump[c]	0	1000	67464.1	Mouse metabolic/ transport/ demand reaction
MMNDP8ex	MMh2o[e] + MMutp[e] -> MMh[e] + MMpi[e] + MMudp[e]	0	1000	21915.1	Mouse metabolic/ transport/ demand reaction
MMNDPK1	MMatp[c] + MMgdp[c] <=> MMadp[c] + MMgtp[c]	-1000	1000	76025.1	Mouse metabolic/ transport/ demand reaction
MMNDPK10	MMatp[c] + MMdtdp[c] <=> MMadp[c] + MMdttp[c]	-1000	1000	18103.1 and 18102.2 or 18102.1 and 18103.1 or 171567.1 or 54369.1 or 79059.1 or 171567.2	Mouse metabolic/ transport/ demand reaction
MMNDPK10m	MMatp[m] + MMdtdp[m] <=> MMadp[m] + MMdttp[m]	-1000	1000	18103.1 and 18102.2 or 18102.1 and 18103.1 or 171567.1 or 54369.1 or 79059.1 or 171567.2	Mouse metabolic/ transport/ demand reaction
MMNDPK10n	MMatp[n] + MMdtdp[n] <=> MMadp[n] + MMdttp[n]	-1000	1000	56520.1	Mouse metabolic/ transport/ demand reaction
MMNDPK1m	MMatp[m] + MMgdp[m] <=> MMadp[m] + MMgtp[m]	-1000	1000	18102.1 and 18103.1 or 18103.1 and 18102.2	Mouse metabolic/ transport/ demand reaction
MMNDPK1n	MMatp[n] + MMgdp[n] <=> MMadp[n] + MMgtp[n]	-1000	1000	56520.1	Mouse metabolic/ transport/ demand reaction
MMNDPK2	MMatp[c] + MMudp[c] <=> MMadp[c] + MMutp[c]	-1000	1000	18102.1 and 18103.1 or 18103.1 and 18102.2	Mouse metabolic/ transport/ demand reaction
MMNDPK2m	MMatp[m] + MMudp[m] <=> MMadp[m] + MMutp[m]	-1000	1000	18103.1 and 18102.2 or 18102.1 and 18103.1 or 171567.1 or 54369.1 or 79059.1 or 171567.2	Mouse metabolic/ transport/ demand reaction
MMNDPK2n	MMatp[n] + MMudp[n] <=> MMutp[n] + MMadp[n]	-1000	1000	56520.1	Mouse metabolic/ transport/ demand reaction
MMNDPK3	MMatp[c] + MMcdp[c] <=> MMadp[c] + MMctp[c]	-1000	1000	18102.1 and 18103.1 or 18103.1 and 18102.2	Mouse metabolic/ transport/ demand reaction
MMNDPK3m	MMatp[m] + MMcdp[m] <=> MMadp[m] + MMctp[m]	-1000	1000	18103.1 and 18102.2 or 18102.1 and 18103.1 or 171567.1 or 54369.1 or 79059.1 or 171567.2	Mouse metabolic/ transport/ demand reaction
MMNDPK3n	MMatp[n] + MMcdp[n] <=> MMctp[n] + MMadp[n]	-1000	1000	56520.1	Mouse metabolic/ transport/ demand reaction
MMNDPK4	MMatp[c] + MMdtdp[c] <=> MMadp[c] + MMdttp[c]	-1000	1000	18102.1 and 18103.1 or 18103.1 and 18102.2	Mouse metabolic/ transport/ demand reaction
MMNDPK4m	MMatp[m] + MMdtdp[m] <=> MMadp[m] + MMdttp[m]	-1000	1000	18103.1 and 18102.2 or 18102.1 and 18103.1 or 171567.1 or 54369.1 or 79059.1 or 171567.2	Mouse metabolic/ transport/ demand reaction
MMNDPK4n	MMatp[n] + MMdtdp[n] <=> MMadp[n] + MMdttp[n]	-1000	1000	56520.1	Mouse metabolic/ transport/ demand reaction
MMNDPK5	MMatp[c] + MMdgdp[c] <=> MMadp[c] + MMdgtp[c]	-1000	1000	18102.1 and 18103.1 or 18103.1 and 18102.2	Mouse metabolic/ transport/ demand reaction
MMNDPK5m	MMatp[m] + MMdgdp[m] <=> MMadp[m] + MMdgtp[m]	-1000	1000	18103.1 and 18102.2 or 18102.1 and 18103.1 or 171567.1 or 54369.1 or 79059.1 or 171567.2	Mouse metabolic/ transport/ demand reaction
MMNDPK5n	MMatp[n] + MMdgdp[n] <=> MMdgtp[n] + MMadp[n]	-1000	1000	56520.1	Mouse metabolic/ transport/ demand reaction
MMNDPK6	MMatp[c] + MMdudp[c] <=> MMadp[c] + MMdutp[c]	-1000	1000	18102.1 and 18103.1 or 18103.1 and 18102.2	Mouse metabolic/ transport/ demand reaction
MMNDPK6m	MMatp[m] + MMdudp[m] <=> MMadp[m] + MMdutp[m]	-1000	1000	18103.1 and 18102.2 or 18102.1 and 18103.1 or 171567.1 or 54369.1 or 79059.1 or 171567.2	Mouse metabolic/ transport/ demand reaction
MMNDPK6n	MMatp[n] + MMdudp[n] <=> MMadp[n] + MMdutp[n]	-1000	1000	56520.1	Mouse metabolic/ transport/ demand reaction
MMNDPK7	MMatp[c] + MMdcdp[c] <=> MMadp[c] + MMdctp[c]	-1000	1000	18102.1 and 18103.1 or 18103.1 and 18102.2	Mouse metabolic/ transport/ demand reaction
MMNDPK7m	MMatp[m] + MMdcdp[m] <=> MMadp[m] + MMdctp[m]	-1000	1000	18103.1 and 18102.2 or 18102.1 and 18103.1 or 171567.1 or 54369.1 or 79059.1 or 171567.2	Mouse metabolic/ transport/ demand reaction
MMNDPK7n	MMatp[n] + MMdcdp[n] <=> MMdctp[n] + MMadp[n]	-1000	1000	56520.1	Mouse metabolic/ transport/ demand reaction
MMNDPK8	MMatp[c] + MMdadp[c] <=> MMadp[c] + MMdatp[c]	-1000	1000	18102.1 and 18103.1 or 18103.1 and 18102.2	Mouse metabolic/ transport/ demand reaction
MMNDPK8m	MMatp[m] + MMdadp[m] <=> MMadp[m] + MMdatp[m]	-1000	1000	18103.1 and 18102.2 or 18102.1 and 18103.1 or 171567.1 or 54369.1 or 79059.1 or 171567.2	Mouse metabolic/ transport/ demand reaction
MMNDPK8n	MMatp[n] + MMdadp[n] <=> MMdatp[n] + MMadp[n]	-1000	1000	56520.1	Mouse metabolic/ transport/ demand reaction
MMNDPK9	MMatp[c] + MMidp[c] <=> MMadp[c] + MMitp[c]	-1000	1000	18102.1 and 18103.1 or 18103.1 and 18102.2	Mouse metabolic/ transport/ demand reaction
MMNDPK9m	MMatp[m] + MMidp[m] <=> MMadp[m] + MMitp[m]	-1000	1000	18103.1 and 18102.2 or 18102.1 and 18103.1 or 171567.1 or 54369.1 or 79059.1 or 171567.2	Mouse metabolic/ transport/ demand reaction
MMNDPK9n	MMatp[n] + MMidp[n] <=> MMadp[n] + MMitp[n]	-1000	1000	56520.1	Mouse metabolic/ transport/ demand reaction
MMNH4t3r	MMnbt4[c] + MM[e] <=> MM[c] + MMnbt4[e]	0	1000	18102.1 and 18103.1 or 18103.1 and 18102.2	Mouse metabolic/ transport/ demand reaction
MMNH4tn	MMnbt4[c] <=> MMnbt4[n]	-1000	1000	19743.1 or 58176.1	Mouse metabolic/ transport/ demand reaction
MMNH4tp	MMnbt4[c] <=> MMnbt4[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMNICRNS	MMatp[c] + MMnicrnn[c] -> MMadp[c] + MMh[c] + MMnicrnt[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMNICRNTtn	MMnicrnt[c] <=> MMnicrnt[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMNIFEDIPINEte	MMnifedipine[e] <=> MMnifedipine[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMNKCC2t	MMna1[e] + MMnbt4[e] + 2 MMcl[e] <=> MMnbt4[c] + MMna1[c] + 2 MMcl[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMNKCCt	MMna1[e] + MMk[e] + 2 MMcl[e] <=> MMna1[c] + 2 MMcl[c] + MMk[c]	-1000	1000	20495.1 or 20496.1	Mouse metabolic/ transport/ demand reaction
MMNMNATm	MMh[m] + MMatp[m] + MMnmn[m] -> MMnmd[m] + MMppi[m]	0	1000	20495.1 or 20496.1	Mouse metabolic/ transport/ demand reaction
MMNMNATn	MMatp[n] + MMh[n] + MMnmn[n] -> MMppi[n] + MMnad[n]	0	1000	74080.1	Mouse metabolic/ transport/ demand reaction

MMNMNATr	MMatp[c] + MMft[c] + MMmnm[c] <=> MMnad[c] + MMppi[c]	-1000	1000	66454.1	Mouse metabolic/ transport/ demand reaction
MMNMNS	MMft[c] + MMprpp[c] + MMncam[c] -> MMppi[c] + MMmni[c]	0	1000	226518.1 or 226518.2 or 74080.1	Mouse metabolic/ transport/ demand reaction
MMNMNtn	MMnmn[c] <=> MMnmn[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMNMPTRCOX	MMo2[c] + MMnmpmrc[c] -> MMh2o2[c] + MMnh4[c] + MM11mpyr[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMNNAT	MMatp[c] + MMft[c] + MMnicrn[c] -> MMppi[c] + MMnad[c]	0	1000	237940.1 or 237940.2 or 11754.1 or 76507.1	Mouse metabolic/ transport/ demand reaction
MMNNATm	MMft[m] + MMatp[m] + MMnicrn[m] -> MMppi[m] + MMnad[m]	0	1000	18605.1 or 18606.1 or 209558.1	Mouse metabolic/ transport/ demand reaction
MMNNATn	MMatp[n] + MMft[n] + MMnicrn[n] -> MMppi[n] + MMnad[n]	0	1000	74080.1	Mouse metabolic/ transport/ demand reaction
MMNNATr	MMatp[c] + MMft[c] + MMnicrn[c] <=> MMppi[c] + MMnad[c]	-1000	1000	66454.1	Mouse metabolic/ transport/ demand reaction
MMNNDPR	2 MMft[c] + MMprpp[c] + MMquln[c] -> MMco2[c] + MMppi[c] + MMnicrn[c]	0	1000	226518.1 or 226518.2 or 74080.1	Mouse metabolic/ transport/ demand reaction
MMNNMT	MMamet[c] + MMncam[c] -> MM1mncam[c] + MMahcys[c]	0	1000	67375.1	Mouse metabolic/ transport/ demand reaction
MMNORANMT	MMamet[c] + MMnrpphr[c] -> MMft[c] + MMahcys[c] + MMadrnl[c]	0	1000	18113.1	Mouse metabolic/ transport/ demand reaction
MMNOS1	MMo2[c] + MMft[c] + MMnadph[c] + MMarg-L[c] -> MMh2o[c] + MMnadp[c] + MMnwharg[c]	0	1000	18948.1	Mouse metabolic/ transport/ demand reaction
MMNOS2	2 MMo2[c] + MMnadph[c] + 2 MMnwharg[c] -> 2 MMh2o[c] + MMft[c] + MMnadp[c] + 2 MMcitr-L[c] + 2 MMno[c]	0	1000	18125.1 or 18126.1 or 18126.2 or 18127.1	Mouse metabolic/ transport/ demand reaction
MMNOt	MMno[e] <=> MMno[c]	0	1000	18125.1 or 18126.1 or 18126.2 or 18127.1	Mouse metabolic/ transport/ demand reaction
MMNP1	MMft[c] + MMnac[c] + MMr1p[c] -> MMpi[c] + MMnicrn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMNPTHLte	MMnpthl[e] <=> MMnpthl[c]	0	1000	667034.1	Mouse metabolic/ transport/ demand reaction
MMNRPPHRSFt	MMnrpphrsf[c] -> MMnrpphrsf[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMNRPPHRVESSEC	MMh2o[c] + MMatp[c] + MMnrpphr[c] -> MMadp[c] + 2 MMft[c] + MMpi[c] + MMnrpphr[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMNRPPHRt4_2_r	2 MMnn1[e] + MMnrpphr[e] <=> 2 MMnn1[c] + MMnrpphr[c]	0	1000	214084.1 or 110877.1	Mouse metabolic/ transport/ demand reaction
MMNRPPHRtu	MMnrpphr[e] <=> MMnrpphr[c]	0	1000	20538.1 or 13162.1	Mouse metabolic/ transport/ demand reaction
MMNRVNCCOAtx	MMnrvnccoa[c] <=> MMnrvnccoa[x]	-1000	1000	20518.1 or 20519.1 or 20518.2	Mouse metabolic/ transport/ demand reaction
MMNRVNCCPT1	MMcrn[c] + MMnrvnccoa[c] -> MMcoa[c] + MMnrvnccrn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMNRVNCCPT2	MMcoa[m] + MMnrvnccrn[m] -> MMcrn[m] + MMnrvnccoa[m]	0	1000	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	Mouse metabolic/ transport/ demand reaction
MMNRVNCCRNt	MMnrvnccrn[c] -> MMnrvnccrn[m]	0	1000	12896.1	Mouse metabolic/ transport/ demand reaction
MMNRVNCt	MMnrvnc[e] <=> MMnrvnc[c]	0	1000	57279.1	Mouse metabolic/ transport/ demand reaction
MMNS26T2g	MMempacna[g] + MMsT_antigen[g] -> MMh[g] + MMcmp[g] + MMdsT_antigen[g]	0	1000		Mouse metabolic/ transport/ demand reaction
MMNS26Tg	MMempacna[g] + MMTn_antigen[g] -> MMh[g] + MMcmp[g] + MMsTn_antigen[g]	0	1000	20445.1	Mouse metabolic/ transport/ demand reaction
MMNT5C	MMh2o[c] + MMnicrnt[c] -> MMpi[c] + MMnicrns[c]	0	1000	20445.1	Mouse metabolic/ transport/ demand reaction
MMNTD1	MMh2o[c] + MMdump[c] -> MMpi[c] + MMdur[c]	0	1000	76952.1	Mouse metabolic/ transport/ demand reaction
MMNTD10	MMh2o[c] + MMxmp[c] -> MMpi[c] + MMxtxt[c]	0	1000	50773.1	Mouse metabolic/ transport/ demand reaction
MMNTD12	MMh2o[c] + MMdmp[c] -> MMpi[c] + MMdin[c]	0	1000	76952.1	Mouse metabolic/ transport/ demand reaction
MMNTD1m	MMh2o[m] + MMdump[m] -> MMpi[m] + MMdur[m]	0	1000	50773.1	Mouse metabolic/ transport/ demand reaction
MMNTD2	MMh2o[c] + MMump[c] -> MMpi[c] + MMuri[c]	0	1000	103850.1	Mouse metabolic/ transport/ demand reaction
MMNTD2e	MMh2o[e] + MMump[e] -> MMpi[e] + MMuri[e]	0	1000	107569.1	Mouse metabolic/ transport/ demand reaction
MMNTD2l	MMh2o[l] + MMump[l] -> MMpi[l] + MMuri[l]	0	1000	23959.1	Mouse metabolic/ transport/ demand reaction
MMNTD2m	MMh2o[m] + MMump[m] -> MMpi[m] + MMuri[m]	0	1000	11432.1	Mouse metabolic/ transport/ demand reaction
MMNTD3l	MMh2o[l] + MMdcmp[l] -> MMpi[l] + MMdcyt[l]	0	1000	103850.1	Mouse metabolic/ transport/ demand reaction
MMNTD4	MMh2o[c] + MMcmp[c] -> MMpi[c] + MMcytd[c]	0	1000	11432.1	Mouse metabolic/ transport/ demand reaction
MMNTD4e	MMh2o[e] + MMcmp[e] -> MMpi[e] + MMcytd[e]	0	1000	107569.1	Mouse metabolic/ transport/ demand reaction
MMNTD4l	MMh2o[l] + MMcmp[l] -> MMpi[l] + MMcytd[l]	0	1000	23959.1	Mouse metabolic/ transport/ demand reaction
MMNTD5	MMh2o[c] + MMdtmp[c] -> MMpi[c] + MMthymd[c]	0	1000	11432.1	Mouse metabolic/ transport/ demand reaction
MMNTD5l	MMh2o[l] + MMdtmp[l] -> MMpi[l] + MMthymd[l]	0	1000	50773.1	Mouse metabolic/ transport/ demand reaction
MMNTD5m	MMh2o[m] + MMdtmp[m] -> MMpi[m] + MMthymd[m]	0	1000	11432.1	Mouse metabolic/ transport/ demand reaction
MMNTD6	MMh2o[c] + MMdamp[c] -> MMpi[c] + MMdad-2[c]	0	1000	103850.1	Mouse metabolic/ transport/ demand reaction
MMNTD6l	MMh2o[l] + MMdamp[l] -> MMpi[l] + MMdad-2[l]	0	1000	76952.1	Mouse metabolic/ transport/ demand reaction
MMNTD7e	MMh2o[e] + MMamp[e] -> MMadn[e] + MMpi[e]	0	1000	11432.1	Mouse metabolic/ transport/ demand reaction
MMNTD7l	MMh2o[l] + MMamp[l] -> MMadn[l] + MMpi[l]	0	1000	23959.1	Mouse metabolic/ transport/ demand reaction
MMNTD8	MMh2o[c] + MMdgmp[c] -> MMpi[c] + MMdgsn[c]	0	1000	11432.1	Mouse metabolic/ transport/ demand reaction
MMNTD8l	MMh2o[l] + MMdgmp[l] -> MMpi[l] + MMdgsn[l]	0	1000	50773.1 or 76952.1	Mouse metabolic/ transport/ demand reaction
MMNTD9	MMh2o[c] + MMgmp[c] -> MMpi[c] + MMgsn[c]	0	1000	11432.1	Mouse metabolic/ transport/ demand reaction
MMNTD9e	MMh2o[e] + MMgmp[e] -> MMpi[e] + MMgsn[e]	0	1000	76952.1	Mouse metabolic/ transport/ demand reaction
MMNTD9l	MMh2o[l] + MMgmp[l] -> MMpi[l] + MMgsn[l]	0	1000	23959.1	Mouse metabolic/ transport/ demand reaction
MMNTMELYSmer	MMNtmelys[n] -> MMNtmelys[r]	0	1000	11432.1	Mouse metabolic/ transport/ demand reaction
MMNTP3e	MMh2o[e] + MMgtp[e] -> MMh[e] + MMpi[e] + MMgslp[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMNTPP10	MMh2o[c] + MMditp[c] -> MMft[c] + MMppi[c] + MMdimp[c]	0	1000	76025.1	Mouse metabolic/ transport/ demand reaction
MMNTPP11	MMh2o[c] + MMxtp[c] -> MMft[c] + MMppi[c] + MMxmp[c]	0	1000	16434.1 or 16434.2	Mouse metabolic/ transport/ demand reaction
MMNTPP9	MMh2o[c] + MMtp[c] -> MMft[c] + MMppi[c] + MMimp[c]	0	1000	16434.1 or 16434.2	Mouse metabolic/ transport/ demand reaction
MMO16G1e	MMh2o[e] + MMglygn4[e] -> MMglc-D[e] + MMglygn5[e]	0	1000	16434.1 or 16434.2	Mouse metabolic/ transport/ demand reaction
MMO16G2e	MMh2o[e] + MMstrch2[e] -> MMglc-D[e] + MMmalt[e]	0	1000	69983.1	Mouse metabolic/ transport/ demand reaction
MMO2St	MMo2s[c] <=> MMo2s[e]	-1000	0	69983.1	Mouse metabolic/ transport/ demand reaction
MMO2Stm	MMo2s[c] <=> MMo2s[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMO2Stn	MMo2s[c] <=> MMo2s[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMO2Stx	MMo2s[c] <=> MMo2s[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMO2t	MMo2[e] <=> MMo2[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMO2ter	MMo2[c] <=> MMo2[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMO2tm	MMo2[c] <=> MMo2[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMO2tn	MMo2[c] <=> MMo2[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMO2tp	MMo2[c] <=> MMo2[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMOAGD3te	MMoagd3_hs[c] <=> MMoagd3_hs[e]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMOAGD3tg	MMoagd3_hs[c] <=> MMoagd3_hs[g]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMOAGT3te	MMoagt3_hs[c] <=> MMoagt3_hs[e]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMOAGT3tg	MMoagt3_hs[c] <=> MMoagt3_hs[g]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMOBDHc	MMnad[c] + MMcoa[c] + MM2obut[c] -> MMnadh[c] + MMco2[c] + MMppcoa[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMOCBTm	MMorn[m] + MMchp[m] -> MMft[m] + MMpi[m] + MMcitr-L[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMOCCOAtm	MMoccoa[c] -> MMoccoa[m]	0	1000	18416.1	Mouse metabolic/ transport/ demand reaction
MMOCCOAtx	MMoccoa[c] <=> MMoccoa[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMOCDCAtr	MMocdca[e] <=> MMocdca[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMOCDCEAtr	MMocdcea[e] <=> MMocdcea[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMOCDEAFABP1tc	2 MMocdcea[c] <=> 2 MMocdcea[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMOCOAT1m	MMacac[m] + MMsuccoa[m] <=> MMaacoa[m] + MMsucc[m]	-1000	1000	14080.1	Mouse metabolic/ transport/ demand reaction
MMOCTAt	MMocta[e] <=> MMocta[c]	0	1000	67041.1 or 64059.1	Mouse metabolic/ transport/ demand reaction
MMODECOAtx	MModecoa[c] <=> MModecoa[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMOIVD1m	MMcoa[m] + MMnad[m] + MM4mop[m] -> MMco2[m] + MMnadh[m] + MMdccoa[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMOIVD2m	MMcoa[m] + MMnad[m] + MM3meb[m] -> MMco2[m] + MMnadh[m] + MMbccoa[m]	0	1000	13171.1 or 12040.1 and 12039.1 or 12039.1 and 12040.2 or 13382.1	Mouse metabolic/ transport/ demand reaction

MMOIVD3m	MMcoa[m] + MMnad[m] + MMcbrasp[m] -> MMco2[m] + MMnadh[m] + MM2mbcoa[m]	0	1000	13171.1 or 12040.1 and 12039.1 or 12039.1 and 12040.2 or 13382.1	Mouse metabolic/ transport/ demand reaction
MMOLEICFATPtc	MMatp[c] + MMcoa[c] + MMocdcea[u] -> MMamp[c] + MMppi[c] + MModecoa[c]	0	1000	13171.1 or 12040.1 and 12039.1 or 12039.1 and 12040.2 or 13382.1	Mouse metabolic/ transport/ demand reaction
MMOMEPRAZOLEte	MMomeprazole[e] <=> MMomeprazole[c]	0	1000	26569.1	Mouse metabolic/ transport/ demand reaction
MMOMPDC	MMh[c] + MMoroa5p[c] -> MMco2[c] + MMumpi[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMONPTHLte	MMonpthl[e] <=> MMonpthl[c]	0	1000	22247.1	Mouse metabolic/ transport/ demand reaction
MMOPAHir	2 MMh2o[c] + MMatp[c] + MMSoxpro[c] -> MMadp[c] + MMh[c] + MMpi[c] + MMglu-L[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMORETNF	MMo2[c] + 2 MMretn[c] -> 2 MMoretn[c]	0	1000	75475.1	Mouse metabolic/ transport/ demand reaction
MMORETNF2	MMo2[c] + 2 MM13-cis-retn[c] -> 2 MM13-cis-oretn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMORETNtn	MMoretn[c] <=> MMoretn[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMORETNtn2	MM13-cis-oretn[c] <=> MM13-cis-oretn[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMORNALArBATIc	MMala-L[c] + MMorn[u] -> MMorn[c] + MMala-L[u]	0	1000		Mouse metabolic/ transport/ demand reaction
MMORNDC	MMh[c] + MMorn[c] -> MMco2[c] + MMptrc[c]	0	1000	(30962.1 and 20532.1)	Mouse metabolic/ transport/ demand reaction
MMORNLEUtBATIc	MMleu-L[c] + MMorn[u] -> MMleu-L[u] + MMorn[c]	0	1000	18263.1	Mouse metabolic/ transport/ demand reaction
MMORNTArm	MMakg[m] + MMorn[m] <=> MMglu-L[m] + MMglu5sa[m]	-1000	1000	(30962.1 and 20532.1)	Mouse metabolic/ transport/ demand reaction
MMORNt	MMorn[e] <=> MMorn[c]	-1000	1000	18242.1	Mouse metabolic/ transport/ demand reaction
MMORNt3m	MMh[c] + MMorn[m] <=> MMh[m] + MMorn[c]	-1000	1000	11987.1	Mouse metabolic/ transport/ demand reaction
MMORNt4m	MMh[c] + MMorn[m] + MMcit-L[c] <=> MMh[m] + MMorn[c] + MMcit-L[m]	-1000	1000	18408.1 or 83885.1	Mouse metabolic/ transport/ demand reaction
MMORNtiDF	MMorn[e] -> MMorn[c]	0	1000	18408.1 or 83885.1	Mouse metabolic/ transport/ demand reaction
MMORPT	MMppi[c] + MMoroa5p[c] <=> MMprpp[c] + MMoroa[c]	-1000	1000	11989.1 or 11988.1 or 11987.1	Mouse metabolic/ transport/ demand reaction
MMOXAHCOtex	2 MMhco3[c] + MMoxa[e] -> 2 MMhco3[e] + MMoxa[c]	0	1000	22247.1	Mouse metabolic/ transport/ demand reaction
MMOXAtp	MMoxa[x] -> MMoxa[c]	0	1000	13487.1 or 231583.1 or 13521.1 or 231583.2 or 231583.3	Mouse metabolic/ transport/ demand reaction
MMP45011A1m	MMh[m] + MMnadph[m] + 2 MMo2[m] + MMchsterol[m] -> 2 MMh2o[m] + MMnadp[m] + MM4mpnt[m] + MMpregalone[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMP45011B11m	MM11docrtstrn[m] + MMh[m] + MMnadph[m] + MMo2[m] -> MMh2o[m] + MMnadp[m] + MMcrtstrn[m]	0	1000	13070.1	Mouse metabolic/ transport/ demand reaction
MMP45011B12m	MM11docrts[m] + MMh[m] + MMnadph[m] + MMo2[m] -> MMh2o[m] + MMnadp[m] + MMcrts[m]	0	1000	110115.1	Mouse metabolic/ transport/ demand reaction
MMP45011B21m	MM11docrtstrn[m] + MMh[m] + MMnadph[m] + 2 MMo2[m] -> 2 MMh2o[m] + MMnadp[m] + MMaldstrn[m]	0	1000	110115.1	Mouse metabolic/ transport/ demand reaction
MMP45017A1r	MMo2[r] + MMh[r] + MMnadph[r] + MMpregalone[r] -> MMh2o[r] + MMnadp[r] + MM17ahpregalone[r]	0	1000	13072.1	Mouse metabolic/ transport/ demand reaction
MMP45017A2r	0.5 MMo2[r] + MMh[r] + MMnadph[r] + MM17ahpregalone[r] -> MMacaldt[r] + MMh2o[r] + MMnadp[r] + MMdhea[r]	0	1000	13074.1	Mouse metabolic/ transport/ demand reaction
MMP45017A3r	MMo2[r] + MMh[r] + MMnadph[r] + MMprgstrn[r] -> MMh2o[r] + MMnadp[r] + MM17ahpregstrn[r]	0	1000	13074.1	Mouse metabolic/ transport/ demand reaction
MMP45017A4r	0.5 MMo2[r] + MMh[r] + MMnadph[r] + MM17ahpregstrn[r] -> MMacaldt[r] + MMh2o[r] + MMnadp[r] + MMandrstndn[r]	0	1000	13074.1	Mouse metabolic/ transport/ demand reaction
MMP45019A1r	2 MMo2[r] + MMnadph[r] + MMandrstndn[r] -> 2 MMh2o[r] + MMnadp[r] + MMestrone[r] + MMfor[r]	0	1000	13074.1	Mouse metabolic/ transport/ demand reaction
MMP45019A2r	2 MMo2[r] + MMnadph[r] + MMteststerone[r] -> 2 MMh2o[r] + MMnadp[r] + MMestradiol[r] + MMfor[r]	0	1000	13075.1 or 13075.2	Mouse metabolic/ transport/ demand reaction
MMP4501B1r	MMo2[r] + MMh[r] + MMnadph[r] + MMestradiol[r] -> MMh2o[r] + MMnadp[r] + MMhestratriol[r]	0	1000	13075.1 or 13075.2	Mouse metabolic/ transport/ demand reaction
MMP45021A1r	MMo2[r] + MMh[r] + MMnadph[r] + MMprgstrn[r] -> MM11docrtstrn[r] + MMh2o[r] + MMnadp[r]	0	1000	13078.1	Mouse metabolic/ transport/ demand reaction
MMP45021A2r	MMo2[r] + MMh[r] + MMnadph[r] + MM17ahpregstrn[r] -> MM11docrts[r] + MMh2o[r] + MMnadp[r]	0	1000	13079.1	Mouse metabolic/ transport/ demand reaction
MMP45027A11m	MMh[m] + MMnadph[m] + MMo2[m] + MMxoltriol[m] -> MMh2o[m] + MMnadp[m] + MMxoltetrol[m]	0	1000	13079.1	Mouse metabolic/ transport/ demand reaction
MMP45027A12m	MMnadp[m] + MMxoltetrol[m] -> MMh[m] + MMnadph[m] + MMthcholst[m]	0	1000	104086.1	Mouse metabolic/ transport/ demand reaction
MMP45027A13m	MMnadph[m] + MMo2[m] + MMthcholst[m] -> MMh2o[m] + MMnadp[m] + MMthcholstoic[m]	0	1000	104086.1	Mouse metabolic/ transport/ demand reaction
MMP45027A14m	MMh[m] + MMnadph[m] + MMo2[m] + MMxol7ah2[m] -> MMh2o[m] + MMnadp[m] + MMxol7ah3[m]	0	1000	104086.1	Mouse metabolic/ transport/ demand reaction
MMP45027A15m	MMh[m] + MMnadph[m] + MMo2[m] + MMxol7ah3[m] -> 2 MMh2o[m] + MMnadp[m] + MMxol7ah2a[m]	0	1000	104086.1	Mouse metabolic/ transport/ demand reaction
MMP45027A16m	MMnadph[m] + MMo2[m] + MMxol7ah2a[m] -> MMh2o[m] + MMnadp[m] + MMdhcholestanate[m]	0	1000	104086.1	Mouse metabolic/ transport/ demand reaction
MMP45027A1m	MMh[m] + MMnadph[m] + MMo2[m] + MMchsterol[m] -> MMh2o[m] + MMnadp[m] + MMxol27oh[m]	0	1000	104086.1	Mouse metabolic/ transport/ demand reaction
MMP4502C18	0.5 MMo2[c] + MMh[c] + MMnadph[c] + MMantipyrene[c] -> MMnadp[c] + MMdmantipyrine[c] + MMmeoh[c]	0	1000	104086.1	Mouse metabolic/ transport/ demand reaction
MMP4502C19	MMo2[c] + MMh[c] + MMnadph[c] + MMomeprazole[c] -> MMh2o[c] + MMnadp[c] + MM5homeprazole[c]	0	1000	72082.1	Mouse metabolic/ transport/ demand reaction
MMP4502C8	MMo2[c] + MMh[c] + MMnadph[c] + MMtaxol[c] -> MMh2o[c] + MMnadp[c] + MMttaxol[c]	0	1000	404195.1	Mouse metabolic/ transport/ demand reaction
MMP4502D6	MMo2[c] + MMh[c] + MMnadph[c] + MMdebrisoquine[c] -> MMh2o[c] + MMnadp[c] + MM4hdebrisoquine[c]	0	1000	69888.1 or 69888.2	Mouse metabolic/ transport/ demand reaction
MMP4502E1	MMo2[c] + MMh[c] + MMnadph[c] + MM4nph[c] -> MMh2o[c] + MM24nph[c] + MMnadp[c]	0	1000	56448.1	Mouse metabolic/ transport/ demand reaction
MMP4502F1	MMo2[c] + MMh[c] + MMnadph[c] + MMapnh[c] -> MMh2o[c] + MMnadp[c] + MMoxpnh[c]	0	1000	13106.1	Mouse metabolic/ transport/ demand reaction
MMP45039A1r	MMo2[r] + MMh[r] + MMnadph[r] + MMxol24oh[r] -> MMh2o[r] + MMnadp[r] + MMxoltri24[r]	0	1000	13107.1	Mouse metabolic/ transport/ demand reaction
MMP4503A4	MMo2[c] + MMh[c] + MMnadph[c] + MMnifedipine[c] -> MMh2o[c] + MMnadp[c] + MMdnifedipine[c]	0	1000	56050.1	Mouse metabolic/ transport/ demand reaction
MMP4503A43r	MMo2[r] + MMh[r] + MMnadph[r] + MMtestosterone[r] -> MMh2o[r] + MMnadp[r] + MMwbteststerone[r]	0	1000	100041375.1	Mouse metabolic/ transport/ demand reaction
MMP4503A5	MMo2[c] + MMh[c] + MMnadph[c] + MMaflatoxin[c] -> MMh2o[c] + MMnadp[c] + MMeaflatoxin[c]	0	1000	56388.1 or 56388.2 or 56388.3	Mouse metabolic/ transport/ demand reaction
MMP4503A7r	MMo2[r] + MMh[r] + MMnadph[r] + MMteststerone[r] -> MM6hteststerone[r] + MMh2o[r] + MMnadp[r]	0	1000		Mouse metabolic/ transport/ demand reaction
MMP45046A1r	MMo2[r] + MMh[r] + MMnadph[r] + MMchsterol[r] -> MMh2o[r] + MMnadp[r] + MMxol24oh[r]	0	1000	13113.1	Mouse metabolic/ transport/ demand reaction
MMP4504B1r	MMo2[r] + MMarachd[r] + MMh[r] + MMnadph[r] -> MMh2o[r] + MMnadp[r] + MM12harachd[r]	0	1000	13116.1	Mouse metabolic/ transport/ demand reaction
MMP4504F121r	MMo2[r] + MMarachd[r] + MMh[r] + MMnadph[r] -> MMh2o[r] + MMnadp[r] + MMwharachd[r]	0	1000	13107.1	Mouse metabolic/ transport/ demand reaction
MMP4504F122r	MMo2[r] + MMh[r] + MMnadph[r] + MMleuktrB4[r] -> MMh2o[r] + MMnadp[r] + MMleuktrB4wcoh[r]	0	1000	64385.1	Mouse metabolic/ transport/ demand reaction
MMP4504F123r	MMo2[r] + MMh[r] + MMnadph[r] + MMebastine[r] -> MMh2o[r] + MMnadp[r] + MMebastineoh[r]	0	1000	106648.1 or 64385.1 or 72054.1	Mouse metabolic/ transport/ demand reaction
MMP4504F81r	MMo2[r] + MMarachd[r] + MMh[r] + MMnadph[r] -> MMh2o[r] + MMnadp[r] + MM18harachd[r]	0	1000	64385.1	Mouse metabolic/ transport/ demand reaction
MMP4507A1r	MMo2[r] + MMh[r] + MMnadph[r] + MMchsterol[r] -> MMh2o[r] + MMnadp[r] + MMxol7a[r]	0	1000	208285.1	Mouse metabolic/ transport/ demand reaction
MMP4507B11r	MMo2[r] + MMh[r] + MMnadph[r] + MMxol25oh[r] -> MMh2o[r] + MMnadp[r] + MMxoltri25[r]	0	1000	13122.1	Mouse metabolic/ transport/ demand reaction
MMP4507B12r	MMo2[r] + MMh[r] + MMnadph[r] + MMxol27oh[r] -> MMh2o[r] + MMnadp[r] + MMxoltri27[r]	0	1000	13123.1	Mouse metabolic/ transport/ demand reaction
MMP4508B11r	MMo2[r] + MMh[r] + MMnadph[r] + MMxol7aone[r] -> MMh2o[r] + MMnadp[r] + MMxoldiolone[r]	0	1000	13123.1	Mouse metabolic/ transport/ demand reaction
MMP4508B13r	MMo2[r] + MMh[r] + MMnadh[r] + MMxol7aone[r] -> MMh2o[r] + MMnad[r] + MMxoldiolone[r]	0	1000	13124.1	Mouse metabolic/ transport/ demand reaction
MMP450LTB4r	1.5 MMo2[r] + MMnadph[r] + MMleuktrB4wodn[r] -> 2 MMh2o[r] + MMnadp[r] + MMleuktrB4wcooh[r]	0	1000	13124.1	Mouse metabolic/ transport/ demand reaction
MMP450SCC1m	MMh[m] + MMnadph[m] + MMo2[m] + MMchsterol[m] <=> MMh2o[m] + MMnadp[m] + MM20ahchsterol[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMP5CDm	2 MMh2o[m] + MMnad[m] + MM1pyr5c[m] -> MMh[m] + MMnadh[m] + MMglu-L[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMP5CR	2 MMh[c] + MMnadph[c] + MM1pyr5c[c] -> MMnadp[c] + MMpro-L[c]	0	1000	212647.1 or 212647.2	Mouse metabolic/ transport/ demand reaction
MMP5CRm	2 MMh[m] + MMnadph[m] + MM1pyr5c[m] -> MMnadp[m] + MMpro-L[m]	0	1000	69051.1 or 66194.1	Mouse metabolic/ transport/ demand reaction
MMP5CRx	2 MMh[c] + MMnadh[c] + MM1pyr5c[c] -> MMnad[c] + MMpro-L[c]	0	1000	209027.1 or 209027.2	Mouse metabolic/ transport/ demand reaction
MMP5CRxm	2 MMh[m] + MMnadh[m] + MM1pyr5c[m] -> MMnad[m] + MMpro-L[m]	0	1000	69051.1 or 66194.1	Mouse metabolic/ transport/ demand reaction
MMPACCOAL	MMatp[c] + MMcoa[c] + MMpac[c] -> MMamp[c] + MMppi[c] + MMphaccoa[c]	0	1000	209027.1 or 209027.2	Mouse metabolic/ transport/ demand reaction
MMPAFH	MMh2o[e] + MMpaf_hs[e] -> MMh[e] + MMac[e] + MMak2lgchol_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPAFHe	MMh2o[e] + MMpaf_hs[e] -> MMh[e] + MMac[e] + MMak2lgchol_hs[e]	0	1000	18476.1 and 18475.1 or 18472.1 and 18476.1 and 18475.1 or 100163.1	Mouse metabolic/ transport/ demand reaction
MMPAFS	MMaccoa[c] + MMak2lgchol_hs[c] -> MMcoa[c] + MMpaf_hs[c]	0	1000	27226.1	Mouse metabolic/ transport/ demand reaction
MMPAFt	MMpaf_hs[e] <=> MMpaf_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPAIL45P_HStn	MMpail45p_hs[c] <=> MMpail45p_hs[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPAIL4P_HStn	MMpail4p_hs[c] <=> MMpail4p_hs[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction

MMPAIL_HStn	MMpail_hs[c] <=> MMpail_hs[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPALFATPtc	MMatp[c] + MMcoa[c] + MMhdca[u] -> MMamp[c] + MMppi[c] + MMpmtcoa[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPAN4PP	MMh2o[c] + MMpan4p[c] -> MMpi[c] + MMpnth[c]	0	1000	26569.1	Mouse metabolic/ transport/ demand reaction
MMPAPStg	MMpaps[c] <=> MMpaps[g]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPAPtg	MMpap[g] -> MMpap[c]	0	1000	73836.1	Mouse metabolic/ transport/ demand reaction
MMPA_HSter	MMpa_hs[c] <=> MMpa_hs[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPA_HStg	MMpa_hs[c] <=> MMpa_hs[g]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPA_HStn	MMpa_hs[c] <=> MMpa_hs[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPCFLOPm	MMh2o[c] + MMatp[c] + MMpchol_hs[m] -> MMadp[c] + MMhc[c] + MMpi[c] + MMpchol_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPCHOLHSTDe	MMpchol_hs[c] -> MMpchol_hs[e]	0	1000	11982.1	Mouse metabolic/ transport/ demand reaction
MMPCHOLP_hs	MMh2o[c] + MMpchol_hs[c] -> MMhc[c] + MMpa_hs[c] + MMchol[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPCHOLPg_hs	MMh2o[g] + MMpchol_hs[g] -> MMhc[g] + MMchol[g] + MMpa_hs[g]	0	1000	18806.1	Mouse metabolic/ transport/ demand reaction
MMPCHOLPm_hs	MMh2o[m] + MMpchol_hs[m] -> MMhc[m] + MMpa_hs[m] + MMchol[m]	0	1000	18805.1	Mouse metabolic/ transport/ demand reaction
MMPCHOLPr_hs	MMh2o[r] + MMpchol_hs[r] -> MMhc[r] + MMchol[r] + MMpa_hs[r]	0	1000	18805.1	Mouse metabolic/ transport/ demand reaction
MMPCHOL_HSter	MMpchol_hs[c] <=> MMpchol_hs[r]	-1000	1000	18805.1	Mouse metabolic/ transport/ demand reaction
MMPCHOL_HStg	MMpchol_hs[c] <=> MMpchol_hs[g]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPCLAD	MMh[c] + MMcmusa[c] -> MMco2[c] + MMam6sa[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPCLYSOX	MMo2[c] + MMalag[c] + MMpcollglys[c] -> MMco2[c] + MMsucc[c] + MMpcollg2hlys[c]	0	1000	266645.1	Mouse metabolic/ transport/ demand reaction
MMPCREATImdiffir	MMpcreat[m] -> MMpcreat[c]	0	1000	26432.1 or 18822.1 or 26432.2 or 26433.1	Mouse metabolic/ transport/ demand reaction
MMPCRNtc	MMpcrn[x] -> MMpcrn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPCRNtm	MMpcrn[c] -> MMpcrn[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPCm	MMpyr[m] + MMatp[m] + MMhco3[m] -> MMh[m] + MMadp[m] + MMpi[m] + MMoaa[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPCt	MMh2o[c] + MMatp[c] + MMpchol_hs[c] <=> MMadp[c] + MMhc[c] + MMpchol_hs[e]	-1000	1000	18563.1 or 18563.2	Mouse metabolic/ transport/ demand reaction
MMPDE1	MMh2o[c] + MMcamp[c] -> MMh[c] + MMamp[c]	0	1000	18670.1 or 18670.2 or 18670.3	Mouse metabolic/ transport/ demand reaction
MMPDE1g	MMh2o[g] + MMcamp[g] -> MMh[g] + MMamp[g]	0	1000	18576.1 or 18584.1 or 18578.1 or 18584.2 or 18583.1 or 18584.3 or 18584.4 or 23984.1 or 241489.1 or 207728.1 or 110385.1 or 18577.1 or 54611.1 or 18576.2 or 29863.1 or 18574.1 or 18573.2 or 18575.1 or 218461.1 or 18584.5 or 238871.1 or 18583.2 or 18573.1	Mouse metabolic/ transport/ demand reaction
MMPDE4	MMh2o[c] + MM35cgmp[c] -> MMh[c] + MMgmp[c]	0	1000	23984.1	Mouse metabolic/ transport/ demand reaction
MMPDE4g	MMh2o[g] + MM35cgmp[g] -> MMh[g] + MMgmp[g]	0	1000	225600.1 and 78600.1 and 18587.1 or 18576.1 or 110855.1 or 18585.1 or 18585.2 or 18585.3 or 18585.4 or 18585.5 or 241489.1 or 207728.1 or 18585.6 or 18585.7 or 18585.8 or 18585.9 or 54611.1 or 18576.1 or 18585.10 or 18574.1 or 18588.1 and 225600.1 and 18582.1 and 110855.1 and 18587.1 or 18573.1 or 18585.11 or 18585.12 or 18585.13 or 18585.14 or 23984.1 or 242202.3 or 18585.15 or 18585.16 or 242202.2 or 242202.1 or 18573.1 or 18575.1 or 18585.17 or 18585.18 or 18585.19	Mouse metabolic/ transport/ demand reaction
MMPDHm	MMcoa[m] + MMnad[m] + MMpyr[m] -> MMco2[m] + MMnadh[m] + MMaccoa[m]	0	1000	23984.1	Mouse metabolic/ transport/ demand reaction
MMPDX5PO	MMo2[c] + MMpdx5p[c] <=> MMh2o2[c] + MMpydx5p[c]	-1000	1000	18597.1 and 68263.1 or 27402.1 and 13382.1 or 68263.1 and 18598.1 or 235339.1	Mouse metabolic/ transport/ demand reaction
MMPDXPP	MMh2o[c] + MMpdx5p[c] -> MMpi[c] + MMpydxn[c]	0	1000	103711.1	Mouse metabolic/ transport/ demand reaction
MMPEAMNO	MMh2o[c] + MMo2[c] + MMpeamn[c] -> MMh2o2[c] + MMnh4[c] + MMpacald[c]	0	1000	57028.1	Mouse metabolic/ transport/ demand reaction
MMPECDCHe	MMh[u] + MMpect[u] + MMdchac[u] -> MMpectindchac[u]	0	1000	109731.1 or 237940.1 or 17161.1 or 237940.2 or 76507.1	Mouse metabolic/ transport/ demand reaction
MMPECDCHt	MMh[e] + MMpectindchac[e] <=> MMh[c] + MMpectindchac[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPECGCHLe	MMh[u] + MMgchola[u] + MMpect[u] -> MMpectingchol[u]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPECGCHLt	MMh[e] + MMpectingchol[e] <=> MMh[c] + MMpectingchol[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPECGONCOATr	MMatp[r] + MMh[r] + MMcoa[r] + MMpecgon[r] -> MMamp[r] + MMppi[r] + MMpecgoncoa[r]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPECTCHLe	MMh[u] + MMtchola[u] + MMpect[u] -> MMpectintchol[u]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPECTCHLt	MMh[e] + MMpectintchol[e] <=> MMh[c] + MMpectintchol[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPECTt	MMh[e] + MMpect[e] <=> MMh[c] + MMpect[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPEFLIP	MMh2o[c] + MMatp[c] + MMpe_hs[e] -> MMadp[c] + MMh[c] + MMpi[c] + MMpe_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPEFLIPm	MMh2o[c] + MMatp[c] + MMpe_hs[c] -> MMadp[c] + MMh[c] + MMpi[c] + MMpe_hs[m]	0	1000	11982.1 or 11980.1	Mouse metabolic/ transport/ demand reaction
MMPEHSFABPe	2 MMpe_hs[c] <=> 2 MMpe_hs[r]	-1000	1000	11982.1 or 11980.1	Mouse metabolic/ transport/ demand reaction
MMPEPCK	MMoaa[c] + MMgtp[c] -> MMco2[c] + MMpep[c] + MMgdp[c]	0	1000	14080.1	Mouse metabolic/ transport/ demand reaction
MMPEPCKm	MMgtp[m] + MMoaa[m] -> MMco2[m] + MMgdp[m] + MMpep[m]	0	1000	18534.1	Mouse metabolic/ transport/ demand reaction
MMPEPLYStn	MMpeplys[e] <=> MMpeplys[n]	-1000	1000	74551.1	Mouse metabolic/ transport/ demand reaction
MMPERILLYLte	MMperillyl[e] <=> MMperillyl[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPEROXx	3 MMnad[x] + 3 MMcoa[x] + 2 MMo2[x] + 3 MMh2o[x] + MMpristcoa[x] -> 3 MMh[x] + 3 MMnadh[x] + MMaccoa[x] + 2 MMh2o2[x] + MMdmnoncoa[x] + 2 MMppcoa[x]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPETHCT	MMh[c] + MMctp[c] + MMethamp[c] -> MMppi[c] + MMcdpea[c]	0	1000	74147.1 and 80911.1 and 113868.1 and 15488.1	Mouse metabolic/ transport/ demand reaction
MMPETOHMm_hs	3 MMamet[m] + MMpe_hs[m] -> 3 MMh[m] + 3 MMahcys[m] + MMpchol_hs[m]	0	1000	68671.1	Mouse metabolic/ transport/ demand reaction
MMPETOHMr_hs	3 MMamet[r] + MMpe_hs[r] -> 3 MMahcys[r] + 3 MMh[r] + MMpchol_hs[r]	0	1000	18618.1 or 18618.2 or 18618.3	Mouse metabolic/ transport/ demand reaction
MMPE_HSter	MMpe_hs[c] <=> MMpe_hs[r]	-1000	1000	18618.1 or 18618.2 or 18618.3	Mouse metabolic/ transport/ demand reaction
MMPE_HStg	MMpe_hs[c] <=> MMpe_hs[g]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPE_HStn	MMpe_hs[c] <=> MMpe_hs[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPEt	MMpe_hs[e] <=> MMpe_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPFK	MMatp[c] + MMf6p[c] -> MMadp[c] + MMh[c] + MMfdp[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPFK26	MMatp[c] + MMf6p[c] -> MMadp[c] + MMh[c] + MM26bp[c]	0	1000	56421.1 or 18641.1 and 18642.1 or 18642.1 and 18641.2 or 18641.1 or 56421.1 and 18642.1 or 18642.1 or 56421.1 and 18641.1 or 18641.2 or 56421.1 and 18641.2	Mouse metabolic/ transport/ demand reaction
MMPGCD	MMnad[c] + MM3pg[c] -> MMh[c] + MMnadh[c] + MM3php[c]	0	1000	18639.1 or 18640.1 or 270198.1 or 170768.1	Mouse metabolic/ transport/ demand reaction
MMPGDI	MMprostgh2[c] <=> MMprostgI2[c]	-1000	1000	236539.1	Mouse metabolic/ transport/ demand reaction
MMPGDIr	MMprostgh2[r] <=> MMprostgI2[r]	-1000	1000	54486.1 or 19215.1	Mouse metabolic/ transport/ demand reaction
MMPGESr	MMprostgh2[r] <=> MMprostge2[r]	-1000	1000	54486.1 or 19215.1	Mouse metabolic/ transport/ demand reaction
MMPGI	MMg6p[c] <=> MMf6p[c]	-1000	1000	96979.1 or 96979.2 or 64292.1 or 96979.3 or 64292.2 or 96979.4	Mouse metabolic/ transport/ demand reaction
MMPGISr	MMprostgh2[r] <=> MMprostgI2[r]	-1000	1000	14751.1	Mouse metabolic/ transport/ demand reaction
MMPGK	MMatp[c] + MM3pg[c] <=> MMadp[c] + MM13dpg[c]	-1000	1000	19223.1	Mouse metabolic/ transport/ demand reaction
MMPGL	MMh2o[c] + MM6pg[c] -> MMh[c] + MM6pgl[c]	0	1000	18663.1 or 18655.1	Mouse metabolic/ transport/ demand reaction
MMPGLYCP	MMh2o[c] + MM2pglyc[c] -> MMpi[c] + MMglycH[c]	0	1000	66171.1	Mouse metabolic/ transport/ demand reaction
MMPGLYCt	MMpglyc_hs[e] <=> MMpglyc_hs[c]	-1000	1000	67078.1	Mouse metabolic/ transport/ demand reaction
MMPGLer	MMh2o[r] + MM6pg[r] -> MMh[r] + MM6pgc[r]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPGM	MM2pg[c] <=> MM3pg[c]	-1000	1000	100198.1	Mouse metabolic/ transport/ demand reaction
MMPGMT	MMg1p[c] <=> MMg6p[c]	-1000	1000	12183.1 or 56012.1 or 18648.1 or 12183.2 or 56012.2	Mouse metabolic/ transport/ demand reaction
MMPGPPT	MMcdpdag_hs[c] + MMglyc3p[c] -> MMh[c] + MMcmp[c] + MMpgp_hs[c]	0	1000	72157.1 or 66681.1	Mouse metabolic/ transport/ demand reaction
MMPGPP_hs	MMh2o[c] + MMpgp_hs[c] -> MMpi[c] + MMpglyc_hs[c]	0	1000	74451.1	Mouse metabolic/ transport/ demand reaction
MMPGS	2 MMo2[c] + MMh[c] + MMnadph[c] + MMarachd[c] -> MMh2o[c] + MMnadp[c] + MMprostgh2[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPGSr	2 MMo2[r] + MMarachd[r] + MMh[r] + MMnadph[r] -> MMh2o[r] + MMnadp[r] + MMprostgh2[r]	0	1000	19225.1 or 19224.1	Mouse metabolic/ transport/ demand reaction
MMPHACCOAGLNAC	MMgln-L[c] + MMphaccoa[c] -> MMcoa[c] + MMpheacgln[c]	0	1000	19225.1 or 19224.1	Mouse metabolic/ transport/ demand reaction
MMPHCDm	2 MMh2o[m] + MMnad[m] + MM1p3h5c[m] -> MMh[m] + MMnadh[m] + MMe4hglu[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPHCHGSm	MMh[m] + MMh2o[m] + MM1p3h5c[m] <=> MM4hglusa[m]	-1000	1000	212647.1 or 212647.2	Mouse metabolic/ transport/ demand reaction
MMPHEACGLNt	MMpheacgln[c] <=> MMpheacgln[e]	-1000	0		Mouse metabolic/ transport/ demand reaction
MMPHEATB0tc	2 MMna1[u] + MMcl[u] + MMphe-L[u] -> 2 MMna1[c] + MMcl[c] + MMphe-L[c]	0	1000		Mouse metabolic/ transport/ demand reaction

MMPHEB0ATtc	MMna1[u] + MMphe-L[u] -> MMna1[c] + MMphe-L[c]	0	1000	56774.1	Mouse metabolic/ transport/ demand reaction
MMPHEILELAT2tc	MMile-L[c] + MMphe-L[e] <=> MMile-L[e] + MMphe-L[c]	-1000	1000	(70008.1 or (74338.1 and 57394.1))	Mouse metabolic/ transport/ demand reaction
MMPHELAT1tc	MMleu-L[c] + MMphe-L[u] -> MMleu-L[u] + MMphe-L[c]	0	1000	(20539.1 and 17254.1)	Mouse metabolic/ transport/ demand reaction
MMPHELAT3tc	MMphe-L[u] <=> MMphe-L[c]	-1000	1000	(20539.1 and 17254.1)	Mouse metabolic/ transport/ demand reaction
MMPHEMEt	MMpheme[e] -> MMpheme[c]	0	1000	72401.1	Mouse metabolic/ transport/ demand reaction
MMPHEMEtm	MMpheme[m] <=> MMpheme[c]	-1000	1000	52466.1	Mouse metabolic/ transport/ demand reaction
MMPHETA1	MMakg[c] + MMphe-L[c] <=> MMglu-L[c] + MMphpyr[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPHETA1m	MMakg[m] + MMphe-L[m] <=> MMglu-L[m] + MMphpyr[m]	-1000	1000	14718.1	Mouse metabolic/ transport/ demand reaction
MMPHETHPTOX2	MMo2[c] + MMphe-L[c] + MMhbpt[c] -> MMtyr-L[c] + MMhbpt4acam[c]	0	1000	234724.1 or 14719.1	Mouse metabolic/ transport/ demand reaction
MMPHEt4	MMna1[e] + MMphe-L[e] -> MMna1[c] + MMphe-L[c]	0	1000	18478.1	Mouse metabolic/ transport/ demand reaction
MMPHEyLATtc	MMna1[e] + MMphe-L[e] + MMarg-L[c] -> MMna1[c] + MMphe-L[c] + MMarg-L[e]	0	1000	105727.1 or 67760.1 or 69354.1 or 56774.1 or 11989.1 or 11988.1 or 11987.1	Mouse metabolic/ transport/ demand reaction
MMPHEyLATthc	MMh[e] + MMphe-L[e] + MMarg-L[c] -> MMh[c] + MMphe-L[c] + MMarg-L[e]	0	1000	(20540.1 or (330836.1 and 17254.1))	Mouse metabolic/ transport/ demand reaction
MMPHYCBOXL	MMh[c] + MMphe-L[c] -> MMcn2[c] + MMpearm[c]	0	1000	(20540.1 or (330836.1 and 17254.1))	Mouse metabolic/ transport/ demand reaction
MMPHYHx	MMo2[x] + MMakg[x] + MMphytrcoa[x] -> MMco2[x] + MMphyh2ohcoa[x] + MMsucc[x]	0	1000	13195.1	Mouse metabolic/ transport/ demand reaction
MMPHYQt	MMh2o[c] + MMatp[c] + MMphyQ[e] -> MMadp[c] + MMh[c] + MMpi[c] + MMphyQ[c]	0	1000	16922.1	Mouse metabolic/ transport/ demand reaction
MMPHYTt	MMphyt[e] <=> MMphyt[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPI345P3P	MMh2o[c] + MMpail345p_hs[c] -> MMpi[c] + MMpail45p_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPI345P3Pn	MMh2o[n] + MMpail345p_hs[n] -> MMpa845p_hs[n] + MMpi[n]	0	1000	19211.1	Mouse metabolic/ transport/ demand reaction
MMPI345P5Pn	MMh2o[n] + MMpail345p_hs[n] -> MMpi[n] + MMpail34p_hs[n]	0	1000	19211.1	Mouse metabolic/ transport/ demand reaction
MMPI34P3Pn	MMh2o[n] + MMpail34p_hs[n] -> MMpa84p_hs[n] + MMpi[n]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPI34P4Pn	MMh2o[n] + MMpail34p_hs[n] -> MMpi[n] + MMpaI3p_hs[n]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPI34P5K	MMatp[c] + MMpail34p_hs[c] -> MMadp[c] + MMh[c] + MMpail345p_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPI34P5Kn	MMatp[n] + MMpail34p_hs[n] -> MMh[n] + MMadp[n] + MMpail345p_hs[n]	0	1000	18719.1 or 18717.1 or 18720.1	Mouse metabolic/ transport/ demand reaction
MMPI35P3P	MMh2o[c] + MMpaiI35p_hs[c] -> MMpi[c] + MMpaiI5p_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPI3P3Pn	MMh2o[n] + MMpaiI3p_hs[n] -> MMpail_hs[n] + MMpi[n]	0	1000	74302.1 or 74302.2 or 74302.3	Mouse metabolic/ transport/ demand reaction
MMPI3P4K	MMatp[c] + MMpaiI3p_hs[c] -> MMadp[c] + MMh[c] + MMpaiI34p_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPI3P4Kn	MMatp[n] + MMpaiI3p_hs[n] -> MMh[n] + MMadp[n] + MMpaiI34p_hs[n]	0	1000	107650.1 or 18719.1 or 224020.1 or 18717.1 or 18720.1 or 84095.1	Mouse metabolic/ transport/ demand reaction
MMPI3P5K	MMatp[c] + MMpaiI3p_hs[c] -> MMadp[c] + MMh[c] + MMpaiI35p_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPI3PP	MMh2o[c] + MMpaiI3p_hs[c] -> MMpi[c] + MMpail_hs[c]	0	1000	18719.1 or 18717.1 or 18720.1	Mouse metabolic/ transport/ demand reaction
MMPI45P3K	MMatp[c] + MMpai845p_hs[c] -> MMadp[c] + MMh[c] + MMpaiI345p_hs[c]	0	1000	74302.1 or 74302.2 or 74302.3	Mouse metabolic/ transport/ demand reaction
MMPI45P3Kn	MMatp[n] + MMpai845p_hs[n] -> MMh[n] + MMadp[n] + MMpaiI345p_hs[n]	0	1000	18710.1 and 18707.1 or 18709.1 and 18706.1 or 74769.1 and 18710.1 or 18708.3 and 18706.1 or 320207.1 and 30955.1 or 18706.1 and 18710.1 or 18709.1 and 74769.1 or 74769.1 and 18708.1 or 18708.3 and 18707.1 or 18709.1 and 74769.1 or 74769.1 and 18708.1 or 18708.3 and 18707.1 or 30955.1 and 23900.1 or 18709.1 and 18707.1 or 18708.2 and 74769.1 or 18708.1 and 18707.1 or 18708.1 and 74769.1 or 18708.1 and 18707.1 or 18708.3 and 18706.1 or 74769.1 and 18710.1 or 18708.3 and 18706.1 or 320207.1 and 30955.1 or 18705.1 or 18706.1 and 18710.1 or 18709.1 and 74769.1 or 74769.1 and 18708.1 or 18708.3 and 18707.1 or 30955.1 and 23900.1 or 18709.1 and 18707.1 or 18704.1 or 18708.2 and 74769.1 or 18708.1 and 18707.1 or 18708.1 and 74769.1 or 18708.1 and 74769.1 or 18708.3 and 18706.1 or 240752.1 or 18708.2 and 18707.1 or 18706.1 and 18708.3 and 18706.1 or 240752.1 or 18708.2 and 18707.1 or 18706.1 and 18708.1	Mouse metabolic/ transport/ demand reaction
MMPI45P4P	MMh2o[c] + MMpai845p_hs[c] -> MMpi[c] + MMpaiI5p_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPI45P5P	MMh2o[c] + MMpai845p_hs[c] -> MMpi[c] + MMpai84p_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPI45P5Pn	MMh2o[n] + MMpai845p_hs[n] -> MMpa84p_hs[n] + MMpi[n]	0	1000	320634.1 or 104015.1 or 320634.2 or 64436.1 or 20975.1 or 16330.1 or 104015.2	Mouse metabolic/ transport/ demand reaction
MMPI45PLC	MMh2o[c] + MMpai845p_hs[c] -> MMh[c] + MMdag_hs[c] + MMmi145p[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPI45PLCn	MMh2o[n] + MMpai845p_hs[n] -> MMh[n] + MMdag_hs[n] + MMmi145p[n]	0	1000	433022.1 or 18797.1 or 18795.1 or 114875.1 or 74055.1 or 227120.1 or 18803.1 or 18798.1 or 18799.1 or 18798.2 or 18803.2 or 18802.1 or 72469.1 or 18796.1 or 269615.1 or 234779.1 or 269437.1 or 18795.2	Mouse metabolic/ transport/ demand reaction
MMPI4P3K	MMatp[c] + MMpai84p_hs[c] -> MMadp[c] + MMh[c] + MMpaiEI4p_hs[c]	0	1000	18795.1 or 18795.2	Mouse metabolic/ transport/ demand reaction
MMPI4P3Ker	MMatp[r] + MMpai84p_hs[r] -> MMadp[r] + MMh[r] + MMpaiI34p_hs[r]	0	1000	18710.1 and 18707.1 or 18709.1 and 18706.1 or 74769.1 and 18710.1 or 18708.3 and 18706.1 or 320207.1 and 30955.1 or 18705.1 or 18706.1 and 18710.1 or 18709.1 and 74769.1 or 74769.1 and 18708.1 or 18708.3 and 18707.1 or 30955.1 and 23900.1 or 18709.1 and 18707.1 or 18704.1 or 18708.2 and 74769.1 or 18708.1 and 18707.1 or 18708.1 and 74769.1 or 18708.1 and 74769.1 or 18708.3 and 18706.1 or 240752.1 or 18708.2 and 18707.1 or 18706.1 and 18708.3 and 18706.1 or 240752.1 or 18708.2 and 18707.1 or 18706.1 and 18708.1	Mouse metabolic/ transport/ demand reaction
MMPI4P3Kn	MMatp[n] + MMpai84p_hs[n] -> MMh[n] + MMadp[n] + MMpaiEI4p_hs[n]	0	1000	240752.1	Mouse metabolic/ transport/ demand reaction
MMPI4P4Pn	MMh2o[n] + MMpai84p_hs[n] -> MMpail_hs[n] + MMpi[n]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPI4P5K	MMatp[c] + MMpai84p_hs[c] -> MMadp[c] + MMh[c] + MMpai845p_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPI4P5Kn	MMatp[n] + MMpai84p_hs[n] -> MMh[n] + MMadp[n] + MMpai845p_hs[n]	0	1000	108083.1 or 18718.1 or 18719.1 or 18717.1 or 18711.1 or 18711.2 or 18711.3 or 18720.1 or 108083.2 or 117150.1	Mouse metabolic/ transport/ demand reaction
MMPI4PLCn	MMh2o[n] + MMpai84p_hs[n] -> MMh[n] + MMdag_hs[n] + MMmi14p[n]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPI4PP	MMh2o[c] + MMpai84p_hs[c] -> MMpi[c] + MMpail_hs[c]	0	1000	18795.1 or 18795.2	Mouse metabolic/ transport/ demand reaction
MMPI5P3K	MMatp[c] + MMpaiI5p_hs[c] -> MMadp[c] + MMh[c] + MMpaiEI5p_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPI5P3Ker	MMatp[r] + MMpaiI5p_hs[r] -> MMadp[r] + MMh[r] + MMpaiI35p_hs[r]	0	1000	18710.1 and 18707.1 or 18709.1 and 18706.1 or 74769.1 and 18710.1 or 18708.1 and 18706.1 or 320207.1 and 30955.1 or 18705.1 or 18706.1 and 18710.1 or 18709.1 and 74769.1 or 225326.1 or 74769.1 and 18708.1 or 18708.1 and 18707.1 or 30955.1 and 23900.1 or 18709.1 and 18707.1 or 18704.1 or 18708.1 and 74769.1 or 18708.1 and 18707.1 or 18708.1 and 74769.1 or 18708.1 and 18706.1 or 240752.1 or 18708.1 and 18707.1 or 18706.1 and 18708.1	Mouse metabolic/ transport/ demand reaction
MMPI5P4K	MMatp[c] + MMpaiI5p_hs[c] -> MMadp[c] + MMh[c] + MMpai845p_hs[c]	0	1000	240752.1	Mouse metabolic/ transport/ demand reaction
MMPI5P4Kn	MMatp[n] + MMpaiI5p_hs[n] -> MMh[n] + MMadp[n] + MMpai845p_hs[n]	0	1000	107650.1 or 224020.1 or 84095.1	Mouse metabolic/ transport/ demand reaction
MMPIACGT	MMpail_hs[c] + MMuacgam[c] -> MMh[c] + MMadp[c] + MMacgpail_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPIK3	MMatp[c] + MMpail_hs[c] -> MMadp[c] + MMh[c] + MMpaiI3p_hs[c]	0	1000	18700.1 or 13481.1 or 56176.2 or 18700.2 or 67292.1 or 13481.2 or 56176.3 or 67292.2 or 56176.1 or 110417.1 or 14755.2 or 18700.3 or 14755.1	Mouse metabolic/ transport/ demand reaction
MMPIK3er	MMatp[r] + MMpail_hs[r] -> MMadp[r] + MMh[r] + MMpaiI3p_hs[r]	0	1000	18710.1 and 18707.1 or 18709.1 and 18706.1 or 74769.1 and 18710.1 or 18708.1 and 18706.1 or 320207.1 and 30955.1 or 18705.1 or 18706.1 and 18710.1 or 18709.1 and 74769.1 or 225326.1 or 74769.1 and 18708.1 or 18708.1 and 18707.1 or 30955.1 and 23900.1 or 18709.1 and 18707.1 or 18704.1 or 18708.1 and 74769.1 or 18708.1 and 18707.1 or 18708.1 and 74769.1 or 18708.1 and 18706.1 or 240752.1 or 18708.1 and 18707.1 or 18706.1 and 18708.1	Mouse metabolic/ transport/ demand reaction
MMPIK3n	MMatp[n] + MMpail_hs[n] -> MMh[n] + MMadp[n] + MMpaiI3p_hs[n]	0	1000	240752.1	Mouse metabolic/ transport/ demand reaction
MMPIK4	MMatp[c] + MMpail_hs[c] -> MMadp[c] + MMh[c] + MMpai84p_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPIK4n	MMatp[n] + MMpail_hs[n] -> MMh[n] + MMadp[n] + MMpai84p_hs[n]	0	1000	107650.1 or 224020.1 or 84095.1	Mouse metabolic/ transport/ demand reaction
MMPIK5	MMatp[c] + MMpail_hs[c] -> MMadp[c] + MMh[c] + MMpaiI5p_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPIK5n	MMatp[n] + MMpail_hs[n] -> MMh[n] + MMadp[n] + MMpaiI5p_hs[n]	0	1000	18719.1 or 18717.1 or 18720.1	Mouse metabolic/ transport/ demand reaction
MMPIPLCn	MMh2o[n] + MMpail_hs[n] -> MMh[n] + MMdag_hs[n] + MMmi1p-D[n]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPIt2m	MMh[c] + MMpi[c] <=> MMh[m] + MMpi[m]	0	0	18795.1 or 18795.2	Mouse metabolic/ transport/ demand reaction
MMPIt2m_2	2 MMh[c] + MMpi[c] <=> 2 MMh[m] + MMpi[m]	-1000	1000	18674.1 or 18674.2 or 18674.3 or 18674.4	Mouse metabolic/ transport/ demand reaction
MMPIt7	3 MMna1[e] + MMpi[e] <=> MMpi[c] + 3 MMna1[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPIt7r	3 MMna1[e] + MMpi[e] -> MMpi[c] + 3 MMna1[c]	0	1000	20505.1 or 20531.1	Mouse metabolic/ transport/ demand reaction
MMPIt8	1.5 MMna1[e] + MMpi[e] <=> MMpi[c] + 1.5 MMna1[c]	0	1000	105355.1 or 218103.1 or 319848.1 or 20504.1	Mouse metabolic/ transport/ demand reaction
MMPIt9	2 MMna1[e] + MMpi[e] <=> MMpi[c] + 2 MMna1[c]	0	1000	20516.1 or 20515.1	Mouse metabolic/ transport/ demand reaction
MMPIter	MMpi[r] <=> MMpi[c]	-1000	1000	142681.1	Mouse metabolic/ transport/ demand reaction
MMPItg	MMpi[g] -> MMpi[c]	0	1000		Mouse metabolic/ transport/ demand reaction

MMPItn	MMpi[n] <=> MMpi[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPItx	MMpi[c] <=> MMpi[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPLA2	MMh2o[c] + MMak2gchol_hs[c] -> MMh[c] + MMRrotal2[c] + MMak2lgchol_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPLYSPSer	MMh2o[r] + MMNtmelys[r] -> MMpeptslys[r] + MMtmlys[r]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPMANM	MMman1p[c] <=> MMman6p[c]	-1000	1000	56529.1 or 66624.1 or 66286.1 or 76687.1 or 69019.1	Mouse metabolic/ transport/ demand reaction
MMPMEVKx	MMatp[x] + MM5pmev[x] -> MMadp[x] + MM5dpmev[x]	0	1000	54128.1 or 66681.1 or 29858.1	Mouse metabolic/ transport/ demand reaction
MMPMI12346PH	MMh2o[c] + MMppmi12346p[c] -> MMh[c] + MMpi[c] + MMminohp[c]	0	1000	68603.1	Mouse metabolic/ transport/ demand reaction
MMPMI12346PHn	MMh2o[n] + MMppmi12346p[n] -> MMh[n] + MMminohp[n] + MMpi[n]	0	1000	27399.2 or 271424.1 or 27399.1	Mouse metabolic/ transport/ demand reaction
MMPMI1346PH	MMh2o[c] + MMppmi1346p[c] -> MMh[c] + MMpi[c] + MMmi13456p[c]	0	1000	76500.1 or 76500.2 or 27399.1 or 76500.3 or 76500.4 or 271424.1 or 27399.2 or 76500.5 or 76500.6	Mouse metabolic/ transport/ demand reaction
MMPMI1346PHn	MMh2o[n] + MMppmi1346p[n] -> MMh[n] + MMmi13456p[n] + MMpi[n]	0	1000	27399.2 or 271424.1 or 27399.1	Mouse metabolic/ transport/ demand reaction
MMPMTCOAFABP1tc	2 MMpmtcoa[c] <=> 2 MMpmtcoa[r]	-1000	1000	76500.1 or 76500.2 or 27399.1 or 76500.3 or 76500.4 or 271424.1 or 27399.2 or 76500.5 or 76500.6	Mouse metabolic/ transport/ demand reaction
MMPMTCOAtx	MMpmtcoa[c] <=> MMpmtcoa[x]	-1000	1000	14080.1	Mouse metabolic/ transport/ demand reaction
MMPNP	MMpi[c] + MMnam[c] <=> MMh[c] + MMncam[c] + MMr1p[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPNTEH	MMh2o[c] + MMpnth[c] -> MMcysam[c] + MMpnto-R[c]	0	1000	667034.1	Mouse metabolic/ transport/ demand reaction
MMPNTK	MMatp[c] + MMpnto-R[c] -> MMadp[c] + MMh[c] + MM4ppan[c]	0	1000	26464.1 or 26464.2 or 56752.1	Mouse metabolic/ transport/ demand reaction
MMPNTKm	MMatp[m] + MMpnto-R[m] -> MMh[m] + MMadp[m] + MM4ppan[m]	0	1000	75735.1 or 269614.1 or 74450.1 or 74450.2 or 75735.2 or 74450.3 or 74450.4 or 75735.3 or 211347.1	Mouse metabolic/ transport/ demand reaction
MMPNTORDe	MMpnto-R[c] -> MMpnto-R[e]	0	1000	74450.5	Mouse metabolic/ transport/ demand reaction
MMPNTOt5	MMh2o[c] + MMatp[c] + 2 MMna1[e] + MMpnto-R[e] -> MMadp[c] + MMh[c] + MMpi[c] + 2 MMna1[c] + MMpnto-R[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPPA	MMh2o[c] + MMppi[c] -> MMh[c] + 2 MMpi[c]	0	1000	330064.1	Mouse metabolic/ transport/ demand reaction
MMPPA2	MMh2o[c] + MMpppi[c] -> MMh[c] + MMpi[c] + MMppi[c]	0	1000	67895.1	Mouse metabolic/ transport/ demand reaction
MMPPA2m	MMh2o[m] + MMpppi[m] -> MMh[m] + MMpi[m] + MMppi[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPPAP	MMh2o[c] + MMpa_hs[c] -> MMpi[c] + MMdag_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPPAer	MMh2o[r] + MMppi[r] -> MMh[r] + 2 MMpi[r]	0	1000	67916.1 or 19012.1 or 50784.1 or 19012.2	Mouse metabolic/ transport/ demand reaction
MMPPAm	MMh2o[m] + MMppi[m] -> MMh[m] + 2 MMpi[m]	0	1000	14378.1 or 14377.1 or 68401.1	Mouse metabolic/ transport/ demand reaction
MMPPAn	MMh2o[n] + MMppi[n] -> MMh[n] + 2 MMpi[n]	0	1000	74776.1 or 74776.2 or 74776.3 or 74776.4	Mouse metabolic/ transport/ demand reaction
MMPPAt	MMppa[e] -> MMppa[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPPAtm	MMppa[c] -> MMppa[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPPBNGS	2 MM5aop[c] -> 2 MMh2o[c] + MMh[c] + MMppbng[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPPCDC	MMh[c] + MM4pccys[c] -> MMco2[c] + MMpan4p[c]	0	1000	17025.1 or 17025.2	Mouse metabolic/ transport/ demand reaction
MMPPCOACm	MMppcoa[m] + MMatp[m] + MMhco3[m] -> MMh[m] + MMadp[m] + MMpi[m] + MMmmcoa-S[m]	0	1000	66812.1	Mouse metabolic/ transport/ demand reaction
MMPPCOAOm	MMppcoa[m] + MMfad[m] -> MMfadh2[m] + MMpropncoa[m]	0	1000	66904.1 and 110821.1	Mouse metabolic/ transport/ demand reaction
MMPPD2CSPp	MM6a2ohxut[x] -> MM1pipdn2c[x] + MMh2o[x]	0	1000	102632.1 or 66948.1 or 11364.1 or 66885.1 or 11409.1 or 71985.1 or 229211.1	Mouse metabolic/ transport/ demand reaction
MMPPDOx	MMh[c] + MMnadh[c] + MMkld-D[c] -> MMnad[c] + MM12ppd-R[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPPDOy	MMh[c] + MMnadph[c] + MMkld-D[c] -> MMnadp[c] + MM12ppd-R[c]	0	1000	110198.1	Mouse metabolic/ transport/ demand reaction
MMPPItr	MMppi[c] <=> MMppi[r]	-1000	1000	110198.1 or 58810.2 or 11677.1 or 58810.1	Mouse metabolic/ transport/ demand reaction
MMPPItx	MMppi[c] <=> MMppi[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPPM	MMr1p[c] <=> MMr5p[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPPMI12346Ptn	MMppmi12346p[c] <=> MMppmi12346p[n]	-1000	1000	72157.1	Mouse metabolic/ transport/ demand reaction
MMPPMI1346Ptn	MMppmi1346p[c] <=> MMppmi1346p[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPPNCL3	MMatp[c] + MMcys-L[c] + MM4ppan[c] -> MMh[c] + MMamp[c] + MMpi[c] + MM4ppcys[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPPOR	MMo2[c] + MMphpyr[c] -> MMco2[c] + MM2hyoxplac[c]	0	1000	106564.1	Mouse metabolic/ transport/ demand reaction
MMPPPG9tm	MMpppg9[c] <=> MMpppg9[m]	-1000	1000	15445.1	Mouse metabolic/ transport/ demand reaction
MMPPPGOm	3 MMo2[m] + 2 MMpppg9[m] -> 6 MMh2o[m] + 2 MMppp9[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPPPItn	MMpppi[c] <=> MMpppi[n]	-1000	1000	19044.1	Mouse metabolic/ transport/ demand reaction
MMPRAGSr	MMatp[c] + MMgly[c] + MMpram[c] <=> MMadp[c] + MMh[c] + MMpi[c] + MMgar[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPRAIS	MMatp[c] + MMfpram[c] -> MMadp[c] + 2 MMh[c] + MMpi[c] + MMair[c]	0	1000	14450.1 or 14450.2	Mouse metabolic/ transport/ demand reaction
MMPRASCS	MMatp[c] + MMasp-L[c] + MM5aizc[c] <=> MMadp[c] + MMh[c] + MMpi[c] + MM25aics[c]	-1000	1000	14450.1 or 14450.2	Mouse metabolic/ transport/ demand reaction
MMPRDX	MMh2o2[c] + MMmeoh[c] -> 2 MMh2o[c] + MMfald[c]	0	1000	67054.1	Mouse metabolic/ transport/ demand reaction
MMPRDXl	MMh2o2[l] + MMmeoh[l] -> 2 MMh2o[l] + MMfald[l]	0	1000	13861.1	Mouse metabolic/ transport/ demand reaction
MMPRFGS	MMh2o[c] + MMatp[c] + MMgln-L[c] + MMfgam[c] -> MMadp[c] + MMh[c] + MMpi[c] + MMglu-L[c] + MMfpram[c]	0	1000	17523.1	Mouse metabolic/ transport/ demand reaction
MMPRGNLONESULT	MMpaps[c] + MMprgnlone[c] -> MMh[c] + MMpap[c] + MMprgnlones[c]	0	1000	237823.1	Mouse metabolic/ transport/ demand reaction
MMPRGNLONEtm	MMprgnlone[c] <=> MMprgnlone[m]	-1000	1000	20859.1 or 54200.2	Mouse metabolic/ transport/ demand reaction
MMPRGNLONEtr	MMprgnlone[c] <=> MMprgnlone[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPRGSTRNt	MMprgstrn[e] <=> MMprgstrn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPRISTANALtx	MMpristanal[x] <=> MMpristanal[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPRISTCOAtx	MMpristcoa[x] <=> MMpristcoa[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPRISTtx	MMprist[x] <=> MMprist[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPRO1x	MMnad[c] + MMpro-L[c] -> 2 MMh[c] + MMnadh[c] + MM1pyr5c[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPRO1xm	MMnad[m] + MMpro-L[m] -> 2 MMh[m] + MMnadh[m] + MM1pyr5c[m]	0	1000	56189.1	Mouse metabolic/ transport/ demand reaction
MMPROAKGOX1r	MMo2[r] + MMakg[r] + MMpro-L[r] -> MMco2[r] + MM4hpro-LT[r] + MMsucc[r]	0	1000	19125.1	Mouse metabolic/ transport/ demand reaction
MMPROB0ATtc	MMna1[u] + MMpro-L[u] -> MMna1[c] + MMpro-L[c]	0	1000	18453.1 or 18452.1 or 18451.1	Mouse metabolic/ transport/ demand reaction
MMPROD2	MMfad[c] + MMpro-L[c] -> MMh[c] + MMfadh2[c] + MM1pre5c[c]	0	1000	(70008.1 or (74338.1 and 57394.1))	Mouse metabolic/ transport/ demand reaction
MMPROD2m	MMfad[m] + MMpro-L[m] -> MMh[m] + MMfadh2[m] + MM1pyr5c[m]	0	1000	56189.1	Mouse metabolic/ transport/ demand reaction
MMPRODPATtc	MMh[u] + MMpro-D[u] -> MMh[c] + MMpro-D[c]	0	1000	19125.1	Mouse metabolic/ transport/ demand reaction
MMPRODt2r	MMh[e] + MMpro-D[e] <=> MMh[c] + MMpro-D[c]	0	1000	215335.1	Mouse metabolic/ transport/ demand reaction
MMPRODt2rL	MMh[l] + MMpro-D[l] <=> MMh[c] + MMpro-D[c]	-1000	1000	215335.1	Mouse metabolic/ transport/ demand reaction
MMPROGLYPEPT1tc	MMh[u] + MMprogly[u] -> MMh[c] + MMprogly[c]	0	1000	215335.1	Mouse metabolic/ transport/ demand reaction
MMPROGLYPRO1c	MMh2o[c] + MMprogly[c] <=> MMgly[c] + MMpro-L[c]	-1000	1000	215335.1	Mouse metabolic/ transport/ demand reaction
MMPROGLYt	MMh[e] + MMprogly[e] -> MMh[c] + MMprogly[c]	0	1000	18624.1	Mouse metabolic/ transport/ demand reaction
MMPROIMINOtc	2 MMna1[u] + MMcl[u] + MMpro-L[u] -> 2 MMna1[c] + MMcl[c] + MMpro-L[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPROLPATtc	MMh[u] + MMpro-L[u] -> MMh[c] + MMpro-L[c]	0	1000	(102680.1 and 57394.1)	Mouse metabolic/ transport/ demand reaction
MMPROSTGD2t	MMhco3[c] + MMprostgd2[e] <=> MMhco3[e] + MMprostgd2[c]	0	1000	215335.1	Mouse metabolic/ transport/ demand reaction
MMPROSTGE1t	MMhco3[c] + MMprostge1[e] <=> MMhco3[e] + MMprostge1[c]	0	1000	24059.1	Mouse metabolic/ transport/ demand reaction
MMPROSTGE1t3	MMh2o[c] + MMatp[c] + MMprostge1[c] -> MMadp[c] + MMh[c] + MMpi[c] + MMprostge1[e]	0	1000	24059.1	Mouse metabolic/ transport/ demand reaction
MMPROSTGE2t	MMhco3[c] + MMprostge2[e] <=> MMhco3[e] + MMprostge2[c]	0	1000	239273.1	Mouse metabolic/ transport/ demand reaction
MMPROSTGE2t2	MMprostge2[e] <=> MMprostge2[c]	0	1000	108116.1 or 108115.1 or 24059.1 or 28250.1	Mouse metabolic/ transport/ demand reaction
MMPROSTGE2t3	MMh2o[c] + MMatp[c] + MMprostge2[c] -> MMadp[c] + MMh[c] + MMpi[c] + MMprostge2[e]	0	1000	20518.1 or 20517.1 or 20518.2	Mouse metabolic/ transport/ demand reaction
MMPROSTGF2t	MMprostgf2[e] <=> MMprostgf2[c]	0	1000	239273.1	Mouse metabolic/ transport/ demand reaction
MMPROSTGH2t	MMhco3[c] + MMprostgh2[e] <=> MMhco3[e] + MMprostgh2[c]	0	1000	20518.1 or 20517.1 or 20518.1	Mouse metabolic/ transport/ demand reaction
MMPROSTGI2t	MMhco3[c] + MMprostgi2[e] <=> MMhco3[e] + MMprostgi2[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPROSTGI2tr	MMprostgi2[c] <=> MMprostgi2[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPROt2r	MMh[e] + MMpro-L[e] <=> MMh[c] + MMpro-L[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPROt2rL	MMh[l] + MMpro-L[l] <=> MMh[c] + MMpro-L[c]	-1000	1000	215335.1	Mouse metabolic/ transport/ demand reaction
MMPROt4	MMna1[e] + MMpro-L[e] -> MMna1[c] + MMpro-L[c]	0	1000	215335.1	Mouse metabolic/ transport/ demand reaction

MMPRO4s4(2)r	2 MMna1[e] + MMpro-L[e] <=> 2 MMna1[c] + MMpro-L[c]	0	1000	105727.1 or 67760.1 or 69354.1	Mouse metabolic/ transport/ demand reaction
MMPROtm	MMpro-L[c] <=> MMpro-L[m]	-1000	1000	240332.1	Mouse metabolic/ transport/ demand reaction
MMPRPNCOAHYDm	MMh2o[m] + MMprpncoa[m] -> MM3hpcoa[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPRPNCOAHYDx	MMh2o[x] + MMprpncoa[x] -> MM3hpcoa[x]	0	1000	11992.1 or 231086.1 or 97212.1 or 93747.1	Mouse metabolic/ transport/ demand reaction
MMPRPPS	MMatp[c] + MMr5p[c] <=> MMh[c] + MMamp[c] + MMprpp[c]	-1000	1000	74147.1	Mouse metabolic/ transport/ demand reaction
MMPSDm_hs	MMh[m] + MMps_hs[m] -> MMco2[m] + MMpe_hs[m]	0	1000	75456.1 or 75456.2 or 19139.1 or 110639.1	Mouse metabolic/ transport/ demand reaction
MMPSERT	MMglu-L[c] + MM3php[c] -> MMakg[c] + MMpser-L[c]	0	1000	320951.1	Mouse metabolic/ transport/ demand reaction
MMPSFLIP	MMh2o[c] + MMatp[c] + MMps_hs[e] -> MMadp[c] + MMh[c] + MMpi[c] + MMps_hs[c]	0	1000	107272.1 or 107272.2	Mouse metabolic/ transport/ demand reaction
MMPSFLIPm	MMh2o[c] + MMatp[c] + MMps_hs[c] -> MMadp[c] + MMh[c] + MMpi[c] + MMps_hs[m]	0	1000	11982.1 or 11980.1	Mouse metabolic/ transport/ demand reaction
MMPSP_L	MMh2o[c] + MMpser-L[c] -> MMpi[c] + MMser-L[c]	0	1000	11982.1 or 11980.1	Mouse metabolic/ transport/ demand reaction
MMPSSA1_hs	MMser-L[c] + MMpchol_hs[c] <=> MMchol[c] + MMps_hs[c]	-1000	1000	100678.1	Mouse metabolic/ transport/ demand reaction
MMPSSA2_hs	MMser-L[c] + MMpe_hs[c] <=> MMetha[c] + MMps_hs[c]	-1000	1000	19210.1	Mouse metabolic/ transport/ demand reaction
MMPSYGCHe	MMgchola[u] + MMpsyl[u] -> MMpsylchol[u]	0	1000	27388.1	Mouse metabolic/ transport/ demand reaction
MMPSYGCHt	MMh[e] + MMpsylchol[e] <=> MMh[c] + MMpsylchol[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPSYLt	MMh[e] + MMpsyl[e] <=> MMh[c] + MMpsyl[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPSYTCHe	MMtchola[u] + MMpsyl[u] -> MMpsyltchol[u]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPSYTCHt	MMh[e] + MMpsyltchol[e] <=> MMh[c] + MMpsyltchol[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPSYTDECHe	MMtdechola[u] + MMpsyl[u] -> MMpsyltdechol[u]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPSYTDECHt	MMh[e] + MMpsyltdechol[e] <=> MMh[c] + MMpsyltdechol[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPS_HSter	MMps_hs[c] <=> MMps_hs[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPS_HStg	MMps_hs[c] <=> MMps_hs[g]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPSt3	MMps_hs[e] <=> MMps_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPTDCACRNCPT1	MMcrn[c] + MMptdcacoa[c] -> MMcoa[c] + MMptdcacrn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPTDCACRNCPT2	MMcoa[m] + MMptdcacrn[m] -> MMcrn[m] + MMptdcacoa[m]	0	1000	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	Mouse metabolic/ transport/ demand reaction
MMPTDCACRNt	MMptdcacrn[c] -> MMptdcacrn[m]	0	1000	12896.1	Mouse metabolic/ transport/ demand reaction
MMPTDCAt	MMptdca[e] <=> MMptdca[c]	0	1000	57279.1	Mouse metabolic/ transport/ demand reaction
MMPTE2x	MMpmtcoa[x] + MMh2o[x] -> MMh[x] + MMcoa[x] + MMhtlca[x]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPTE3x	MMh2o[x] + MMpristcoa[x] -> MMh[x] + MMcoa[x] + MMprist[x]	0	1000	170789.1 or 171210.1 or 170789.2 or 170789.3	Mouse metabolic/ transport/ demand reaction
MMPTE4x	MMh2o[x] + MMphytcoa[x] -> MMh[x] + MMcoa[x] + MMphyt[x]	0	1000	171210.1	Mouse metabolic/ transport/ demand reaction
MMPTE5x	MMh2o[x] + MMadmcoa[x] -> MMh[x] + MMcoa[x] + MMadmt[x]	0	1000	171210.1	Mouse metabolic/ transport/ demand reaction
MMPTHPS	MMahtd[c] -> MMpppi[c] + MM6pthp[c]	0	1000	171210.1	Mouse metabolic/ transport/ demand reaction
MMPTHPSn	MMahtd[n] -> MMpppi[n] + MM6pthp[n]	0	1000	19286.1	Mouse metabolic/ transport/ demand reaction
MMPTPAT	MMatp[c] + MMh[c] + MMpan4p[c] <=> MMppi[c] + MMdpcoa[c]	-1000	1000	19286.1	Mouse metabolic/ transport/ demand reaction
MMPTRCAT1	MMaccoa[c] + MMptrc[c] -> MMh[c] + MMcoa[c] + MMaprut[c]	0	1000	71743.1	Mouse metabolic/ transport/ demand reaction
MMPTRCOX1	MMh2o[c] + MMo2[c] + MMptrc[c] -> MMh2o2[c] + MMnh4[c] + MM4abutn[c]	0	1000	69215.1 or 20229.1	Mouse metabolic/ transport/ demand reaction
MMPUNP1	MMpi[c] + MMadn[c] <=> MMade[c] + MMr1p[c]	-1000	1000	237940.1 or 237940.2 or 11754.1 or 76507.1	Mouse metabolic/ transport/ demand reaction
MMPUNP2	MMpi[c] + MMdad-2[c] <=> MM2dr1p[c] + MMade[c]	-1000	1000	667034.1	Mouse metabolic/ transport/ demand reaction
MMPUNP3	MMpi[c] + MMgsn[c] <=> MMgua[c] + MMr1p[c]	-1000	1000	667034.1	Mouse metabolic/ transport/ demand reaction
MMPUNP4	MMpi[c] + MMdgsn[c] <=> MM2dr1p[c] + MMgua[c]	-1000	1000	667034.1	Mouse metabolic/ transport/ demand reaction
MMPUNP5	MMpi[c] + MMins[c] <=> MMhxan[c] + MMr1p[c]	-1000	1000	667034.1	Mouse metabolic/ transport/ demand reaction
MMPUNP6	MMpi[c] + MMdin[c] <=> MM2dr1p[c] + MMhxan[c]	-1000	1000	667034.1	Mouse metabolic/ transport/ demand reaction
MMPUNP7	MMpi[c] + MMxtsn[c] <=> MMxan[c] + MMr1p[c]	-1000	1000	667034.1	Mouse metabolic/ transport/ demand reaction
MMPVD3	MM7dhchsterol[c] <=> MMpd3[c]	-1000	1000	667034.1	Mouse metabolic/ transport/ demand reaction
MMPYAM5POr	MMh2o[c] + MMo2[c] + MMpyam5p[c] <=> MMh2o2[c] + MMnh4[c] + MMpydx5p[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPYAM5Ptm	MMpyam5p[c] <=> MMpyam5p[m]	-1000	1000	103711.1	Mouse metabolic/ transport/ demand reaction
MMPYDAMK	MMatp[c] + MMpydam[c] -> MMadp[c] + MMh[c] + MMpyam5p[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPYDAMtr	MMpydam[e] <=> MMpydam[c]	0	1000	216134.1	Mouse metabolic/ transport/ demand reaction
MMPYDX5Ptm	MMpydx5p[c] <=> MMpydx5p[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMPYDXDH	MMh2o[c] + MMo2[c] + MMpydx[c] -> MMh2o2[c] + MM4pyrdx[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPYDXK	MMatp[c] + MMpydx[c] -> MMadp[c] + MMh[c] + MMpydx5p[c]	0	1000	11761.1	Mouse metabolic/ transport/ demand reaction
MMPYDXNK	MMatp[c] + MMpydxn[c] -> MMadp[c] + MMh[c] + MMpdx5p[c]	0	1000	216134.1	Mouse metabolic/ transport/ demand reaction
MMPYDXNtr	MMpydxn[e] <=> MMpydxn[c]	0	1000	216134.1	Mouse metabolic/ transport/ demand reaction
MMPYDXPP	MMh2o[c] + MMpydx5p[c] -> MMpi[c] + MMpydx[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPYDXtr	MMpydx[e] <=> MMpydx[c]	0	1000	57028.1	Mouse metabolic/ transport/ demand reaction
MMPYK	MMadp[c] + MMh[c] + MMpep[c] -> MMatp[c] + MMpyr[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMPYLALDOX	MMh2o[c] + MMnaal[c] + MMpylald[c] -> 2 MMh[c] + MMnadh[c] + MMpteracd[c]	0	1000	18746.1 or 66260.1 or 18770.1 or 18746.2 or 18770.2 or 18746.3	Mouse metabolic/ transport/ demand reaction
MMPYLALDOXm	MMh2o[m] + MMnaal[m] + MMpylald[m] -> 2 MMh[m] + MMnadh[m] + MMperacd[m]	0	1000	19378.1 or 56752.1 or 110695.1 or 11668.1 or 11671.1 or 19378.2 or 19378.3	Mouse metabolic/ transport/ demand reaction
MMPYNP2r	MMpi[c] + MMurr[c] <=> MMura[c] + MMr1p[c]	-1000	1000	11669.1 or 212647.1 or 212647.2 or 72535.1	Mouse metabolic/ transport/ demand reaction
MMPYRt2m	MMh[c] + MMpyr[c] <=> MMh[m] + MMpyr[m]	-1000	1000	22271.1 or 22271.2 or 76654.1	Mouse metabolic/ transport/ demand reaction
MMPYRt2p	MMh[c] + MMpyr[c] <=> MMh[x] + MMpyr[x]	-1000	1000	20501.1	Mouse metabolic/ transport/ demand reaction
MMPYRt2r	MMh[e] + MMpyr[e] <=> MMh[c] + MMpyr[c]	0	1000	20503.1 or 20501.1	Mouse metabolic/ transport/ demand reaction
MMQUILSYN	MMcrnusa[c] -> MMh2o[c] + MMh[c] + MMquln[c]	0	1000	20503.1 or 80879.1 or 20501.1	Mouse metabolic/ transport/ demand reaction
MMRADH	MMh2o[c] + MMnad[c] + MMretinal[c] <=> 2 MMh[c] + MMnadh[c] + MMretn[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMRADH2	MMh2o[c] + MMnadp[c] + MMretinal[c] <=> 2 MMh[c] + MMnadph[c] + MMretn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRADH3	MMh2o[c] + MMnad[c] + MMretinal-cis-13[c] <=> 2 MMh[c] + MMnadh[c] + MM13-cis-retn[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMRADH4	MMh2o[c] + MMnadp[c] + MMretinal-cis-13[c] <=> 2 MMh[c] + MMnadph[c] + MM13-cis-retn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRAHY	MMo2[c] + MMh[c] + MMnadph[c] + MMretn[c] -> MMh2o[c] + MMnadp[c] + MMretn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRAI1	MMretinal[c] <=> MMretinal-11-cis[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMRAI2	MMretinal[c] <=> MMretinal-cis-9[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMRAI3	MMretn[c] <=> MM13-cis-retn[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMRAI4	MMoretn[c] <=> MM13-cis-oretn[c]	-1000	1000	14863.1 or 14863.2	Mouse metabolic/ transport/ demand reaction
MMRAtn	MMretn[c] <=> MMretn[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMRAtn3	MM13-cis-retn[c] <=> MM13-cis-retn[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMRBK	MMatp[c] + MMrib-D[c] -> MMadp[c] + MMh[c] + MMr5p[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRBK_D	MMatp[c] + MMrbl-D[c] -> MMadp[c] + MMh[c] + MMru5p-D[c]	0	1000	71336.1	Mouse metabolic/ transport/ demand reaction
MMRBTi	MMrib[c] -> MMrib[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRDH1	MMnad[c] + MMretinol[c] <=> MMh[c] + MMnadh[c] + MMretinal[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMRDH1a	MMnadp[c] + MMretinol[c] <=> MMh[c] + MMnadph[c] + MMretinal[c]	0	1000	107605.1 or 19682.1	Mouse metabolic/ transport/ demand reaction
MMRDH2	MMnad[c] + MMretinol-9-cis[c] <=> MMh[c] + MMnadh[c] + MMretinal-cis-9[c]	-1000	1000	105014.1 or 235033.1 or 98711.1 or 108841.1 or 242285.1 or 17252.1 or 77974.1	Mouse metabolic/ transport/ demand reaction
MMRDH2a	MMnadp[c] + MMretinol-9-cis[c] <=> MMh[c] + MMnadph[c] + MMretinal-cis-9[c]	0	1000	19682.1	Mouse metabolic/ transport/ demand reaction
MMRDH3	MMnad[c] + MMretinol-cis-11[c] <=> MMh[c] + MMnadh[c] + MMretinal-11-cis[c]	-1000	1000	105014.1 or 235033.1 or 108841.1 or 242285.1 or 17252.1 or 77974.1	Mouse metabolic/ transport/ demand reaction
MMRDH3a	MMnadp[c] + MMretinol-cis-11[c] <=> MMh[c] + MMnadph[c] + MMretinal-11-cis[c]	0	1000	19682.1	Mouse metabolic/ transport/ demand reaction
MMRDH4	MMnad[c] + MMretinol-cis-13[c] <=> MMh[c] + MMnadh[c] + MMretinal-cis-13[c]	-1000	1000	105014.1 or 108841.1 or 242285.1 or 17252.1 or 77974.1	Mouse metabolic/ transport/ demand reaction
MMRE2666G	MMadpgal[g] + MMgalskafe_hs[g] -> MMh[g] + MMadp[g] + MMdigalskafe_hs[g]	0	1000	19682.1	Mouse metabolic/ transport/ demand reaction
MMRETFA	MMRtotal2coa[c] + MMretinol[c] -> MMcoa[c] + MMretfa[c]	0	1000		Mouse metabolic/ transport/ demand reaction

MMRETFAt	MMretfa[c] -> MMretfa[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRETFAt1	MM9-cis-retfa[c] -> MM9-cis-retfa[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRETFAt2	MM11-cis-retfa[c] -> MM11-cis-retfa[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRETH1	MMlh2o[c] + MM9-cis-retfa[c] -> MMlh[c] + MMRtotal2[c] + MMretinol-9-cis[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRETH1e	MMlh2o[e] + MM9-cis-retfa[e] -> MMlh[e] + MMRtotal2[e] + MMretinol-9-cis[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRETH2	MMlh2o[c] + MM11-cis-retfa[c] -> MMlh[c] + MMRtotal2[c] + MMretinol-cis-11[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRETH2e	MMlh2o[e] + MM11-cis-retfa[e] -> MMlh[e] + MMRtotal2[e] + MMretinol-cis-11[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRETHe	MMlh2o[e] + MMretfa[e] -> MMlh[e] + MMRtotal2[e] + MMretinol[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRETI1	MMretinol[c] <=> MMretinol-cis-11[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMRETI2	MMretinol[c] <=> MMretinol-9-cis[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMRETI3	MMretinol[c] <=> MMretinol-cis-13[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMRETINOLtc	MMretinol[u] -> MMretinol[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRETNCOA	MMatp[c] + MMcoa[c] + MMretn[c] -> MMamp[c] + MMppi[c] + MMretncoa[c]	0	1000	(19660.1 or (19662.1 and 20897.1 and 19659.1))	Mouse metabolic/ transport/ demand reaction
MMRETNGLCt	MMretngk[c] -> MMretngk[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRETNGLCt2	MM13-cis-retngk[c] -> MM13-cis-retngk[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRETNGLCt2r	MM13-cis-retngk[r] -> MM13-cis-retngk[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRETNGLCtr	MMretngk[r] -> MMretngk[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRETNt	MMretn[c] <=> MMretn[e]	-1000	0		Mouse metabolic/ transport/ demand reaction
MMRETNtr	MMretn[c] -> MMretn[r]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRETNtr2	MM13-cis-retn[c] -> MM13-cis-retn[r]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRETt	MMretinol[e] -> MMretinol[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRIBFLVIu	MMribflv[u] -> MMribflv[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRIBFLVt3	MMlh2o[c] + MMatp[c] + MMribflv[e] -> MMadp[c] + MMhi[c] + MMpi[c] + MMribflv[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRIBFLVte	MMlh2o[c] + MMatp[c] + MMribflv[c] -> MMadp[c] + MMhi[c] + MMpi[c] + MMribflv[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRIBt	MMrib-D[e] <=> MMrib-D[c]	-1000	1000	52710.1	Mouse metabolic/ transport/ demand reaction
MMRIBt2	MMhi[e] + MMrib-D[e] -> MMhi[c] + MMrib-D[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRNDR1	MMadp[c] + MMtrdrd[c] -> MMlh2o[c] + MMdadp[c] + MMtrdox[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRNDR2	MMgdp[c] + MMtrdrd[c] -> MMlh2o[c] + MMdgdp[c] + MMtrdox[c]	0	1000	20135.1 and 20133.1	Mouse metabolic/ transport/ demand reaction
MMRNDR3	MMcdp[c] + MMtrdrd[c] -> MMlh2o[c] + MMdcdp[c] + MMtrdox[c]	0	1000	20135.1 and 20133.1	Mouse metabolic/ transport/ demand reaction
MMRNDR4	MMudp[c] + MMtrdrd[c] -> MMlh2o[c] + MMdudp[c] + MMtrdox[c]	0	1000	20135.1 and 20133.1	Mouse metabolic/ transport/ demand reaction
MMRNMK	MMatp[c] + MMrnam[c] -> MMadp[c] + MMhi[c] + MMrnm[c]	0	1000	20135.1 and 20133.1	Mouse metabolic/ transport/ demand reaction
MMRPE	MMru5p-D[c] <=> MMxu5p-D[c]	-1000	1000	225994.1	Mouse metabolic/ transport/ demand reaction
MMRPI	MMr5p[c] <=> MMru5p-D[c]	-1000	1000	66646.1 or 66646.2	Mouse metabolic/ transport/ demand reaction
MMRTOT1	MMR1coa_hs[c] -> MMRtotalcoa[c]	0	1000	19895.1	Mouse metabolic/ transport/ demand reaction
MMRTOT2	MMR2coa_hs[c] -> MMRtotalcoa[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRTOT3	MMR3coa_hs[c] -> MMRtotalcoa[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRTOT4	MMR4coa_hs[c] -> MMRtotalcoa[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRTOT5	MMR5coa_hs[c] -> MMRtotalcoa[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRTOT6	MMR6coa_hs[c] -> MMRtotalcoa[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRTOTAL2CRNCPT1	MMcrn[c] + MMRtotal2coa[c] -> MMcoa[c] + MMRtotal2crn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRTOTAL2CRNCPT2	MMcoa[m] + MMRtotal2crn[m] -> MMcrn[m] + MMRtotal2coa[m]	0	1000	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	Mouse metabolic/ transport/ demand reaction
MMRTOTAL2CRNt	MMRtotal2crn[c] -> MMRtotal2crn[m]	0	1000	12896.1	Mouse metabolic/ transport/ demand reaction
MMRTOTAL2TDIu	MMRtotal2[u] <=> MMRtotal2[c]	-1000	1000	57279.1	Mouse metabolic/ transport/ demand reaction
MMRTOTAL2t	MMRtotal2[e] <=> MMRtotal2[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRTOTAL3CRNCPT1	MMcrn[c] + MMRtotal3coa[c] -> MMcoa[c] + MMRtotal3crn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRTOTAL3CRNCPT2	MMcoa[m] + MMRtotal3crn[m] -> MMcrn[m] + MMRtotal3coa[m]	0	1000	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3	Mouse metabolic/ transport/ demand reaction
MMRTOTAL3CRNt	MMRtotal3crn[c] -> MMRtotal3crn[m]	0	1000	12896.1	Mouse metabolic/ transport/ demand reaction
MMRTOTAL3TDIu	MMRtotal3[u] <=> MMRtotal3[c]	-1000	1000	57279.1	Mouse metabolic/ transport/ demand reaction
MMRTOTAL3t	MMRtotal3[e] <=> MMRtotal3[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRTOTALCRNCPT1	MMcrn[c] + MMRtotalcoa[c] -> MMcoa[c] + MMRtotalcrn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRTOTALCRNCPT2	MMcoa[m] + MMRtotalcrn[m] -> MMcrn[m] + MMRtotalcoa[m]	0	1000	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	Mouse metabolic/ transport/ demand reaction
MMRTOTALCRNt	MMRtotalcrn[c] -> MMRtotalcrn[m]	0	1000	12896.1	Mouse metabolic/ transport/ demand reaction
MMRTOTALDIu	MMRtotal[u] <=> MMRtotal[c]	-1000	1000	57279.1	Mouse metabolic/ transport/ demand reaction
MMRTOTALt	MMRtotal[e] <=> MMRtotal[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRTOT_2	MMR2coa_hs[c] + MMR4coa_hs[c] -> 2 MMRtotal2coa[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRTOT_3	MMR1coa_hs[c] + MMR2coa_hs[c] -> 2 MMRtotal3coa[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMRtotakl	MMRtotal[c] <=> MMRtotal[l]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMRtotaltp	MMRtotal[c] <=> MMRtotal[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMS23T2g	MMcore2[g] + MMcmpacna[g] -> MMh[g] + MMcmp[g] + MMksii_core2_pre1[g]	0	1000		Mouse metabolic/ transport/ demand reaction
MMS23T3g	MMcmpacna[g] + MM2fn2m2masn[g] -> MMh[g] + MMksi_pre1[g] + MMcmp[g]	0	1000	20442.1 or 20444.1 or 20442.2 or 20443.1	Mouse metabolic/ transport/ demand reaction
MMS23T4g	MMcmpacna[g] + MMksii_core4_pre1[g] -> MMh[g] + MMksii_core4_pre2[g] + MMcmp[g]	0	1000	20441.1 or 20441.2 or 20441.3 or 20441.4 or 20441.5 or 20441.6 or 20441.7 or 20441.8 or 20441.9 or 20441.10 or 20441.11	Mouse metabolic/ transport/ demand reaction
MMS23Tg	MMT_antigen[g] + MMcmpacna[g] -> MMh[g] + MMcmp[g] + MMsT_antigen[g]	0	1000	20442.1 or 20444.1 or 20442.2 or 20443.1	Mouse metabolic/ transport/ demand reaction
MMS26Tg	2 MMcmpacna[g] + MM2fn2m2masn[g] -> 2 MMh[g] + 2 MMcmp[g] + MMs2f2fn2m2masn[g]	0	1000	20442.1 or 20442.2	Mouse metabolic/ transport/ demand reaction
MMS2L2FN2M2MASNt	MMs2f2fn2m2masn[g] -> MMs2f2fn2m2masn[e]	0	1000	20440.1 or 20440.2 or 20440.3	Mouse metabolic/ transport/ demand reaction
MMS2L2FN2M2MASNtly	MMs2f2fn2m2masn[e] -> MMs2f2fn2m2masn[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MMS2L2N2M2MASNtly	MMs2f2n2m2masn[e] -> MMs2f2n2m2masn[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MMS2L2N2M2Mt	MMs2f2n2m2m[l] <=> MMs2f2n2m2m[e]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMS2T1g	MMpaps[g] + MMcs_c_d_e_pre1[g] -> MMh[g] + MMpap[g] + MMcs_d_pre2[g]	0	1000		Mouse metabolic/ transport/ demand reaction
MMS2T2g	MMpaps[g] + MMcs_d_pre5[g] -> MMh[g] + MMcspg_d[g] + MMpap[g]	0	1000	338362.1	Mouse metabolic/ transport/ demand reaction
MMS2T3g	MMpaps[g] + MMcs_b_pre5[g] -> MMh[g] + MMcspg_b[g] + MMpap[g]	0	1000	338362.1	Mouse metabolic/ transport/ demand reaction
MMS2T4g	2 MMpaps[g] + MMhs_pre11[g] -> 2 MMh[g] + 2 MMpap[g] + MMhs_pre12[g]	0	1000	338362.1	Mouse metabolic/ transport/ demand reaction
MMS2TASE1ly	MMlh2o[l] + MMhs_deg15[l] -> MMh[l] + MMso4[l] + MMhs_deg16[l]	0	1000	23908.1	Mouse metabolic/ transport/ demand reaction
MMS2TASE2ly	MMlh2o[l] + MMhs_deg21[l] -> MMh[l] + MMso4[l] + MMhs_deg22[l]	0	1000	15931.1 or 15931.2	Mouse metabolic/ transport/ demand reaction
MMS2TASE3ly	MMlh2o[l] + MMcs_b_deg2[l] -> MMh[l] + MMso4[l] + MMcs_b_deg3[l]	0	1000	15931.1 or 15931.2	Mouse metabolic/ transport/ demand reaction
MMS2TASE4ly	MMlh2o[l] + MMcs_d_deg2[l] -> MMh[l] + MMso4[l] + MMcs_d_deg3[l]	0	1000	15931.1 or 15931.2	Mouse metabolic/ transport/ demand reaction
MMS2TASE5ly	MMlh2o[l] + MMcs_d_deg6[l] -> MMh[l] + MMso4[l] + MMcs_c_deg5[l]	0	1000		Mouse metabolic/ transport/ demand reaction
MMS3T1g	MMpaps[g] + MMhs_pre13[g] -> MMh[g] + MMpap[g] + MMhs_pre14[g]	0	1000		Mouse metabolic/ transport/ demand reaction
MMS3T2g	MMpaps[g] + MMhs_pre14[g] -> MMh[g] + MMpap[g] + MMhs_pre15[g]	0	1000	15476.1 or 628779.1 or 319415.1	Mouse metabolic/ transport/ demand reaction
MMS3T3g	MMpaps[g] + MMhs_pre15[g] -> MMh[g] + MMpap[g] + MMhspg[g]	0	1000	628779.1 or 319415.1 or 195646.1	Mouse metabolic/ transport/ demand reaction
MMS3TASE1ly	MMlh2o[l] + MMhs_deg10[l] <=> MMh[l] + MMso4[l] + MMhs_deg11[l]	-1000	1000	15478.1 or 54710.1 or 328779.1 or 628779.1	Mouse metabolic/ transport/ demand reaction
MMS3TASE2ly	MMlh2o[l] + MMhs_deg17[l] <=> MMh[l] + MMso4[l] + MMhs_deg18[l]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMS3TASE3ly	MMlh2o[l] + MMhs_deg23[l] <=> MMh[l] + MMso4[l] + MMhs_deg24[l]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMS4T1g	2 MMpaps[g] + MMcs_pre[g] -> 2 MMh[g] + 2 MMpap[g] + MMcs_a_b_e_pre1[g]	0	1000		Mouse metabolic/ transport/ demand reaction
MMS4T2g	MMpaps[g] + MMcs_a_b_pre3[g] -> MMh[g] + MMcspg_a[g] + MMpap[g]	0	1000	71797.1 or 58250.1 or 59031.1 or 72136.1	Mouse metabolic/ transport/ demand reaction

MMS4T3g	MMpaps[g] + MMcs_e_pre4[g] -> MMh[g] + MMpap[g] + MMcs_e_pre5d[g]	0	1000	71797.1 or 58250.1 or 59031.1 or 72136.1	Mouse metabolic/ transport/ demand reaction
MMS4T4g	2 MMpaps[g] + MMcs_c_d_e_pre1[g] -> 2 MMh[g] + 2 MMpap[g] + MMcs_e_pre2[g]	0	1000	71797.1 or 58250.1 or 59031.1 or 72136.1	Mouse metabolic/ transport/ demand reaction
MMS4T5g	MMpaps[g] + MMcs_e_pre5b[g] -> MMh[g] + MMcspg_e[g] + MMfnnap[g]	0	1000		Mouse metabolic/ transport/ demand reaction
MMS4T6g	MMpaps[g] + MMcs_b_pre4[g] -> MMh[g] + MMpap[g] + MMcs_b_pre5[g]	0	1000		Mouse metabolic/ transport/ demand reaction
MMS4TASE1ly	MMh2o[l] + MMcs_a[l] <=> MMh[l] + MMso4[l] + MMcs_a_deg1[l]	-1000	1000	71797.1 or 58250.1 or 59031.1 or 72136.1	Mouse metabolic/ transport/ demand reaction
MMS4TASE2ly	MMh2o[l] + MMcs_a_deg3[l] <=> MMh[l] + MMso4[l] + MMcs_a_deg4[l]	-1000	1000	11881.1 or 11881.2	Mouse metabolic/ transport/ demand reaction
MMS4TASE3ly	MMh2o[l] + MMcs_b[l] <=> MMh[l] + MMso4[l] + MMcs_b_deg1[l]	-1000	1000	11881.1 or 11881.2	Mouse metabolic/ transport/ demand reaction
MMS4TASE4ly	MMh2o[l] + MMcs_e[l] <=> MMh[l] + MMso4[l] + MMcs_e_deg1[l]	-1000	1000	11881.1 or 11881.2	Mouse metabolic/ transport/ demand reaction
MMS4TASE5ly	MMh2o[l] + MMcs_e_deg4[l] <=> MMh[l] + MMso4[l] + MMcs_e_deg5[l]	-1000	1000	11881.1 or 11881.2	Mouse metabolic/ transport/ demand reaction
MMS6T10g	MMksi_pre22[g] + MMpaps[g] -> MMh[g] + MMksi_pre23[g] + MMpap[g]	0	1000	11881.1 or 11881.2	Mouse metabolic/ transport/ demand reaction
MMS6T11g	MMksi_pre25[g] + MMpaps[g] -> MMh[g] + MMksi_pre26[g] + MMpap[g]	0	1000	26887.1 or 54371.1 or 56773.1 or 56773.2	Mouse metabolic/ transport/ demand reaction
MMS6T12g	MMksi_pre28[g] + MMpaps[g] -> MMh[g] + MMksi_pre29[g] + MMpap[g]	0	1000	26887.1 or 56773.1 or 54342.1 or 56773.1 or 56773.1	Mouse metabolic/ transport/ demand reaction
MMS6T13g	MMksi_pre31[g] + MMpaps[g] -> MMh[g] + MMksi_pre32[g] + MMpap[g]	0	1000	26887.1 or 56773.1 or 54342.1 or 56773.1 or 56773.1	Mouse metabolic/ transport/ demand reaction
MMS6T14g	MMksi_pre34[g] + MMpaps[g] -> MMh[g] + MMksi_pre35[g] + MMpap[g]	0	1000	26887.1 or 56773.1 or 54342.1 or 56773.1 or 56773.1	Mouse metabolic/ transport/ demand reaction
MMS6T15g	MMksi_pre36[g] + MMpaps[g] -> MMh[g] + MMpap[g] + MMksi[g]	0	1000	26887.1 or 56773.1 or 54342.1 or 56773.1 or 56773.1	Mouse metabolic/ transport/ demand reaction
MMS6T16g	MMksii_core4_pre5[g] + MMpaps[g] -> MMh[g] + MMksii_core4_pre6[g] + MMpap[g]	0	1000	53374.1 or 76969.1	Mouse metabolic/ transport/ demand reaction
MMS6T17g	MMksii_core4_pre8[g] + MMpaps[g] -> MMh[g] + MMksii_core4_pre9[g] + MMpap[g]	0	1000	26887.1 or 56773.1 or 54342.1 or 56773.1 or 56773.1	Mouse metabolic/ transport/ demand reaction
MMS6T18g	MMksii_core4_pre10[g] + MMpaps[g] -> MMh[g] + MMpap[g] + MMksii_core4[g]	0	1000	26887.1 or 56773.1 or 54342.1 or 56773.1 or 56773.1	Mouse metabolic/ transport/ demand reaction
MMS6T19g	2 MMpaps[g] + MMcs_pre[g] -> 2 MMh[g] + 2 MMpap[g] + MMcs_c_d_e_pre1[g]	0	1000	53374.1 or 76969.1	Mouse metabolic/ transport/ demand reaction
MMS6T1g	MMksii_core2_pre5[g] + MMpaps[g] -> MMh[g] + MMksii_core2_pre6[g] + MMpap[g]	0	1000	60322.1 or 53374.1	Mouse metabolic/ transport/ demand reaction
MMS6T20g	MMpaps[g] + MMcs_c_pre3[g] -> MMh[g] + MMcspg_c[g] + MMpap[g]	0	1000	26887.1 or 56773.1 or 54342.1 or 56773.1 or 56773.1	Mouse metabolic/ transport/ demand reaction
MMS6T21g	MMpaps[g] + MMcs_d_pre4[g] -> MMh[g] + MMpap[g] + MMcs_d_pre5[g]	0	1000	60322.1 or 53374.1	Mouse metabolic/ transport/ demand reaction
MMS6T22g	2 MMpaps[g] + MMcs_a_b_e_pre1[g] -> 2 MMh[g] + 2 MMpap[g] + MMcs_e_pre2[g]	0	1000	60322.1 or 53374.1	Mouse metabolic/ transport/ demand reaction
MMS6T23g	MMpaps[g] + MMcs_e_pre5a[g] -> MMh[g] + MMcspg_e[g] + MMpap[g]	0	1000	60322.1	Mouse metabolic/ transport/ demand reaction
MMS6T24g	MMpaps[g] + MMcs_e_pre4[g] -> MMh[g] + MMpap[g] + MMcs_e_pre5b[g]	0	1000	60322.1	Mouse metabolic/ transport/ demand reaction
MMS6T25g	3 MMpaps[g] + MMhs_pre12[g] -> 3 MMh[g] + 3 MMpap[g] + MMhs_pre13[g]	0	1000	60322.1 or 53374.1	Mouse metabolic/ transport/ demand reaction
MMS6T2g	MMksii_core2_pre8[g] + MMpaps[g] -> MMh[g] + MMksii_core2_pre9[g] + MMpap[g]	0	1000	50785.1 or 50787.1 or 50786.2 or 50786.1	Mouse metabolic/ transport/ demand reaction
MMS6T3g	MMksii_core2_pre10[g] + MMpaps[g] -> MMh[g] + MMpap[g] + MMksii_core2[g]	0	1000	26887.1 or 56773.1 or 54342.1 or 56773.1 or 56773.1	Mouse metabolic/ transport/ demand reaction
MMS6T4g	MMksi_pre4[g] + MMpaps[g] -> MMh[g] + MMksi_pre5[g] + MMpap[g]	0	1000	53374.1 or 76969.1	Mouse metabolic/ transport/ demand reaction
MMS6T5g	MMksi_pre7[g] + MMpaps[g] -> MMh[g] + MMksi_pre8[g] + MMpap[g]	0	1000	26887.1 or 56773.1 or 54342.1 or 56773.1 or 56773.1	Mouse metabolic/ transport/ demand reaction
MMS6T6g	MMksi_pre10[g] + MMpaps[g] -> MMh[g] + MMksi_pre11[g] + MMpap[g]	0	1000	26887.1 or 56773.1 or 54342.1 or 56773.1 or 56773.1	Mouse metabolic/ transport/ demand reaction
MMS6T7g	MMksi_pre13[g] + MMpaps[g] -> MMh[g] + MMksi_pre14[g] + MMpap[g]	0	1000	26887.1 or 56773.1 or 54342.1 or 56773.1 or 56773.1	Mouse metabolic/ transport/ demand reaction
MMS6T8g	MMksi_pre16[g] + MMpaps[g] -> MMh[g] + MMksi_pre17[g] + MMpap[g]	0	1000	26887.1 or 56773.1 or 54342.1 or 56773.1 or 56773.1	Mouse metabolic/ transport/ demand reaction
MMS6T9g	MMksi_pre19[g] + MMpaps[g] -> MMh[g] + MMksi_pre20[g] + MMpap[g]	0	1000	26887.1 or 56773.1 or 54342.1 or 56773.1 or 56773.1	Mouse metabolic/ transport/ demand reaction
MMS6TASE10ly	MMh2o[l] + MMksi_deg4[l] <=> MMh[l] + MMso4[l] + MMksi_deg5[l]	-1000	1000	26887.1 or 56773.1 or 54342.1 or 56773.1 or 56773.1	Mouse metabolic/ transport/ demand reaction
MMS6TASE11ly	MMh2o[l] + MMksi_deg6[l] <=> MMh[l] + MMso4[l] + MMksi_deg7[l]	-1000	1000	50917.1 or 19025.1 or 12091.1 or 18010.1	Mouse metabolic/ transport/ demand reaction
MMS6TASE12ly	MMh2o[l] + MMksi_deg9[l] <=> MMh[l] + MMso4[l] + MMksi_deg10[l]	-1000	1000	75612.1	Mouse metabolic/ transport/ demand reaction
MMS6TASE13ly	MMh2o[l] + MMksi_deg12[l] <=> MMh[l] + MMso4[l] + MMksi_deg13[l]	-1000	1000	75612.1	Mouse metabolic/ transport/ demand reaction
MMS6TASE14ly	MMh2o[l] + MMksi_deg15[l] <=> MMh[l] + MMso4[l] + MMksi_deg16[l]	-1000	1000	75612.1	Mouse metabolic/ transport/ demand reaction
MMS6TASE15ly	MMh2o[l] + MMksi_deg18[l] <=> MMh[l] + MMso4[l] + MMksi_deg19[l]	-1000	1000	75612.1	Mouse metabolic/ transport/ demand reaction
MMS6TASE16ly	MMh2o[l] + MMksi_deg21[l] <=> MMh[l] + MMso4[l] + MMksi_deg22[l]	-1000	1000	75612.1	Mouse metabolic/ transport/ demand reaction
MMS6TASE17ly	MMh2o[l] + MMksi_deg24[l] <=> MMh[l] + MMso4[l] + MMksi_deg25[l]	-1000	1000	75612.1	Mouse metabolic/ transport/ demand reaction
MMS6TASE18ly	MMh2o[l] + MMksi_deg27[l] <=> MMh[l] + MMso4[l] + MMksi_deg28[l]	-1000	1000	75612.1	Mouse metabolic/ transport/ demand reaction
MMS6TASE19ly	MMh2o[l] + MMksi_deg30[l] <=> MMh[l] + MMso4[l] + MMksi_deg31[l]	-1000	1000	75612.1	Mouse metabolic/ transport/ demand reaction
MMS6TASE1ly	MMh2o[l] + MMhs[l] <=> MMh[l] + MMso4[l] + MMhs_deg1[l]	-1000	1000	75612.1	Mouse metabolic/ transport/ demand reaction
MMS6TASE20ly	MMh2o[l] + MMksi_deg33[l] <=> MMh[l] + MMso4[l] + MMksi_deg34[l]	-1000	1000	75612.1	Mouse metabolic/ transport/ demand reaction
MMS6TASE21ly	MMh2o[l] + MMksi_deg36[l] <=> MMh[l] + MMso4[l] + MMksi_deg37[l]	-1000	1000	75612.1	Mouse metabolic/ transport/ demand reaction
MMS6TASE22ly	MMh2o[l] + MMksii_core2_deg1[l] <=> MMh[l] + MMso4[l] + MMksii_core2_deg2[l]	-1000	1000	75612.1	Mouse metabolic/ transport/ demand reaction
MMS6TASE23ly	MMh2o[l] + MMksii_core2_deg3[l] <=> MMh[l] + MMso4[l] + MMksii_core2_deg4[l]	-1000	1000	50917.1 or 19025.1 or 12091.1 or 18010.1	Mouse metabolic/ transport/ demand reaction
MMS6TASE24ly	MMh2o[l] + MMksii_core2_deg6[l] <=> MMh[l] + MMso4[l] + MMksii_core2_deg7[l]	-1000	1000	75612.1	Mouse metabolic/ transport/ demand reaction
MMS6TASE25ly	MMh2o[l] + MMksii_core4_deg1[l] <=> MMh[l] + MMso4[l] + MMksii_core4_deg2[l]	-1000	1000	75612.1	Mouse metabolic/ transport/ demand reaction
MMS6TASE26ly	MMh2o[l] + MMksii_core4_deg3[l] <=> MMh[l] + MMso4[l] + MMksii_core4_deg4[l]	-1000	1000	50917.1 or 19025.1 or 12091.1 or 18010.1	Mouse metabolic/ transport/ demand reaction
MMS6TASE2ly	MMh2o[l] + MMhs_deg5[l] <=> MMh[l] + MMso4[l] + MMhs_deg6[l]	-1000	1000	75612.1	Mouse metabolic/ transport/ demand reaction
MMS6TASE3ly	MMh2o[l] + MMhs_deg11[l] <=> MMh[l] + MMso4[l] + MMhs_deg12[l]	-1000	1000	75612.1	Mouse metabolic/ transport/ demand reaction
MMS6TASE4ly	MMh2o[l] + MMcs_c[l] <=> MMh[l] + MMso4[l] + MMcs_c_deg1[l]	-1000	1000	75612.1	Mouse metabolic/ transport/ demand reaction
MMS6TASE5ly	MMh2o[l] + MMcs_c_deg3[l] <=> MMh[l] + MMso4[l] + MMcs_c_deg4[l]	-1000	1000	50917.1 or 19025.1 or 12091.1 or 18010.1	Mouse metabolic/ transport/ demand reaction
MMS6TASE6ly	MMh2o[l] + MMcs_d[l] <=> MMh[l] + MMso4[l] + MMcs_d_deg1[l]	-1000	1000	50917.1 or 19025.1 or 12091.1 or 18010.1	Mouse metabolic/ transport/ demand reaction
MMS6TASE7ly	MMh2o[l] + MMcs_d_deg4[l] <=> MMh[l] + MMso4[l] + MMcs_d_deg5[l]	-1000	1000	50917.1 or 19025.1 or 12091.1 or 18010.1	Mouse metabolic/ transport/ demand reaction
MMS6TASE8ly	MMh2o[l] + MMcs_e_deg1[l] <=> MMh[l] + MMso4[l] + MMcs_e_deg2[l]	-1000	1000	50917.1 or 19025.1 or 12091.1 or 18010.1	Mouse metabolic/ transport/ demand reaction
MMS6TASE9ly	MMh2o[l] + MMcs_e_deg5[l] <=> MMh[l] + MMso4[l] + MMcs_e_deg6[l]	-1000	1000	50917.1 or 19025.1 or 12091.1 or 18010.1	Mouse metabolic/ transport/ demand reaction
MMSACCD3m	MMh[m] + MMnadph[m] + MMakg[m] + MMlys-L[m] -> MMh2o[m] + MMnadp[m] + MMsaccrp-L[m]	0	1000	50917.1 or 19025.1 or 12091.1 or 18010.1	Mouse metabolic/ transport/ demand reaction
MMSACCD4m	MMh2o[m] + MMnadp[m] + MMsaccrp-L[m] -> MMh[m] + MMnadph[m] + MMglu-L[m] + MML2aadp6sa[m]	0	1000	30956.1	Mouse metabolic/ transport/ demand reaction
MMSADT	MMatp[c] + MMh[c] + MMso4[c] -> MMppi[c] + MMaps[c]	0	1000	30956.1	Mouse metabolic/ transport/ demand reaction
MMSALMCOM	MMamet[c] + MMurpph[c] -> MMh[c] + MMahcys[c] + MMmormte-L[c]	0	1000	23972.1 or 23971.1	Mouse metabolic/ transport/ demand reaction
MMSALMCOM2	MMamet[c] + MMadrnl[c] -> MMh[c] + MMahcys[c] + MMmepi[c]	0	1000	12846.1 or 69156.1 or 12846.2	Mouse metabolic/ transport/ demand reaction
MMSAMHISTA	MMamet[c] + MMhista[c] -> MMh[c] + MMahcys[c] + MMmhista[c]	0	1000	69156.1	Mouse metabolic/ transport/ demand reaction
MMSARCOXp	MMo2[x] + MMh2o[x] + MMsarcs[x] -> MMh2o2[x] + MMgly[x] + MMald[x]	0	1000	140483.1	Mouse metabolic/ transport/ demand reaction
MMSARCStex	MMsarcs[e] -> MMsarcs[c]	0	1000	19193.1	Mouse metabolic/ transport/ demand reaction
MMSARCStm	MMsarcs[c] -> MMsarcs[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMSARCStp	MMsarcs[c] -> MMsarcs[x]	0	1000		Mouse metabolic/ transport/ demand reaction
MMSARDHm	MMfad[m] + MMsarcs[m] + MMthf[m] -> MMfadh2[m] + MMgly[m] + MMmthf[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMSBPP1er	MMh2o[r] + MMsph1p[r] -> MMpi[r] + MMsphgn[r]	0	1000	192166.1	Mouse metabolic/ transport/ demand reaction
MMSBPP3er	MMh2o[r] + MMsphn1p[r] -> MMpi[r] + MMsphings[r]	0	1000	81535.1	Mouse metabolic/ transport/ demand reaction
MMSBTD_D2	MMnad[c] + MMsbt-D[c] -> MMh[c] + MMnadh[c] + MMfru[c]	0	1000	81535.1	Mouse metabolic/ transport/ demand reaction
MMSBTR	MMh[c] + MMnadph[c] + MMglc-D[c] -> MMnadp[c] + MMsbt-D[c]	0	1000	20322.1	Mouse metabolic/ transport/ demand reaction
MMSBTtu	MMsbt-D[u] -> MMsbt-D[c]	0	1000	110198.1 or 58810.2 or 11677.1 or 58810.1	Mouse metabolic/ transport/ demand reaction
MMSBTt	MMsbt-D[e] <=> MMsbt-D[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMSCP21x	MMphytcoa[c] <=> MMphytcoa[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMSCP22x	MMdmnoncoa[c] <=> MMdmnoncoa[x]	-1000	1000	20280.1	Mouse metabolic/ transport/ demand reaction
MMSCP2x	MMcoa[x] + MMdhochololeylcoa[x] -> MMdgchrolcoa[x] + MMppcoa[x]	0	1000	20280.1	Mouse metabolic/ transport/ demand reaction
MMSCP3x	MMcoa[x] + MMo2[x] + MMdhcholestancoa[x] -> MMh2o[x] + MMdchrlcoa[x] + MMppcoa[x]	0	1000	20280.1	Mouse metabolic/ transport/ demand reaction
MMSCPx	MMcoa[x] + MMcholenaone[x] -> MMcholcoa[x] + MMppcoa[x]	0	1000	20280.1	Mouse metabolic/ transport/ demand reaction
MMSEAHCYSHYD	MMh2o[c] + MMsealhcys[c] -> MMadrl[c] + MMselhcys[c]	0	1000	20280.1	Mouse metabolic/ transport/ demand reaction
MMSEAHCYStn	MMsealhcys[c] <=> MMsealhcys[n]	-1000	1000	74340.1 or 229709.1 or 229709.2 or 269378.1	Mouse metabolic/ transport/ demand reaction

MMSEASMETtn	MMseasmet[c] <=> MMseasmet[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMSELADT	MMatp[c] + MMth[c] + MMser[c] -> MMpp[c] + MMadser[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMSELCYSLY	MMdtt[c] + MMselcys[c] -> MMh[c] + MMala-L[c] + MMdttOX[c] + MMselx[c]	0	1000	23972.1 or 23971.1	Mouse metabolic/ transport/ demand reaction
MMSELCYSLY2	MMpds5p[c] + MMselcys[c] -> MMth[c] + MMala-L[c] + MMpyds5p[c] + MMselx[c]	0	1000	50880.1	Mouse metabolic/ transport/ demand reaction
MMSELCYSTGL	MMh2o[c] + MMselcyst[c] -> MMlnb4[c] + MM2obut[c] + MMselcys[c]	0	1000	50880.1	Mouse metabolic/ transport/ demand reaction
MMSELCYSTS	MMser-L[c] + MMselhcys[c] -> MMh2o[c] + MMselcyst[c]	0	1000	107869.1 or 107869.2	Mouse metabolic/ transport/ demand reaction
MMSELMETAT	MMth2o[c] + MMatp[c] + MMselmeth[c] -> MMpi[c] + MMppi[c] + MMseasmet[c]	0	1000	12411.1	Mouse metabolic/ transport/ demand reaction
MMSELNPS	MMh2o[c] + MMatp[c] + MMselnh[c] -> MMpi[c] + MMamp[c] + MMselnp[c]	0	1000	232087.1 and 108645.1 or 108645.2 and 232087.1 or 11720.1	Mouse metabolic/ transport/ demand reaction
MMSELt4_3	3 MMnu1[e] + MMsel[e] <=> 3 MMnu1[c] + MMsel[c]	0	1000	109079.1 or 20768.1	Mouse metabolic/ transport/ demand reaction
MMSERALANaEx	MMnu1[e] + MMala-L[c] + MMser-L[e] -> MMnu1[c] + MMala-L[e] + MMser-L[c]	0	1000	55961.1	Mouse metabolic/ transport/ demand reaction
MMSERASNNaEx	MMnu1[e] + MMasn-L[c] + MMser-L[e] -> MMnu1[c] + MMasn-L[e] + MMser-L[c]	0	1000	20514.1 or 55963.1	Mouse metabolic/ transport/ demand reaction
MMSERATB0tc	2 MMnu1[u] + MMcit[u] + MMser-L[u] -> 2 MMnu1[c] + MMcit[c] + MMser-L[c]	0	1000	20514.1	Mouse metabolic/ transport/ demand reaction
MMSERB0AT1tc	MMnu1[u] + MMser-L[u] -> MMnu1[c] + MMser-L[c]	0	1000	56774.1	Mouse metabolic/ transport/ demand reaction
MMSERCYSNaEx	MMnu1[e] + MMcys-L[c] + MMser-L[e] -> MMnu1[c] + MMcys-L[e] + MMser-L[c]	0	1000	(70008.1 or (74338.1 and 57394.1))	Mouse metabolic/ transport/ demand reaction
MMSERDGLNexR	MMgln-L[c] + MMser-D[e] <=> MMgln-L[e] + MMser-D[c]	-1000	1000	20514.1 or 55963.1	Mouse metabolic/ transport/ demand reaction
MMSERDGLYexR	MMgly[c] + MMser-D[e] <=> MMgly[e] + MMser-D[c]	-1000	1000	53896.1 or 17254.1	Mouse metabolic/ transport/ demand reaction
MMSERGLNNaEx	MMnu1[e] + MMgln-L[c] + MMser-L[e] -> MMnu1[c] + MMgln-L[e] + MMser-L[c]	0	1000	53896.1 or 17254.1	Mouse metabolic/ transport/ demand reaction
MMSERGLNexR	MMgln-L[c] + MMser-L[e] <=> MMgln-L[e] + MMser-L[c]	-1000	1000	20514.1	Mouse metabolic/ transport/ demand reaction
MMSERGLYALAGLYt	MMSer_Gly_Ala_X_Gly[l] -> MMSer_Gly_Ala_X_Gly[r]	0	1000	53896.1 or 17254.1	Mouse metabolic/ transport/ demand reaction
MMSERGLYexR	MMgly[c] + MMser-L[e] <=> MMgly[e] + MMser-L[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMSERHL	MMser-L[c] -> MMh2o[c] + MM2amac[c]	0	1000	53896.1 or 17254.1	Mouse metabolic/ transport/ demand reaction
MMSERILELAT2tc	MMile-L[c] + MMser-L[e] -> MMile-L[e] + MMser-L[c]	0	1000	231691.1	Mouse metabolic/ transport/ demand reaction
MMSERLYSNaex	MMnu1[e] + MMser-L[e] + MMlys-L[c] -> MMnu1[c] + MMser-L[c] + MMlys-L[e]	0	1000	(20539.1 and 17254.1)	Mouse metabolic/ transport/ demand reaction
MMSERPHELAT2tc	MMphe-L[c] + MMser-L[e] -> MMphe-L[e] + MMser-L[c]	0	1000	20540.1 and 20532.1	Mouse metabolic/ transport/ demand reaction
MMSERPT	MMh[c] + MMser-L[c] + MMpmtcoa[c] -> MMco2[c] + MM3dsphgn[c] + MMcoa[c]	0	1000	(20539.1 and 17254.1)	Mouse metabolic/ transport/ demand reaction
MMSERTHRNaEx	MMnu1[e] + MMser-L[e] + MMthr-L[c] -> MMnu1[c] + MMser-L[c] + MMthr-L[e]	0	1000	20773.1 and 268656.1	Mouse metabolic/ transport/ demand reaction
MMSERt4	MMnu1[e] + MMser-L[e] -> MMnu1[c] + MMser-L[c]	0	1000	20514.1 or 55963.1	Mouse metabolic/ transport/ demand reaction
MMSERtN1	MMh[c] + 2 MMnu1[e] + MMser-L[e] <=> MMh[e] + 2 MMnu1[c] + MMser-L[c]	-1000	1000	105727.1 or 67760.1 or 69354.1 or 56774.1	Mouse metabolic/ transport/ demand reaction
MMSERtp	MMser-L[c] <=> MMser-L[x]	-1000	1000	209837.1	Mouse metabolic/ transport/ demand reaction
MMSFGTH	MMh2o[c] + MMSfglutnh[c] <=> MMh[c] + MMfor[c] + MMglyhrd[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMSGALSIDEtg	MMsgalside_hs[c] <=> MMsgalside_hs[g]	-1000	1000	13885.1	Mouse metabolic/ transport/ demand reaction
MMSGALSIDEtl	MMsgalside_hs[c] <=> MMsgalside_hs[l]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMSGPL11r	MMsph1p[r] -> MMethamp[r] + MMhxdcal[r]	0	1000		Mouse metabolic/ transport/ demand reaction
MMSGPL12r	MMh2o[r] + MMsphs1p[r] -> MMh[r] + MMethamp[r] + MMhtdcal[r]	0	1000	20397.1	Mouse metabolic/ transport/ demand reaction
MMSIAASE	2 MMh2o[c] + MMs2fn2m2mm[c] -> 2 MMacnam[c] + MM2n2m2mm[c]	0	1000	20397.1	Mouse metabolic/ transport/ demand reaction
MMSIAASE2ly	MMih2o[l] + MMksi_deg3[l] -> MMacnam[l] + MMksi_deg4[l]	0	1000	241159.1 or 23956.1	Mouse metabolic/ transport/ demand reaction
MMSIAASE3ly	MMh2o[l] + MMksii_core2[l] -> MMacnam[l] + MMksii_core2_deg1[l]	0	1000	50917.1 or 19025.1 or 12091.1 or 18010.1	Mouse metabolic/ transport/ demand reaction
MMSIAASE4ly	MMh2o[l] + MMksii_core4[l] -> MMacnam[l] + MMksii_core4_deg1[l]	0	1000	50917.1 or 19025.1 or 12091.1 or 18010.1	Mouse metabolic/ transport/ demand reaction
MMSIAASEly	2 MMh2o[l] + MMs2fn2m2mm[l] -> 2 MMacnam[l] + MM2n2m2mm[l]	0	1000	50917.1 or 19025.1 or 12091.1 or 18010.1	Mouse metabolic/ transport/ demand reaction
MMSIAT4Bg	MMgalglside_hs[g] + MMcrnpacna[g] -> MMh[g] + MMcrnp[g] + MMacngalglside_hs[g]	0	1000	50917.1 or 19025.1 or 12091.1 or 18010.1	Mouse metabolic/ transport/ demand reaction
MMSIAT9g	MMgalglside_hs[g] + MMcrnpacna[g] -> MMh[g] + MMcrnp[g] + MMgm3_hs[g]	0	1000	20444.1	Mouse metabolic/ transport/ demand reaction
MMSLCBK1	MMatp[c] + MMsphgn[c] -> MMadp[c] + MMh[c] + MMsph1p[c]	0	1000	20454.1	Mouse metabolic/ transport/ demand reaction
MMSLDt	MMsl-L[c] -> MMsl-L[e]	0	1000	56632.1	Mouse metabolic/ transport/ demand reaction
MMSLDx	MMnadl[c] + MMsl-L[c] <=> MMh[c] + MMnadh[c] + MM3spyr[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMSLDxm	MMnadl[m] + MMsl-L[m] <=> MMh[m] + MMnadh[m] + MM3spyr[m]	-1000	1000	76668.1 or 17449.1	Mouse metabolic/ transport/ demand reaction
MMSMPD3g	MMh2o[g] + MMsphmyln_hs[g] -> MMh[g] + MMcrm_hs[g] + MMchol(p[g]	0	1000	17448.1	Mouse metabolic/ transport/ demand reaction
MMSMPD3l	MMh2o[l] + MMsphmyln_hs[l] -> MMh[l] + MMcrm_hs[l] + MMchol(p[l]	0	1000	58994.1 or 58994.2	Mouse metabolic/ transport/ demand reaction
MMSMPD4	MMh2o[c] + MMspc_hs[c] -> MMh[c] + MMchol(p[c] + MMsphings[c]	0	1000	58994.1 or 58994.2	Mouse metabolic/ transport/ demand reaction
MMSMS	MMpchol_hs[c] + MMcrm_hs[c] -> MMdag_hs[c] + MMsphmyln_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMSO4CLtex2	MMcl[c] + 2 MMso4[e] -> MMcl[e] + 2 MMso4[c]	0	1000	208449.1	Mouse metabolic/ transport/ demand reaction
MMSO4HCOtex	2 MMhco3[c] + MMso4[e] -> 2 MMhco3[e] + MMso4[c]	0	1000	171429.1 or 171429.2 or 171429.3	Mouse metabolic/ transport/ demand reaction
MMSO4OXAtex2	MMoxa[c] + 2 MMso4[e] -> MMoxa[e] + 2 MMso4[c]	0	1000	13487.1 or 224661.1 or 231583.1 or 208890.1 or 224661.2 or 320718.1 or 13521.1 or 231583.2 or 208890.2 or 231583.3 or 268512.1 or 320718.2	Mouse metabolic/ transport/ demand reaction
MMSO4t4_2	2 MMnu1[e] + MMso4[e] <=> 2 MMnu1[c] + MMso4[c]	0	1000	171429.1 or 171429.2 or 171429.3	Mouse metabolic/ transport/ demand reaction
MMSO4t4_3	3 MMnu1[e] + MMso4[e] <=> 3 MMnu1[c] + MMso4[c]	0	1000	243755.1	Mouse metabolic/ transport/ demand reaction
MMSO4tl	MMso4[l] <=> MMso4[c]	-1000	1000	55961.1	Mouse metabolic/ transport/ demand reaction
MMSOAT11	MMR1coa_hs[c] + MMchsterol[c] -> MMcoa[c] + MMsulest_hs[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMSOAT11r	MMchsterol[r] + MMR1coa_hs[r] -> MMcoa[r] + MMsulest_hs[r]	0	1000	20652.1	Mouse metabolic/ transport/ demand reaction
MMSOAT12	MMR2coa_hs[c] + MMchsterol[c] -> MMcoa[c] + MMsulest_hs[c]	0	1000	20652.1	Mouse metabolic/ transport/ demand reaction
MMSOAT12r	MMchsterol[r] + MMR2coa_hs[r] -> MMcoa[r] + MMsulest_hs[r]	0	1000	20652.1	Mouse metabolic/ transport/ demand reaction
MMSOProd	MMo2[m] + MMe-[m] -> MMo2s[m]	0	1000	20652.1	Mouse metabolic/ transport/ demand reaction
MMSPC_HSt	MMspc_hs[c] <=> MMspc_hs[e]	-1000	0		Mouse metabolic/ transport/ demand reaction
MMSPH1Pte	MMsph1p[c] <=> MMsph1p[e]	-1000	0		Mouse metabolic/ transport/ demand reaction
MMSPH1Ptr	MMsph1p[c] <=> MMsph1p[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMSPHGNtr	MMsphgn[r] <=> MMsphgn[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMSPHINGStl	MMsphings[c] <=> MMsphings[l]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMSPHINGStr	MMsphings[c] <=> MMsphings[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMSPHK21c	MMatp[c] + MMsphings[c] -> MMadp[c] + MMh[c] + MMsphs1p[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMSPHMDAc	MMh2o[c] + MMsphmyln_hs[c] -> MMRttotal[c] + MMspc_hs[c]	0	1000	56632.1	Mouse metabolic/ transport/ demand reaction
MMSPHMYLNtg	MMsphmyln_hs[c] <=> MMsphmyln_hs[g]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMSPHMYLNtl	MMsphmyln_hs[c] <=> MMsphmyln_hs[l]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMSPHS1Pte	MMsphs1p[c] <=> MMsphs1p[e]	-1000	0		Mouse metabolic/ transport/ demand reaction
MMSPHS1Ptr	MMsphs1p[c] <=> MMsphs1p[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMSPMDOX	MMh2o[c] + MMo2[c] + MMspmd[c] -> MM13damspp[c] + MMh2o2[c] + MM4abutn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMSPMS	MMametam[c] + MMptrc[c] -> MMh[c] + MM5mta[c] + MMspmd[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMSPODM	2 MMh[c] + 2 MMo2s[c] -> MMo2[c] + MMh2o2[c]	0	1000	20810.1	Mouse metabolic/ transport/ demand reaction
MMSPODMe	2 MMh[e] + 2 MMo2s[e] -> MMh2o2[e] + MMo2[e]	0	1000	20655.1	Mouse metabolic/ transport/ demand reaction
MMSPODMm	2 MMh[m] + 2 MMo2s[m] -> MMo2[m] + MMh2o2[m]	0	1000	20657.1	Mouse metabolic/ transport/ demand reaction
MMSPODMn	2 MMh[n] + 2 MMo2s[n] -> MMh2o2[n] + MMo2[n]	0	1000	20656.1	Mouse metabolic/ transport/ demand reaction
MMSPODMx	2 MMh[x] + 2 MMo2s[x] -> MMo2[x] + MMh2o2[x]	0	1000	20655.1	Mouse metabolic/ transport/ demand reaction
MMSPR	2 MMh[c] + 2 MMnadph[c] + MM6pthp[c] -> 2 MMnadp[c] + MMthbpt[c]	0	1000	20655.1	Mouse metabolic/ transport/ demand reaction
MMSPRMS	MMametam[c] + MMspmd[c] -> MMh[c] + MMspmt[c] + MM5mta[c]	0	1000	20751.1	Mouse metabolic/ transport/ demand reaction
MMSPRn	2 MMh[n] + MM6pthp[n] + 2 MMnadph[n] -> 2 MMnadp[n] + MMthbpt[n]	0	1000	20603.1	Mouse metabolic/ transport/ demand reaction
MMSPTtx	MMpyr[x] + MMser-L[x] -> MMala-L[x] + MMhpyr[x]	0	1000	20751.1	Mouse metabolic/ transport/ demand reaction
MMSQLEr	MMo2[r] + MMh[r] + MMnadph[r] + MMsql[r] -> MMh2o[r] + MMnadp[r] + MMSsq23epx[r]	0	1000	11611.1	Mouse metabolic/ transport/ demand reaction

MMSQLSr	MMft[r] + MMnadph[r] + 2 MMftdp[r] -> MMnadp[r] + 2 MMpp[r] + MMsq[r]	0	1000	20775.1	Mouse metabolic/ transport/ demand reaction
MMSR5AR2r	MMft[r] + MMnadph[r] + MMandrstndn[r] -> MMnadp[r] + MMandrstandn[r]	0	1000	14137.1	Mouse metabolic/ transport/ demand reaction
MMSR5ARr	MMft[r] + MMnadph[r] + MMtststerone[r] -> MM5adtststerone[r] + MMnadp[r]	0	1000	94224.1 or 78925.1	Mouse metabolic/ transport/ demand reaction
MMSRTN23OX	MMo2[c] + MMsrtn[c] -> MM5hoxkyn[c]	0	1000	94224.1 or 78925.1	Mouse metabolic/ transport/ demand reaction
MMSRTNACT	MMsrtn[c] + MMacccoa[c] -> MMft[c] + MMcoa[c] + MMNacsrtn[c]	0	1000	15930.1	Mouse metabolic/ transport/ demand reaction
MMSRTNMTX	MMamet[c] + MMsrtn[c] -> MMft[c] + MMahcys[c] + MMmmhsrtn[c]	0	1000	11298.1	Mouse metabolic/ transport/ demand reaction
MMSRTN6_2_r	2 MMna1[e] + 2 MMfk[c] + MMsrtn[e] <=> 2 MMna1[c] + MMsrtn[c] + 2 MMk[e]	0	1000	21743.1	Mouse metabolic/ transport/ demand reaction
MMSRTNtu	MMsrtn[e] <=> MMsrtn[c]	0	1000	15567.1	Mouse metabolic/ transport/ demand reaction
MMSSALxm	MMft2o[m] + MMnad[m] + MMsucsal[m] -> 2 MMft[m] + MMnadh[m] + MMsucc[m]	0	1000	20518.1 or 20517.1 or 20518.2	Mouse metabolic/ transport/ demand reaction
MMST3GAL21g	MMga1_hs[g] + MMcmpacna[g] -> MMft[g] + MMcmp[g] + MMgm1b_hs[g]	0	1000	214579.1 or 214579.2	Mouse metabolic/ transport/ demand reaction
MMST3GAL22g	MMgm1_hs[g] + MMcmpacna[g] -> MMft[g] + MMcmp[g] + MMgt1a_hs[g]	0	1000	20444.1	Mouse metabolic/ transport/ demand reaction
MMST3GAL23g	MMgt1b_hs[g] + MMcmpacna[g] -> MMft[g] + MMcmp[g] + MMgt1b_hs[g]	0	1000	20444.1	Mouse metabolic/ transport/ demand reaction
MMST3GAL61g	MMgal14acglcgalglxside_hs[g] + MMcmpacna[g] -> MMft[g] + MMcmp[g] + MMacngal14acglcgalglxside_hs[g]	0	1000	20444.1	Mouse metabolic/ transport/ demand reaction
MMST3GAL62g	MMgalacglcgal14acglcgalglxside_hs[g] + MMcmpacna[g] -> MMft[g] + MMacngalacglcgal14acglcgalglxside_hs[g] + MMcmp[g]	0	1000	54613.1	Mouse metabolic/ transport/ demand reaction
MMST6GALNAC21	MMcmpacna[g] + MMacngalglxside_hs[g] -> MMft[g] + MMacm13acngalglxside_hs[g] + MMcmp[g]	0	1000	54613.1	Mouse metabolic/ transport/ demand reaction
MMST6GALNAC22	MMcmpacna[g] + MMacngalglxside_hs[g] -> MMft[g] + MMacm23acngalglxside_hs[g] + MMcmp[g]	0	1000	20446.1	Mouse metabolic/ transport/ demand reaction
MMST6GALNAC23	MMga2_hs[g] + MMcmpacna[g] -> MMft[g] + MMgm2a_hs[g] + MMcmp[g]	0	1000	20446.1	Mouse metabolic/ transport/ demand reaction
MMST6GALNAC24	MMgm1a_hs[g] + MMcmpacna[g] -> MMft[g] + MMcmp[g] + MMgt1b2_hs[g]	0	1000	20446.1	Mouse metabolic/ transport/ demand reaction
MMST6GALNAC25	MMcmpacna[g] + MMgt1a_hs[g] -> MMft[g] + MMcmp[g] + MMgt1alpha_hs[g]	0	1000	20446.1	Mouse metabolic/ transport/ demand reaction
MMST6GALNAC26	MMcmpacna[g] + MMgt1alpha_hs[g] -> MMft[g] + MMcmp[g] + MMgg1balpha_hs[g]	0	1000	50935.1	Mouse metabolic/ transport/ demand reaction
MMST6GALNAC27	MMgt1c_hs[g] + MMcmpacna[g] -> MMft[g] + MMcmp[g] + MMggt1c_hs[g]	0	1000	20446.1	Mouse metabolic/ transport/ demand reaction
MMST6GALNAC28	MMcmpacna[g] + MMggt1c_hs[g] -> MMft[g] + MMcmp[g] + MMgp1c_hs[g]	0	1000	20446.1	Mouse metabolic/ transport/ demand reaction
MMST6GALNAC31	MMcmpacna[g] + MMgm1b_hs[g] -> MMft[g] + MMcmp[g] + MMgd1a_hs[g]	0	1000	20446.1	Mouse metabolic/ transport/ demand reaction
MMST6GALNAC61	MMcmpacna[g] + MMgd1alpha_hs[g] -> MMft[g] + MMcmp[g] + MMgt1alpha_hs[g]	0	1000	50935.1 or 26938.1 or 20447.1	Mouse metabolic/ transport/ demand reaction
MMST6GALNAC62	MMcmpacna[g] + MMgt1b_hs[g] -> MMft[g] + MMcmp[g] + MMgg1balpha_hs[g]	0	1000	20446.1	Mouse metabolic/ transport/ demand reaction
MMSTBSIA11	MMcmpacna[g] + MMacngalglxside_hs[g] -> MMft[g] + MMacnacngalglxside_hs[g] + MMcmp[g]	0	1000	50935.1	Mouse metabolic/ transport/ demand reaction
MMSTBSIA12	MMcmpacna[g] + MMgm3_hs[g] -> MMft[g] + MMcmp[g] + MMgt3_hs[g]	0	1000	20449.1	Mouse metabolic/ transport/ demand reaction
MMST8SIA51g	MMcmpacna[g] + MMgt3_hs[g] -> MMft[g] + MMcmp[g] + MMgt3_hs[g]	0	1000	20449.1	Mouse metabolic/ transport/ demand reaction
MMST8SIA52g	MMcmpacna[g] + MMgt1b_hs[g] -> MMft[g] + MMcmp[g] + MMgg1b_hs[g]	0	1000	225742.1	Mouse metabolic/ transport/ demand reaction
MMST8SIA53g	MMcmpacna[g] + MMgd1a_hs[g] -> MMft[g] + MMcmp[g] + MMgt1a_hs[g]	0	1000	225742.1	Mouse metabolic/ transport/ demand reaction
MMST8SIA54g	MMcmpacna[g] + MMgm1b_hs[g] -> MMft[g] + MMcmp[g] + MMgd1c_hs[g]	0	1000	225742.1	Mouse metabolic/ transport/ demand reaction
MMST8SIA55g	MMcmpacna[g] + MMgg1c_hs[g] -> MMft[g] + MMcmp[g] + MMgp1calpha_hs[g]	0	1000	225742.1	Mouse metabolic/ transport/ demand reaction
MMST8SIA56g	MMcmpacna[g] + MMacngal14acglcgalglxside_hs[g] -> MMft[g] + MMacnacngal14acglcgalglxside_hs[g] + MMcmp[g]	0	1000	225742.1	Mouse metabolic/ transport/ demand reaction
MMSTCOAtx	MMstcoa[c] <=> MMstcoa[x]	-1000	1000	225742.1	Mouse metabolic/ transport/ demand reaction
MMSTN_ANTIGENt	MMsTn_antigen[g] -> MMsTn_antigen[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMSTRDNCCPT1	MMcrn[c] + MMstrdnccoa[c] -> MMcoa[c] + MMstrdnccrn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMSTRDNCCPT2	MMcoa[m] + MMstrdnccrn[m] -> MMcrn[m] + MMstrdnccoa[m]	0	1000	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	Mouse metabolic/ transport/ demand reaction
MMSTRDNCCRNt	MMstrdnccrn[c] -> MMstrdnccrn[m]	0	1000	12896.1	Mouse metabolic/ transport/ demand reaction
MMSTRDNCt	MMstrdnc[e] <=> MMstrdnc[c]	0	1000	57279.1	Mouse metabolic/ transport/ demand reaction
MMSUCC2m	MMpi[m] + MMsucc[c] <=> MMpi[c] + MMsucc[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMSUCC4_2	2 MMna1[e] + MMsucc[e] <=> 2 MMna1[c] + MMsucc[c]	0	1000	27376.1	Mouse metabolic/ transport/ demand reaction
MMSUCC4_3	3 MMna1[e] + MMsucc[e] <=> 3 MMna1[c] + MMsucc[c]	0	1000	20500.1	Mouse metabolic/ transport/ demand reaction
MMSUCCtp	MMsucc[c] <=> MMsucc[x]	-1000	1000	114644.1 or 114644.2	Mouse metabolic/ transport/ demand reaction
MMSUCD1m	MMfad[m] + MMsucc[m] <=> MMfadh2[m] + MMum[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMSUCOAS1m	MMcoa[m] + MMgtp[m] + MMsucc[m] <=> MMp[m] + MMgdp[m] + MMsuccoa[m]	-1000	1000	66945.1 and 66052.1 and 67680.1 and 66925.1	Mouse metabolic/ transport/ demand reaction
MMSUCOASm	MMcoa[m] + MMatp[m] + MMsucc[m] <=> MMadp[m] + MMp[m] + MMsuccoa[m]	-1000	1000	20917.1 and 56451.1	Mouse metabolic/ transport/ demand reaction
MMSUCRe	MMft2o[e] + MMsucr[e] -> MMglc-D[e] + MMfru[e]	0	1000	56451.1 and 20916.1	Mouse metabolic/ transport/ demand reaction
MMSULFOX	MMft2o[c] + MMso3[c] + 2 MMficytC[m] -> 2 MMft[c] + 2 MMficytC[m] + MMso4[c]	0	1000	232714.1 or 69983.1	Mouse metabolic/ transport/ demand reaction
MMSer_Thrg	MMSer_Thr[g] <=> MMSer_Thr[l]	-1000	1000	211389.1	Mouse metabolic/ transport/ demand reaction
MMT2M26DCOAHLm	MMft2o[m] + MMt2m26dcoa[m] <=> MM3h26dm5coa[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMT2M26DCOAHLx	MMft2o[x] + MMt2m26dcoa[x] <=> MM3h26dm5coa[x]	-1000	1000	11992.1 or 231086.1 or 97212.1	Mouse metabolic/ transport/ demand reaction
MMT4HCINNMFM	MM34hpl[m] -> MMft2o[m] + MMT4hcinnm[m]	0	1000	74147.1 or 51798.1	Mouse metabolic/ transport/ demand reaction
MMT4HCINNOX	MMo2[c] + 2 MMT4hcinnm[c] -> 2 MM34dhcinn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMTAGAT_Dt	MMtagat-D[e] -> MMtagat-D[c]	0	1000	22173.1	Mouse metabolic/ transport/ demand reaction
MMTAGHSTDe	MMtag_hs[c] -> MMtag_hs[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMTAGt	MMtag_hs[e] <=> MMtag_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMTALA	MMg3p[c] + MMs7p[c] <=> MMf6p[c] + MMe4p[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMTAUBETAtc	2 MMna1[u] + MMcf[u] + MMtaur[u] -> 2 MMna1[c] + MMcf[c] + MMtaur[c]	0	1000	21351.1	Mouse metabolic/ transport/ demand reaction
MMTAUPAT1c	MMft[u] + MMtaur[u] -> MMft[c] + MMtaur[c]	0	1000	21366.1	Mouse metabolic/ transport/ demand reaction
MMTAURt4_2_r	2 MMna1[e] + MMtaur[e] <=> 2 MMna1[c] + MMtaur[c]	0	1000	215335.1	Mouse metabolic/ transport/ demand reaction
MMTAURtcx	MMna1[c] + MMtaur[c] <=> MMtaur[x] + MMna1[x]	-1000	1000	21366.1	Mouse metabolic/ transport/ demand reaction
MMTAXOLte	MMtaxol[e] <=> MMtaxol[c]	0	1000	21366.1	Mouse metabolic/ transport/ demand reaction
MMTCHOLAt2	2 MMna1[e] + MMtchola[e] -> 2 MMna1[c] + MMtchola[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMTCHOLAt3	MMft2o[c] + MMatp[c] + MMtchola[c] -> MMadp[c] + MMf[c] + MMp[c] + MMtchola[e]	0	1000	20494.1 or 20493.1	Mouse metabolic/ transport/ demand reaction
MMTCHOLAte	MMtchola[e] <=> MMtchola[c]	-1000	1000	27413.1 or 76408.2 or 76408.3 or 76408.1	Mouse metabolic/ transport/ demand reaction
MMTCHOLAtx	MMtchola[x] <=> MMtchola[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMTCYNTt	MMtcynt[c] -> MMtcynt[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMTCYNTtm	MMtcynt[m] -> MMtcynt[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMTDCHOLAte	MMtdchola[e] <=> MMtdchola[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMTDCHOLAtx	MMtdchola[x] <=> MMtdchola[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMTDECHOLAt	MMtdechola[e] <=> MMtdechola[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMTDP	MMft2o[c] + MMtdmpp[c] -> MMft[c] + MMpi[c] + MMthmmp[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMTDPDRE	MMdtdp4d6dg[c] -> MMdtdp4d6dm[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMTDPDRR	MMft[c] + MMnadph[c] + MMdtdp4d6dm[c] -> MMnadp[c] + MMdtdprrm[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMTDPGDH	MMdtdpgluk[c] -> MMft2o[c] + MMdtdp4d6dg[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMTDPtm	MMft2o[m] + MMthmpp[m] -> MMft[m] + MMpi[m] + MMthmmp[m]	0	1000	76355.1	Mouse metabolic/ transport/ demand reaction
MMTETHEX3COAtx	MMtethex3coa[c] <=> MMtethex3coa[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMTETHEX3t	MMtethex3[e] <=> MMtethex3[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMTETPENT3COAtx	MMtetpent3coa[c] <=> MMtetpent3coa[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMTETPENT3CPT1	MMcrn[c] + MMtetpent3coa[c] -> MMcoa[c] + MMtetpent3crn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMTETPENT3CPT2	MMcoa[m] + MMtetpent3crn[m] -> MMcrn[m] + MMtetpent3coa[m]	0	1000	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	Mouse metabolic/ transport/ demand reaction
MMTETPENT3CRNt	MMtetpent3crn[c] -> MMtetpent3crn[m]	0	1000	12896.1	Mouse metabolic/ transport/ demand reaction
MMTETPENT3t	MMtetpent3[e] <=> MMtetpent3[c]	0	1000	57279.1	Mouse metabolic/ transport/ demand reaction

MMTETPENT6COAtx	MMtetpent6coa[c] <=> MMtetpent6coa[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMTETPENT6CPT1	MMcrn[c] + MMtetpent6coa[c] -> MMcoa[c] + MMtetpent6crn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMTETPENT6CPT2	MMcoa[m] + MMtetpent6crn[m] -> MMcrn[m] + MMtetpent6coa[m]	0	1000	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	Mouse metabolic/ transport/ demand reaction
MMTETPENT6CRNt	MMtetpent6crn[c] -> MMtetpent6crn[m]	0	1000	12896.1	Mouse metabolic/ transport/ demand reaction
MMTETPENT6t	MMtetpent6[e] <=> MMtetpent6[c]	0	1000	57279.1	Mouse metabolic/ transport/ demand reaction
MMTETTET6COAtx	MMtettet6coa[c] <=> MMtettet6coa[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMTETTET6CPT1	MMcrn[c] + MMtettet6coa[c] -> MMcoa[c] + MMtettet6crn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMTETTET6CPT2	MMcoa[m] + MMtettet6crn[m] -> MMcrn[m] + MMtettet6coa[m]	0	1000	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	Mouse metabolic/ transport/ demand reaction
MMTETTET6CRNt	MMtettet6crn[c] -> MMtettet6crn[m]	0	1000	12896.1	Mouse metabolic/ transport/ demand reaction
MMTETTET6t	MMtettet6[e] <=> MMtettet6[c]	0	1000	57279.1	Mouse metabolic/ transport/ demand reaction
MMTHBPT4ACAMDASE	MMthbpt4acam[c] -> MMh2o[c] + MMdhbpt[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMTHCHOLSTOICtm	MMthcholstoic[m] <=> MMthcholstoic[x]	-1000	1000	13180.1 or 13180.2	Mouse metabolic/ transport/ demand reaction
MMTHD1m	MMh[c] + MMnadp[m] + MMnadh[m] <=> MMh[m] + MMnadph[m] + MMnad[m]	0	0		Mouse metabolic/ transport/ demand reaction
MMTHFt2	MMoh1[c] + MMthf[e] <=> MMoh1[e] + MMthf[c]	0	1000	18115.1 or 18115.2	Mouse metabolic/ transport/ demand reaction
MMTHFtl	MMthf[c] <=> MMthf[l]	-1000	1000	20509.1 or 20509.2	Mouse metabolic/ transport/ demand reaction
MMTHFtm	MMthf[c] <=> MMthf[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMTHMATPe	MMh2o[c] + MMatp[c] + MMthm[c] -> MMadp[c] + MMh[c] + MMpi[c] + MMthm[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMTHMDt4	MMna1[e] + MMthymd[e] -> MMna1[c] + MMthymd[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMTHMDt5	2 MMna1[e] + MMthymd[e] -> 2 MMna1[c] + MMthymd[c]	0	1000	114304.1 or 434203.1 or 434203.2	Mouse metabolic/ transport/ demand reaction
MMTHMMPt4	MMoh1[c] + MMthmmp[e] <=> MMoh1[e] + MMthmmp[c]	0	1000	114304.1	Mouse metabolic/ transport/ demand reaction
MMTHMMPtm	MMthmmp[c] + MMoh1[m] <=> MMoh1[c] + MMthmmp[m]	0	1000	20509.1 or 20509.2	Mouse metabolic/ transport/ demand reaction
MMTHMP	MMh2o[c] + MMthmmp[c] -> MMpi[c] + MMthm[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMTHMPPtm	MMthmpp[c] + 2 MMoh1[m] -> 2 MMoh1[c] + MMthmpp[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMTHMTP	MMh2o[c] + MMthmtp[c] -> MMh[c] + MMpi[c] + MMthmpp[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMTHMTPt	3 MMoh1[e] + MMthmtp[c] -> 3 MMoh1[c] + MMthmtp[e]	0	1000	105663.1	Mouse metabolic/ transport/ demand reaction
MMTHMt2m	MMh[c] + MMthm[c] -> MMh[m] + MMthm[m]	-1000	1000	20509.1 or 20509.2	Mouse metabolic/ transport/ demand reaction
MMTHMt3	MMh[c] + MMthm[e] <=> MMh[e] + MMthm[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMTHP2Ctp	MMthp2c[c] <=> MMthp2c[x]	-1000	1000	116914.1 or 80721.1	Mouse metabolic/ transport/ demand reaction
MMTHRALANaEx	MMna1[e] + MMala-L[c] + MMthr-L[e] -> MMna1[c] + MMala-L[e] + MMthr-L[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMTHRASNNaEx	MMna1[e] + MMasn-L[c] + MMthr-L[e] -> MMna1[c] + MMasn-L[e] + MMthr-L[c]	0	1000	20514.1 or 55963.1	Mouse metabolic/ transport/ demand reaction
MMTHRATB0tc	2 MMna1[u] + MMcl[u] + MMthr-L[u] -> 2 MMna1[c] + MMcl[c] + MMthr-L[c]	0	1000	20514.1	Mouse metabolic/ transport/ demand reaction
MMTHRB0AT1tc	MMna1[u] + MMthr-L[u] -> MMna1[c] + MMthr-L[c]	0	1000	56774.1	Mouse metabolic/ transport/ demand reaction
MMTHRCYSNaEx	MMna1[e] + MMcys-L[c] + MMthr-L[e] -> MMna1[c] + MMcys-L[e] + MMthr-L[c]	0	1000	(70008.1 or (74338.1 and 57394.1))	Mouse metabolic/ transport/ demand reaction
MMTHRD_L	MMthr-L[c] -> MMnh4[c] + MM2obut[c]	0	1000	20514.1 or 55963.1	Mouse metabolic/ transport/ demand reaction
MMTHRGLNNaEx	MMna1[e] + MMgln-L[c] + MMthr-L[e] -> MMna1[c] + MMgln-L[e] + MMthr-L[c]	0	1000	231691.1	Mouse metabolic/ transport/ demand reaction
MMTHRGLNexR	MMgln-L[c] + MMthr-L[e] <=> MMgln-L[e] + MMthr-L[c]	-1000	1000	20514.1	Mouse metabolic/ transport/ demand reaction
MMTHRGLYexR	MMgly[c] + MMthr-L[e] <=> MMgly[e] + MMthr-L[c]	-1000	1000	53896.1 or 17254.1	Mouse metabolic/ transport/ demand reaction
MMTHRILELAT2tc	MMile-L[c] + MMthr-L[e] -> MMile-L[e] + MMthr-L[c]	0	1000	53896.1 or 17254.1	Mouse metabolic/ transport/ demand reaction
MMTHRPHELAT2tc	MMphe-L[c] + MMthr-L[e] -> MMphe-L[e] + MMthr-L[c]	0	1000	(20539.1 and 17254.1)	Mouse metabolic/ transport/ demand reaction
MMTHRS	MMh2o[c] + MMphom[c] -> MMpi[c] + MMthr-L[c]	0	1000	(20539.1 and 17254.1)	Mouse metabolic/ transport/ demand reaction
MMTHRSERNaEx	MMna1[e] + MMser-L[c] + MMthr-L[e] -> MMna1[c] + MMser-L[e] + MMthr-L[c]	0	1000	208967.1	Mouse metabolic/ transport/ demand reaction
MMTHRt4	MMna1[e] + MMthr-L[e] -> MMna1[c] + MMthr-L[c]	0	1000	20514.1 or 55963.1	Mouse metabolic/ transport/ demand reaction
MMTHYMDt1	MMthymd[e] -> MMthymd[c]	0	1000	105727.1 or 67760.1 or 56774.1	Mouse metabolic/ transport/ demand reaction
MMTHYMDtl	MMthymd[l] <=> MMthymd[c]	-1000	1000	13340.1 or 63959.1	Mouse metabolic/ transport/ demand reaction
MMTHYMDtm	MMthymd[c] <=> MMthymd[m]	-1000	1000	71279.1	Mouse metabolic/ transport/ demand reaction
MMTHYMt	MMthym[e] <=> MMthym[c]	0	1000	63959.1	Mouse metabolic/ transport/ demand reaction
MMTHYOXt2	MMthyox-L[e] <=> MMthyox-L[c]	0	1000	13340.1	Mouse metabolic/ transport/ demand reaction
MMTHYPX	MMh2o2[c] + 2 MMh[c] + 2 MMi[c] -> 2 MMh2o[c] + MMiodine[c]	0	1000	20502.1	Mouse metabolic/ transport/ demand reaction
MMTKT1	MMr5p[c] + MMxu5p-D[c] <=> MMg3p[c] + MMs7p[c]	-1000	1000	22018.1 or 22018.2 or 22018.3 or 22018.4 or 22018.5	Mouse metabolic/ transport/ demand reaction
MMTKT2	MMxu5p-D[c] + MMe4p[c] <=> MMg3p[c] + MMf6p[c]	-1000	1000	74419.1 or 11670.1 or 83553.1 or 21881.1	Mouse metabolic/ transport/ demand reaction
MMTMABADH	MMh2o[c] + MMnad[c] + MM4tmeabut[c] -> 2 MMh[c] + MMnadh[c] + MM4tmeabutn[c]	0	1000	74419.1 or 11670.1 or 83553.1	Mouse metabolic/ transport/ demand reaction
MMTMDK1	MMatp[c] + MMthymd[c] -> MMadp[c] + MMh[c] + MMdtmp[c]	0	1000	56752.1	Mouse metabolic/ transport/ demand reaction
MMTMDK1m	MMatp[m] + MMthymd[m] -> MMh[m] + MMadp[m] + MMdtmp[m]	0	1000	57813.1 or 619653.1	Mouse metabolic/ transport/ demand reaction
MMTMDPK	MMatp[c] + MMthm[c] -> MMh[c] + MMamp[c] + MMthmpp[c]	0	1000	57813.1	Mouse metabolic/ transport/ demand reaction
MMTMDPP	MMpi[c] + MMthymd[c] <=> MM2dr1p[c] + MMthym[c]	-1000	1000	29807.1	Mouse metabolic/ transport/ demand reaction
MMTMDPPK	MMatp[c] + MMthmpp[c] -> MMadp[c] + MMthmtp[c]	0	1000	72962.1	Mouse metabolic/ transport/ demand reaction
MMTMDS	MMdump[c] + MMmlthf[c] -> MMdhf[c] + MMdtmp[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMTMLYSOX	MMo2[c] + MMakg[c] + MMtmlys[c] -> MMco2[c] + MMsucc[c] + MM3htmelys[c]	0	1000	22171.1	Mouse metabolic/ transport/ demand reaction
MMTMLYSter	MMtmlys[r] -> MMtmlys[c]	0	1000	192289.1	Mouse metabolic/ transport/ demand reaction
MMTMNDNCCOAtx	MMtmndnccoa[c] <=> MMtmndnccoa[x]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMTMNDNCCPT1	MMcrn[c] + MMtmndnccoa[c] -> MMcoa[c] + MMtmndnccrn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMTMNDNCCPT2	MMcoa[m] + MMtmndnccrn[m] -> MMcrn[m] + MMtmndnccoa[m]	0	1000	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	Mouse metabolic/ transport/ demand reaction
MMTMNDNCCRNt	MMtmndnccrn[c] -> MMtmndnccrn[m]	0	1000	12896.1	Mouse metabolic/ transport/ demand reaction
MMTMNDNCt	MMtmndnc[e] <=> MMtmndnc[c]	0	1000	57279.1	Mouse metabolic/ transport/ demand reaction
MMTOLBUTAMIDEte	MMtolbutamide[e] <=> MMtolbutamide[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMTPI	MMdhap[c] <=> MMg3p[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMTRDR	MMh[c] + MMnadph[c] + MMtrdox[c] -> MMnadp[c] + MMtrdrd[c]	0	1000	21991.1	Mouse metabolic/ transport/ demand reaction
MMTRDR2	MMh[c] + MMnadph[c] + MMq10[c] -> MMnadp[c] + MMq10h2[c]	0	1000	50493.1 or 50493.2 or 50493.3 or 50493.4	Mouse metabolic/ transport/ demand reaction
MMTRDR3	MMh[c] + MMnadh[c] + MMq10[c] -> MMnad[c] + MMq10h2[c]	0	1000	50493.1 or 50493.2 or 50493.3 or 50493.4	Mouse metabolic/ transport/ demand reaction
MMTRDRm	MMh[m] + MMnadph[m] + MMtrdox[m] -> MMnadp[m] + MMtrdrd[m]	0	1000	50493.1 or 50493.2 or 50493.3 or 50493.4	Mouse metabolic/ transport/ demand reaction
MMTREH	MMh2o[c] + MMtre[c] -> 2 MMglc-D[c]	0	1000	26462.1 or 232223.1 or 26462.2 or 26462.3	Mouse metabolic/ transport/ demand reaction
MMTREHe	MMh2o[e] + MMtre[e] -> 2 MMglc-D[e]	0	1000	212974.1	Mouse metabolic/ transport/ demand reaction
MMTRIODTHYSUFt	MMtriodthysuf[c] -> MMtriodthysuf[e]	0	1000	58866.1	Mouse metabolic/ transport/ demand reaction
MMTRIODTHYSULT	MMpaps[c] + MMtriodthy[c] -> MMh[c] + MMpap[c] + MMtriodthysuf[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMTRIODTHYt2	MMtriodthy[e] <=> MMtriodthy[c]	0	1000	20887.1 or 20887.2 or 20887.3 or 20887.4 or 20887.5	Mouse metabolic/ transport/ demand reaction
MMTRIOK	MMatp[c] + MMglyald[c] -> MMadp[c] + MMh[c] + MMg3p[c]	0	1000	20502.1	Mouse metabolic/ transport/ demand reaction
MMTRPATB0tc	2 MMna1[u] + MMcl[u] + MMtrp-L[u] -> 2 MMna1[c] + MMcl[c] + MMtrp-L[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMTRPB0AT1tc	MMna1[u] + MMtrp-L[u] -> MMna1[c] + MMtrp-L[c]	0	1000	56774.1	Mouse metabolic/ transport/ demand reaction
MMTRPHYDRO2	MMo2[c] + MMthbpt[c] + MMtrp-L[c] -> MM5htrp[c] + MMthbpt4acam[c]	0	1000	(70008.1 or (74338.1 and 57394.1))	Mouse metabolic/ transport/ demand reaction
MMTRPILELAT2tc	MMile-L[c] + MMtrp-L[e] -> MMile-L[e] + MMtrp-L[c]	0	1000	21990.1 or 216343.1	Mouse metabolic/ transport/ demand reaction
MMTRPLAT1tc	MMleu-L[c] + MMtrp-L[u] -> MMleu-L[u] + MMtrp-L[c]	0	1000	(20539.1 and 17254.1)	Mouse metabolic/ transport/ demand reaction
MMTRPO2	MMo2[c] + MMtrp-L[c] -> MMLfmkynr[c]	0	1000	(20539.1 and 17254.1)	Mouse metabolic/ transport/ demand reaction
MMTRPPHELAT1tc	MMphe-L[c] + MMtrp-L[e] -> MMphe-L[e] + MMtrp-L[c]	0	1000	56720.1	Mouse metabolic/ transport/ demand reaction
MMTRPt4	MMna1[e] + MMtrp-L[e] -> MMna1[c] + MMtrp-L[c]	0	1000	(20539.1 and 17254.1)	Mouse metabolic/ transport/ demand reaction
MMTRYPTAOX	MMh2o[c] + MMo2[c] + MMtrypta[c] -> MMh2o2[c] + MMnh4[c] + MMid3acald[c]	0	1000	56774.1	Mouse metabolic/ transport/ demand reaction

MMTS3	MMpd3[c] <=> MMts3[c]	-1000	1000	109731.1 or 237940.1 or 17161.1 or 237940.2 or 76507.1	Mouse metabolic/ transport/ demand reaction
MMTSTSTERONEGLCte	MMh2o[c] + MMatp[c] + MMtststeroneglc[c] -> MMadp[c] + MMh[c] + MMpi[c] + MMtststeroneglc[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMTSTSTERONEGLCtr	MMtststeroneglc[c] <=> MMtststeroneglc[r]	-1000	1000	17250.1	Mouse metabolic/ transport/ demand reaction
MMTSTSTERONESULT	MMpaps[c] + MMtststerone[c] -> MMh[c] + MMpap[c] + MMtststerones[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMTSTSTERONESte	MMtststerones[c] <=> MMtststerones[e]	-1000	0	20859.1	Mouse metabolic/ transport/ demand reaction
MMTSTSTERONEt	MMtststerone[e] <=> MMtststerone[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMTSTSTERONEtr	MMtststerone[r] <=> MMtststerone[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMTSULt4_3	3 MMna1[e] + MMtsul[e] <=> 3 MMna1[c] + MMtsul[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMTTDCAt	MMttdca[e] -> MMttdca[c]	0	1000	55961.1	Mouse metabolic/ transport/ demand reaction
MMTTDCAtr	MMttdca[e] <=> MMttdca[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMTTDCPT1	MMcrn[c] + MMtdcoa[c] -> MMcoa[c] + MMttdcrn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMTTDCPT2	MMcoa[m] + MMttdcrn[m] -> MMcrn[m] + MMtdcoa[m]	0	1000	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	Mouse metabolic/ transport/ demand reaction
MMTTDCRNt	MMttdcrn[c] -> MMttdcrn[m]	0	1000	12896.1	Mouse metabolic/ transport/ demand reaction
MMTXA2te	MMtxa2[e] <=> MMtxa2[c]	0	1000	57279.1	Mouse metabolic/ transport/ demand reaction
MMTXA2tr	MMtxa2[c] <=> MMtxa2[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMTXASr	MMprostgh2[r] -> MMtxa2[r]	0	1000		Mouse metabolic/ transport/ demand reaction
MMTYMSFt	MMtymsf[c] -> MMtymsf[e]	0	1000	21391.1	Mouse metabolic/ transport/ demand reaction
MMTYR3MO2	MMo2[c] + MMthbpt[c] + MMtyr-L[c] -> MM34dhphe[c] + MMthbpt4acam[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMTYRASE	MM56dihindlcrbxlt[c] -> MMmelanin[c]	0	1000	21823.1 or 21823.2 or 21823.3	Mouse metabolic/ transport/ demand reaction
MMTYRATB0tc	2 MMna1[u] + MMcl[u] + MMtyr-L[u] -> 2 MMna1[c] + MMcl[c] + MMtyr-L[c]	0	1000	22178.1	Mouse metabolic/ transport/ demand reaction
MMTYRB0AT1tc	MMna1[u] + MMtyr-L[u] -> MMna1[c] + MMtyr-L[c]	0	1000	56774.1	Mouse metabolic/ transport/ demand reaction
MMTYRCBOX	MMh[c] + MMtyr-L[c] -> MMco2[c] + MMtym[c]	0	1000	(70008.1 or (74338.1 and 57394.1))	Mouse metabolic/ transport/ demand reaction
MMTYRDOPO	MMo2[c] + 2 MMtyr-L[c] -> 2 MM34dhphe[c]	0	1000	13195.1	Mouse metabolic/ transport/ demand reaction
MMTYRDOPO3	MMo2[c] + 2 MM34dhphe[c] -> 2 MMh2o[c] + 2 MMdopaqn[c]	0	1000	22173.1	Mouse metabolic/ transport/ demand reaction
MMTYRILELAT2tc	MMile-L[c] + MMtyr-L[e] -> MMile-L[e] + MMtyr-L[c]	0	1000	22173.1	Mouse metabolic/ transport/ demand reaction
MMTYRLAT1tc	MMleu-L[c] + MMtyr-L[u] -> MMleu-L[u] + MMtyr-L[c]	0	1000	(20539.1 and 17254.1)	Mouse metabolic/ transport/ demand reaction
MMTYROXDAc	MMh2o[c] + MMo2[c] + MMtym[c] -> MMh2o2[c] + MMnh4[c] + MM4hoxpacd[c]	0	1000	(20539.1 and 17254.1)	Mouse metabolic/ transport/ demand reaction
MMTYRPHELAT2tc	MMphe-L[c] + MMtyr-L[e] -> MMphe-L[e] + MMtyr-L[c]	0	1000	109731.1 or 17161.1	Mouse metabolic/ transport/ demand reaction
MMTYRTA	MMakg[c] + MMtyr-L[c] <=> MM34hpp[c] + MMglu-L[c]	-1000	1000	(20539.1 and 17254.1)	Mouse metabolic/ transport/ demand reaction
MMTYRTAm	MMakg[m] + MMtyr-L[m] <=> MM34hpp[m] + MMglu-L[m]	-1000	1000	14718.1	Mouse metabolic/ transport/ demand reaction
MMTYRt4	MMna1[e] + MMtyr-L[e] -> MMna1[c] + MMtyr-L[c]	0	1000	234724.1 or 14719.1	Mouse metabolic/ transport/ demand reaction
MMUAG2EMAi	MMh2o[c] + MMuacgam[c] -> MMh[c] + MMudp[c] + MMacmana[c]	0	1000	56774.1	Mouse metabolic/ transport/ demand reaction
MMUAG4E	MMuacgam[c] <=> MMudpacgal[c]	-1000	1000	50798.1	Mouse metabolic/ transport/ demand reaction
MMUAGALDP	MMh[c] + MMacgal1p[c] + MMutp[c] -> MMppi[c] + MMudpacgal[c]	0	1000	74246.1 or 74246.2	Mouse metabolic/ transport/ demand reaction
MMUAGDP	MMh[c] + MMacgam1p[c] + MMutp[c] -> MMppi[c] + MMuacgam[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMUDPACGALtl	MMudpacgal[c] <=> MMudpacgal[l]	-1000	1000	227620.1 or 107652.1	Mouse metabolic/ transport/ demand reaction
MMUDPDOLPT_L	0.1 MMdolp_L[c] + MMudpg[c] -> MMudp[c] + 0.1 MMdolglcp_L[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMUDPDOLPT_U	0.1 MMdolp_U[c] + MMudpg[c] -> MMudp[c] + 0.1 MMdolglcp_U[c]	0	1000	66248.1	Mouse metabolic/ transport/ demand reaction
MMUDPG1P	MMh2o[c] + MMudpglcur[c] -> 2 MMh[c] + MMump[c] + MMglcur1p[c]	0	1000	66248.1	Mouse metabolic/ transport/ demand reaction
MMUDPG4E	MMudpg[c] <=> MMudpgal[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMUDPGALt2g	MMudpgal[c] -> MMudpgal[g]	0	1000	74246.1 or 74246.2	Mouse metabolic/ transport/ demand reaction
MMUDPGALtg	MMudpgal[c] + MMump[g] <=> MMudpgal[g] + MMump[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMUDPGD	MMh2o[c] + 2 MMnad[c] + MMudpg[c] -> 3 MMh[c] + 2 MMnadh[c] + MMudpglcur[c]	0	1000	22232.1	Mouse metabolic/ transport/ demand reaction
MMUDPGLCAter	MMump[c] + MMudpglcur[r] <=> MMudpglcur[c] + MMump[r]	-1000	1000	22235.1	Mouse metabolic/ transport/ demand reaction
MMUDPGLCAtg	MMudpglcur[g] + MMump[c] <=> MMudpglcur[c] + MMump[g]	-1000	1000	242585.1	Mouse metabolic/ transport/ demand reaction
MMUDPGLCter	MMudpg[c] + MMump[r] <=> MMump[c] + MMudpg[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMUDPGLCtg	MMudpg[c] + MMump[g] <=> MMump[c] + MMudpg[g]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMUDPGLDCg	MMh[g] + MMudpglcur[g] -> MMco2[g] + MMudpxyl[g]	0	1000	58246.1 or 229782.1 or 70484.1	Mouse metabolic/ transport/ demand reaction
MMUDPGNP	MMh2o[c] + MMudpglcur[c] -> MMh[c] + MMudp[c] + MMglcur[c]	0	1000	67883.1	Mouse metabolic/ transport/ demand reaction
MMUDPGP	MMh2o[c] + MMudpg[c] -> 2 MMh[c] + MMg1p[c] + MMump[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMUDPXYLter	MMump[r] + MMudpxyl[c] <=> MMump[c] + MMudpxyl[r]	-1000	1000	18605.1 or 18606.1 or 209558.1	Mouse metabolic/ transport/ demand reaction
MMUDPXYLtg	MMump[g] + MMudpxyl[c] <=> MMump[c] + MMudpxyl[g]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMUDPtl	MMudp[c] <=> MMudp[l]	-1000	1000	58246.1	Mouse metabolic/ transport/ demand reaction
MMUGALGTg	MMudpgal[g] + MMglc-D[g] -> MMh[g] + MMudp[g] + MMlcts[g]	0	1000		Mouse metabolic/ transport/ demand reaction
MMUGALNACter	MMump[r] + MMudpacgal[c] <=> MMump[c] + MMudpacgal[r]	-1000	1000	16770.1 or 14595.1 or 53418.1 or 53418.2	Mouse metabolic/ transport/ demand reaction
MMUGALNACtg	MMump[g] + MMudpacgal[c] <=> MMudpacgal[g] + MMump[c]	-1000	1000	242585.1	Mouse metabolic/ transport/ demand reaction
MMUGCG	MMcrm_hs[r] + MMudpg[r] -> MMh[r] + MMgluside_hs[r] + MMudp[r]	0	1000	22232.1	Mouse metabolic/ transport/ demand reaction
MMUGLCNACtg	MMuacgam[c] + MMump[g] <=> MMuacgam[g] + MMump[c]	-1000	1000	22234.1	Mouse metabolic/ transport/ demand reaction
MMUGLT	MMgal1p[c] + MMudpg[c] <=> MMudpgal[c] + MMg1p[c]	-1000	1000	70484.1	Mouse metabolic/ transport/ demand reaction
MMUGT1A9r	MM5adtststerone[r] + MMudpglcur[r] -> MM5adtststeroneglc[r] + MMudp[r]	0	1000	14430.1 or 14430.2 or 14430.3	Mouse metabolic/ transport/ demand reaction
MMUMPK	MMatp[c] + MMump[c] <=> MMadp[c] + MMudp[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMUMPK2	MMctp[c] + MMump[c] <=> MMudp[c] + MMcdp[c]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMUMPK2n	MMctp[n] + MMump[n] <=> MMcdp[n] + MMudp[n]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMUMPK3	MMutp[c] + MMump[c] <=> 2 MMudp[c]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMUMPK3n	MMutp[n] + MMump[n] <=> 2 MMudp[n]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMUMPK4	MMgtp[c] + MMump[c] <=> MMudp[c] + MMgdp[c]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMUMPK4n	MMgtp[n] + MMump[n] <=> MMudp[n] + MMgdp[n]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMUMPK5	MMdatp[c] + MMump[c] <=> MMudp[c] + MMdadp[c]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMUMPK5n	MMdatp[n] + MMump[n] <=> MMdadp[n] + MMudp[n]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMUMPK6	MMdctp[c] + MMump[c] <=> MMudp[c] + MMdcdp[c]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMUMPK6n	MMdctp[n] + MMump[n] <=> MMdcdp[n] + MMudp[n]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMUMPK7	MMdgtp[c] + MMump[c] <=> MMudp[c] + MMdgdp[c]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMUMPK7n	MMdgtp[n] + MMump[n] <=> MMdgdp[n] + MMudp[n]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMUMPKm	MMatp[m] + MMump[m] <=> MMadp[m] + MMudp[m]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMUMPKn	MMatp[n] + MMump[n] <=> MMudp[n] + MMadp[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMUMPtr	MMump[c] <=> MMump[r]	-1000	1000	66588.1	Mouse metabolic/ transport/ demand reaction
MMUNK2	MMh[c] + MMgln-L[c] + MM2kmb[c] -> MMglu-L[c] + MMmet-L[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMUNK3	MMglu-L[c] + MM2kmb[c] -> MMakg[c] + MMmet-L[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMUPP3S	MMhmbil[c] -> MMh2o[c] + MMuppg3[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMUPPDC1	4 MMh[c] + MMuppg3[c] -> 4 MMco2[c] + MMcpppg3[c]	0	1000	22276.1	Mouse metabolic/ transport/ demand reaction
MMUPPN	MMh2o[c] + 2 MMh[c] + MMcala[c] -> MMnh4[c] + MMco2[c] + MMala-B[c]	0	1000	22275.1	Mouse metabolic/ transport/ demand reaction
MMURATEt	MMurate[c] -> MMurate[e]	0	1000	103149.1	Mouse metabolic/ transport/ demand reaction
MMURATEtx	MMurate[x] -> MMurate[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMURAt	MMura[e] <=> MMura[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMURCN	MMh2o[c] + MMurcan[c] -> MM4izp[c]	0	1000	13340.1	Mouse metabolic/ transport/ demand reaction

MMUREAt	MMurea[e] <=> MMurea[c]	0	1000	243537.1	Mouse metabolic/ transport/ demand reaction
MMUREAt5	MMh2o[e] + MMurea[e] <=> MMh2o[c] + MMurea[c]	0	1000	108052.1 or 27411.1 or 20537.1 or 114479.1	Mouse metabolic/ transport/ demand reaction
MMUREAtm	MMurea[c] <=> MMurea[m]	-1000	1000	20537.1	Mouse metabolic/ transport/ demand reaction
MMURIDK2m	MMatp[m] + MMdump[m] <=> MMadp[m] + MMdudp[m]	-1000	1000	64008.1	Mouse metabolic/ transport/ demand reaction
MMURIK1	MMatp[c] + MMuri[c] -> MMadp[c] + MMh[c] + MMump[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMURIt	MMuri[e] <=> MMuri[c]	0	1000	22245.1 or 80914.1	Mouse metabolic/ transport/ demand reaction
MMURIt4	MMna1[e] + MMuri[e] -> MMna1[c] + MMuri[c]	0	1000	13340.1 or 63959.1	Mouse metabolic/ transport/ demand reaction
MMURIt5	2 MMna1[e] + MMuri[e] -> 2 MMna1[c] + MMuri[c]	0	1000	114304.1 or 434203.1 or 434203.2 or 269346.1	Mouse metabolic/ transport/ demand reaction
MMUROLACer	MMh[r] + MMglcur[r] <=> MMh2o[r] + MMglac[r]	-1000	1000	114304.1	Mouse metabolic/ transport/ demand reaction
MMUTPtn	MMutp[c] <=> MMutp[n]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMUritl	MMuri[l] <=> MMuri[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMUritm	MMuri[c] <=> MMuri[m]	-1000	1000	71279.1	Mouse metabolic/ transport/ demand reaction
MMUritn	MMuri[c] <=> MMuri[n]	-1000	1000	63959.1	Mouse metabolic/ transport/ demand reaction
MMVACCCPT1	MMcrn[c] + MMvacccoa[c] -> MMcoa[c] + MMvacccrn[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMVACCCPT2	MMcoa[m] + MMvacccrn[m] -> MMcrn[m] + MMvacccoa[m]	0	1000	12895.4 or 12894.1 or 78070.1 or 12895.2 or 12895.3 or 12895.1	Mouse metabolic/ transport/ demand reaction
MMVACCCRNt	MMvacccrn[c] -> MMvacccrn[m]	0	1000	12896.1	Mouse metabolic/ transport/ demand reaction
MMVACCt	MMvacc[e] <=> MMvacc[c]	0	1000	57279.1	Mouse metabolic/ transport/ demand reaction
MMVALATB0tc	2 MMna1[u] + MMcl[u] + MMval-L[u] -> 2 MMna1[c] + MMcl[c] + MMval-L[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMVALB0ATtc	MMna1[u] + MMval-L[u] -> MMna1[c] + MMval-L[c]	0	1000	56774.1	Mouse metabolic/ transport/ demand reaction
MMVALILELAT2tc	MMile-L[c] + MMval-L[e] -> MMile-L[e] + MMval-L[c]	0	1000	(70008.1 or (74338.1 and 57394.1))	Mouse metabolic/ transport/ demand reaction
MMVALLAT1tc	MMleu-L[c] + MMval-L[u] -> MMleu-L[u] + MMval-L[c]	0	1000	(20539.1 and 17254.1)	Mouse metabolic/ transport/ demand reaction
MMVALPHELAT2tc	MMphe-L[c] + MMval-L[e] -> MMphe-L[e] + MMval-L[c]	0	1000	(20539.1 and 17254.1)	Mouse metabolic/ transport/ demand reaction
MMVALTA	MMakg[c] + MMval-L[c] <=> MMglu-L[c] + MM3mob[c]	-1000	1000	(20539.1 and 17254.1)	Mouse metabolic/ transport/ demand reaction
MMVALTAm	MMakg[m] + MMval-L[m] <=> MMglu-L[m] + MM3mob[m]	-1000	1000	12035.1	Mouse metabolic/ transport/ demand reaction
MMVALt4	MMna1[e] + MMval-L[e] -> MMna1[c] + MMval-L[c]	0	1000	12036.1	Mouse metabolic/ transport/ demand reaction
MMVALt5m	MMval-L[c] <=> MMval-L[m]	-1000	1000	56774.1	Mouse metabolic/ transport/ demand reaction
MMVALtec	MMval-L[e] <=> MMval-L[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMVD3	MMpd3[c] <=> MMvitd3[c]	-1000	1000	215113.1 or 72401.1	Mouse metabolic/ transport/ demand reaction
MMVITD2Hm	MMh[m] + MMnadph[m] + MMo2[m] + MMvitd2[m] -> MMh2o[m] + MMnadp[m] + MM25hvitd2[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMVITD2t	MMvitd2[c] -> MMvitd2[e]	0	1000	104086.1	Mouse metabolic/ transport/ demand reaction
MMVITD2tm	MMvitd2[m] <=> MMvitd2[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMVITD3Hm	MMh[m] + MMnadph[m] + MMo2[m] + MMvitd3[m] -> MMh2o[m] + MMnadp[m] + MM25hvitd3[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMVITD3Te	MMvitd3[c] <=> MMvitd3[e]	-1000	1000	104086.1	Mouse metabolic/ transport/ demand reaction
MMVITD3lu	MMvitd3[u] <=> MMvitd3[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMVITD3t	MMvitd3[c] -> MMvitd3[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMVITD3t2	MMvitd3[e] -> MMvitd3[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMVITD3tm	MMvitd3[m] -> MMvitd3[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMVITD3tm3	MMvitd3[c] -> MMvitd3[m]	0	1000		Mouse metabolic/ transport/ demand reaction
MMVITEtc	MMavite1[u] -> MMavite1[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMVITEtl	MMh2o[c] + MMatp[c] + MMavite1[c] -> MMadp[c] + MMh[c] + MMpi[c] + MMavite1[e]	0	1000	(20778.1 and 237636.1)	Mouse metabolic/ transport/ demand reaction
MMVITKtl	MMphyQ[c] -> MMphyQ[e]	0	1000	11303.1	Mouse metabolic/ transport/ demand reaction
MMVLCS2p	MMcoa[x] + MMatp[x] + MMdhcholestanate[x] -> MMdhcholestancoa[x] + MMamp[x] + MMppi[x]	0	1000		Mouse metabolic/ transport/ demand reaction
MMVLCS2r	MMatp[r] + MMcoa[r] + MMdhcholestanate[r] -> MMdhcholestancoa[r] + MMamp[r] + MMppi[r]	0	1000	26458.1	Mouse metabolic/ transport/ demand reaction
MMVLCSp	MMcoa[x] + MMatp[x] + MMthcholstoic[x] -> MMcholcoar[x] + MMamp[x] + MMppi[x]	0	1000	26458.1	Mouse metabolic/ transport/ demand reaction
MMVLCSr	MMatp[r] + MMcoa[r] + MMthcholstoic[r] -> MMcholcoar[r] + MMamp[r] + MMppi[r]	0	1000	26458.1	Mouse metabolic/ transport/ demand reaction
MMWHDDCAte	MMwhddca[e] <=> MMwhddca[c]	0	1000	26458.1	Mouse metabolic/ transport/ demand reaction
MMWHHDCAte	MMwhhdca[e] <=> MMwhhdca[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMWHTSTSTERONEte	MMwhtststerone[c] <=> MMwhtststerone[e]	-1000	0		Mouse metabolic/ transport/ demand reaction
MMWHTTDCAte	MMwhttdca[e] <=> MMwhttdca[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMXANDp	MMnad[x] + MMh2o[x] + MMxan[x] -> MMh[x] + MMnadh[x] + MMurate[x]	0	1000		Mouse metabolic/ transport/ demand reaction
MMXANtx	MMxan[c] -> MMxan[x]	0	1000	22436.1	Mouse metabolic/ transport/ demand reaction
MMXAO2x	MMo2[x] + MMh2o[x] + MMfoxan[x] -> MMh2o2[x] + MMxan[x]	0	1000		Mouse metabolic/ transport/ demand reaction
MMXAOx	MMo2[x] + MMh2o[x] + MMxan[x] -> MMh2o2[x] + MMurate[x]	0	1000	22436.1	Mouse metabolic/ transport/ demand reaction
MMXOL27OHtm	MMxol27oh[r] <=> MMxol27oh[m]	-1000	1000	22436.1	Mouse metabolic/ transport/ demand reaction
MMXOL7AH2tm	MMxol7ah2[c] <=> MMxol7ah2[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMXOL7AH2tr	MMxol7ah2[c] <=> MMxol7ah2[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMXOL7AONEtr	MMxol7aone[c] <=> MMxol7aone[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMXOLDIOLONEt	MMxoldiolone[c] <=> MMxoldiolone[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMXOLDIOLONEtm	MMxoldiolone[m] <=> MMxoldiolone[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMXOLEST2HSTDlu	MMxolest2_hs[c] -> MMxolest2_hs[e]	0	1000		Mouse metabolic/ transport/ demand reaction
MMXOLEST2te	MMxolest2_hs[e] <=> MMxolest2_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMXOLESTte	MMxolest_hs[e] <=> MMxolest_hs[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMXOLTRI24tc	MMxoltri24[r] <=> MMxoltri24[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMXOLTRI24te	MMxoltri24[c] <=> MMxoltri24[e]	-1000	0		Mouse metabolic/ transport/ demand reaction
MMXOLTRI25tc	MMxoltri25[r] <=> MMxoltri25[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMXOLTRI25te	MMxoltri25[c] <=> MMxoltri25[e]	-1000	0		Mouse metabolic/ transport/ demand reaction
MMXOLTRI27tc	MMxoltri27[r] <=> MMxoltri27[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMXOLTRI27te	MMxoltri27[c] <=> MMxoltri27[e]	-1000	0		Mouse metabolic/ transport/ demand reaction
MMXOLTRIOLtm	MMxoltriol[c] <=> MMxoltriol[m]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMXOLTRIOLtr	MMxoltriol[c] <=> MMxoltriol[r]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMXSERtg	MMxser[r] -> MMxser[g]	0	1000		Mouse metabolic/ transport/ demand reaction
MMXYLK	MMatp[c] + MMxylu-D[c] -> MMadp[c] + MMh[c] + MMxu5p-D[c]	0	1000		Mouse metabolic/ transport/ demand reaction
MMXYLTD_Dr	MMnad[c] + MMxylt[c] <=> MMh[c] + MMnadh[c] + MMxylu-D[c]	-1000	1000	102448.1	Mouse metabolic/ transport/ demand reaction
MMXYLTer	MMSer_Gly_Ala_X_Gly[r] + MMudpxyl[r] -> MMh[r] + MMudp[r] + MMxser[r]	0	1000		Mouse metabolic/ transport/ demand reaction
MMXYLTt	MMxylt[e] <=> MMxylt[c]	0	1000	217119.1 or 233781.1	Mouse metabolic/ transport/ demand reaction
MMXYLUR	MMh[c] + MMnadph[c] + MMxylu-L[c] <=> MMnadp[c] + MMxylt[c]	-1000	1000		Mouse metabolic/ transport/ demand reaction
MMXYLt	MMxyl-D[e] <=> MMxyl-D[c]	0	1000	67880.1	Mouse metabolic/ transport/ demand reaction
MMXYLtly	MMxyl-D[l] -> MMxyl-D[c]	0	1000	20527.1	Mouse metabolic/ transport/ demand reaction
MMYVITEt	MMyvite[e] -> MMyvite[c]	0	1000		Mouse metabolic/ transport/ demand reaction

MMbiomass_mm_1_no_glygln	43.153 MMh2o[c] + 43.153 MMatp[c] + 0.564 MMleu-L[c] + 0.386 MMglu-L[c] + 0.359 MMasp-L[c] + 0.033 MMamp[c] + 0.0148 MMdamp[c] + 0.0521 MMcmp[c] + 0.6 MMala-L[c] + 0.2881 MMasn-L[c] + 0.145 MMcys-L[c] + 0.322 MMglu-L[c] + 0.538 MMgly[c] + 0.324 MMile-L[c] + 0.219 MMphe-L[c] + 0.43 MMser-L[c] + 0.386 MMthr-L[c] + 0.377 MMarg-L[c] + 0.57 MMlys-L[c] + 0.138 MMmet-L[c] + 0.143 MMhis-L[c] + 0.01 MMpail_hs[c] + 0.069 MMpchol_hs[c] + 0.026 MMpe_hs[c] + 0.018 MMchitersfa[c] + 0.001 MMpglyc_hs[c] + 0.003 MMclpn_hs[c] + 0.0099 MMdcmp[c] + 0.0099 MMdgmp[c] + 0.0148 MMdtmp[c] + 0.0624 MMgmp[c] + 0.033 MMump[c] + 0.313 MMpro-L[c] + 0.182 MMtyr-L[c] + 0.044 MMtrp-L[c] + 0.416 MMval-L[c] + 0.003 MMps_hs[c] + 0.008 MMsphmyln_hs[c] -> 43.153 MMadp[c] + 43.153 MMh[c] + 43.153 MMpi[c]	0	0		Mouse metabolic/ transport/ demand reaction
MMsink_ctr-L	MMctr-L[c] <=>	0	0		Mouse metabolic/ transport/ demand reaction
MMsink_pre_pro(er)	MMpre_pro[r] <=>	-1	1000		Mouse metabolic/ transport/ demand reaction
MM1MNCAMtb	MMh2o[c] + MM1mncam[c] + MMatp[c] -> MMadp[c] + MMh[c] + MMpi[c] + MM1mncam[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_1mncam(e)b	MM1mncam[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MM24NPHteb	MM24nph[b] <=> MM24nph[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_24nph(e)b	MM24nph[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MM24_25DHVITD2tb	MM2425dhvitd2[c] -> MM2425dhvitd2[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_2425dhvitd2(e)b	MM2425dhvitd2[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MM24_25DHVITD3tb	MM2425dhvitd3[c] -> MM2425dhvitd3[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_2425dhvitd3(e)b	MM2425dhvitd3[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MM25HVITD2tb	MM25hvitd2[c] -> MM25hvitd2[b]	0	1000		Mouse secretion to outlet (body fluids)
MM25HVITD2tmb	MM25hvitd2[b] -> MM25hvitd2[c]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_25hvitd2(e)b	MM25hvitd2[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MM25HVITD3tb	MM25hvitd3[c] -> MM25hvitd3[b]	0	1000		Mouse secretion to outlet (body fluids)
MM25HVITD3tmb	MM25hvitd3[b] -> MM25hvitd3[c]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_25hvitd3(e)b	MM25hvitd3[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MM2HBt2b	MM2hb[b] + MMh[b] <=> MMh[c] + MM2hb[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_2hb(e)b	MM2hb[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MM4HPRO_LTtb	MMh[b] + MM4hpro-LT[b] <=> MMh[c] + MM4hpro-LT[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMABUTt2rb	MMh[b] + MM4abut[b] <=> MMh[c] + MM4abut[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMACACt2b	MMh[b] + MMacac[b] <=> MMh[c] + MMacac[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMACETONEt2b	MMh[b] + MMacetone[b] <=> MMh[c] + MMacetone[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMACHEeb	MMach[b] + MMh2o[b] -> MMh[b] + MMac[b] + MMchol[b]	0	1000		Mouse secretion to outlet (body fluids)
MMACt2rb	MMh[b] + MMac[b] <=> MMh[c] + MMac[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMADAeb	MMh[b] + MMh2o[b] + MMadn[b] -> MMins[b] + MMnh4[b]	0	1000		Mouse secretion to outlet (body fluids)
MMALAt2rb	MMh[b] + MMala-L[b] <=> MMh[c] + MMala-L[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMALAtN1b	MMh[c] + MMala-L[b] + 2 MMna1[b] <=> 2 MMna1[c] + MMala-L[c] + MMh[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMALAyLATIhcb	MMarg-L[c] + MMh[b] + MMala-L[b] -> MMh[c] + MMala-L[c] + MMarg-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMASNtN1b	MMh[c] + 2 MMna1[b] + MMasn-L[b] <=> 2 MMna1[c] + MMasn-L[c] + MMh[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMASPDt6b	MMk[c] + MMh[b] + 3 MMna1[b] + MMasp-D[b] -> MMh[c] + 3 MMna1[c] + MMasp-D[c] + MMk[b]	0	1000		Mouse secretion to outlet (body fluids)
MMASPt6b	MMk[c] + MMh[b] + 3 MMna1[b] + MMasp-L[b] -> MMh[c] + 3 MMna1[c] + MMasp-L[c] + MMk[b]	0	1000		Mouse secretion to outlet (body fluids)
MMATPH1eb	2 MMh2o[b] + MMatp[b] -> 2 MMh[b] + MMamp[b] + 2 MMpi[b]	0	1000		Mouse secretion to outlet (body fluids)
MMATPH2eb	MMh2o[b] + MMadp[b] -> MMh[b] + MMamp[b] + MMpi[b]	0	1000		Mouse secretion to outlet (body fluids)
MMBGLCtb	MMh[b] + MMbglc[b] <=> MMh[c] + MMbglc[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMBGLUGCHtb	MMh[b] + MMglgchlo[b] <=> MMh[c] + MMglgchlo[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMBGLUTCHLtb	MMh[b] + MMgltcho[b] <=> MMh[c] + MMgltcho[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMBGLUTDECHOtb	MMh[b] + MMgltdecho[b] <=> MMh[c] + MMgltdecho[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMBHBtb	MMh[b] + MMbhb[b] <=> MMh[c] + MMbhb[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMBTN2b	MMh[b] + MMbtn[b] <=> MMh[c] + MMbtn[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMBTNt4b	MMh[c] + MMbtn[b] -> MMbtn[c] + MMh[b]	0	1000		Mouse secretion to outlet (body fluids)
MMBUTt2rb	MMh[b] + MMbut[b] <=> MMh[c] + MMbut[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMCAATPSb	MMh2o[c] + MMatp[c] + 2 MMca2[c] -> MMadp[c] + MMpi[c] + MMh[b] + 2 MMca2[b]	0	1000		Mouse secretion to outlet (body fluids)
MMCGLYt3_2_b	2 MMh[b] + MMcgly[b] -> 2 MMh[c] + MMcgly[c]	0	1000		Mouse secretion to outlet (body fluids)
MMCRNtHab	MMcrn[c] + MMh[b] -> MMh[c] + MMcrn[b]	0	1000		Mouse secretion to outlet (body fluids)
MMDADAeb	MMh[b] + MMh2o[b] + MMdad-2[b] -> MMnh4[b] + MMdin[b]	0	1000		Mouse secretion to outlet (body fluids)
MMDALAt2rb	MMh[b] + MMala-D[b] <=> MMh[c] + MMala-D[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMD_LACt2b	MMh[b] + MMlac-D[b] <=> MMh[c] + MMlac-D[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_h(e)b	MMh[b] <=>	-100	1000		Mouse secretion to outlet (body fluids)
MMFE3R2eb	MMascb-L[b] + 2 MMfe3[b] -> 2 MMh[b] + MMdhdascb[b] + 2 MMfe2[b]	0	1000		Mouse secretion to outlet (body fluids)
MMGALt2_2b	2 MMh[b] + MMgal[b] <=> 2 MMh[c] + MMgal[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMGLCt2_2b	2 MMh[b] + MMglc-D[b] <=> 2 MMh[c] + MMglc-D[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMGLCt2rb	MMh[b] + MMglc-D[b] <=> MMh[c] + MMglc-D[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMGLNtN1b	MMh[c] + 2 MMna1[b] + MMgln-L[b] <=> 2 MMna1[c] + MMgln-L[c] + MMh[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMGLNyLATIhcb	MMarg-L[c] + MMh[b] + MMgln-L[b] -> MMh[c] + MMgln-L[c] + MMarg-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMGLUt6b	MMk[c] + MMh[b] + 3 MMna1[b] + MMglu-L[b] -> MMh[c] + 3 MMna1[c] + MMglu-L[c] + MMk[b]	0	1000		Mouse secretion to outlet (body fluids)
MMGLYGLYtb	MMh[b] + MMglygly[b] <=> MMh[c] + MMglygly[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMGLYPHEtb	MMh[b] + MMglyphe[b] <=> MMh[c] + MMglyphe[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMGLYSARtb	MMh[b] + MMglysar[b] <=> MMh[c] + MMglysar[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMGLYt2rb	MMh[b] + MMgly[b] <=> MMh[c] + MMgly[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMGUMDCHAtb	MMh[b] + MMgumdchac[b] <=> MMh[c] + MMgumdchac[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMGUMGCHLtb	MMh[b] + MMgumgcho[b] <=> MMh[c] + MMgumgcho[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMGUMTCHOLtb	MMh[b] + MMgumtcho[b] <=> MMh[c] + MMgumtcho[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMGUMtb	MMh[b] + MMgum[b] <=> MMh[c] + MMgum[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMHIStN1b	MMh[c] + 2 MMna1[b] + MMhis-L[b] <=> 2 MMna1[c] + MMhis-L[c] + MMh[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMHISyLATIhcb	MMarg-L[c] + MMh[b] + MMhis-L[b] -> MMh[c] + MMhis-L[c] + MMarg-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMHKtb	MMh2o[c] + MMatp[c] + MMk[b] -> MMadp[c] + MMpi[c] + MMk[c] + MMh[b]	0	1000		Mouse secretion to outlet (body fluids)
MMINSTt2rb	MMh[b] + MMinost[b] <=> MMh[c] + MMinost[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMLEUGLYtb	MMh[b] + MMleugly[b] -> MMh[c] + MMleugly[c]	0	1000		Mouse secretion to outlet (body fluids)
MMLEULEUtb	MMh[b] + MMleuleu[b] -> MMh[c] + MMleuleu[c]	0	1000		Mouse secretion to outlet (body fluids)
MMLEUyLATIhtcb	MMarg-L[c] + MMh[b] + MMleu-L[b] -> MMh[c] + MMleu-L[c] + MMarg-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMLPS2eb	MMh2o[b] + MMdag_hs[b] -> MMh[b] + MMRiotaIb[b] + MMmag_hs[b]	0	1000		Mouse secretion to outlet (body fluids)
MMLPS3eb	MMh2o[b] + MMmag_hs[b] -> MMh[b] + MMRiotaI2[b] + MMghyc[b]	0	1000		Mouse secretion to outlet (body fluids)
MMLPS4eb	MMh2o[b] + MMpglyc_hs[b] -> MMh[b] + MMRiotaI2[b] + MM1glyc_hs[b]	0	1000		Mouse secretion to outlet (body fluids)
MMLPSeb	MMh2o[b] + MMtag_hs[b] -> MMh[b] + MMdag_hs[b] + MMRiotaI3[b]	0	1000		Mouse secretion to outlet (body fluids)
MML_LACt2rb	MMh[b] + MMlac-L[b] <=> MMh[c] + MMlac-L[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMMETyLATIhcb	MMarg-L[c] + MMh[b] + MMmet-L[b] -> MMh[c] + MMmet-L[c] + MMarg-L[b]	0	1000		Mouse secretion to outlet (body fluids)

MMNADNeb	MMh2o[b] + MMnad[b] -> MMh[b] + MMadprib[b] + MMncam[b]	0	1000		Mouse secretion to outlet (body fluids)
MMNADPNeb	MMh2o[b] + MMnadp[b] -> MMh[b] + MMncam[b] + MMadprbp[b]	0	1000		Mouse secretion to outlet (body fluids)
MMNAHCO3_HCLtb	MMh[c] + MMcl[c] + MMna1[b] + MMhco3[b] <=> MMhco3[c] + MMna1[c] + MMh[b] + MMcl[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMNAt3_1b	MMna1[c] + MMh[b] <=> MMh[c] + MMna1[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMNDP10exb	MMh2o[b] + MMtdp[b] -> MMh[b] + MMp[b] + MMimp[b]	0	1000		Mouse secretion to outlet (body fluids)
MMNDP3exb	MMh2o[b] + MMgdp[b] -> MMh[b] + MMp[b] + MMgmp[b]	0	1000		Mouse secretion to outlet (body fluids)
MMNDP7exb	MMh2o[b] + MMudp[b] -> MMh[b] + MMp[b] + MMump[b]	0	1000		Mouse secretion to outlet (body fluids)
MMNDP8exb	MMh2o[b] + MMutp[b] -> MMh[b] + MMp[b] + MMudp[b]	0	1000		Mouse secretion to outlet (body fluids)
MMNH4t3rb	MMnh4[c] + MMh[b] <=> MMh[c] + MMnh4[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMNTP3eb	MMh2o[b] + MMgtp[b] -> MMh[b] + MMp[b] + MMgdp[b]	0	1000		Mouse secretion to outlet (body fluids)
MMPAFHeb	MMh2o[b] + MMpaf_hs[b] -> MMh[b] + MMac[b] + MMak2lgchol_hs[b]	0	1000		Mouse secretion to outlet (body fluids)
MMPECDCHtb	MMh[b] + MMpectindchac[b] <=> MMh[c] + MMpectindchac[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMPECGCHLtb	MMh[b] + MMpectingchol[b] <=> MMh[c] + MMpectingchol[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMPECTCHLtb	MMh[b] + MMpectintchol[b] <=> MMh[c] + MMpectintchol[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMPECTtb	MMh[b] + MMpect[b] <=> MMh[c] + MMpect[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMPHEyLATthcb	MMarg-L[c] + MMh[b] + MMphe-L[b] -> MMh[c] + MMphe-L[c] + MMarg-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMPRODt2rb	MMh[b] + MMpro-D[b] <=> MMh[c] + MMpro-D[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMPROGLYtb	MMh[b] + MMprogly[b] -> MMh[c] + MMprogly[c]	0	1000		Mouse secretion to outlet (body fluids)
MMPROt2rb	MMh[b] + MMpro-L[b] <=> MMh[c] + MMpro-L[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMPSYGCHtb	MMh[b] + MMpsylchol[b] <=> MMh[c] + MMpsylchol[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMPSYLtb	MMh[b] + MMpsyl[b] <=> MMh[c] + MMpsyl[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMPSYTCHtb	MMh[b] + MMpsyltchol[b] <=> MMh[c] + MMpsyltchol[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMPSYTDECHtb	MMh[b] + MMpsyltdechol[b] <=> MMh[c] + MMpsyltdechol[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMPYRt2rb	MMh[b] + MMpyr[b] <=> MMh[c] + MMpyr[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMRETH1eb	MMh2o[b] + MM9-cis-retfa[b] -> MMh[b] + MMRiotal2[b] + MMretinol-9-cis[b]	0	1000		Mouse secretion to outlet (body fluids)
MMRETH2eb	MMh2o[b] + MM11-cis-retfa[b] -> MMh[b] + MMRiotal2[b] + MMretinol-cis-11[b]	0	1000		Mouse secretion to outlet (body fluids)
MMRETHeb	MMh2o[b] + MMretfa[b] -> MMh[b] + MMRiotal2[b] + MMretinol[b]	0	1000		Mouse secretion to outlet (body fluids)
MMRIBt2b	MMh[b] + MMrib-D[b] -> MMh[c] + MMrib-D[c]	0	1000		Mouse secretion to outlet (body fluids)
MMSERtN1b	MMh[c] + 2 MMna1[b] + MMser-L[b] <=> 2 MMna1[c] + MMser-L[c] + MMh[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMSPODMeb	2 MMh[b] + 2 MMo2s[b] -> MMh2o2[b] + MMo2[b]	0	1000		Mouse secretion to outlet (body fluids)
MMTHMt3b	MMh[c] + MMthm[b] <=> MMthm[c] + MMh[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MM2HCO3_NAtb	MMna1[b] + 2 MMhco3[b] <=> 2 MMhco3[c] + MMna1[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MM3HCO3_NAtb	MMna1[b] + 3 MMhco3[b] <=> 3 MMhco3[c] + MMna1[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMBILIRUBt2b	MMhco3[c] + MMbilirub[b] <=> MMbilirub[c] + MMhco3[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMCLHCO3tex2b	MMhco3[c] + 2 MMcl[b] -> 2 MMcl[c] + MMhco3[b]	0	1000		Mouse secretion to outlet (body fluids)
MMCLHCOtexb	2 MMhco3[c] + MMcl[b] -> MMcl[c] + 2 MMhco3[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_hco3(e)b	MMhco3[b] <=>	-100	1000		Mouse secretion to outlet (body fluids)
MMHCO3_CLtb	MMcl[c] + MMhco3[b] <=> MMhco3[c] + MMcl[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMHCO3_NAtb	MMna1[b] + MMhco3[b] <=> MMhco3[c] + MMna1[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMOXAHCOtexb	2 MMhco3[c] + MMoxa[b] -> MMoxa[c] + 2 MMhco3[b]	0	1000		Mouse secretion to outlet (body fluids)
MMPROSTGD2tb	MMhco3[c] + MMprostgd2[b] <=> MMprostgd2[c] + MMhco3[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMPROSTGE1tb	MMhco3[c] + MMprostge1[b] <=> MMprostge1[c] + MMhco3[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMPROSTGE2tb	MMhco3[c] + MMprostge2[b] <=> MMprostge2[c] + MMhco3[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMPROSTGH2tb	MMhco3[c] + MMprostgh2[b] <=> MMprostgh2[c] + MMhco3[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMPROSTGI2tb	MMhco3[c] + MMprostgi2[b] <=> MMprostgi2[c] + MMhco3[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMSO4HCOtexb	2 MMhco3[c] + MMso4[b] -> MMso4[c] + 2 MMhco3[b]	0	1000		Mouse secretion to outlet (body fluids)
MMABUTt4_2_rb	MM4abut[b] + 2 MMna1[b] <=> 2 MMna1[c] + MM4abut[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMADNt4b	MMadn[b] + MMna1[b] -> MMna1[c] + MMadn[c]	0	1000		Mouse secretion to outlet (body fluids)
MMADNt5b	MMadn[b] + 2 MMna1[b] -> 2 MMna1[c] + MMadn[c]	0	1000		Mouse secretion to outlet (body fluids)
MMAKGt4_3b	3 MMna1[b] + MMakg[b] <=> MMakg[c] + 3 MMna1[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMALAASNNaExb	MMasn-L[c] + MMala-L[b] + MMna1[b] -> MMna1[c] + MMala-L[c] + MMasn-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMALACYSNaExb	MMcys-L[c] + MMala-L[b] + MMna1[b] -> MMna1[c] + MMala-L[c] + MMcys-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMALAGLNNaExb	MMgln-L[c] + MMala-L[b] + MMna1[b] -> MMna1[c] + MMala-L[c] + MMgln-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMALASERNaExb	MMser-L[c] + MMala-L[b] + MMna1[b] -> MMna1[c] + MMala-L[c] + MMser-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMALATHRNaExb	MMthr-L[c] + MMala-L[b] + MMna1[b] -> MMna1[c] + MMala-L[c] + MMthr-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMALAt4b	MMala-L[b] + MMna1[b] -> MMna1[c] + MMala-L[c]	0	1000		Mouse secretion to outlet (body fluids)
MMALAyLATtcb	MMarg-L[c] + MMala-L[b] + MMna1[b] -> MMna1[c] + MMala-L[c] + MMarg-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMARGt4b	MMna1[b] + MMarg-L[b] -> MMna1[c] + MMarg-L[c]	0	1000		Mouse secretion to outlet (body fluids)
MMASCBt4b	MMna1[b] + MMascb-L[b] <=> MMna1[c] + MMascb-L[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMASNALANaExb	MMala-L[c] + MMna1[b] + MMasn-L[b] -> MMna1[c] + MMasn-L[c] + MMala-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMASNCYSNaExb	MMcys-L[c] + MMna1[b] + MMasn-L[b] -> MMna1[c] + MMasn-L[c] + MMcys-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMASNGLNNaExb	MMgln-L[c] + MMna1[b] + MMasn-L[b] -> MMna1[c] + MMasn-L[c] + MMgln-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMASNSERNaExb	MMser-L[c] + MMna1[b] + MMasn-L[b] -> MMna1[c] + MMasn-L[c] + MMser-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMASNTHRNaExb	MMthr-L[c] + MMna1[b] + MMasn-L[b] -> MMna1[c] + MMasn-L[c] + MMthr-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMASNt4b	MMna1[b] + MMasn-L[b] -> MMna1[c] + MMasn-L[c]	0	1000		Mouse secretion to outlet (body fluids)
MMBTNt3b	MMh2o[c] + MMatp[c] + 2 MMna1[b] + MMbtn[b] -> MMadp[c] + MMh[c] + MMpi[c] + 2 MMna1[c] + MMbtn[c]	0	1000		Mouse secretion to outlet (body fluids)
MMCAt7rb	MMca2[c] + 3 MMna1[b] <=> 3 MMna1[c] + MMca2[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMCHOLATEt2b	2 MMna1[b] + MMcholate[b] -> 2 MMna1[c] + MMcholate[c]	0	1000		Mouse secretion to outlet (body fluids)
MMCHOLt4b	MMchol[b] + MMna1[b] <=> MMna1[c] + MMchol[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMCITt4_2b	2 MMna1[b] + MMcit[b] <=> 2 MMna1[c] + MMcit[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMCITt4_4b	4 MMna1[b] + MMcit[b] <=> 4 MMna1[c] + MMcit[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMCREATt4_2_rb	2 MMna1[b] + MMcreat[b] <=> 2 MMna1[c] + MMcreat[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMCRNtuNab	MMna1[b] + MMcrn[b] -> MMna1[c] + MMcrn[c]	0	1000		Mouse secretion to outlet (body fluids)
MMCYSALANaExb	MMala-L[c] + MMna1[b] + MMcys-L[b] -> MMna1[c] + MMcys-L[c] + MMala-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMCYSASNNaExb	MMasn-L[c] + MMna1[b] + MMcys-L[b] -> MMna1[c] + MMcys-L[c] + MMasn-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMCYSGLNNaExb	MMgln-L[c] + MMna1[b] + MMcys-L[b] -> MMna1[c] + MMcys-L[c] + MMgln-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMCYSSERNaExb	MMser-L[c] + MMna1[b] + MMcys-L[b] -> MMna1[c] + MMcys-L[c] + MMser-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMCYSTHRNaExb	MMthr-L[c] + MMna1[b] + MMcys-L[b] -> MMna1[c] + MMcys-L[c] + MMthr-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMCYSt4b	MMna1[b] + MMcys-L[b] -> MMna1[c] + MMcys-L[c]	0	1000		Mouse secretion to outlet (body fluids)
MMCYTDt4b	MMna1[b] + MMcytd[b] -> MMna1[c] + MMcytd[c]	0	1000		Mouse secretion to outlet (body fluids)
MMCYTDt5b	2 MMna1[b] + MMcytd[b] -> 2 MMna1[c] + MMcytd[c]	0	1000		Mouse secretion to outlet (body fluids)
MMDOPAt4_2_rb	2 MMna1[b] + MMdopa[b] <=> 2 MMna1[c] + MMdopa[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMESTRONESt2b	2 MMna1[b] + MMestrones[b] -> 2 MMna1[c] + MMestrones[c]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_na1(e)b	MMna1[b] <=>	-100	1000		Mouse secretion to outlet (body fluids)

MMFATP1tb	MMna1[c] + MMhdca[c] <=> MMna1[b] + MMhdca[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMFATP2tb	MMna1[c] + MMocdcea[c] <=> MMna1[b] + MMocdcea[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMFATP3tb	MMna1[c] + MMocdca[c] <=> MMna1[b] + MMocdca[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMFATP4tb	MMna1[c] + MMarach[c] <=> MMna1[b] + MMarach[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMFATP5tb	MMna1[c] + MMarachd[c] <=> MMna1[b] + MMarachd[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMFATP6tb	MMna1[c] + MMadrn[c] <=> MMna1[b] + MMadrn[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMFATP7tb	MMna1[c] + MMcrvnc[c] <=> MMna1[b] + MMcrvnc[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMFATP8tb	MMna1[c] + MMlgnc[c] <=> MMna1[b] + MMlgnc[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMFATP9tb	MMna1[c] + MMnrvnc[c] <=> MMna1[b] + MMnrvnc[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMFRUt4b	MMna1[b] + MMfru[b] <=> MMna1[c] + MMfru[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMGALt4b	MMna1[b] + MMgal[b] <=> MMna1[c] + MMgal[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMGALt4_2b	2 MMna1[b] + MMgal[b] <=> 2 MMna1[c] + MMgal[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMGCHOLA2b	2 MMna1[b] + MMgchola[b] -> 2 MMna1[c] + MMgchola[c]	0	1000		Mouse secretion to outlet (body fluids)
MMGLCt4b	MMna1[b] + MMglc-D[b] <=> MMna1[c] + MMglc-D[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMGLCt4_2b	2 MMna1[b] + MMglc-D[b] <=> 2 MMna1[c] + MMglc-D[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMGLNALANaExb	MMala-L[c] + MMna1[b] + MMgln-L[b] -> MMna1[c] + MMgln-L[c] + MMala-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMGLNASNNaExb	MMasn-L[c] + MMna1[b] + MMgln-L[b] -> MMna1[c] + MMgln-L[c] + MMasn-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMGLNCYSNaExb	MMcys-L[c] + MMna1[b] + MMgln-L[b] -> MMna1[c] + MMgln-L[c] + MMcys-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMGLNSERNaExb	MMser-L[c] + MMna1[b] + MMgln-L[b] -> MMna1[c] + MMgln-L[c] + MMser-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMGLNTHRNaExb	MMthr-L[c] + MMna1[b] + MMgln-L[b] -> MMna1[c] + MMgln-L[c] + MMthr-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMGLNt4b	MMna1[b] + MMgln-L[b] -> MMna1[c] + MMgln-L[c]	0	1000		Mouse secretion to outlet (body fluids)
MMGLNtyLATIctb	MMarg-L[c] + MMna1[b] + MMgln-L[b] -> MMna1[c] + MMgln-L[c] + MMarg-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMGLYBt4_2_rb	2 MMna1[b] + MMglyb[b] <=> 2 MMna1[c] + MMglyb[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMGLYt4b	MMna1[b] + MMgly[b] -> MMna1[c] + MMgly[c]	0	1000		Mouse secretion to outlet (body fluids)
MMGLY7_211_rb	2 MMna1[b] + MMgly[b] + MMcl[b] <=> 2 MMna1[c] + MMcl[c] + MMgly[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMGLY7_311_rb	3 MMna1[b] + MMgly[b] + MMcl[b] <=> 3 MMna1[c] + MMcl[c] + MMgly[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMGSNt4b	MMna1[b] + MMgsn[b] -> MMna1[c] + MMgsn[c]	0	1000		Mouse secretion to outlet (body fluids)
MMGSNt5b	2 MMna1[b] + MMgsn[b] -> 2 MMna1[c] + MMgsn[c]	0	1000		Mouse secretion to outlet (body fluids)
MMHISt4b	MMna1[b] + MMhis-L[b] -> MMna1[c] + MMhis-L[c]	0	1000		Mouse secretion to outlet (body fluids)
MMHISyLATIctb	MMarg-L[c] + MMna1[b] + MMhis-L[b] -> MMna1[c] + MMhis-L[c] + MMarg-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMHOMt4b	MMna1[b] + MMhom-L[b] -> MMna1[c] + MMhom-L[c]	0	1000		Mouse secretion to outlet (body fluids)
MMILEt4b	MMna1[b] + MMile-L[b] -> MMna1[c] + MMile-L[c]	0	1000		Mouse secretion to outlet (body fluids)
MMINSTt4b	MMna1[b] + MMinost[b] <=> MMna1[c] + MMinost[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMINSTt4_2b	2 MMna1[b] + MMinost[b] <=> 2 MMna1[c] + MMinost[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMINSt4b	MMins[b] + MMna1[b] -> MMna1[c] + MMins[c]	0	1000		Mouse secretion to outlet (body fluids)
MMINSt5b	MMins[b] + 2 MMna1[b] -> 2 MMna1[c] + MMins[c]	0	1000		Mouse secretion to outlet (body fluids)
MMLEUt4b	MMna1[b] + MMleu-L[b] -> MMna1[c] + MMleu-L[c]	0	1000		Mouse secretion to outlet (body fluids)
MMLEUyLATIctb	MMarg-L[c] + MMna1[b] + MMleu-L[b] -> MMna1[c] + MMleu-L[c] + MMarg-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMLIPOtb	MMh2o[c] + MMatp[c] + 2 MMna1[b] + MMlipoate[b] -> MMadp[c] + MMh[c] + MMpi[c] + 2 MMna1[c] + MMlipoate[c]	0	1000		Mouse secretion to outlet (body fluids)
MMLYSt4b	MMna1[b] + MMlys-L[b] -> MMna1[c] + MMlys-L[c]	0	1000		Mouse secretion to outlet (body fluids)
MML_LACt4rb	MMna1[b] + MMlac-L[b] <=> MMna1[c] + MMlac-L[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMMANt4b	MMna1[b] + MMman[b] <=> MMna1[c] + MMman[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMMETt4b	MMna1[b] + MMmet-L[b] -> MMna1[c] + MMmet-L[c]	0	1000		Mouse secretion to outlet (body fluids)
MMMETyLATIctb	MMarg-L[c] + MMna1[b] + MMmet-L[b] -> MMna1[c] + MMmet-L[c] + MMarg-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMNAHtb	2 MMna1[b] + MMh[b] <=> 2 MMna1[c] + MMh[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMNAtb	MMna1[b] <=> MMna1[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMNAt5b	MMna1[c] + MMnh4[b] <=> MMnh4[c] + MMna1[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMNCCtb	MMna1[b] + MMcl[b] -> MMna1[c] + MMcl[c]	0	1000		Mouse secretion to outlet (body fluids)
MMNCKtb	4 MMna1[c] + MMk[b] + MMca2[b] <=> MMk[c] + MMca2[c] + 4 MMna1[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMNCNtb	4 MMna1[c] + MMnh4[b] + MMca2[b] <=> MMnh4[c] + MMca2[c] + 4 MMna1[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMNKCC2tb	MMnh4[b] + MMna1[b] + 2 MMcl[b] <=> MMnh4[c] + MMna1[c] + 2 MMcl[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMNKCCtb	MMna1[b] + MMk[b] + 2 MMcl[b] <=> MMna1[c] + 2 MMcl[c] + MMk[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMNRPPHR4_2_rb	2 MMna1[b] + MMnrpphr[b] <=> 2 MMna1[c] + MMnrpphr[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMPHEt4b	MMna1[b] + MMphe-L[b] -> MMna1[c] + MMphe-L[c]	0	1000		Mouse secretion to outlet (body fluids)
MMPHEyLATIctb	MMarg-L[c] + MMna1[b] + MMphe-L[b] -> MMna1[c] + MMphe-L[c] + MMarg-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMPIt7b	3 MMna1[b] + MMpi[b] <=> MMpi[c] + 3 MMna1[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMPIt8b	1.5 MMna1[b] + MMpi[b] <=> MMpi[c] + 1.5 MMna1[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMPIt9b	2 MMna1[b] + MMpi[b] <=> MMpi[c] + 2 MMna1[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMPNTOt5b	MMh2o[c] + MMatp[c] + 2 MMna1[b] + MMpnto-R[b] -> MMadp[c] + MMh[c] + MMpi[c] + 2 MMna1[c] + MMpnto-R[c]	0	1000		Mouse secretion to outlet (body fluids)
MMPROt4b	MMna1[b] + MMpro-L[b] -> MMna1[c] + MMpro-L[c]	0	1000		Mouse secretion to outlet (body fluids)
MMPROt4(2)rb	2 MMna1[b] + MMpro-L[b] <=> 2 MMna1[c] + MMpro-L[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMSELt4_3b	3 MMna1[b] + MMse[b] <=> 3 MMna1[c] + MMse[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMSERALANaExb	MMala-L[c] + MMna1[b] + MMser-L[b] -> MMna1[c] + MMser-L[c] + MMala-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMSERASNNaExb	MMasn-L[c] + MMna1[b] + MMser-L[b] -> MMna1[c] + MMser-L[c] + MMasn-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMSERCYSNaExb	MMcys-L[c] + MMna1[b] + MMser-L[b] -> MMna1[c] + MMser-L[c] + MMcys-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMSERGLNNaExb	MMgln-L[c] + MMna1[b] + MMser-L[b] -> MMna1[c] + MMser-L[c] + MMgln-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMSERLYSNaexb	MMlys-L[c] + MMna1[b] + MMser-L[b] -> MMna1[c] + MMser-L[c] + MMlys-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMSERTHRNaExb	MMthr-L[c] + MMna1[b] + MMser-L[b] -> MMna1[c] + MMser-L[c] + MMthr-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMSERt4b	MMna1[b] + MMser-L[b] -> MMna1[c] + MMser-L[c]	0	1000		Mouse secretion to outlet (body fluids)
MMSO4t4_2b	2 MMna1[b] + MMso4[b] <=> 2 MMna1[c] + MMso4[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMSO4t4_3b	3 MMna1[b] + MMso4[b] <=> 3 MMna1[c] + MMso4[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMSRTN6_2_rb	2 MMk[c] + 2 MMna1[b] + MMsrtn[b] <=> 2 MMna1[c] + MMsrtn[c] + 2 MMk[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMSUCCt4_2b	2 MMna1[b] + MMsucc[b] <=> 2 MMna1[c] + MMsucc[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMSUCCt4_3b	3 MMna1[b] + MMsucc[b] <=> 3 MMna1[c] + MMsucc[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMTAURt4_2_rb	2 MMna1[b] + MMtaur[b] <=> 2 MMna1[c] + MMtaur[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMTCHOLAt2b	2 MMna1[b] + MMtchola[b] -> 2 MMna1[c] + MMtchola[c]	0	1000		Mouse secretion to outlet (body fluids)
MMTHMDt4b	MMna1[b] + MMthymd[b] -> MMna1[c] + MMthymd[c]	0	1000		Mouse secretion to outlet (body fluids)
MMTHMDt5b	2 MMna1[b] + MMthymd[b] -> 2 MMna1[c] + MMthymd[c]	0	1000		Mouse secretion to outlet (body fluids)
MMTHRALANaExb	MMala-L[c] + MMna1[b] + MMthr-L[b] -> MMna1[c] + MMthr-L[c] + MMala-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMTHRASNNaExb	MMasn-L[c] + MMna1[b] + MMthr-L[b] -> MMna1[c] + MMthr-L[c] + MMasn-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMTHRCYSNaExb	MMcys-L[c] + MMna1[b] + MMthr-L[b] -> MMna1[c] + MMthr-L[c] + MMcys-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMTHRGLNNaExb	MMgln-L[c] + MMna1[b] + MMthr-L[b] -> MMna1[c] + MMthr-L[c] + MMgln-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMTHRSERNaExb	MMser-L[c] + MMna1[b] + MMthr-L[b] -> MMna1[c] + MMthr-L[c] + MMser-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMTHRt4b	MMna1[b] + MMthr-L[b] -> MMna1[c] + MMthr-L[c]	0	1000		Mouse secretion to outlet (body fluids)

MMTRPt4b	MMna1[b] + MMtrp-L[b] -> MMna1[c] + MMtrp-L[c]	0	1000		Mouse secretion to outlet (body fluids)
MMTSUL4_3b	3 MMna1[b] + MMtsul[b] <=> 3 MMna1[c] + MMtsul[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMTYRt4b	MMna1[b] + MMtyr-L[b] -> MMna1[c] + MMtyr-L[c]	0	1000		Mouse secretion to outlet (body fluids)
MMURIt4b	MMna1[b] + MMuri[b] -> MMna1[c] + MMuri[c]	0	1000		Mouse secretion to outlet (body fluids)
MMURIt5b	2 MMna1[b] + MMuri[b] -> 2 MMna1[c] + MMuri[c]	0	1000		Mouse secretion to outlet (body fluids)
MMVALt4b	MMna1[b] + MMval-L[b] -> MMna1[c] + MMval-L[c]	0	1000		Mouse secretion to outlet (body fluids)
MM2MCITtb	MM2mci[c] <=> MM2mci[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_2mci(e)b	MM2mci[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MM34DHOXPEGtb	MM34dhoxpeg[c] <=> MM34dhoxpeg[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_34dhoxpeg(e)b	MM34dhoxpeg[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MM3AIBtb	MM3aib[c] -> MM3aib[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_3aib(e)b	MM3aib[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MM3MLDAtb	MM3mlda[c] <=> MM3mlda[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_3mlda(e)b	MM3mlda[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MM4HDEBRISOQUINEteb	MM4hdebrisoquine[b] <=> MM4hdebrisoquine[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_4hdebrisoquine(e)b	MM4hdebrisoquine[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MM4MPTNLteb	MM4mptnl[c] <=> MM4mptnl[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_4mptnl(e)b	MM4mptnl[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MM4MTOLBUTAMIDEteb	MM4mtolbutamide[b] <=> MM4mtolbutamide[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_4mtolbutamide(e)b	MM4mtolbutamide[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MM4NPHSFteb	MM4nphsf[c] <=> MM4nphsf[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_4nphsf(e)b	MM4nphsf[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MM4NPHteb	MM4nph[b] <=> MM4nph[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_4nph(e)b	MM4nph[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MM4PYRDXb	MMh2o[c] + MMatp[c] + MM4pyrdx[c] -> MMadp[c] + MMhi[c] + MMpi[c] + MM4pyrdx[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_4pyrdx(e)b	MM4pyrdx[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MM5ADTSTSTERONEGLCteb	MMh2o[c] + MMatp[c] + MM5adtststeronegglc[c] -> MMadp[c] + MMhi[c] + MMpi[c] + MM5adtststeronegglc[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_5adtststeronegglc(e)b	MM5adtststeronegglc[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MM5ADTSTSTERONESteb	MM5adtststerones[c] <=> MM5adtststerones[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_5adtststerones(e)b	MM5adtststerones[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MM5ADTSTSTERONEteb	MM5adtststerone[b] <=> MM5adtststerone[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_5adtststerone(e)b	MM5adtststerone[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MM5FTHFt2b	MMoh1[c] + MM5thf[b] <=> MM5thf[c] + MMoh1[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_5thf(e)b	MM5thf[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MM5MTHFt2b	MMoh1[c] + MM5mthf[b] <=> MM5mthf[c] + MMoh1[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMCLOHtex2b	MMoh1[c] + 2 MMcl[b] -> 2 MMcl[c] + MMoh1[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_oh1b	MMoh1[b] <=>	-100	1000		Mouse secretion to outlet (body fluids)
MMFOLt2b	MMoh1[c] + MMfol[b] <=> MMfol[c] + MMoh1[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMTHFt2b	MMoh1[c] + MMthf[b] <=> MMthf[c] + MMoh1[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMTHMMPt4b	MMoh1[c] + MMthmmp[b] <=> MMthmmp[c] + MMoh1[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMTHMTPtb	MMthmtp[c] + 3 MMoh1[b] -> 3 MMoh1[c] + MMthmtp[b]	0	1000		Mouse secretion to outlet (body fluids)
MM5HOMEPRAZOLEteb	MM5homeprazole[b] <=> MM5homeprazole[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_5homeprazole(e)b	MM5homeprazole[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MM5HTRPVESSECb	2 MMh2o[c] + 2 MMatp[c] + 3 MM5htrp[c] -> 2 MMadp[c] + 2 MMhi[c] + 2 MMpi[c] + 3 MM5htrp[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_5htrp(e)b	MM5htrp[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_5mthf(e)b	MM5mthf[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMMTHFTeb	MM5mthf[c] -> MM5mthf[b]	0	1000		Mouse secretion to outlet (body fluids)
MM6HTSTSTERONEteb	MM6htststerone[c] <=> MM6htststerone[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_6htststerone(e)b	MM6htststerone[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMABTtb	MMabt[c] -> MMabt[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_abt(e)b	MMabt[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_4abut(e)b	MM4abut[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMGABAVESSECb	MMh2o[c] + MMatp[c] + 3 MM4abut[c] -> MMadp[c] + MMhi[c] + MMpi[c] + 3 MM4abut[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_acac(e)b	MMacac[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMACALDtb	MMacald[b] <=> MMacald[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_acald(e)b	MMacald[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_acetone(e)b	MMacetone[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMACGALFUCGALACGALFUC12GAL14ACGLCGALGLUSIDEteb	MMacgalfucgalacgalfuc12gal14acglcgalgluside_hs[b] <=> MMacgalfucgalacgalfuc12gal14acglcgalgluside_hs[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_acgalfucgalacgalfuc12gal14acglcgalgluside_hs(e)b	MMacgalfucgalacgalfuc12gal14acglcgalgluside_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMACGALFUCGALACGALFUCGALACGLCGAL14ACGLCGALGLUSIDEteb	MMacgalfucgalacgalfucgalacglcgal14acglcgalgluside_hs[b] <=> MMacgalfucgalacgalfucgalacglcgal14acglcgalgluside_hs[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_acgalfucgalacgalfucgalacglcgal14acglcgalgluside_hs(e)b	MMacgalfucgalacgalfucgalacglcgal14acglcgalgluside_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMACGALtrb	MMacgal[c] -> MMacgal[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_acgal(e)b	MMacgal[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMACHVESSECb	2 MMh2o[c] + 2 MMatp[c] + 3 MMach[c] -> 2 MMadp[c] + 2 MMhi[c] + 2 MMpi[c] + 3 MMach[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_ach(e)b	MMach[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMAMPTASECGeb	MMh2o[b] + MMcgly[b] -> MMgly[b] + MMcys-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMAMY1eb	8 MMh2o[b] + MMstrch1[b] -> 8 MMglc-D[b] + MMstrch2[b]	0	1000		Mouse secretion to outlet (body fluids)
MMAMY2eb	8 MMh2o[b] + MMglygn2[b] -> 8 MMglc-D[b] + MMglygn4[b]	0	1000		Mouse secretion to outlet (body fluids)
MMBTNDeb	MMh2o[b] + MMbtocyt[b] -> MMbtn[b] + MMlys-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMCHTNASEeb	2 MMh2o[b] + MMchtn[b] -> 3 MMacgam[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_h2o(e)b	MMh2o[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMFUCASE2eb	MMh2o[b] + MMksi[b] -> MMfuc-L[b] + MMksi_deg1[b]	0	1000		Mouse secretion to outlet (body fluids)
MMFUCASEeb	MMh2o[b] + MMs2f3f4m2mnstr[b] -> MMfuc-L[b] + MMs2f2m2m2mnstr[b]	0	1000		Mouse secretion to outlet (body fluids)
MMGAMYeb	MMh2o[b] + MMglygn5[b] -> MMTyr-ggp[b] + MMmalt[b]	0	1000		Mouse secretion to outlet (body fluids)
MMGGH_10FTHF5GLUeb	4 MMh2o[b] + MM10fthf5glu[b] -> 4 MMglu-L[b] + MM10fthf[b]	0	1000		Mouse secretion to outlet (body fluids)
MMGGH_10FTHF6GLUeb	MMh2o[b] + MM10fthf6glu[b] -> MMglu-L[b] + MM10fthf5glu[b]	0	1000		Mouse secretion to outlet (body fluids)
MMGGH_10FTHF7GLUeb	MMh2o[b] + MM10fthf7glu[b] -> MMglu-L[b] + MM10fthf6glu[b]	0	1000		Mouse secretion to outlet (body fluids)
MMGGH_5DHFeb	4 MMh2o[b] + MM5dhf[b] -> 4 MMglu-L[b] + MMdhf[b]	0	1000		Mouse secretion to outlet (body fluids)
MMGGH_5THFeb	4 MMh2o[b] + MM5thf[b] -> 4 MMglu-L[b] + MMthf[b]	0	1000		Mouse secretion to outlet (body fluids)
MMGGH_6DHFeb	MMh2o[b] + MM6dhf[b] -> MMglu-L[b] + MM5dhf[b]	0	1000		Mouse secretion to outlet (body fluids)
MMGGH_6THFeb	MMh2o[b] + MM6thf[b] -> MMglu-L[b] + MM5thf[b]	0	1000		Mouse secretion to outlet (body fluids)
MMGGH_7DHFeb	MMh2o[b] + MM7dhf[b] -> MMglu-L[b] + MM6dhf[b]	0	1000		Mouse secretion to outlet (body fluids)
MMGGH_7THFeb	MMh2o[b] + MM7thf[b] -> MMglu-L[b] + MM6thf[b]	0	1000		Mouse secretion to outlet (body fluids)

MMGTHPeb	MMh2o2[b] + 2 MMgthrd[b] <=> 2 MMh2o[b] + MMgthox[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMH2Otb	MMh2o[b] <=> MMh2o[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMLACZeb	MMh2o[b] + MMlcts[b] -> MMgal[b] + MMglc-D[b]	0	1000		Mouse secretion to outlet (body fluids)
MMMALTeb	MMh2o[b] + MMmalt[b] -> 2 MMglc-D[b]	0	1000		Mouse secretion to outlet (body fluids)
MMMLTG1eb	MMh2o[b] + MMmalttr[b] -> MMglc-D[b] + MMmalt[b]	0	1000		Mouse secretion to outlet (body fluids)
MMNTD2eb	MMh2o[b] + MMump[b] -> MMpi[b] + MMuri[b]	0	1000		Mouse secretion to outlet (body fluids)
MMNTD4eb	MMh2o[b] + MMcmp[b] -> MMpi[b] + MMcytd[b]	0	1000		Mouse secretion to outlet (body fluids)
MMNTD7eb	MMh2o[b] + MMamp[b] -> MMadn[b] + MMpi[b]	0	1000		Mouse secretion to outlet (body fluids)
MMNTD9eb	MMh2o[b] + MMgmp[b] -> MMpi[b] + MMgsn[b]	0	1000		Mouse secretion to outlet (body fluids)
MMO16G1eb	MMh2o[b] + MMglygn4[b] -> MMglc-D[b] + MMglygn5[b]	0	1000		Mouse secretion to outlet (body fluids)
MMO16G2eb	MMh2o[b] + MMstrch2[b] -> MMglc-D[b] + MMmalt[b]	0	1000		Mouse secretion to outlet (body fluids)
MMSUCReb	MMh2o[b] + MMsucr[b] -> MMglc-D[b] + MMfru[b]	0	1000		Mouse secretion to outlet (body fluids)
MMTREHeb	MMh2o[b] + MMtre[b] -> 2 MMglc-D[b]	0	1000		Mouse secretion to outlet (body fluids)
MMUREAt5b	MMh2o[b] + MMurea[b] <=> MMh2o[c] + MMurea[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_ac(e)b	MMac[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMCHOLtub	MMchol[b] <=> MMchol[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_chol(e)b	MMchol[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMACN13ACNGALGBSIDEteb	MMacn13acngalgbside_hs[c] <=> MMacn13acngalgbside_hs[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_acn13acngalgbside_hs(e)b	MMacn13acngalgbside_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMACN23ACNGALGBSIDEteb	MMacn23acngalgbside_hs[c] <=> MMacn23acngalgbside_hs[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_acn23acngalgbside_hs(e)b	MMacn23acngalgbside_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMACNACNGALGAL14ACGLCGALGLUSIDEteb	MMacnacngal14acglcgalgluside_hs[b] <=> MMacnacngal14acglcgalgluside_hs[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_acnacngal14acglcgalgluside_hs(e)b	MMacnacngal14acglcgalgluside_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMACNACNGALGBSIDEteb	MMacnacngalgbside_hs[c] <=> MMacnacngalgbside_hs[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_acnacngalgbside_hs(e)b	MMacnacngalgbside_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMACNAMtrb	MMacnam[c] -> MMacnam[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_acnam(e)b	MMacnam[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMACNGALACGLCGAL14ACGLCGALGLUSIDEteb	MMacngalacglcgal14acglcgalgluside_hs[b] <=> MMacngalacglcgal14acglcgalgluside_hs[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_acngalacglcgal14acglcgalgluside_hs(e)b	MMacngalacglcgal14acglcgalgluside_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMADNtb	MMadn[b] <=> MMadn[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_adn(e)b	MMadn[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_ins(e)b	MMins[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMINStb	MMins[b] <=> MMins[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_nh4(e)b	MMnh4[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMKCC2tb	MMnh4[b] + MMcl[b] <=> MMnh4[c] + MMcl[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMADEtb	MMade[b] <=> MMade[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_ade(e)b	MMade[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMADPRIBtb	MMadprib[b] -> MMadprib[c]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_adprib(e)b	MMadprib[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMADRNLPVESSECb	2 MMh2o[c] + 2 MMatp[c] + 3 MMadrnl[c] -> 2 MMadp[c] + 2 MMh[c] + 2 MMpi[c] + 3 MMadrnl[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_adrnl(e)b	MMadrnl[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMADRNtb	MMadrn[b] <=> MMadrn[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_adrn(e)b	MMadrn[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMAFLATOXINteb	MMaflatoxin[b] <=> MMaflatoxin[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_aflatoxin(e)b	MMaflatoxin[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMAHANDROSTANGLCteb	MMh2o[c] + MMatp[c] + MMahandrostangl[c] -> MMadp[c] + MMh[c] + MMpi[c] + MMahandrostangl[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_ahandrostangl(e)b	MMahandrostangl[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMAK2LGCHOLtb	MMak2lgchol_hs[b] <=> MMak2lgchol_hs[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_ak2lgchol_hs(e)b	MMak2lgchol_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_akg(e)b	MMakg[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMALAGLNexRb	MMgln-L[c] + MMala-L[b] <=> MMala-L[c] + MMgln-L[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMALAGLYexRb	MMgly[c] + MMala-L[b] <=> MMala-L[c] + MMgly[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMALAILELAT2tcb	MMile-L[c] + MMala-L[b] -> MMala-L[c] + MMile-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMALAPHELAT2tcb	MMphe-L[c] + MMala-L[b] -> MMala-L[c] + MMphe-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_ala_L(e)b	MMala-L[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMASNILELAT2tcb	MMile-L[c] + MMasn-L[b] -> MMasn-L[c] + MMile-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMASNPHELAT2tcb	MMphe-L[c] + MMasn-L[b] -> MMasn-L[c] + MMphe-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_asn_L(e)b	MMasn-L[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMCYSGLUexRb	MMgln-L[c] + MMcys-L[b] <=> MMcys-L[c] + MMgln-L[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMCYSGLYexb	MMcys-L[c] + MMgly[b] -> MMgly[c] + MMcys-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMCYSILELAT2tcb	MMile-L[c] + MMcys-L[b] -> MMcys-L[c] + MMile-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMCYSPHELAT2tcb	MMphe-L[c] + MMcys-L[b] -> MMcys-L[c] + MMphe-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMCYStectb	MMcys-L[b] <=> MMcys-L[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_cys_L(e)b	MMcys-L[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMALADGLNexRb	MMgln-L[c] + MMala-D[b] <=> MMala-D[c] + MMgln-L[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMALADGLYexRb	MMgly[c] + MMala-D[b] <=> MMala-D[c] + MMgly[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_ala_D(e)b	MMala-D[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_gln_L(e)b	MMgln-L[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMGLNILELAT2tcb	MMile-L[c] + MMgln-L[b] -> MMgln-L[c] + MMile-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMGLNPHELAT2tcb	MMphe-L[c] + MMgln-L[b] -> MMgln-L[c] + MMphe-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMSERDGLNexRb	MMgln-L[c] + MMser-D[b] <=> MMser-D[c] + MMgln-L[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMSERGLNexRb	MMgln-L[c] + MMser-L[b] <=> MMser-L[c] + MMgln-L[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMTHRGLNexRb	MMgln-L[c] + MMthr-L[b] <=> MMthr-L[c] + MMgln-L[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_gly(e)b	MMgly[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMGLYVESSECb	MMh2o[c] + MMatp[c] + 3 MMgly[c] -> MMadp[c] + MMh[c] + MMpi[c] + 3 MMgly[b]	0	1000		Mouse secretion to outlet (body fluids)
MMSERDGLYexRb	MMgly[c] + MMser-D[b] <=> MMser-D[c] + MMgly[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMSERGLYexRb	MMgly[c] + MMser-L[b] <=> MMser-L[c] + MMgly[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMTHRGLYexRb	MMgly[c] + MMthr-L[b] <=> MMthr-L[c] + MMgly[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_ile_L(e)b	MMile-L[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMHISILELAT2tcb	MMile-L[c] + MMhis-L[b] -> MMhis-L[c] + MMile-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMILEATB0tcb	2 MMna1[u] + MMcl[u] + MMile-L[b] -> 2 MMna1[c] + MMcl[c] + MMile-L[c]	0	1000		Mouse secretion to outlet (body fluids)
MMILEPHELAT2tcb	MMphe-L[c] + MMile-L[b] -> MMile-L[c] + MMphe-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMILEtectb	MMile-L[b] <=> MMile-L[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMLEUILELAT2tcb	MMile-L[c] + MMleu-L[b] <=> MMleu-L[c] + MMile-L[b]	-1000	1000		Mouse secretion to outlet (body fluids)

MMMETILELAT2tcb	MMile-L[c] + MMmet-L[b] -> MMmet-L[c] + MMile-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMPHEILELAT2tcb	MMile-L[c] + MMphe-L[b] <=> MMphe-L[c] + MMile-L[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMSERILELAT2tcb	MMile-L[c] + MMser-L[b] -> MMser-L[c] + MMile-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMTHRILELAT2tcb	MMile-L[c] + MMthr-L[b] -> MMthr-L[c] + MMile-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMTRPILELAT2tcb	MMile-L[c] + MMtrp-L[b] -> MMtrp-L[c] + MMile-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMTYRILELAT2tcb	MMile-L[c] + MMtyr-L[b] -> MMtyr-L[c] + MMile-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMVALILELAT2tcb	MMile-L[c] + MMval-L[b] -> MMval-L[c] + MMile-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_phe_L(e)b	MMphe-L[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMHISPHELAT2tcb	MMphe-L[c] + MMhis-L[b] -> MMhis-L[c] + MMphe-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMLEUPHELAT2tcb	MMphe-L[c] + MMleu-L[b] <=> MMleu-L[c] + MMphe-L[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMMETPHELAT2tcb	MMphe-L[c] + MMmet-L[b] -> MMmet-L[c] + MMphe-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMSERPHELAT2tcb	MMphe-L[c] + MMser-L[b] -> MMser-L[c] + MMphe-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMTHRPHELAT2tcb	MMphe-L[c] + MMthr-L[b] -> MMthr-L[c] + MMphe-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMTRPPHELAT1tcb	MMphe-L[c] + MMtrp-L[b] -> MMtrp-L[c] + MMphe-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMTYRPHELAT2tcb	MMphe-L[c] + MMtyr-L[b] -> MMtyr-L[c] + MMphe-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMVALPHELAT2tcb	MMphe-L[c] + MMval-L[b] -> MMval-L[c] + MMphe-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMCYSTSERexb	MMser-L[c] + MMLcystin[b] -> MMLcystin[c] + MMser-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_ser_L(e)b	MMser-L[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_thr_L(e)b	MMthr-L[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMARGLYSexb	MMlys-L[c] + MMarg-L[b] -> MMarg-L[c] + MMlys-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMARGGSrb	MMarg-L[b] <=> MMarg-L[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_arg_L(e)b	MMarg-L[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMALDSTRNteb	MMaldstrn[c] <=> MMaldstrn[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_aldstrn(e)b	MMaldstrn[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_cgly(e)b	MMcgly[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMGTMLTeb	MMala-L[c] + MMgthrd[c] -> MMcgly[b] + MMgluala[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_strch1(e)b	MMstrch1[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_glc(e)b	MMglc-D[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMGLCMtetb	MMglc-D[r] -> MMglc-D[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_strch2(e)b	MMstrch2[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_glygn2(e)b	MMglygn2[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_glygn4(e)b	MMglygn4[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMANDRSTRNGLCteb	MMfth2o[c] + MMatp[c] + MMandrstrnglc[c] -> MMadp[c] + MMfth[c] + MMpi[c] + MMandrstrnglc[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_andrstrnglc(e)b	MMandrstrnglc[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMANDRSTRNteb	MMandrstrn[b] <=> MMandrstrn[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_andrstrn(e)b	MMandrstrn[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMANTIPYRENEteb	MMantipyrene[b] <=> MMantipyrene[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_antipyrene(e)b	MMantipyrene[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMAPNNOXteb	MMapnnox[b] <=> MMapnnox[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_apnnox(e)b	MMapnnox[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMAPPNNteb	MMappnn[b] <=> MMappnn[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_appnn(e)b	MMappnn[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMAPRGSTRNteb	MMaprgstrn[b] <=> MMaprgstrn[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_aprgstrn(e)b	MMaprgstrn[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMAQCOBALtb	MMaqcobal[b] -> MMaqcobal[c]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_aqcobal(e)b	MMaqcobal[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMARAB_Ltb	MMarab-L[b] <=> MMarab-L[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_arab_L(e)b	MMarab-L[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMARACHD2b	MMarachd[b] <=> MMarachd[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_arachd(e)b	MMarachd[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMARACHtb	MMarach[b] <=> MMarach[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_arach(e)b	MMarach[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_lys_L(e)b	MMlys-L[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMLYSt6rb	MMlys-L[b] <=> MMlys-L[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMASCBtb	MMascb-L[b] <=> MMascb-L[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_ascb_L(e)b	MMascb-L[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_asp_D(e)b	MMasp-D[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_k(e)b	MMk[b] <=>	-100	1000		Mouse secretion to outlet (body fluids)
MMKCCtb	MMk[b] + MMcl[b] <=> MMcl[c] + MMk[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_asp_L(e)b	MMasp-L[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_atp(e)b	MMatp[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_amp(e)b	MMamp[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_pi(e)b	MMpi[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_adpb	MMadp[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMAVITE1tb	MMavite1[b] -> MMavite1[c]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_avite1(e)b	MMavite1[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMVITEtb	MMfth2o[c] + MMatp[c] + MMavite1[c] -> MMadp[c] + MMfth[c] + MMpi[c] + MMavite1[b]	0	1000		Mouse secretion to outlet (body fluids)
MMAVITE2tb	MMavite2[b] -> MMavite2[c]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_avite2(e)b	MMavite2[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMBALAVECSECb	MMfth2o[c] + MMatp[c] + 3 MMala-B[c] -> MMadp[c] + MMfth[c] + MMpi[c] + 3 MMala-B[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_ala_B(e)b	MMala-B[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_bglc(e)b	MMbglc[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_glgchlo(e)b	MMglgchlo[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_glchco(e)b	MMglchco[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_glhdechol(e)b	MMglhdechol[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_hhb(e)b	MMhhb[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMBILDGLCURteb	MMfth2o[c] + MMatp[c] + MMbildglcur[c] <=> MMadp[c] + MMfth[c] + MMpi[c] + MMbildglcur[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_bildglcur(e)b	MMbildglcur[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMBILGLCURteb	MMfth2o[c] + MMatp[c] + MMbilglcur[c] <=> MMadp[c] + MMfth[c] + MMpi[c] + MMbilglcur[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_bilglcur(e)b	MMbilglcur[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_bilirub(e)b	MMbilirub[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_biocyt(e)b	MMbiocyt[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMBTNTeb	MMbtn[c] -> MMbtn[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_btn(e)b	MMbtn[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_but(e)b	MMbut[b] <=>	0	1000		Mouse secretion to outlet (body fluids)

MMBVITEtb	MMbvite[b] -> MMbvite[c]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_bvite(e)b	MMbvite[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMBZtb	MMbz[b] <=> MMbz[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_bz(e)b	MMbz[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_ca2(e)b	MMca2[b] <=>	-100	1000		Mouse secretion to outlet (body fluids)
MMCAMPtb	MMh2o[c] + MMatp[c] + MMcamp[c] -> MMadp[c] + MMh[c] + MMpi[c] + MMcamp[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_camp(e)b	MMcamp[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMCAROtrb	MMcaro[b] <=> MMcaro[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_caro(e)b	MMcaro[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMCARVEOLteb	MMcarveol[b] <=> MMcarveol[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_carveol(e)b	MMcarveol[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMCBLTDe_rb	MMadocbl[c] <=> MMadocbl[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_adocbl(e)b	MMadocbl[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMCCA_D3tb	MMcca_d3[c] -> MMcca_d3[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_cca_d3(e)b	MMcca_d3[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMCGMPtb	MMh2o[c] + MMatp[c] + MM35cgmp[c] -> MMadp[c] + MMh[c] + MMpi[c] + MM35cgmp[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_35cgmp(e)b	MM35cgmp[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMCHOLABCAetb	MMh2o[c] + MMatp[c] + MMchsterol[c] -> MMadp[c] + MMh[c] + MMpi[c] + MMchsterol[b]	0	1000		Mouse secretion to outlet (body fluids)
MMCHOLESTTDeb	MMchsterol[c] -> MMchsterol[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_chsterol(e)b	MMchsterol[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMLCAT1eb	MMchsterol[b] + MMpchol_hs[b] -> MMlpchol_hs[b] + MMxolest2_hs[b]	0	1000		Mouse secretion to outlet (body fluids)
MMCHOLATE3b	MMh2o[c] + MMatp[c] + MMcholate[c] -> MMadp[c] + MMh[c] + MMpi[c] + MMcholate[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_cholate(e)b	MMcholate[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_c1tn(e)b	MMc1tn[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_acgam(e)b	MMacgam[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_ci(e)b	MMci[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMCLFORtexb	2 MMfor[c] + MMcl[b] -> MMcl[c] + 2 MMfor[b]	0	1000		Mouse secretion to outlet (body fluids)
MMCLFORtex2b	MMfor[c] + 2 MMcl[b] -> 2 MMcl[c] + MMfor[b]	0	1000		Mouse secretion to outlet (body fluids)
MMCLI2texb	2 MMI[c] + MMcl[b] -> MMcl[c] + 2 MMI[b]	0	1000		Mouse secretion to outlet (body fluids)
MMCLOXAtex2b	MMoxa[c] + 2 MMcl[b] -> 2 MMcl[c] + MMoxa[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_cl(e)b	MMcl[b] <=>	-100	1000		Mouse secretion to outlet (body fluids)
MMSO4CLtex2b	MMcl[c] + 2 MMso4[b] -> 2 MMso4[c] + MMcl[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_for(e)b	MMfor[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_i(e)b	MMi[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMItb	MMi[b] <=> MMi[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_oxa(e)b	MMoxa[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMSO4OXAtex2b	MMoxa[c] + 2 MMso4[b] -> 2 MMso4[c] + MMoxa[b]	0	1000		Mouse secretion to outlet (body fluids)
MMCLPNDtb	MMclpnd[b] <=> MMclpnd[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_CLPND(e)b	MMclpnd[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMCO2tb	MMco2[b] <=> MMco2[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_co2(e)b	MMco2[b] <=>	-100	1000		Mouse secretion to outlet (body fluids)
MMCORE4tb	MMcore4[g] -> MMcore4[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_core4(e)b	MMcore4[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMCORE5tb	MMcore5[g] -> MMcore5[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_core5(e)b	MMcore5[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMCORE7tb	MMcore7[g] -> MMcore7[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_core7(e)b	MMcore7[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMCORE8tb	MMcore8[g] -> MMcore8[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_core8(e)b	MMcore8[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMCOUMARINteb	MMcoumarin[b] <=> MMcoumarin[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_coumarin(e)b	MMcoumarin[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMCOtb	MMco[c] <=> MMco[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_co(e)b	MMco[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_creat(e)b	MMcreat[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMCRMPteb	MMcrmp_hs[c] <=> MMcrmp_hs[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_crmp_hs(e)b	MMcrmp_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMCRNtb	MMcrn[b] <=> MMcrn[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_crn(e)b	MMcrn[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMCRTSLtb	MMcrtsl[b] <=> MMcrtsl[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_crtsl(e)b	MMcrtsl[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMCRTSTRNtb	MMcrtstrn[b] <=> MMcrtstrn[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_crtstrn(e)b	MMcrtstrn[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMCRVNCtrb	MMcrvnc[b] <=> MMcrvnc[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_crvnc(e)b	MMcrvnc[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMCSNtb	MMcsn[b] <=> MMcsn[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_csn(e)b	MMcsn[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMCSPG_Atb	MMcspg_a[g] -> MMcspg_a[b]	0	1000		Mouse secretion to outlet (body fluids)
MMCSPG_Atlyb	MMcspg_a[b] -> MMcspg_a[l]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_cspg_a(e)b	MMcspg_a[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMCSPG_Btb	MMcspg_b[g] -> MMcspg_b[b]	0	1000		Mouse secretion to outlet (body fluids)
MMCSPG_Btlyb	MMcspg_b[b] -> MMcspg_b[l]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_cspg_b(e)b	MMcspg_b[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMCSPG_Ctb	MMcspg_c[g] -> MMcspg_c[b]	0	1000		Mouse secretion to outlet (body fluids)
MMCSPG_Ctlyb	MMcspg_c[b] -> MMcspg_c[l]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_cspg_c(e)b	MMcspg_c[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMCSPG_Dtb	MMcspg_d[g] -> MMcspg_d[b]	0	1000		Mouse secretion to outlet (body fluids)
MMCSPG_Dtlyb	MMcspg_d[b] -> MMcspg_d[l]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_cspg_d(e)b	MMcspg_d[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMCSPG_Etb	MMcspg_e[g] -> MMcspg_e[b]	0	1000		Mouse secretion to outlet (body fluids)
MMCSPG_Etlyb	MMcspg_e[b] -> MMcspg_e[l]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_cspg_e(e)b	MMcspg_e[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMCYANtb	MMcyan[b] <=> MMcyan[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_cyan(e)b	MMcyan[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMCYSTGLUexb	MMglu-L[c] + MMLcystin[b] -> MMLcystin[c] + MMglu-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_Lcystin(e)b	MMLcystin[b] <=>	0	1000		Mouse secretion to outlet (body fluids)

MMEX_glu_L(e)b	MMglu-L[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMCYTDtb	MMcytd[b] <=> MMcytd[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_cytd(e)b	MMcytd[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMDADNt4b	MMdad-2[b] <=> MMdad-2[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_dad_2(e)b	MMdad-2[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMDINtb	MMdin[b] <=> MMdin[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_din(e)b	MMdin[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMDAGtb	MMdag_hs[b] <=> MMdag_hs[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_dag_hs(e)b	MMdag_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMDCSPTN1tb	MMdcsptn1[b] <=> MMdcsptn1[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_dcsptn1(e)b	MMdcsptn1[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMDCYTtb	MMdcyt[b] <=> MMdcyt[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_dcyt(e)b	MMdcyt[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMDEBRISOQUINEtb	MMdebrisoquine[b] <=> MMdebrisoquine[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_debrisoquine(e)b	MMdebrisoquine[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMDGCHOLtetb	MMdgchol[b] <=> MMdgchol[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_dgchol(e)b	MMdgchol[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMDGSNtb	MMdgsn[b] <=> MMdgsn[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_dgsn(e)b	MMdgsn[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMDHAAt1rb	MMdhdascb[b] <=> MMdhdascb[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_dhdascb(e)b	MMdhdascb[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMDIGALSGALSIDEteb	MMdigalsgalside_hs[c] <=> MMdigalsgalside_hs[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_digalsgalside_hs(e)b	MMdigalsgalside_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMDLNLCGtb	MMdlnlcg[b] <=> MMdlnlcg[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_dlnlcg(e)b	MMdlnlcg[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMDMANTIPYRINEteb	MMdmantipyrine[b] <=> MMdmantipyrine[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_dmantipyrine(e)b	MMdmantipyrine[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMDMHPTCRNteb	MMdmhptcrn[c] <=> MMdmhptcrn[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_dmhptcrn(e)b	MMdmhptcrn[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMDOPASFtb	MMdopasf[c] -> MMdopasf[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_dopasf(e)b	MMdopasf[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMDOPAVESSECb	2 MMfb2o[c] + 2 MMatp[c] + 3 MMdopa[c] -> 2 MMadp[c] + 2 MMh[c] + 2 MMpi[c] + 3 MMdopa[b]	0	1000		Mouse secretion to outlet (body fluids)
MMDOPAtub	MMdopa[b] <=> MMdopa[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_dopa(e)b	MMdopa[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMDRIBtb	MMdrib[b] <=> MMdrib[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_drib(e)b	MMdrib[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMDST_ANTIGENtb	MMdsT_antigen[g] -> MMdsT_antigen[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_dsT_antigen(e)b	MMdsT_antigen[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMDURItb	MMduri[b] <=> MMduri[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_duri(e)b	MMduri[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMD_3AIBtb	MM3aib-D[c] -> MM3aib-D[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_3aib_D(e)b	MM3aib-D[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_lac_D(e)b	MMlac-D[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEAFLATOXINteb	MMeaflatoxin[b] <=> MMeaflatoxin[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_eaflatoxin(e)b	MMeaflatoxin[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEBASTINEOHteb	MMebastineoh[b] <=> MMebastineoh[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_ebastineoh(e)b	MMebastineoh[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEBASTINEteb	MMebastine[b] <=> MMebastine[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_ebastine(e)b	MMebastine[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEICOSTETtb	MMeicostet[b] <=> MMeicostet[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_eicostet(e)b	MMeicostet[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMELAIDtb	MMelaid[b] <=> MMelaid[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_elaid(e)b	MMelaid[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMESTRADIOLGLCt2b	MMfb2o[c] + MMatp[c] + MMestradiolglc[c] -> MMadp[c] + MMh[c] + MMpi[c] + MMestradiolglc[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_estradiolglc(e)b	MMestradiolglc[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMESTRADIOLtb	MMestradiol[b] <=> MMestradiol[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_estradiol(e)b	MMestradiol[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMESTRIOLGLCteb	MMfb2o[c] + MMatp[c] + MMestriolglc[c] -> MMadp[c] + MMh[c] + MMpi[c] + MMestriolglc[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_estriolglc(e)b	MMestriolglc[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMESTRONEGLCtb	MMfb2o[c] + MMatp[c] + MMestronegk[c] -> MMadp[c] + MMh[c] + MMpi[c] + MMestronegk[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_estronegk(e)b	MMestronegk[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_estrones(e)b	MMestrones[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMETHAtrb	MMetha[c] -> MMetha[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_etha(e)b	MMetha[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMETOHtb	MMetoh[b] <=> MMetoh[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_etoh(e)b	MMetoh[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_10thf(e)b	MM10thf[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_10thf5glu(e)b	MM10thf5glu[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_10thf6glu(e)b	MM10thf6glu[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_10thf7glu(e)b	MM10thf7glu[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_11_cis_retfa(e)b	MM11-cis-retfa[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMRETFAt2b	MM11-cis-retfa[c] -> MM11-cis-retfa[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_13_cis_retngk(e)b	MM13-cis-retngk[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMRETNGLCt2b	MM13-cis-retngk[c] -> MM13-cis-retngk[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_1glyc_hs(e)b	MM1glyc_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_34dhphe(e)b	MM34dhphe[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_4HPRO(e)b	MM4hpro_LT[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_4hphac(e)b	MM4hphac[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MM4HPACtrb	MM4hphac[c] <=> MM4hphac[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_5dhf(e)b	MM5dhf[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_5thf(e)b	MM5thf[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_6dhf(e)b	MM6dhf[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_6thf(e)b	MM6thf[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_7dhf(e)b	MM7dhf[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_7thf(e)b	MM7thf[b] <=>	0	1000		Mouse secretion to outlet (body fluids)

MMEX_9_cis_retfa(e)b	MM9-cis-retfa[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMRETFAt1b	MM9-cis-retfa[c] -> MM9-cis-retfa[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_Rtotal(e)b	MMRtotal[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMRTOTALtb	MMRtotal[b] <=> MMRtotal[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_Rtotal2(e)b	MMRtotal2[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMRTOTAL2tb	MMRtotal2[b] <=> MMRtotal2[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_Rtotal3(e)b	MMRtotal3[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMRTOTAL3tb	MMRtotal3[b] <=> MMRtotal3[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_Tyr_ggn(e)b	MMTyr-ggn[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_adprbp(e)b	MMadprbp[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_alaala(e)b	MMalaala[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_cam(e)b	MMcam[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_cmp(e)b	MMcmp[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_dad-5(e)b	MMdad-5[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_dheas(e)b	MMdheas[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_dhf(e)b	MMdhf[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_f1a(e)b	MMf1a[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMF1Atb	MMf1a[g] -> MMf1a[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_fe2(e)b	MMfe2[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMFE2tb	MMfe2[b] -> MMfe2[c]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_fe3(e)b	MMfe3[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_fol(e)b	MMfol[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_fru(e)b	MMfru[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_fuc13galacglcgal14acglcgalgluside_hs(e)b	MMfuc13galacglcgal14acglcgalgluside_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMFUC13GALACGLCGAL14ACGLCGALGLUSIDEteb	MMfuc13galacglcgal14acglcgalgluside_hs[b] <=> MMfuc13galacglcgal14acglcgalgluside_hs[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_fuc14galacglcgalgluside_hs(e)b	MMfuc14galacglcgalgluside_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMFUC14GALACGLCGALGLUSIDEteh	MMfuc14galacglcgalgluside_hs[b] <=> MMfuc14galacglcgalgluside_hs[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_fuc_L(e)b	MMfuc-L[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_fucacgalfucgalacglcgalgluside_hs(e)b	MMfucacgalfucgalacglcgalgluside_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMFUCACGALFUCGALACGLCGALGLUSIDEteb	MMfucacgalfucgalacglcgalgluside_hs[b] <=> MMfucacgalfucgalacglcgalgluside_hs[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_fucacngal14acglcgalgluside_hs(e)b	MMfucacngal14acglcgalgluside_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMFUCACNGAL14ACGLCGALGLUSIDEteb	MMfucacngal14acglcgalgluside_hs[b] <=> MMfucacngal14acglcgalgluside_hs[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_fucacngalacglcgalgluside_hs(e)b	MMfucacngalacglcgalgluside_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMFUCACNGALACGLCGALGLUSIDEteb	MMfucacngalacglcgalgluside_hs[b] <=> MMfucacngalacglcgalgluside_hs[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_fucfuc12gal14acglcgalgluside_hs(e)b	MMfucfuc12gal14acglcgalgluside_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMFUCFUC12GAL14ACGLCGALGLUSIDEteb	MMfucfuc12gal14acglcgalgluside_hs[b] <=> MMfucfuc12gal14acglcgalgluside_hs[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_fucfuc132galacglcgal14acglcgalgluside_hs(e)b	MMfucfuc132galacglcgal14acglcgalgluside_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMFUCFUC132GALACGLCGAL14ACGLCGALGLUSIDEteb	MMfucfuc132galacglcgal14acglcgalgluside_hs[b] <=> MMfucfuc132galacglcgal14acglcgalgluside_hs[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_fucfucfucgalacglc13galacglcgal14acglcgalgluside_hs(e)b	MMfucfucfucgalacglc13galacglcgal14acglcgalgluside_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMFUCFUCFUCGALACGLC13GALACGLCGAL14ACGLCGALGLUSIDEteb	MMfucfucfucgalacglc13galacglcgal14acglcgalgluside_hs[b] <=> MMfucfucfucgalacglc13galacglcgal14acglcgalgluside_hs[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_fucfucfucgalacglcgal14acglcgalgluside_hs(e)b	MMfucfucfucgalacglcgal14acglcgalgluside_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMFUCFUCFUCGALACGLCGAL14ACGLCGALGLUSIDEteb	MMfucfucfucgalacglcgal14acglcgalgluside_hs[b] <=> MMfucfucfucgalacglcgal14acglcgalgluside_hs[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_fucfucgalacglcgalgluside_hs(e)b	MMfucfucgalacglcgalgluside_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMFUCFUCGALACGLCGALGLUSIDEteb	MMfucfucgalacglcgalgluside_hs[b] <=> MMfucfucgalacglcgalgluside_hs[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_fucgal14acglcgalglusite_hs(e)b	MMfucgal14acglcgalgluside_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMFUCGAL14ACGLCGALGLUSIDEteb	MMfucgal14acglcgalgluside_hs[b] <=> MMfucgal14acglcgalgluside_hs[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_fucgalfucgalacglcgalgluside_hs(e)b	MMfucgalfucgalacglcgalgluside_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMFUCGALFUCGALACGLCGALGLUSIDEteb	MMfucgalfucgalacglcgalgluside_hs[b] <=> MMfucgalfucgalacglcgalgluside_hs[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_fucgalglbside_hs(e)b	MMfucgalglbside_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMFUCGALGBSIDEteb	MMfucgalglbside_hs[c] <=> MMfucgalglbside_hs[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_gal(e)b	MMgal[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMGAL1tb	MMgal[b] <=> MMgal[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_galacglcgalglbside_hs(e)b	MMgalacglcgalglbside_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMGALACGLCGALGBSIDEteb	MMgalacglcgalglbside_hs[c] <=> MMgalacglcgalglbside_hs[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_galam(e)b	MMgalam[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMGALAMtrb	MMgalam[b] <=> MMgalam[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_galfuc12gal14acglcgalglusite_hs(e)b	MMgalfuc12gal14acglcgalgluside_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMGALFUC12GAL14ACGLCGALGLUSIDEteb	MMgalfuc12gal14acglcgalgluside_hs[b] <=> MMgalfuc12gal14acglcgalgluside_hs[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_galfucgalacglcgal14acglcgalglusite_hs(e)b	MMgalfucgalacglcgal14acglcgalgluside_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMGALFUCGALACGLCGAL14ACGLCGALGLUSIDEteb	MMgalfucgalacglcgal14acglcgalgluside_hs[b] <=> MMgalfucgalacglcgal14acglcgalglusite_hs[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_galgalfucfucgalacglcgalacglcgal14acglcgalglusite_hs(e)b	MMgalgalfucfucgalacglcgalacglcgal14acglcgalglusite_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMGALGALFUCFUCGALACGLCGALACGLCGAL14ACGLCGALGLUSIDEteb	MMgalgalfucfucgalacglcgalacglcgal14acglcgalglusite_hs[b] <=> MMgalgalfucfucgalacglcgalacglcgal14acglcgalglusite_hs[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_galgalgalgalthcrm_hs(e)b	MMgalgalgalgalthcrm_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMGALGALGALTHCRMteb	MMgalgalgalgalthcrm_hs[c] <=> MMgalgalgalgalthcrm_hs[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_gam(e)b	MMgam[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMGAMt1rb	MMgam[b] <=> MMgam[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_gbside_hs(e)b	MMgbside_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMGBSIDEteb	MMgbside_hs[c] <=> MMgbside_hs[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_gchola(e)b	MMgchola[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMGCHOLAt3b	MMh2o[c] + MMatp[c] + MMgchola[c] -> MMadp[c] + MMh[c] + MMp[c] + MMgchola[b]	0	1000		Mouse secretion to outlet (body fluids)
MMGCHOLAteb	MMgchola[b] <=> MMgchola[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_gd1b2_hs(e)b	MMgd1b2_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMGD1B2teb	MMgd1b2_hs[c] <=> MMgd1b2_hs[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_gd1c_hs(e)b	MMgd1c_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMGD1Cteb	MMgd1c_hs[c] <=> MMgd1c_hs[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_gdchola(e)b	MMgdchola[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMGDCHOLAteb	MMgdchola[b] <=> MMgdchola[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_gdp(e)b	MMgdp[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_glcur(e)b	MMglcur[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMGLCURtrb	MMglcur[c] -> MMglcur[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_gluala(e)b	MMgluala[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMGGLUCTb	MMgluala[b] -> MMala-L[c] + MM5oxpro[c]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_glyb(e)b	MMglyb[b] <=>	0	1000		Mouse secretion to outlet (body fluids)

MMEX_glyc(e)b	MMglyc[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMGLYCtb	MMglyc[c] <=> MMglyc[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_glyc_S(e)b	MMglyc-S[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMGLYC_Stb	MMglyc-S[c] -> MMglyc-S[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_glygly(e)b	MMglygly[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_glygn5(e)b	MMglygn5[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_glyleu(e)b	MMglyleu[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_glyphe(e)b	MMglyphe[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_glypro(e)b	MMglypro[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_glysar(e)b	MMglysar[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_gmp(e)b	MMgmp[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_gncore1(e)b	MMgncore1[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMGNCORE1tb	MMgncore1[g] -> MMgncore1[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_gncore2(e)b	MMgncore2[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMGNCORE2tb	MMgncore2[g] -> MMgncore2[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_gp1c_hs(e)b	MMgp1c_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMGP1Ctetb	MMgp1c_hs[c] <=> MMgp1c_hs[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_gp1calpha_hs(e)b	MMgp1calpha_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMGP1CALPHAtetb	MMgp1calpha_hs[c] <=> MMgp1calpha_hs[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_gq1b_hs(e)b	MMgq1b_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMGQ1Btetb	MMgq1b_hs[c] <=> MMgq1b_hs[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_gq1balpha_hs(e)b	MMgq1balpha_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMGQ1BALPHAtetb	MMgq1balpha_hs[c] <=> MMgq1balpha_hs[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_gsn(e)b	MMgsn[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMGSNtb	MMgsn[b] <=> MMgsn[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_gt1a_hs(e)b	MMgt1a_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMGT1Atetb	MMgt1a_hs[c] <=> MMgt1a_hs[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_gthox(e)b	MMgthox[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_gthrd(e)b	MMgthrd[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_gtp(e)b	MMgtp[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_gua(e)b	MMgua[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMGUAtb	MMgua[b] <=> MMgua[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_gum(e)b	MMgum[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_gumdchac(e)b	MMgumdchac[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_gumgcho(e)b	MMgumgcho[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_gumtcho(e)b	MMgumtcho[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_h2o2(e)b	MMh2o2[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMH2O2tb	MMh2o2[b] <=> MMh2o2[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_ha(e)b	MMha[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMHAS2b	MMuacgam[c] + MMudpglcur[c] + MMha_pre1[b] -> 2 MMh[c] + 2 MMudp[c] + MMha[b]	0	1000		Mouse secretion to outlet (body fluids)
MMHAtlyb	MMha[b] -> MMha[l]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_ha_pre1(e)b	MMha_pre1[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMHAS1b	MMuacgam[c] + MMudpglcur[c] -> 2 MMH[c] + 2 MMudp[c] + MMha_pre1[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_hcoumarin(e)b	MMhcoumarin[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMHCOUMARINtetb	MMhcoumarin[b] <=> MMhcoumarin[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_hdca(e)b	MMhdca[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMHDCAtrb	MMhdca[b] <=> MMhdca[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_hdcea(e)b	MMhdcea[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMHDCEAtrb	MMhdcea[b] <=> MMhdcea[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_hestratriol(e)b	MMhestratriol[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMHESTRATRIOLtetb	MMhestratriol[c] <=> MMhestratriol[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_hexc(e)b	MMhexc[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMHEXCtb	MMhexc[b] <=> MMhexc[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_his_L(e)b	MMhis-L[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMHISCAT1b	MMhis-L[c] <=> MMhis-L[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMHISdDFb	MMhis-L[b] -> MMhis-L[c]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_hista(e)b	MMhista[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMHISTAVESSECb	2 MMh2o2[c] + 2 MMatp[c] + 3 MMhista[c] -> 2 MMadp[c] + 2 MMh[c] + 2 MMpi[c] + 3 MMhista[b]	0	1000		Mouse secretion to outlet (body fluids)
MMHISTAtub	MMhista[b] <=> MMhista[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_hom_L(e)b	MMhom-L[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_hpdca(e)b	MMhpdca[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMHPDCAtb	MMhpdca[b] <=> MMhpdca[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_hspg(e)b	MMhspg[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMHSPGtb	MMhspg[g] -> MMhspg[b]	0	1000		Mouse secretion to outlet (body fluids)
MMHSPGtlyb	MMhspg[b] -> MMhspg[l]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_htaxol(e)b	MMhtaxol[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMHTAXOLtetb	MMhtaxol[b] <=> MMhtaxol[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_hxan(e)b	MMhxan[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMHYXNtb	MMhxan[b] <=> MMhxan[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_idp(e)b	MMidp[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_imp(e)b	MMimp[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_inost(e)b	MMinost[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_ksi(e)b	MMksi[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMKSItb	MMksi[g] -> MMksi[b]	0	1000		Mouse secretion to outlet (body fluids)
MMKSItlyb	MMksi[b] -> MMksi[l]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_ksi_deg1(e)b	MMksi_deg1[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_ksii_core2(e)b	MMksii_core2[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMKSII_CORE2tb	MMksii_core2[g] -> MMksii_core2[b]	0	1000		Mouse secretion to outlet (body fluids)
MMKSII_CORE2tlyb	MMksii_core2[b] -> MMksii_core2[l]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_ksii_core4(e)b	MMksii_core4[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMKSII_CORE4tb	MMksii_core4[g] -> MMksii_core4[b]	0	1000		Mouse secretion to outlet (body fluids)
MMKSII_CORE4tlyb	MMksii_core4[b] -> MMksii_core4[l]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_lac_L(e)b	MMlac-L[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_lcts(e)b	MMlcts[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMLCTStgb	MMlcts[g] -> MMlcts[b]	0	1000		Mouse secretion to outlet (body fluids)

MMEX_leu_L(e)b	MMleu-L[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMLEUtecb	MMleu-L[b] <=> MMleu-L[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMMETLEUexb	MMleu-L[c] + MMmet-L[b] -> MMmet-L[c] + MMleu-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_leugly(e)b	MMleugly[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_leuktrA4(e)b	MMleuktrA4[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMLEUKTRA4tb	MMleuktrA4[b] <=> MMleuktrA4[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_leuktrB4(e)b	MMleuktrB4[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMLEUKTRB4tb	MMleuktrB4[b] <=> MMleuktrB4[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_leuktrC4(e)b	MMleuktrC4[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_leuktrD4(e)b	MMleuktrD4[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMLEUKTRD4tb	MMleuktrD4[b] <=> MMleuktrD4[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_leuktrE4(e)b	MMleuktrE4[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMLEUKTRE4tb	MMleuktrE4[b] <=> MMleuktrE4[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_leuktrF4(e)b	MMleuktrF4[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMLEUKTRF4tb	MMleuktrF4[b] <=> MMleuktrF4[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_leuleu(e)b	MMleuleu[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_lgnc(e)b	MMlgnc[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMLGNCtb	MMlgnc[b] <=> MMlgnc[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_limnen(e)b	MMlimnen[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMLIMNENteb	MMlimnen[b] <=> MMlimnen[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_lipoate(e)b	MMlipoate[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_lneldc(e)b	MMlneldc[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMLNELDCtb	MMlneldc[b] <=> MMlneldc[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_lnk(e)b	MMlnk[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMLNLCtb	MMlnlc[b] <=> MMlnlc[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_lnlnca(e)b	MMlnlnca[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMLNLNCAtb	MMlnlnca[b] <=> MMlnlnca[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_lnlncg(e)b	MMlnlncg[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMLNLNCGtb	MMlnlncg[b] <=> MMlnlncg[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_lpchol_hs(e)b	MMlpchol_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMLPCHOLtb	MMlpchol_hs[b] <=> MMlpchol_hs[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_mag_hs(e)b	MMmag_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMMAGtb	MMmag_hs[b] <=> MMmag_hs[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_malt(e)b	MMmalt[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMMALTt1rb	MMmalt[b] <=> MMmalt[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_maltttr(e)b	MMmaltttr[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_man(e)b	MMman[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMMANt1rb	MMman[b] <=> MMman[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_meoh(e)b	MMmeoh[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMMEOHt2b	MMmeoh[b] <=> MMmeoh[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_mepi(e)b	MMmepi[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMMEPIVESSteb	2 MMh2o[c] + 2 MMatp[c] + 3 MMmepi[c] -> 2 MMadp[c] + 2 MMit[c] + 2 MMpi[c] + 3 MMmrpi[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_mercplaccys(e)b	MMmercplaccys[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMMERCPLACCYStb	MMmercplaccys[c] -> MMmercplaccys[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_met_L(e)b	MMmet-L[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMMETtecb	MMmet-L[b] <=> MMmet-L[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_mqn10(e)b	MMmqn10[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMMK10tb	MMmqn10[c] <=> MMmqn10[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_mqn11(e)b	MMmqn11[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMMK11tb	MMmqn11[c] <=> MMmqn11[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_mqn7(e)b	MMmqn7[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMMK7tb	MMmqn7[c] <=> MMmqn7[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_mqn8(e)b	MMmqn8[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMMK8tb	MMmqn8[c] <=> MMmqn8[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_mqn9(e)b	MMmqn9[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMMK9tb	MMmqn9[c] <=> MMmqn9[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_mthgxd(e)b	MMmthgxd[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMMTHGXLtb	MMmthgxd[c] -> MMmthgxd[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_n2m2mmasn(e)b	MMn2m2mmasn[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMN2M2NMASNtb	MMn2m2mmasn[g] -> MMn2m2mmasn[b]	0	1000		Mouse secretion to outlet (body fluids)
MMN2M2NMASNtlyb	MMn2m2mmasn[b] -> MMn2m2mmasn[l]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_nac(e)b	MMnac[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMNACDeb	MMnac[c] -> MMnac[b]	0	1000		Mouse secretion to outlet (body fluids)
MMNACUPb	MMnac[b] -> MMnac[c]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_nad(e)b	MMnad[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_nadp(e)b	MMnadp[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_ncam(e)b	MMncam[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMNCAMDeb	MMncam[c] -> MMncam[b]	0	1000		Mouse secretion to outlet (body fluids)
MMNCAMUPb	MMncam[b] -> MMncam[c]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_nifedipine(e)b	MMnifedipine[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMNIFEDIPINEteb	MMnifedipine[b] <=> MMnifedipine[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_no(e)b	MMno[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMNOtb	MMno[b] <=> MMno[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_npthl(e)b	MMnpthl[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMNPTHLteb	MMnpthl[b] <=> MMnpthl[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_nrpphr(e)b	MMnrpphr[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMNRPPHRVESSECb	MMh2o[c] + MMatp[c] + MMnrpphr[c] -> MMadp[c] + 2 MMit[c] + MMpi[c] + MMnrpphr[b]	0	1000		Mouse secretion to outlet (body fluids)
MMNRPPHRtub	MMnrpphr[b] <=> MMnrpphr[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_nrpphrsf(e)b	MMnrpphrsf[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMNRPPHRSFtb	MMnrpphrsf[c] -> MMnrpphrsf[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_nrvnc(e)b	MMnrvnc[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMNRVNCtb	MMnrvnc[b] <=> MMnrvnc[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_o2(e)b	MMo2[b] <=>	-100	1000		Mouse secretion to outlet (body fluids)
MMO2tb	MMo2[b] <=> MMo2[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_o2s(e)b	MMo2s[b] <=>	0	1000		Mouse secretion to outlet (body fluids)

MMO2Stb	MMo2s[c] <=> MMo2s[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_oagt3_hs(e)b	MMoagt3_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMOAGD3teb	MMoagt3_hs[c] <=> MMoagt3_hs[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_oagt3_hs(e)b	MMoagt3_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMOAGT3teb	MMoagt3_hs[c] <=> MMoagt3_hs[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_ocdca(e)b	MMocdca[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMOCDCAtrb	MMocdca[b] <=> MMocdca[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_ocdcea(e)b	MMocdcea[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMOCDCEAtrb	MMocdcea[b] <=> MMocdcea[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_octa(e)b	MMocta[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMOCTAtb	MMocta[b] <=> MMocta[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_omeprazole(e)b	MMomeprazole[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMOMEPRAZOLEteb	MMomeprazole[b] <=> MMomeprazole[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_ompth(e)b	MMompth[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMONPTHLteb	MMompth[b] <=> MMompth[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_orn(e)b	MMorn[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMORNtb	MMorn[b] <=> MMorn[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_paf_hs(e)b	MMpaf_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMPAFtb	MMpaf_hs[b] <=> MMpaf_hs[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_pchol_hs(e)b	MMpchol_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMPCHOLHSTDeb	MMpchol_hs[c] -> MMpchol_hs[b]	0	1000		Mouse secretion to outlet (body fluids)
MMPCtb	MMh2o[c] + MMatp[c] + MMpchol_hs[c] <=> MMadp[c] + MMh[c] + MMpi[c] + MMpchol_hs[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_pe_hs(e)b	MMpe_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMPEFLIPtb	MMh2o[c] + MMatp[c] + MMpe_hs[b] -> MMadp[c] + MMh[c] + MMpi[c] + MMpe_hs[c]	0	1000		Mouse secretion to outlet (body fluids)
MMPEtb	MMpe_hs[b] <=> MMpe_hs[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_pect(e)b	MMpect[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_pectindchac(e)b	MMpectindchac[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_pectingchol(e)b	MMpectingchol[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_pectintchol(e)b	MMpectintchol[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_peplys(e)b	MMpeplys[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMPEPLYStmb	MMpeplys[b] <=> MMpeplys[n]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_perilly(e)b	MMperilly[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMPERILLYLteb	MMperilly[b] <=> MMperilly[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_pglyc_hs(e)b	MMpglyc_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMPGLYCtb	MMpglyc_hs[b] <=> MMpglyc_hs[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_pheacglu(e)b	MMpheacglu[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMPHEACGLNtb	MMpheacglu[c] <=> MMpheacglu[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_pheme(e)b	MMpheme[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMPHEMEtb	MMpheme[b] -> MMpheme[c]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_phyQ(e)b	MMphyQ[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMPHYQtb	MMh2o[c] + MMatp[c] + MMphyQ[b] -> MMadp[c] + MMh[c] + MMpi[c] + MMphyQ[c]	0	1000		Mouse secretion to outlet (body fluids)
MMVITKtlb	MMphyQ[c] -> MMphyQ[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_phyt(e)b	MMphyt[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMPHYTtb	MMphyt[b] <=> MMphyt[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_proto_R(e)b	MMproto-R[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMPNTORDeb	MMproto-R[c] -> MMproto-R[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_ppa(e)b	MMppa[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMPPAtb	MMppa[b] -> MMppa[c]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_prgstrn(e)b	MMprgstrn[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMPRGSTRNtb	MMprgstrn[b] <=> MMprgstrn[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_pro_D(e)b	MMpro-D[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_pro_L(e)b	MMpro-L[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_progly(e)b	MMprogly[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_prostgd2(e)b	MMprostgd2[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_prostge1(e)b	MMprostge1[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMPROSTGE1t3b	MMh2o[c] + MMatp[c] + MMprostge1[c] -> MMadp[c] + MMh[c] + MMpi[c] + MMprostge1[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_prostge2(e)b	MMprostge2[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMPROSTGE2t2b	MMprostge2[b] <=> MMprostge2[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMPROSTGE2t3b	MMh2o[c] + MMatp[c] + MMprostge2[c] -> MMadp[c] + MMh[c] + MMpi[c] + MMprostge2[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_prostgf2(e)b	MMprostgf2[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMPROSTGF2tb	MMprostgf2[b] <=> MMprostgf2[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_ps_hs(e)b	MMps_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMPSFLIPtb	MMh2o[c] + MMatp[c] + MMps_hs[b] -> MMadp[c] + MMh[c] + MMpi[c] + MMps_hs[c]	0	1000		Mouse secretion to outlet (body fluids)
MMPSt3b	MMps_hs[b] <=> MMps_hs[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_psyl(e)b	MMpsyl[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_psylchol(e)b	MMpsylchol[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_psyltchol(e)b	MMpsyltchol[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_psyltdechol(e)b	MMpsyltdechol[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_ptdca(e)b	MMptdca[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMPTDCAtb	MMptdca[b] <=> MMptdca[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_pydam(e)b	MMpydam[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMPYDAMtrb	MMpydam[b] <=> MMpydam[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_pydx(e)b	MMpydx[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMPYDXtrb	MMpydx[b] <=> MMpydx[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_pydxn(e)b	MMpydxn[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMPYDXNtrb	MMpydxn[b] <=> MMpydxn[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_pyr(e)b	MMpyr[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_rbt(e)b	MMrbt[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMRBTtb	MMrbt[c] -> MMrbt[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_retfa(e)b	MMretfa[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMRETFAtb	MMretfa[c] -> MMretfa[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_retinol(e)b	MMretinol[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMRETtb	MMretinol[b] -> MMretinol[c]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_retinol_9_cis(e)b	MMretinol-9-cis[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_retinol_cis_11(e)b	MMretinol-cis-11[b] <=>	0	1000		Mouse secretion to outlet (body fluids)

MMEX_retn(e)b	MMretn[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMRETNtb	MMretn[c] <=> MMretn[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_retngk(e)b	MMretngk[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMRETNGLCtb	MMretngk[c] -> MMretngk[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_rib_D(e)b	MMrib-D[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMRIBtb	MMrib-D[b] <=> MMrib-D[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_ribflv(e)b	MMribflv[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMRIBFLVCl3b	MMh2o[c] + MMatp[c] + MMribflv[b] -> MMadp[c] + MMh[c] + MMpi[c] + MMribflv[c]	0	1000		Mouse secretion to outlet (body fluids)
MMRIBFLVtrib	MMh2o[c] + MMatp[c] + MMribflv[c] -> MMadp[c] + MMh[c] + MMpi[c] + MMribflv[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_s2l2fn2m2masn(e)b	MMs2l2fn2m2masn[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMS2L2FN2M2MASNtb	MMs2l2fn2m2masn[g] -> MMs2l2fn2m2masn[b]	0	1000		Mouse secretion to outlet (body fluids)
MMS2L2FN2M2MASNtlyb	MMs2l2fn2m2masn[b] -> MMs2l2fn2m2masn[l]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_s2l2n2m2m(e)b	MMs2l2n2m2m[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMS2L2N2M2Mtb	MMs2l2n2m2m[l] <=> MMs2l2n2m2m[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_s2l2n2m2masn(e)b	MMs2l2n2m2masn[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMS2L2N2M2MASNtlyb	MMs2l2n2m2masn[b] -> MMs2l2n2m2masn[l]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_sTn_antigen(e)b	MMsTn_antigen[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMSTN_ANTIGENtb	MMsTn_antigen[g] -> MMsTn_antigen[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_sarcs(e)b	MMsarcs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMSARCStesb	MMsarcs[b] -> MMsarcs[c]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_sbt_D(e)b	MMsbt-D[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMSBTtb	MMsbt-D[b] <=> MMsbt-D[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_sel(e)b	MMsel[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_ser_D(e)b	MMser-D[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_sl_L(e)b	MMsl-L[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMSLDtb	MMsl-L[c] -> MMsl-L[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_so4(e)b	MMso4[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_spc_hs(e)b	MMspc_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMSPC_HStb	MMspc_hs[c] <=> MMspc_hs[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_sph1p(e)b	MMsph1p[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMSPH1Ptetb	MMsph1p[c] <=> MMsph1p[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_sphs1p(e)b	MMsphs1p[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMSPHS1Ptetb	MMsphs1p[c] <=> MMsphs1p[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_srtn(e)b	MMsrtn[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMSRTNtub	MMsrtn[b] <=> MMsrtn[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_strdnc(e)b	MMstrdnc[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMSTRDNCtb	MMstrdnc[b] <=> MMstrdnc[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_succ(e)b	MMsucc[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_sucr(e)b	MMsucr[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_tag_hs(e)b	MMtag_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMTAGHSTDeb	MMtag_hs[c] -> MMtag_hs[b]	0	1000		Mouse secretion to outlet (body fluids)
MMTAGtb	MMtag_hs[b] <=> MMtag_hs[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_tagat_D(e)b	MMtagat-D[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMTAGAT_Dtb	MMtagat-D[b] -> MMtagat-D[c]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_taur(e)b	MMtaur[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_taxol(e)b	MMtaxol[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMTAXOLteb	MMtaxol[b] <=> MMtaxol[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_tchola(e)b	MMtchola[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMTCHOLAtCl3b	MMh2o[c] + MMatp[c] + MMtchola[c] -> MMadp[c] + MMh[c] + MMpi[c] + MMtchola[b]	0	1000		Mouse secretion to outlet (body fluids)
MMTCHOLAteb	MMtchola[b] <=> MMtchola[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_tcynt(e)b	MMtcynt[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMTCYNTtb	MMtcynt[c] -> MMtcynt[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_tdchola(e)b	MMtdchola[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMTDCHOLAteb	MMtdchola[b] <=> MMtdchola[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_tdechola(e)b	MMtdechola[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMTDECHOLAtb	MMtdechola[b] <=> MMtdechola[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_tethex3(e)b	MMtethex3[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMTETHEX3tb	MMtethex3[b] <=> MMtethex3[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_tetpent3(e)b	MMtetpent3[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMTETPENT3tb	MMtetpent3[b] <=> MMtetpent3[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_tetpent6(e)b	MMtetpent6[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMTETPENT6tb	MMtetpent6[b] <=> MMtetpent6[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_tetter6(e)b	MMtetter6[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMTETTET6tb	MMtetter6[b] <=> MMtetter6[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_thf(e)b	MMthf[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_thm(e)b	MMthm[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMTHMATPeb	MMh2o[c] + MMatp[c] + MMthm[c] -> MMadp[c] + MMh[c] + MMpi[c] + MMthm[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_thmmp(e)b	MMthmmp[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_thmtp(e)b	MMthmtp[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_thym(e)b	MMthym[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMTHYMtb	MMthym[b] <=> MMthym[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_thymd(e)b	MMthymd[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMTHYMDc1b	MMthymd[b] -> MMthymd[c]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_thyox_L(e)b	MMthyox-L[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMTHYOXt2b	MMthyox-L[b] <=> MMthyox-L[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_tmndnc(e)b	MMtmndnc[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMTMNDNCtb	MMtmndnc[b] <=> MMtmndnc[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_tolbutamide(e)b	MMtolbutamide[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMTOLBUTAMIDEteb	MMtolbutamide[b] <=> MMtolbutamide[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_tre(e)b	MMtre[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_triodthy(e)b	MMtriodthy[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMTRIODTHYt2b	MMtriodthy[b] <=> MMtriodthy[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_triodthysuf(e)b	MMtriodthysuf[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMTRIODTHYSUFtb	MMtriodthysuf[c] -> MMtriodthysuf[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_trp_L(e)b	MMtrp-L[b] <=>	0	1000		Mouse secretion to outlet (body fluids)

MMEX_tststerone(e)b	MMtststerone[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMTSTSTERONEtb	MMtststerone[b] <=> MMtststerone[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_tststeronegk(e)b	MMtststeronegk[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMTSTSTERONEGLCteb	MMtb2o[c] + MMasp[c] + MMtststeronegk[c] -> MMasdp[c] + MMtb[c] + MMpi[c] + MMtststeronegk[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_tststerones(e)b	MMtststerones[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMTSTSTERONEStеb	MMtststerones[c] <=> MMtststerones[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_tsul(e)b	MMtsul[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_ttdca(e)b	MMttdca[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMTTDCAtb	MMttdca[b] -> MMttdca[c]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_txa2(e)b	MMtxa2[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMTXA2teb	MMtxa2[b] <=> MMtxa2[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_tymsf(e)b	MMtymsf[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMTYMSFtb	MMtymsf[c] -> MMtymsf[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_tyr_L(e)b	MMtyr-L[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_udp(e)b	MMudp[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_ump(e)b	MMump[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_ura(e)b	MMura[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMURAtb	MMura[b] <=> MMura[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_urate(e)b	MMurate[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMURATEtb	MMurate[c] -> MMurate[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_urea(e)b	MMurea[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMUREAtb	MMurea[b] <=> MMurea[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_uri(e)b	MMuri[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMURItb	MMuri[b] <=> MMuri[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_utp(e)b	MMutp[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMEX_vacc(e)b	MMvacc[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMVACCtb	MMvacc[b] <=> MMvacc[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_val_L(e)b	MMval-L[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMVALtecb	MMval-L[b] <=> MMval-L[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_vitd2(e)b	MMvitd2[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMVITD2tb	MMvitd2[c] -> MMvitd2[b]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_vitd3(e)b	MMvitd3[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMVITD3Teb	MMvitd3[c] <=> MMvitd3[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMVITD3tc2b	MMvitd3[b] -> MMvitd3[c]	0	1000		Mouse secretion to outlet (body fluids)
MMEX_whddca(e)b	MMwhddca[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMWHDDCAteb	MMwhddca[b] <=> MMwhddca[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_whhdca(e)b	MMwhhdca[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMWHHDCAteb	MMwhhdca[b] <=> MMwhhdca[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_whtststerone(e)b	MMwhtststerone[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMWHTSTSTERONEteb	MMwhtststerone[c] <=> MMwhtststerone[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_whttdca(e)b	MMwhttdca[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMWHTTDCAteb	MMwhttdca[b] <=> MMwhttdca[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_xolest2_hs(e)b	MMxolest2_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMXOLEST2HSTDtub	MMxolest2_hs[c] -> MMxolest2_hs[b]	0	1000		Mouse secretion to outlet (body fluids)
MMXOLEST2teb	MMxolest2_hs[b] <=> MMxolest2_hs[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_xolest_hs(e)b	MMxolest_hs[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMXOLESTteb	MMxolest_hs[b] <=> MMxolest_hs[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_xoltri24(e)b	MMxoltri24[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMXOLTRI24teb	MMxoltri24[c] <=> MMxoltri24[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_xoltri25(e)b	MMxoltri25[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMXOLTRI25teb	MMxoltri25[c] <=> MMxoltri25[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_xoltri27(e)b	MMxoltri27[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMXOLTRI27teb	MMxoltri27[c] <=> MMxoltri27[b]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_xyl_D(e)b	MMxyl-D[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMXYLtb	MMxyl-D[b] <=> MMxyl-D[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_xylt(e)b	MMxylt[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMXYLTtb	MMxylt[b] <=> MMxylt[c]	-1000	1000		Mouse secretion to outlet (body fluids)
MMEX_yvite(e)b	MMyvite[b] <=>	0	1000		Mouse secretion to outlet (body fluids)
MMYVITEtb	MMyvite[b] -> MMyvite[c]	0	1000		Mouse secretion to outlet (body fluids)
MM1mncam[u]tr	MM1mncam[e] <=> 1mncam[u]	0	0		Internal exchange reaction mouse <=> lumen
MM24nph[u]tr	MM24nph[e] <=> 24nph[u]	0	0		Internal exchange reaction mouse <=> lumen
MM2425dhvitd2[u]tr	MM2425dhvitd2[e] <=> 2425dhvitd2[u]	0	0		Internal exchange reaction mouse <=> lumen
MM2425dhvitd3[u]tr	MM2425dhvitd3[e] <=> 2425dhvitd3[u]	0	0		Internal exchange reaction mouse <=> lumen
MM25hvitd2[u]tr	MM25hvitd2[e] <=> 25hvitd2[u]	0	0		Internal exchange reaction mouse <=> lumen
MM25hvitd3[u]tr	MM25hvitd3[e] <=> 25hvitd3[u]	0	0		Internal exchange reaction mouse <=> lumen
MM2hb[u]tr	MM2hb[e] <=> 2hb[u]	0	0		Internal exchange reaction mouse <=> lumen
MMh[u]tr	MMh[e] <=> h[u]	0	0		Internal exchange reaction mouse <=> lumen
MMhco3[u]tr	MMhco3[e] <=> hco3[u]	0	0		Internal exchange reaction mouse <=> lumen
MMna1[u]tr	MMna1[e] <=> na1[u]	0	0		Internal exchange reaction mouse <=> lumen
MM2mcit[u]tr	MM2mcit[e] <=> 2mcit[u]	0	0		Internal exchange reaction mouse <=> lumen
MM34dhoxpeg[u]tr	MM34dhoxpeg[e] <=> 34dhoxpeg[u]	0	0		Internal exchange reaction mouse <=> lumen
MM3aib[u]tr	MM3aib[e] <=> 3aib[u]	0	0		Internal exchange reaction mouse <=> lumen
MM3mlda[u]tr	MM3mlda[e] <=> 3mlda[u]	0	0		Internal exchange reaction mouse <=> lumen
MM4hdebrisoquine[u]tr	MM4hdebrisoquine[e] <=> 4hdebrisoquine[u]	0	0		Internal exchange reaction mouse <=> lumen
MM4hpro-LT[u]tr	MM4hpro-LT[e] <=> 4hpro-LT[u]	0	0		Internal exchange reaction mouse <=> lumen
MM4mptn[u]tr	MM4mptn[e] <=> 4mptn[u]	0	0		Internal exchange reaction mouse <=> lumen
MM4mtolbutamide[u]tr	MM4mtolbutamide[e] <=> 4mtolbutamide[u]	0	0		Internal exchange reaction mouse <=> lumen
MM4nphs[u]tr	MM4nphs[e] <=> 4nphs[u]	0	0		Internal exchange reaction mouse <=> lumen
MM4nph[u]tr	MM4nph[e] <=> 4nph[u]	0	0		Internal exchange reaction mouse <=> lumen
MM4pyrdx[u]tr	MM4pyrdx[e] <=> 4pyrdx[u]	0	0		Internal exchange reaction mouse <=> lumen
MM5adtststeronegk[u]tr	MM5adtststeronegk[e] <=> 5adtststeronegk[u]	0	0		Internal exchange reaction mouse <=> lumen
MM5adtststerones[u]tr	MM5adtststerones[e] <=> 5adtststerones[u]	0	0		Internal exchange reaction mouse <=> lumen
MM5adtststerone[u]tr	MM5adtststerone[e] <=> 5adtststerone[u]	0	0		Internal exchange reaction mouse <=> lumen
MM5thf[u]tr	MM5thf[e] <=> 5thf[u]	0	0		Internal exchange reaction mouse <=> lumen
MMohi1[u]tr	MMohi1[e] <=> ohi1[u]	0	0		Internal exchange reaction mouse <=> lumen

MM5homeprazole[u]tr	MM5homeprazole[e] <=> 5homeprazole[u]	0	0		Internal exchange reaction mouse <=> lumen
MM5htrp[u]tr	MM5htrp[e] <=> 5htrp[u]	0	0		Internal exchange reaction mouse <=> lumen
MM5mthf[u]tr	MM5mthf[e] <=> 5mthf[u]	0	0		Internal exchange reaction mouse <=> lumen
MM6htststerone[u]tr	MM6htststerone[e] <=> 6htststerone[u]	0	0		Internal exchange reaction mouse <=> lumen
MMabt[u]tr	MMabt[e] <=> abt[u]	0	0		Internal exchange reaction mouse <=> lumen
MM4abut[u]tr	MM4abut[e] <=> 4abut[u]	0	0		Internal exchange reaction mouse <=> lumen
MMacac[u]tr	MMacac[e] <=> acac[u]	0	0		Internal exchange reaction mouse <=> lumen
MMacald[u]tr	MMacald[e] <=> acald[u]	0	0		Internal exchange reaction mouse <=> lumen
MMacetone[u]tr	MMacetone[e] <=> acetone[u]	0	0		Internal exchange reaction mouse <=> lumen
MMacgalfucgalacgalfuc12gal14acglcgalglukside_hs[u]tr	MMacgalfucgalacgalfuc12gal14acglcgalglukside_hs[e] <=> acgalfucgalacgalfuc12gal14acglcgalglukside_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMacgalfucgalacgalfucgalacglcgal14acglcgalglukside_hs[u]tr	MMacgalfucgalacgalfucgalacglcgal14acglcgalglukside_hs[e] <=> acgalfucgalacgalfucgalacglcgal14acglcgalglukside_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMacgal[u]tr	MMacgal[e] <=> acgal[u]	0	0		Internal exchange reaction mouse <=> lumen
MMach[u]tr	MMach[e] <=> ach[u]	0	0		Internal exchange reaction mouse <=> lumen
MMh2o[u]tr	MMh2o[e] <=> h2o[u]	0	0		Internal exchange reaction mouse <=> lumen
MMac[u]tr	MMac[e] <=> ac[u]	0	0		Internal exchange reaction mouse <=> lumen
MMchol[u]tr	MMchol[e] <=> chol[u]	0	0		Internal exchange reaction mouse <=> lumen
MMacn13acngalglxside_hs[u]tr	MMacn13acngalglxside_hs[e] <=> acn13acngalglxside_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMacn23acngalglxside_hs[u]tr	MMacn23acngalglxside_hs[e] <=> acn23acngalglxside_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMacnacngal14acglcgalglukside_hs[u]tr	MMacnacngal14acglcgalglukside_hs[e] <=> acnacngal14acglcgalglukside_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMacnacngalglxside_hs[u]tr	MMacnacngalglxside_hs[e] <=> acnacngalglxside_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMacnam[u]tr	MMacnam[e] <=> acnam[u]	0	0		Internal exchange reaction mouse <=> lumen
MMacngalacglcgal14acglcgalglukside_hs[u]tr	MMacngalacglcgal14acglcgalglukside_hs[e] <=> acngalacglcgal14acglcgalglukside_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMadn[u]tr	MMadn[e] <=> adn[u]	0	0		Internal exchange reaction mouse <=> lumen
MMins[u]tr	MMins[e] <=> ins[u]	0	0		Internal exchange reaction mouse <=> lumen
MMmbt4[u]tr	MMmbt4[e] <=> mbt4[u]	0	0		Internal exchange reaction mouse <=> lumen
MMade[u]tr	MMade[e] <=> ade[u]	0	0		Internal exchange reaction mouse <=> lumen
MMadprib[u]tr	MMadprib[e] <=> adprib[u]	0	0		Internal exchange reaction mouse <=> lumen
MMadrnl[u]tr	MMadrnl[e] <=> adrnl[u]	0	0		Internal exchange reaction mouse <=> lumen
MMadrn[u]tr	MMadrn[e] <=> adrn[u]	0	0		Internal exchange reaction mouse <=> lumen
MMaflatoxin[u]tr	MMaflatoxin[e] <=> aflatoxin[u]	0	0		Internal exchange reaction mouse <=> lumen
MMahandrostangk[u]tr	MMahandrostangk[e] <=> ahandrostangk[u]	0	0		Internal exchange reaction mouse <=> lumen
MMak2lgchol_hs[u]tr	MMak2lgchol_hs[e] <=> ak2lgchol_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMakg[u]tr	MMakg[e] <=> akg[u]	0	0		Internal exchange reaction mouse <=> lumen
MMala-L[u]tr	MMala-L[e] <=> ala-L[u]	0	0		Internal exchange reaction mouse <=> lumen
MMasn-L[u]tr	MMasn-L[e] <=> asn-L[u]	0	0		Internal exchange reaction mouse <=> lumen
MMcys-L[u]tr	MMcys-L[e] <=> cys-L[u]	0	0		Internal exchange reaction mouse <=> lumen
MMala-D[u]tr	MMala-D[e] <=> ala-D[u]	0	0		Internal exchange reaction mouse <=> lumen
MMglu-L[u]tr	MMglu-L[e] <=> glu-L[u]	0	0		Internal exchange reaction mouse <=> lumen
MMgly[u]tr	MMgly[e] <=> gly[u]	0	0		Internal exchange reaction mouse <=> lumen
MMile-L[u]tr	MMile-L[e] <=> ile-L[u]	0	0		Internal exchange reaction mouse <=> lumen
MMphe-L[u]tr	MMphe-L[e] <=> phe-L[u]	0	0		Internal exchange reaction mouse <=> lumen
MMser-L[u]tr	MMser-L[e] <=> ser-L[u]	0	0		Internal exchange reaction mouse <=> lumen
MMthr-L[u]tr	MMthr-L[e] <=> thr-L[u]	0	0		Internal exchange reaction mouse <=> lumen
MMarg-L[u]tr	MMarg-L[e] <=> arg-L[u]	0	0		Internal exchange reaction mouse <=> lumen
MMaldstrn[u]tr	MMaldstrn[e] <=> aldstrn[u]	0	0		Internal exchange reaction mouse <=> lumen
MMcgly[u]tr	MMcgly[e] <=> cgly[u]	0	0		Internal exchange reaction mouse <=> lumen
MMstrch1[u]tr	MMstrch1[e] <=> strch1[u]	0	0		Internal exchange reaction mouse <=> lumen
MMglc-D[u]tr	MMglc-D[e] <=> glc-D[u]	0	0		Internal exchange reaction mouse <=> lumen
MMstrch2[u]tr	MMstrch2[e] <=> strch2[u]	0	0		Internal exchange reaction mouse <=> lumen
MMglygn2[u]tr	MMglygn2[e] <=> glygn2[u]	0	0		Internal exchange reaction mouse <=> lumen
MMglygs4[u]tr	MMglygs4[e] <=> glygs4[u]	0	0		Internal exchange reaction mouse <=> lumen
MMandrstrngk[u]tr	MMandrstrngk[e] <=> andrstrngk[u]	0	0		Internal exchange reaction mouse <=> lumen
MMandrstrn[u]tr	MMandrstrn[e] <=> andrstrn[u]	0	0		Internal exchange reaction mouse <=> lumen
MMantipyrene[u]tr	MMantipyrene[e] <=> antipyrene[u]	0	0		Internal exchange reaction mouse <=> lumen
MMapnnox[u]tr	MMapnnox[e] <=> apnnox[u]	0	0		Internal exchange reaction mouse <=> lumen
MMappnn[u]tr	MMappnn[e] <=> appnn[u]	0	0		Internal exchange reaction mouse <=> lumen
MMaprgstrn[u]tr	MMaprgstrn[e] <=> aprgstrn[u]	0	0		Internal exchange reaction mouse <=> lumen
MMaqcoba[u]tr	MMaqcoba[e] <=> aqcoba[u]	0	0		Internal exchange reaction mouse <=> lumen
MMarab-L[u]tr	MMarab-L[e] <=> arab-L[u]	0	0		Internal exchange reaction mouse <=> lumen
MMarachd[u]tr	MMarachd[e] <=> arachd[u]	0	0		Internal exchange reaction mouse <=> lumen
MMarach[u]tr	MMarach[e] <=> arach[u]	0	0		Internal exchange reaction mouse <=> lumen
MMlys-L[u]tr	MMlys-L[e] <=> lys-L[u]	0	0		Internal exchange reaction mouse <=> lumen
MMascb-L[u]tr	MMascb-L[e] <=> ascb-L[u]	0	0		Internal exchange reaction mouse <=> lumen
MMasp-D[u]tr	MMasp-D[e] <=> asp-D[u]	0	0		Internal exchange reaction mouse <=> lumen
MMk[u]tr	MMk[e] <=> k[u]	0	0		Internal exchange reaction mouse <=> lumen
MMasp-L[u]tr	MMasp-L[e] <=> asp-L[u]	0	0		Internal exchange reaction mouse <=> lumen
MMatp[u]tr	MMatp[e] <=> atp[u]	0	0		Internal exchange reaction mouse <=> lumen
MMamp[u]tr	MMamp[e] <=> amp[u]	0	0		Internal exchange reaction mouse <=> lumen
MMpi[u]tr	MMpi[e] <=> pi[u]	0	0		Internal exchange reaction mouse <=> lumen
MMadp[u]tr	MMadp[e] <=> adp[u]	0	0		Internal exchange reaction mouse <=> lumen
MMavite1[u]tr	MMavite1[e] <=> avite1[u]	0	0		Internal exchange reaction mouse <=> lumen
MMavite2[u]tr	MMavite2[e] <=> avite2[u]	0	0		Internal exchange reaction mouse <=> lumen
MMala-B[u]tr	MMala-B[e] <=> ala-B[u]	0	0		Internal exchange reaction mouse <=> lumen
MMbglc[u]tr	MMbglc[e] <=> bglc[u]	0	0		Internal exchange reaction mouse <=> lumen
MMglgchlo[u]tr	MMglgchlo[e] <=> glgchlo[u]	0	0		Internal exchange reaction mouse <=> lumen
MMglchco[u]tr	MMglchco[e] <=> glchco[u]	0	0		Internal exchange reaction mouse <=> lumen
MMgldechol[u]tr	MMgldechol[e] <=> gldechol[u]	0	0		Internal exchange reaction mouse <=> lumen
MMbhb[u]tr	MMbhb[e] <=> bhb[u]	0	0		Internal exchange reaction mouse <=> lumen
MMbildglcur[u]tr	MMbildglcur[e] <=> bildglcur[u]	0	0		Internal exchange reaction mouse <=> lumen
MMbilglcur[u]tr	MMbilglcur[e] <=> bilglcur[u]	0	0		Internal exchange reaction mouse <=> lumen
MMbilirub[u]tr	MMbilirub[e] <=> bilirub[u]	0	0		Internal exchange reaction mouse <=> lumen
MMbiocyt[u]tr	MMbiocyt[e] <=> biocyt[u]	0	0		Internal exchange reaction mouse <=> lumen
MMbtn[u]tr	MMbtn[e] <=> btn[u]	0	0		Internal exchange reaction mouse <=> lumen
MMbut[u]tr	MMbut[e] <=> but[u]	0	0		Internal exchange reaction mouse <=> lumen

MMbvite[u]tr	MMbvite[e] <=> bvite[u]	0	0		Internal exchange reaction mouse <=> lumen
MMbz[u]tr	MMbz[e] <=> bz[u]	0	0		Internal exchange reaction mouse <=> lumen
MMca2[u]tr	MMca2[e] <=> ca2[u]	0	0		Internal exchange reaction mouse <=> lumen
MMcamp[u]tr	MMcamp[e] <=> camp[u]	0	0		Internal exchange reaction mouse <=> lumen
MMcaro[u]tr	MMcaro[e] <=> caro[u]	0	0		Internal exchange reaction mouse <=> lumen
MMcarveol[u]tr	MMcarveol[e] <=> carveol[u]	0	0		Internal exchange reaction mouse <=> lumen
MMadocbl[u]tr	MMadocbl[e] <=> adocbl[u]	0	0		Internal exchange reaction mouse <=> lumen
MMcca_d3[u]tr	MMcca_d3[e] <=> cca_d3[u]	0	0		Internal exchange reaction mouse <=> lumen
MM35cgmp[u]tr	MM35cgmp[e] <=> 35cgmp[u]	0	0		Internal exchange reaction mouse <=> lumen
MMchstero[u]tr	MMchstero[e] <=> chstero[u]	0	0		Internal exchange reaction mouse <=> lumen
MMcholate[u]tr	MMcholate[e] <=> cholate[u]	0	0		Internal exchange reaction mouse <=> lumen
MMchtn[u]tr	MMchtn[e] <=> chtn[u]	0	0		Internal exchange reaction mouse <=> lumen
MMacgam[u]tr	MMacgam[e] <=> acgam[u]	0	0		Internal exchange reaction mouse <=> lumen
MMcit[u]tr	MMcit[e] <=> cit[u]	0	0		Internal exchange reaction mouse <=> lumen
MMcl[u]tr	MMcl[e] <=> cl[u]	0	0		Internal exchange reaction mouse <=> lumen
MMfor[u]tr	MMfor[e] <=> for[u]	0	0		Internal exchange reaction mouse <=> lumen
MMf[u]tr	MMf[e] <=> f[u]	0	0		Internal exchange reaction mouse <=> lumen
MMoxa[u]tr	MMoxa[e] <=> oxa[u]	0	0		Internal exchange reaction mouse <=> lumen
MMclpnd[u]tr	MMclpnd[e] <=> clpnd[u]	0	0		Internal exchange reaction mouse <=> lumen
MMco2[u]tr	MMco2[e] <=> co2[u]	0	0		Internal exchange reaction mouse <=> lumen
MMcore4[u]tr	MMcore4[e] <=> core4[u]	-1000	1000		Internal exchange reaction mouse <=> lumen
MMcore5[u]tr	MMcore5[e] <=> core5[u]	-1000	1000		Internal exchange reaction mouse <=> lumen
MMcore7[u]tr	MMcore7[e] <=> core7[u]	-1000	1000		Internal exchange reaction mouse <=> lumen
MMcore8[u]tr	MMcore8[e] <=> core8[u]	-1000	1000		Internal exchange reaction mouse <=> lumen
MMcoumarin[u]tr	MMcoumarin[e] <=> coumarin[u]	0	0		Internal exchange reaction mouse <=> lumen
MMco[u]tr	MMco[e] <=> co[u]	0	0		Internal exchange reaction mouse <=> lumen
MMcreat[u]tr	MMcreat[e] <=> creat[u]	0	0		Internal exchange reaction mouse <=> lumen
MMcrmp_hs[u]tr	MMcrmp_hs[e] <=> crmp_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMcrn[u]tr	MMcrn[e] <=> crn[u]	0	0		Internal exchange reaction mouse <=> lumen
MMcrns[u]tr	MMcrns[e] <=> crns[u]	0	0		Internal exchange reaction mouse <=> lumen
MMcrtstrn[u]tr	MMcrtstrn[e] <=> crtstrn[u]	0	0		Internal exchange reaction mouse <=> lumen
MMcrvnc[u]tr	MMcrvnc[e] <=> crvnc[u]	0	0		Internal exchange reaction mouse <=> lumen
MMcsn[u]tr	MMcsn[e] <=> csn[u]	0	0		Internal exchange reaction mouse <=> lumen
MMcspg_a[u]tr	MMcspg_a[e] <=> cspg_a[u]	0	0		Internal exchange reaction mouse <=> lumen
MMcspg_b[u]tr	MMcspg_b[e] <=> cspg_b[u]	0	0		Internal exchange reaction mouse <=> lumen
MMcspg_c[u]tr	MMcspg_c[e] <=> cspg_c[u]	0	0		Internal exchange reaction mouse <=> lumen
MMcspg_d[u]tr	MMcspg_d[e] <=> cspg_d[u]	0	0		Internal exchange reaction mouse <=> lumen
MMcspg_e[u]tr	MMcspg_e[e] <=> cspg_e[u]	0	0		Internal exchange reaction mouse <=> lumen
MMcyan[u]tr	MMcyan[e] <=> cyan[u]	0	0		Internal exchange reaction mouse <=> lumen
MMLcystin[u]tr	MMLcystin[e] <=> Lcystin[u]	0	0		Internal exchange reaction mouse <=> lumen
MMglu-L[u]tr	MMglu-L[e] <=> glu-L[u]	0	0		Internal exchange reaction mouse <=> lumen
MMcytd[u]tr	MMcytd[e] <=> cytd[u]	0	0		Internal exchange reaction mouse <=> lumen
MMdad-2[u]tr	MMdad-2[e] <=> dad-2[u]	0	0		Internal exchange reaction mouse <=> lumen
MMdin[u]tr	MMdin[e] <=> din[u]	0	0		Internal exchange reaction mouse <=> lumen
MMdag_hs[u]tr	MMdag_hs[e] <=> dag_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMdcsptn1[u]tr	MMdcsptn1[e] <=> dcsptn1[u]	0	0		Internal exchange reaction mouse <=> lumen
MMdcyt[u]tr	MMdcyt[e] <=> dcyt[u]	0	0		Internal exchange reaction mouse <=> lumen
MMdebrisoquine[u]tr	MMdebrisoquine[e] <=> debrisoquine[u]	0	0		Internal exchange reaction mouse <=> lumen
MMdgchol[u]tr	MMdgchol[e] <=> dgchol[u]	0	0		Internal exchange reaction mouse <=> lumen
MMdgsn[u]tr	MMdgsn[e] <=> dgsn[u]	0	0		Internal exchange reaction mouse <=> lumen
MMdhdascb[u]tr	MMdhdascb[e] <=> dhdascb[u]	0	0		Internal exchange reaction mouse <=> lumen
MMdigalsgalside_hs[u]tr	MMdigalsgalside_hs[e] <=> digalsgalside_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMdlnlcg[u]tr	MMdlnlcg[e] <=> dlnlcg[u]	0	0		Internal exchange reaction mouse <=> lumen
MMdmantipyrine[u]tr	MMdmantipyrine[e] <=> dmantipyrine[u]	0	0		Internal exchange reaction mouse <=> lumen
MMdmhptcrn[u]tr	MMdmhptcrn[e] <=> dmhptcrn[u]	0	0		Internal exchange reaction mouse <=> lumen
MMdopasf[u]tr	MMdopasf[e] <=> dopasf[u]	0	0		Internal exchange reaction mouse <=> lumen
MMdopa[u]tr	MMdopa[e] <=> dopa[u]	0	0		Internal exchange reaction mouse <=> lumen
MMdrib[u]tr	MMdrib[e] <=> drib[u]	0	0		Internal exchange reaction mouse <=> lumen
MMdsT_antigen[u]tr	MMdsT_antigen[e] <=> dsT_antigen[u]	-1000	1000		Internal exchange reaction mouse <=> lumen
MMdur[u]tr	MMdur[e] <=> dur[u]	0	0		Internal exchange reaction mouse <=> lumen
MM3aib-D[u]tr	MM3aib-D[e] <=> 3aib-D[u]	0	0		Internal exchange reaction mouse <=> lumen
MMlac-D[u]tr	MMlac-D[e] <=> lac-D[u]	0	0		Internal exchange reaction mouse <=> lumen
MMeaflatoxin[u]tr	MMeaflatoxin[e] <=> eaflatoxin[u]	0	0		Internal exchange reaction mouse <=> lumen
MMebastineoh[u]tr	MMebastineoh[e] <=> ebastineoh[u]	0	0		Internal exchange reaction mouse <=> lumen
MMebastine[u]tr	MMebastine[e] <=> ebastine[u]	0	0		Internal exchange reaction mouse <=> lumen
MMeicosterl[u]tr	MMeicosterl[e] <=> eicosterl[u]	0	0		Internal exchange reaction mouse <=> lumen
MMelaid[u]tr	MMelaid[e] <=> elaid[u]	0	0		Internal exchange reaction mouse <=> lumen
MMestradiolglc[u]tr	MMestradiolglc[e] <=> estradiolglc[u]	0	0		Internal exchange reaction mouse <=> lumen
MMestradiol[u]tr	MMestradiol[e] <=> estradiol[u]	0	0		Internal exchange reaction mouse <=> lumen
MMestriolglc[u]tr	MMestriolglc[e] <=> estriolglc[u]	0	0		Internal exchange reaction mouse <=> lumen
MMestronesglc[u]tr	MMestronesglc[e] <=> estronesglc[u]	0	0		Internal exchange reaction mouse <=> lumen
MMestrones[u]tr	MMestrones[e] <=> estrones[u]	0	0		Internal exchange reaction mouse <=> lumen
MMetha[u]tr	MMetha[e] <=> etha[u]	0	0		Internal exchange reaction mouse <=> lumen
MMetoh[u]tr	MMetoh[e] <=> etoh[u]	0	0		Internal exchange reaction mouse <=> lumen
MM10thf[u]tr	MM10thf[e] <=> 10thf[u]	0	0		Internal exchange reaction mouse <=> lumen
MM10thf5glu[u]tr	MM10thf5glu[e] <=> 10thf5glu[u]	0	0		Internal exchange reaction mouse <=> lumen
MM10thf6glu[u]tr	MM10thf6glu[e] <=> 10thf6glu[u]	0	0		Internal exchange reaction mouse <=> lumen
MM10thf7glu[u]tr	MM10thf7glu[e] <=> 10thf7glu[u]	0	0		Internal exchange reaction mouse <=> lumen
MM11-cis-retfa[u]tr	MM11-cis-retfa[e] <=> 11-cis-retfa[u]	0	0		Internal exchange reaction mouse <=> lumen
MM13-cis-retnglc[u]tr	MM13-cis-retnglc[e] <=> 13-cis-retnglc[u]	0	0		Internal exchange reaction mouse <=> lumen
MM1glyc_hs[u]tr	MM1glyc_hs[e] <=> 1glyc_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MM4hphac[u]tr	MM4hphac[e] <=> 4hphac[u]	0	0		Internal exchange reaction mouse <=> lumen
MM5dhf[u]tr	MM5dhf[e] <=> 5dhf[u]	0	0		Internal exchange reaction mouse <=> lumen
MM5thf[u]tr	MM5thf[e] <=> 5thf[u]	0	0		Internal exchange reaction mouse <=> lumen
MM6dhf[u]tr	MM6dhf[e] <=> 6dhf[u]	0	0		Internal exchange reaction mouse <=> lumen

MM6thf[u]tr	MM6thf[e] <=> 6thf[u]	0	0		Internal exchange reaction mouse <=> lumen
MM7thf[e]tr	MM7thf[e] <=> 7thf[u]	0	0		Internal exchange reaction mouse <=> lumen
MM7thf[u]tr	MM7thf[e] <=> 7thf[u]	0	0		Internal exchange reaction mouse <=> lumen
MM9-cis-retfa[u]tr	MM9-cis-retfa[e] <=> 9-cis-retfa[u]	0	0		Internal exchange reaction mouse <=> lumen
MMRtotal[u]tr	MMRtotal[e] <=> Rtotal[u]	0	0		Internal exchange reaction mouse <=> lumen
MMRtotal2[u]tr	MMRtotal2[e] <=> Rtotal2[u]	0	0		Internal exchange reaction mouse <=> lumen
MMRtotal3[u]tr	MMRtotal3[e] <=> Rtotal3[u]	0	0		Internal exchange reaction mouse <=> lumen
MMTyr-ggn[u]tr	MMTyr-ggn[e] <=> Tyr-ggn[u]	0	0		Internal exchange reaction mouse <=> lumen
MMadprhp[u]tr	MMadprhp[e] <=> adprhp[u]	0	0		Internal exchange reaction mouse <=> lumen
MMcmp[u]tr	MMcmp[e] <=> cmp[u]	0	0		Internal exchange reaction mouse <=> lumen
MMdhf[u]tr	MMdhf[e] <=> dhf[u]	0	0		Internal exchange reaction mouse <=> lumen
MMf1a[u]tr	MMf1a[e] <=> f1a[u]	-1000	1000		Internal exchange reaction mouse <=> lumen
MMfe2[u]tr	MMfe2[e] <=> fe2[u]	0	0		Internal exchange reaction mouse <=> lumen
MMfe3[u]tr	MMfe3[e] <=> fe3[u]	0	0		Internal exchange reaction mouse <=> lumen
MMfol[u]tr	MMfol[e] <=> fol[u]	0	0		Internal exchange reaction mouse <=> lumen
MMfru[u]tr	MMfru[e] <=> fru[u]	0	0		Internal exchange reaction mouse <=> lumen
MMfuc13galacglcgal14acglcgalglcside_hs[u]tr	MMfuc13galacglcgal14acglcgalglcside_hs[e] <=> fuc13galacglcgal14acglcgalglcside_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMfuc14galacglcgalglcside_hs[u]tr	MMfuc14galacglcgalglcside_hs[e] <=> fuc14galacglcgalglcside_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMfuc-L[u]tr	MMfuc-L[e] <=> fuc-L[u]	0	0		Internal exchange reaction mouse <=> lumen
MMfucacgalfucgalacglcgalglcside_hs[u]tr	MMfucacgalfucgalacglcgalglcside_hs[e] <=> fucacgalfucgalacglcgalglcside_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMfucacngal14acglcgalglcside_hs[u]tr	MMfucacngal14acglcgalglcside_hs[e] <=> fucacngal14acglcgalglcside_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMfucacngalacglcgalglcside_hs[u]tr	MMfucacngalacglcgalglcside_hs[e] <=> fucacngalacglcgalglcside_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMfucfuc12gal14acglcgalglcside_hs[u]tr	MMfucfuc12gal14acglcgalglcside_hs[e] <=> fucfuc12gal14acglcgalglcside_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMfucfuc132galacglcgal14acglcgalglcside_hs[u]tr	MMfucfuc132galacglcgal14acglcgalglcside_hs[e] <=> fucfuc132galacglcgal14acglcgalglcside_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMfucfucfucgalacglc13galacglcgal14acglcgalglcside_hs[u]tr	MMfucfucfucgalacglc13galacglcgal14acglcgalglcside_hs[e] <=> fucfucfucgalacglc13galacglcgal14acglcgalglcside_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMfucfucfucgalacglcgal14acglcgalglcside_hs[u]tr	MMfucfucfucgalacglcgal14acglcgalglcside_hs[e] <=> fucfucfucgalacglcgal14acglcgalglcside_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMfucfucgalacglcgalglcside_hs[u]tr	MMfucfucgalacglcgalglcside_hs[e] <=> fucfucgalacglcgalglcside_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMfucgal14acglcgalglcside_hs[u]tr	MMfucgal14acglcgalglcside_hs[e] <=> fucgal14acglcgalglcside_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMfucgalfucgalacglcgalglcside_hs[u]tr	MMfucgalfucgalacglcgalglcside_hs[e] <=> fucgalfucgalacglcgalglcside_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMfucgalglcside_hs[u]tr	MMfucgalglcside_hs[e] <=> fucgalglcside_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMgal[u]tr	MMgal[e] <=> gal[u]	0	0		Internal exchange reaction mouse <=> lumen
MMgalacglcgalglcside_hs[u]tr	MMgalacglcgalglcside_hs[e] <=> galacglcgalglcside_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMgalam[u]tr	MMgalam[e] <=> galam[u]	0	0		Internal exchange reaction mouse <=> lumen
MMgalfuc12gal14acglcgalglcside_hs[u]tr	MMgalfuc12gal14acglcgalglcside_hs[e] <=> galfuc12gal14acglcgalglcside_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMgalfucgalacglcgal14acglcgalglcside_hs[u]tr	MMgalfucgalacglcgal14acglcgalglcside_hs[e] <=> galfucgalacglcgal14acglcgalglcside_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMgalgalfucfucgalacglcgalacglcgal14acglcgalglcside_hs[u]tr	MMgalgalfucfucgalacglcgalacglcgal14acglcgalglcside_hs[e] <=> galgalfucfucgalacglcgalacglcgal14acglcgalglcside_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMgalgalgalthcrm_hs[u]tr	MMgalgalgalthcrm_hs[e] <=> galgalgalthcrm_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMgam[u]tr	MMgam[e] <=> gam[u]	0	0		Internal exchange reaction mouse <=> lumen
MMglnside_hs[u]tr	MMglnside_hs[e] <=> glnside_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMgchola[u]tr	MMgchola[e] <=> gchola[u]	0	0		Internal exchange reaction mouse <=> lumen
MMgd1b2_hs[u]tr	MMgd1b2_hs[e] <=> gd1b2_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMgd1c_hs[u]tr	MMgd1c_hs[e] <=> gd1c_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMgdchola[u]tr	MMgdchola[e] <=> gdchola[u]	0	0		Internal exchange reaction mouse <=> lumen
MMgdp[u]tr	MMgdp[e] <=> gdp[u]	0	0		Internal exchange reaction mouse <=> lumen
MMgkcur[u]tr	MMgkcur[e] <=> gkcur[u]	0	0		Internal exchange reaction mouse <=> lumen
MMgluala[u]tr	MMgluala[e] <=> gluala[u]	0	0		Internal exchange reaction mouse <=> lumen
MMglyb[u]tr	MMglyb[e] <=> glyb[u]	0	0		Internal exchange reaction mouse <=> lumen
MMglyc[u]tr	MMglyc[e] <=> glyc[u]	0	0		Internal exchange reaction mouse <=> lumen
MMglyc-S[u]tr	MMglyc-S[e] <=> glyc-S[u]	0	0		Internal exchange reaction mouse <=> lumen
MMglygly[u]tr	MMglygly[e] <=> glygly[u]	0	0		Internal exchange reaction mouse <=> lumen
MMglygpf5[u]tr	MMglygpf5[e] <=> glygpf5[u]	0	0		Internal exchange reaction mouse <=> lumen
MMglyphe[u]tr	MMglyphe[e] <=> glyphe[u]	0	0		Internal exchange reaction mouse <=> lumen
MMglysar[u]tr	MMglysar[e] <=> glysar[u]	0	0		Internal exchange reaction mouse <=> lumen
MMgmp[u]tr	MMgmp[e] <=> gmp[u]	0	0		Internal exchange reaction mouse <=> lumen
MMgncore1[u]tr	MMgncore1[e] <=> gncore1[u]	-1000	1000		Internal exchange reaction mouse <=> lumen
MMgncore2[u]tr	MMgncore2[e] <=> gncore2[u]	-1000	1000		Internal exchange reaction mouse <=> lumen
MMgp1c_hs[u]tr	MMgp1c_hs[e] <=> gp1c_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMgp1calpha_hs[u]tr	MMgp1calpha_hs[e] <=> gp1calpha_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMgq1b_hs[u]tr	MMgq1b_hs[e] <=> gq1b_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMgq1balpha_hs[u]tr	MMgq1balpha_hs[e] <=> gq1balpha_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMgsn[u]tr	MMgsn[e] <=> gsn[u]	0	0		Internal exchange reaction mouse <=> lumen
MMgt1a_hs[u]tr	MMgt1a_hs[e] <=> gt1a_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMgthox[u]tr	MMgthox[e] <=> gthox[u]	0	0		Internal exchange reaction mouse <=> lumen
MMgthrd[u]tr	MMgthrd[e] <=> gthrd[u]	0	0		Internal exchange reaction mouse <=> lumen
MMgtp[u]tr	MMgtp[e] <=> gtp[u]	0	0		Internal exchange reaction mouse <=> lumen
MMgua[u]tr	MMgua[e] <=> gua[u]	0	0		Internal exchange reaction mouse <=> lumen
MMgum[u]tr	MMgum[e] <=> gum[u]	0	0		Internal exchange reaction mouse <=> lumen
MMgumdchac[u]tr	MMgumdchac[e] <=> gumdchac[u]	0	0		Internal exchange reaction mouse <=> lumen
MMgumgchol[u]tr	MMgumgchol[e] <=> gumgchol[u]	0	0		Internal exchange reaction mouse <=> lumen
MMgumtchol[u]tr	MMgumtchol[e] <=> gumtchol[u]	0	0		Internal exchange reaction mouse <=> lumen
MMh2o2[u]tr	MMh2o2[e] <=> h2o2[u]	0	0		Internal exchange reaction mouse <=> lumen
MMha[u]tr	MMha[e] <=> ha[u]	0	0		Internal exchange reaction mouse <=> lumen
MMha_pre1[u]tr	MMha_pre1[e] <=> ha_pre1[u]	0	0		Internal exchange reaction mouse <=> lumen
MMhcoumarin[u]tr	MMhcoumarin[e] <=> hcoumarin[u]	0	0		Internal exchange reaction mouse <=> lumen
MMhdca[u]tr	MMhdca[e] <=> hdca[u]	0	0		Internal exchange reaction mouse <=> lumen
MMhdcea[u]tr	MMhdcea[e] <=> hdcea[u]	0	0		Internal exchange reaction mouse <=> lumen
MMhestratriol[u]tr	MMhestratriol[e] <=> hestratriol[u]	0	0		Internal exchange reaction mouse <=> lumen
MMhexc[u]tr	MMhexc[e] <=> hexc[u]	0	0		Internal exchange reaction mouse <=> lumen
MMhis-L[u]tr	MMhis-L[e] <=> his-L[u]	0	0		Internal exchange reaction mouse <=> lumen
MMhista[u]tr	MMhista[e] <=> hista[u]	0	0		Internal exchange reaction mouse <=> lumen
MMhom-L[u]tr	MMhom-L[e] <=> hom-L[u]	0	0		Internal exchange reaction mouse <=> lumen
MMhpdca[u]tr	MMhpdca[e] <=> hpdca[u]	0	0		Internal exchange reaction mouse <=> lumen
MMhspg[u]tr	MMhspg[e] <=> hspg[u]	0	0		Internal exchange reaction mouse <=> lumen
MMhtaxol[u]tr	MMhtaxol[e] <=> htaxol[u]	0	0		Internal exchange reaction mouse <=> lumen

MMhxan[u]tr	MMhxan[e] <=> hxan[u]	0	0		Internal exchange reaction mouse <=> lumen
MMidp[u]tr	MMidp[e] <=> idp[u]	0	0		Internal exchange reaction mouse <=> lumen
MMimp[u]tr	MMimp[e] <=> imp[u]	0	0		Internal exchange reaction mouse <=> lumen
MMinost[u]tr	MMinost[e] <=> inost[u]	0	0		Internal exchange reaction mouse <=> lumen
MMksi[u]tr	MMksi[e] <=> ksi[u]	0	0		Internal exchange reaction mouse <=> lumen
MMksi_deg1[u]tr	MMksi_deg1[e] <=> ksi_deg1[u]	0	0		Internal exchange reaction mouse <=> lumen
MMksii_core2[u]tr	MMksii_core2[e] <=> ksii_core2[u]	0	0		Internal exchange reaction mouse <=> lumen
MMksii_core4[u]tr	MMksii_core4[e] <=> ksii_core4[u]	0	0		Internal exchange reaction mouse <=> lumen
MMlac-L[u]tr	MMlac-L[e] <=> lac-L[u]	0	0		Internal exchange reaction mouse <=> lumen
MMlcts[u]tr	MMlcts[e] <=> lcts[u]	0	0		Internal exchange reaction mouse <=> lumen
MMles-L[u]tr	MMles-L[e] <=> les-L[u]	0	0		Internal exchange reaction mouse <=> lumen
MMleugly[u]tr	MMleugly[e] <=> leugly[u]	0	0		Internal exchange reaction mouse <=> lumen
MMleuktrA4[u]tr	MMleuktrA4[e] <=> leuktrA4[u]	0	0		Internal exchange reaction mouse <=> lumen
MMleuktrB4[u]tr	MMleuktrB4[e] <=> leuktrB4[u]	0	0		Internal exchange reaction mouse <=> lumen
MMleuktrD4[u]tr	MMleuktrD4[e] <=> leuktrD4[u]	0	0		Internal exchange reaction mouse <=> lumen
MMleuktrE4[u]tr	MMleuktrE4[e] <=> leuktrE4[u]	0	0		Internal exchange reaction mouse <=> lumen
MMleuktrF4[u]tr	MMleuktrF4[e] <=> leuktrF4[u]	0	0		Internal exchange reaction mouse <=> lumen
MMleules[u]tr	MMleules[e] <=> leules[u]	0	0		Internal exchange reaction mouse <=> lumen
MMlgnc[u]tr	MMlgnc[e] <=> lgnc[u]	0	0		Internal exchange reaction mouse <=> lumen
MMlimmen[u]tr	MMlimmen[e] <=> limmen[u]	0	0		Internal exchange reaction mouse <=> lumen
MMlipoate[u]tr	MMlipoate[e] <=> lipoate[u]	0	0		Internal exchange reaction mouse <=> lumen
MMlneldc[u]tr	MMlneldc[e] <=> lneldc[u]	0	0		Internal exchange reaction mouse <=> lumen
MMlnlc[u]tr	MMlnlc[e] <=> lnlc[u]	0	0		Internal exchange reaction mouse <=> lumen
MMlnlnca[u]tr	MMlnlnca[e] <=> lnlnca[u]	0	0		Internal exchange reaction mouse <=> lumen
MMlnlncg[u]tr	MMlnlncg[e] <=> lnlncg[u]	0	0		Internal exchange reaction mouse <=> lumen
MMlpchol_hs[u]tr	MMlpchol_hs[e] <=> lpchol_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMmag_hs[u]tr	MMmag_hs[e] <=> mag_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMmalt[u]tr	MMmalt[e] <=> malt[u]	0	0		Internal exchange reaction mouse <=> lumen
MMmalttr[u]tr	MMmalttr[e] <=> malttr[u]	0	0		Internal exchange reaction mouse <=> lumen
MMmant[u]tr	MMmant[e] <=> mant[u]	0	0		Internal exchange reaction mouse <=> lumen
MMmeoh[u]tr	MMmeoh[e] <=> meoh[u]	0	0		Internal exchange reaction mouse <=> lumen
MMmepi[u]tr	MMmepi[e] <=> mepi[u]	0	0		Internal exchange reaction mouse <=> lumen
MMmercplaccys[u]tr	MMmercplaccys[e] <=> mercplaccys[u]	0	0		Internal exchange reaction mouse <=> lumen
MMmet-L[u]tr	MMmet-L[e] <=> met-L[u]	0	0		Internal exchange reaction mouse <=> lumen
MMmqn10[u]tr	MMmqn10[e] <=> mqn10[u]	0	0		Internal exchange reaction mouse <=> lumen
MMmqn11[u]tr	MMmqn11[e] <=> mqn11[u]	0	0		Internal exchange reaction mouse <=> lumen
MMmqn7[u]tr	MMmqn7[e] <=> mqn7[u]	0	0		Internal exchange reaction mouse <=> lumen
MMmqn8[u]tr	MMmqn8[e] <=> mqn8[u]	0	0		Internal exchange reaction mouse <=> lumen
MMmqn9[u]tr	MMmqn9[e] <=> mqn9[u]	0	0		Internal exchange reaction mouse <=> lumen
MMmthgx[u]tr	MMmthgx[e] <=> mthgx[u]	0	0		Internal exchange reaction mouse <=> lumen
MMn2m2nmasn[u]tr	MMn2m2nmasn[e] <=> n2m2nmasn[u]	0	0		Internal exchange reaction mouse <=> lumen
MMnac[u]tr	MMnac[e] <=> nac[u]	0	0		Internal exchange reaction mouse <=> lumen
MMnad[u]tr	MMnad[e] <=> nad[u]	0	0		Internal exchange reaction mouse <=> lumen
MMnadp[u]tr	MMnadp[e] <=> nadp[u]	0	0		Internal exchange reaction mouse <=> lumen
MMncam[u]tr	MMncam[e] <=> ncam[u]	0	0		Internal exchange reaction mouse <=> lumen
MMnifedipine[u]tr	MMnifedipine[e] <=> nifedipine[u]	0	0		Internal exchange reaction mouse <=> lumen
MMno[u]tr	MMno[e] <=> no[u]	0	0		Internal exchange reaction mouse <=> lumen
MMnpthl[u]tr	MMnpthl[e] <=> npthl[u]	0	0		Internal exchange reaction mouse <=> lumen
MMnrpphr[u]tr	MMnrpphr[e] <=> nrpphr[u]	0	0		Internal exchange reaction mouse <=> lumen
MMnrpphrsf[u]tr	MMnrpphrsf[e] <=> nrpphrsf[u]	0	0		Internal exchange reaction mouse <=> lumen
MMnrvnc[u]tr	MMnrvnc[e] <=> nrvnc[u]	0	0		Internal exchange reaction mouse <=> lumen
MMo2[u]tr	MMo2[e] <=> o2[u]	0	0		Internal exchange reaction mouse <=> lumen
MMo2s[u]tr	MMo2s[e] <=> o2s[u]	0	0		Internal exchange reaction mouse <=> lumen
MMoagtf3_hs[u]tr	MMoagtf3_hs[e] <=> oagtf3_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMoagt3_hs[u]tr	MMoagt3_hs[e] <=> oagt3_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMocdca[u]tr	MMocdca[e] <=> ocdca[u]	0	0		Internal exchange reaction mouse <=> lumen
MMocdcea[u]tr	MMocdcea[e] <=> ocdcea[u]	0	0		Internal exchange reaction mouse <=> lumen
MMocta[u]tr	MMocta[e] <=> octa[u]	0	0		Internal exchange reaction mouse <=> lumen
MMomeprazole[u]tr	MMomeprazole[e] <=> omeprazole[u]	0	0		Internal exchange reaction mouse <=> lumen
MMonpthl[u]tr	MMonpthl[e] <=> onpthl[u]	0	0		Internal exchange reaction mouse <=> lumen
MMorn[u]tr	MMorn[e] <=> orn[u]	0	0		Internal exchange reaction mouse <=> lumen
MMpaf_hs[u]tr	MMpaf_hs[e] <=> paf_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMpchol_hs[u]tr	MMpchol_hs[e] <=> pchol_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMpe_hs[u]tr	MMpe_hs[e] <=> pe_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMpect[u]tr	MMpect[e] <=> pect[u]	0	0		Internal exchange reaction mouse <=> lumen
MMpectindchac[u]tr	MMpectindchac[e] <=> pectindchac[u]	0	0		Internal exchange reaction mouse <=> lumen
MMpectingchol[u]tr	MMpectingchol[e] <=> pectingchol[u]	0	0		Internal exchange reaction mouse <=> lumen
MMpectintchol[u]tr	MMpectintchol[e] <=> pectintchol[u]	0	0		Internal exchange reaction mouse <=> lumen
MMpephys[u]tr	MMpephys[e] <=> pephys[u]	0	0		Internal exchange reaction mouse <=> lumen
MMperilly[u]tr	MMperilly[e] <=> perilly[u]	0	0		Internal exchange reaction mouse <=> lumen
MMpglyc_hs[u]tr	MMpglyc_hs[e] <=> pglyc_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMpheacglnt[u]tr	MMpheacglnt[e] <=> pheacglnt[u]	0	0		Internal exchange reaction mouse <=> lumen
MMpheme[u]tr	MMpheme[e] <=> pheme[u]	0	0		Internal exchange reaction mouse <=> lumen
MMphyQ[u]tr	MMphyQ[e] <=> phyQ[u]	0	0		Internal exchange reaction mouse <=> lumen
MMphyt[u]tr	MMphyt[e] <=> phyt[u]	0	0		Internal exchange reaction mouse <=> lumen
MMpnto-R[u]tr	MMpnto-R[e] <=> pnto-R[u]	0	0		Internal exchange reaction mouse <=> lumen
MMppa[u]tr	MMppa[e] <=> ppa[u]	0	0		Internal exchange reaction mouse <=> lumen
MMprgstrn[u]tr	MMprgstrn[e] <=> prgstrn[u]	0	0		Internal exchange reaction mouse <=> lumen
MMpro-D[u]tr	MMpro-D[e] <=> pro-D[u]	0	0		Internal exchange reaction mouse <=> lumen
MMpro-L[u]tr	MMpro-L[e] <=> pro-L[u]	0	0		Internal exchange reaction mouse <=> lumen
MMprogly[u]tr	MMprogly[e] <=> progly[u]	0	0		Internal exchange reaction mouse <=> lumen
MMprostgd2[u]tr	MMprostgd2[e] <=> prostgd2[u]	0	0		Internal exchange reaction mouse <=> lumen
MMprostge1[u]tr	MMprostge1[e] <=> prostge1[u]	0	0		Internal exchange reaction mouse <=> lumen
MMprostge2[u]tr	MMprostge2[e] <=> prostge2[u]	0	0		Internal exchange reaction mouse <=> lumen
MMprostgf2[u]tr	MMprostgf2[e] <=> prostgf2[u]	0	0		Internal exchange reaction mouse <=> lumen

MMps_hs[u]tr	MMps_hs[e] <=> ps_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMpsyl[u]tr	MMpsyl[e] <=> psyl[u]	0	0		Internal exchange reaction mouse <=> lumen
MMpsylchol[u]tr	MMpsylchol[e] <=> psylchol[u]	0	0		Internal exchange reaction mouse <=> lumen
MMpsylchol[u]tr	MMpsylchol[e] <=> psylchol[u]	0	0		Internal exchange reaction mouse <=> lumen
MMpsyldecchol[u]tr	MMpsyldecchol[e] <=> psyldecchol[u]	0	0		Internal exchange reaction mouse <=> lumen
MMptdca[u]tr	MMptdca[e] <=> ptdca[u]	0	0		Internal exchange reaction mouse <=> lumen
MMpydam[u]tr	MMpydam[e] <=> pydam[u]	0	0		Internal exchange reaction mouse <=> lumen
MMpydx[u]tr	MMpydx[e] <=> pydx[u]	0	0		Internal exchange reaction mouse <=> lumen
MMpydxn[u]tr	MMpydxn[e] <=> pydxn[u]	0	0		Internal exchange reaction mouse <=> lumen
MMpyr[u]tr	MMpyr[e] <=> pyr[u]	0	0		Internal exchange reaction mouse <=> lumen
MMrbt[u]tr	MMrbt[e] <=> rbt[u]	0	0		Internal exchange reaction mouse <=> lumen
MMretfa[u]tr	MMretfa[e] <=> retfa[u]	0	0		Internal exchange reaction mouse <=> lumen
MMretinol[u]tr	MMretinol[e] <=> retinol[u]	0	0		Internal exchange reaction mouse <=> lumen
MMretinol-9-cis[u]tr	MMretinol-9-cis[e] <=> retinol-9-cis[u]	0	0		Internal exchange reaction mouse <=> lumen
MMretinol-cis-11[u]tr	MMretinol-cis-11[e] <=> retinol-cis-11[u]	0	0		Internal exchange reaction mouse <=> lumen
MMretn[u]tr	MMretn[e] <=> retn[u]	0	0		Internal exchange reaction mouse <=> lumen
MMretnglc[u]tr	MMretnglc[e] <=> retnglc[u]	0	0		Internal exchange reaction mouse <=> lumen
MMrib-D[u]tr	MMrib-D[e] <=> rib-D[u]	0	0		Internal exchange reaction mouse <=> lumen
MMribflv[u]tr	MMribflv[e] <=> ribflv[u]	0	0		Internal exchange reaction mouse <=> lumen
MMs2f2fn2m2mnsn[u]tr	MMs2f2fn2m2mnsn[e] <=> s2f2fn2m2mnsn[u]	0	0		Internal exchange reaction mouse <=> lumen
MMs2f2n2m2m[u]tr	MMs2f2n2m2m[e] <=> s2f2n2m2m[u]	-1000	1000		Internal exchange reaction mouse <=> lumen
MMs2f2n2m2mnsn[u]tr	MMs2f2n2m2mnsn[e] <=> s2f2n2m2mnsn[u]	0	0		Internal exchange reaction mouse <=> lumen
MMsTn_antigen[u]tr	MMsTn_antigen[e] <=> sTn_antigen[u]	-1000	1000		Internal exchange reaction mouse <=> lumen
MMsarcs[u]tr	MMsarcs[e] <=> sarcs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMsbt-D[u]tr	MMsbt-D[e] <=> sbt-D[u]	0	0		Internal exchange reaction mouse <=> lumen
MMsel[u]tr	MMsel[e] <=> sel[u]	0	0		Internal exchange reaction mouse <=> lumen
MMser-D[u]tr	MMser-D[e] <=> ser-D[u]	0	0		Internal exchange reaction mouse <=> lumen
MMsl-L[u]tr	MMsl-L[e] <=> sl-L[u]	0	0		Internal exchange reaction mouse <=> lumen
MMso4[u]tr	MMso4[e] <=> so4[u]	0	0		Internal exchange reaction mouse <=> lumen
MMspc_hs[u]tr	MMspc_hs[e] <=> spc_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMsph1p[u]tr	MMsph1p[e] <=> sph1p[u]	0	0		Internal exchange reaction mouse <=> lumen
MMsphn1p[u]tr	MMsphn1p[e] <=> sphn1p[u]	0	0		Internal exchange reaction mouse <=> lumen
MMsrnt[u]tr	MMsrnt[e] <=> srnt[u]	0	0		Internal exchange reaction mouse <=> lumen
MMstrdnc[u]tr	MMstrdnc[e] <=> strdnc[u]	0	0		Internal exchange reaction mouse <=> lumen
MMsucc[u]tr	MMsucc[e] <=> succ[u]	0	0		Internal exchange reaction mouse <=> lumen
MMsucr[u]tr	MMsucr[e] <=> sucr[u]	0	0		Internal exchange reaction mouse <=> lumen
MMtag_hs[u]tr	MMtag_hs[e] <=> tag_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMtagat-D[u]tr	MMtagat-D[e] <=> tagat-D[u]	0	0		Internal exchange reaction mouse <=> lumen
MMtaur[u]tr	MMtaur[e] <=> taur[u]	0	0		Internal exchange reaction mouse <=> lumen
MMtaxol[u]tr	MMtaxol[e] <=> taxol[u]	0	0		Internal exchange reaction mouse <=> lumen
MMtchola[u]tr	MMtchola[e] <=> tchola[u]	0	0		Internal exchange reaction mouse <=> lumen
MMtcynt[u]tr	MMtcynt[e] <=> tcynt[u]	0	0		Internal exchange reaction mouse <=> lumen
MMtdchola[u]tr	MMtdchola[e] <=> tdchola[u]	0	0		Internal exchange reaction mouse <=> lumen
MMtdechola[u]tr	MMtdechola[e] <=> tdechola[u]	0	0		Internal exchange reaction mouse <=> lumen
MMtethex3[u]tr	MMtethex3[e] <=> tethex3[u]	0	0		Internal exchange reaction mouse <=> lumen
MMtetpent3[u]tr	MMtetpent3[e] <=> tetpent3[u]	0	0		Internal exchange reaction mouse <=> lumen
MMtetpent6[u]tr	MMtetpent6[e] <=> tetpent6[u]	0	0		Internal exchange reaction mouse <=> lumen
MMtetrt6[u]tr	MMtetrt6[e] <=> tetrt6[u]	0	0		Internal exchange reaction mouse <=> lumen
MMthf[u]tr	MMthf[e] <=> thf[u]	0	0		Internal exchange reaction mouse <=> lumen
MMthm[u]tr	MMthm[e] <=> thm[u]	0	0		Internal exchange reaction mouse <=> lumen
MMthmmp[u]tr	MMthmmp[e] <=> thmmp[u]	0	0		Internal exchange reaction mouse <=> lumen
MMthmtp[u]tr	MMthmtp[e] <=> thmtp[u]	0	0		Internal exchange reaction mouse <=> lumen
MMthym[u]tr	MMthym[e] <=> thym[u]	0	0		Internal exchange reaction mouse <=> lumen
MMthymd[u]tr	MMthymd[e] <=> thymd[u]	0	0		Internal exchange reaction mouse <=> lumen
MMthyox-L[u]tr	MMthyox-L[e] <=> thyox-L[u]	0	0		Internal exchange reaction mouse <=> lumen
MMtmndnc[u]tr	MMtmndnc[e] <=> tmndnc[u]	0	0		Internal exchange reaction mouse <=> lumen
MMtolbutamide[u]tr	MMtolbutamide[e] <=> tolbutamide[u]	0	0		Internal exchange reaction mouse <=> lumen
MMtre[u]tr	MMtre[e] <=> tre[u]	0	0		Internal exchange reaction mouse <=> lumen
MMtriodthy[u]tr	MMtriodthy[e] <=> triodthy[u]	0	0		Internal exchange reaction mouse <=> lumen
MMtriodthysul[u]tr	MMtriodthysul[e] <=> triodthysul[u]	0	0		Internal exchange reaction mouse <=> lumen
MMtrp-L[u]tr	MMtrp-L[e] <=> trp-L[u]	0	0		Internal exchange reaction mouse <=> lumen
MMtststerone[u]tr	MMtststerone[e] <=> tststerone[u]	0	0		Internal exchange reaction mouse <=> lumen
MMtststeroneglc[u]tr	MMtststeroneglc[e] <=> tststeroneglc[u]	0	0		Internal exchange reaction mouse <=> lumen
MMtststerones[u]tr	MMtststerones[e] <=> tststerones[u]	0	0		Internal exchange reaction mouse <=> lumen
MMtsul[u]tr	MMtsul[e] <=> tsul[u]	0	0		Internal exchange reaction mouse <=> lumen
MMtudca[u]tr	MMtudca[e] <=> tudca[u]	0	0		Internal exchange reaction mouse <=> lumen
MMtxa2[u]tr	MMtxa2[e] <=> txa2[u]	0	0		Internal exchange reaction mouse <=> lumen
MMtymsl[u]tr	MMtymsl[e] <=> tymsl[u]	0	0		Internal exchange reaction mouse <=> lumen
MMtyr-L[u]tr	MMtyr-L[e] <=> tyr-L[u]	0	0		Internal exchange reaction mouse <=> lumen
MMudp[u]tr	MMudp[e] <=> udp[u]	0	0		Internal exchange reaction mouse <=> lumen
MMump[u]tr	MMump[e] <=> ump[u]	0	0		Internal exchange reaction mouse <=> lumen
MMura[u]tr	MMura[e] <=> ura[u]	0	0		Internal exchange reaction mouse <=> lumen
MMurate[u]tr	MMurate[e] <=> urate[u]	0	0		Internal exchange reaction mouse <=> lumen
MMurea[u]tr	MMurea[e] <=> urea[u]	0	0		Internal exchange reaction mouse <=> lumen
MMuri[u]tr	MMuri[e] <=> uri[u]	0	0		Internal exchange reaction mouse <=> lumen
MMutp[u]tr	MMutp[e] <=> utp[u]	0	0		Internal exchange reaction mouse <=> lumen
MMvacc[u]tr	MMvacc[e] <=> vacc[u]	0	0		Internal exchange reaction mouse <=> lumen
MMval-L[u]tr	MMval-L[e] <=> val-L[u]	0	0		Internal exchange reaction mouse <=> lumen
MMvitd2[u]tr	MMvitd2[e] <=> vitd2[u]	0	0		Internal exchange reaction mouse <=> lumen
MMvitd3[u]tr	MMvitd3[e] <=> vitd3[u]	0	0		Internal exchange reaction mouse <=> lumen
MMwhddca[u]tr	MMwhddca[e] <=> whddca[u]	0	0		Internal exchange reaction mouse <=> lumen
MMwhhdca[u]tr	MMwhhdca[e] <=> whhdca[u]	0	0		Internal exchange reaction mouse <=> lumen
MMwhtststerone[u]tr	MMwhtststerone[e] <=> whtststerone[u]	0	0		Internal exchange reaction mouse <=> lumen
MMwhttdca[u]tr	MMwhttdca[e] <=> whttdca[u]	0	0		Internal exchange reaction mouse <=> lumen
MMxolest2_hs[u]tr	MMxolest2_hs[e] <=> xolest2_hs[u]	0	0		Internal exchange reaction mouse <=> lumen

MMxolest_hs[u]tr	MMxolest_hs[e] <=> xolest_hs[u]	0	0		Internal exchange reaction mouse <=> lumen
MMxoltri24[u]tr	MMxoltri24[e] <=> xoltri24[u]	0	0		Internal exchange reaction mouse <=> lumen
MMxoltri25[u]tr	MMxoltri25[e] <=> xoltri25[u]	0	0		Internal exchange reaction mouse <=> lumen
MMxoltri27[u]tr	MMxoltri27[e] <=> xoltri27[u]	0	0		Internal exchange reaction mouse <=> lumen
MMxyl-D[u]tr	MMxyl-D[e] <=> xyl-D[u]	0	0		Internal exchange reaction mouse <=> lumen
MMxylt[u]tr	MMxylt[e] <=> xylt[u]	0	0		Internal exchange reaction mouse <=> lumen
MMyvite[u]tr	MMyvite[e] <=> yvite[u]	0	0		Internal exchange reaction mouse <=> lumen
MMprostgh2[u]tr	MMprostgh2[e] <=> prostgh2[u]	0	0		Internal exchange reaction mouse <=> lumen
MMprostgi2[u]tr	MMprostgi2[e] <=> prostgi2[u]	0	0		Internal exchange reaction mouse <=> lumen
Ex_10fhf5gk[u]	10fhf5gk[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_10fhf6gk[u]	10fhf6gk[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_10fhf7gk[u]	10fhf7gk[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_10fhf[u]	10fhf[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_11-cis-retfa[u]	11-cis-retfa[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_12ethdl[u]	12ethdl[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_12ppd-R[u]	12ppd-R[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_12ppd-S[u]	12ppd-S[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_13-cis-retngk[u]	13-cis-retngk[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_1glyc_hs[u]	1glyc_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_1mncam[u]	1mncam[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_2425dhvitd2[u]	2425dhvitd2[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_2425dhvitd3[u]	2425dhvitd3[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_24mph[u]	24mph[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_25hvitd2[u]	25hvitd2[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_25hvitd3[u]	25hvitd3[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_2fuclac[u]	2fuclac[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_2hb[u]	2hb[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_2mcit[u]	2mcit[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_2omfuc[u]	2omfuc[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_2omxyl[u]	2omxyl[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_34dhoxpeg[u]	34dhoxpeg[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_35cgmp[u]	35cgmp[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_3aib-D[u]	3aib-D[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_3aib[u]	3aib[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_3ddlhept[u]	3ddlhept[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_3fuclac[u]	3fuclac[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_3mlda[u]	3mlda[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_4abut[u]	4abut[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_4hdebrisoquine[u]	4hdebrisoquine[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_4hphac[u]	4hphac[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_4hpro-LT[u]	4hpro-LT[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_4mptnl[u]	4mptnl[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_4mtolbutamide[u]	4mtolbutamide[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_4nph[u]	4nph[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_4nphs[u]	4nphs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_4pyrdx[u]	4pyrdx[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_5adtststerone[u]	5adtststerone[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_5adtststeronegk[u]	5adtststeronegk[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_5adtststerones[u]	5adtststerones[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_5dhf[u]	5dhf[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_5fthf[u]	5fthf[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_5homeprazole[u]	5homeprazole[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_5htrp[u]	5htrp[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_5mthf[u]	5mthf[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_5thf[u]	5thf[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_6dhf[u]	6dhf[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_6htststerone[u]	6htststerone[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_6thf[u]	6thf[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_7dhf[u]	7dhf[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen

Ex_7ocholate[u]	7ocholate[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_7thf[u]	7thf[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_9-cis-retfa[u]	9-cis-retfa[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_Lcystin[u]	Lcystin[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_Rtotal2[u]	Rtotal2[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_Rtotal3[u]	Rtotal3[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_Rtotal[u]	Rtotal[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_Ser_Thr[u]	Ser_Thr[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_T_antigen[u]	T_antigen[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_Tn_antigen[u]	Tn_antigen[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_Tyr_ggn[u]	Tyr_ggn[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_abt[u]	abt[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_ac[u]	ac[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_acac[u]	acac[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_acald[u]	acald[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_acerA[u]	acerA[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_aceto[u]	aceto[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_acetone[u]	acetone[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_acgal[u]	acgal[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_acgalfucgalacgalfuc12gal14acglcgalglcside_hs[u]	acgalfucgalacgalfuc12gal14acglcgalglcside_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_acgalfucgalacgalfucgalacglcgal14acglcgalglcside_hs[u]	acgalfucgalacgalfucgalacglcgal14acglcgalglcside_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_acgalglcur[u]	acgalglcur[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_acgalidour2s[u]	acgalidour2s[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_acgalidour[u]	acgalidour[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_acgam[u]	acgam[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_ach[u]	ach[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_acn13acngalglcside_hs[u]	acn13acngalglcside_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_acn23acngalglcside_hs[u]	acn23acngalglcside_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_acnacngal14acglcgalglcside_hs[u]	acnacngal14acglcgalglcside_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_acnacngalglcside_hs[u]	acnacngalglcside_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_acnam[u]	acnam[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_acngalacglcgal14acglcgalglcside_hs[u]	acngalacglcgal14acglcgalglcside_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_ade[u]	ade[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_adn[u]	adn[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_adocbl[u]	adocbl[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_adp[u]	adp[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_adprbp[u]	adprbp[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_adprib[u]	adprib[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_adrn[u]	adrn[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_adrnl[u]	adrnl[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_aflatoxin[u]	aflatoxin[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_ahandrostangl[u]	ahandrostangl[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_ak2lgchol_hs[u]	ak2lgchol_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_akg[u]	akg[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_ala-B[u]	ala-B[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_ala-D[u]	ala-D[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_ala-L[u]	ala-L[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_alaala[u]	alaala[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_alaasp[u]	alaasp[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_alagln[u]	alagln[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_alagly[u]	alagly[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_alahis[u]	alahis[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_alaleu[u]	alaleu[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_alathr[u]	alathr[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_aldstrn[u]	aldstrn[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen

Ex_amannan140[u]	amannan140[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_amp[u]	amp[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_amylose300[u]	amylose300[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_andrstrn[u]	andrstrn[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_andrstrngk[u]	andrstrngk[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_antipyrene[u]	antipyrene[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_apio-D[u]	apio-D[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_apnnox[u]	apnnox[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_appnn[u]	appnn[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_aprgstrn[u]	aprgstrn[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_aqcoba[u]	aqcoba[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_arab-L[u]	arab-L[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_arabinan101[u]	arabinan101[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_arabinogal[u]	arabinogal[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_arabttr[u]	arabttr[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_arach[u]	arach[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_arachd[u]	arachd[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_arg-L[u]	arg-L[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_argarg[u]	argarg[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_ascb-L[u]	ascb-L[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_asn-L[u]	asn-L[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_asp-D[u]	asp-D[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_asp-L[u]	asp-L[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_atp[u]	atp[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_avite1[u]	avite1[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_avite2[u]	avite2[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_bglc[u]	bglc[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_bhb[u]	bhb[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_bildglcur[u]	bildglcur[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_bilglcur[u]	bilglcur[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_bilirub[u]	bilirub[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_biocyt[u]	biocyt[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_btn[u]	btn[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_but[u]	but[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_bvite[u]	bvite[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_bz[u]	bz[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_ca2[u]	ca2[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_camp[u]	camp[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_carn[u]	carn[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_caro[u]	caro[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_carveol[u]	carveol[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_cbl1[u]	cbl1[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_cca_d3[u]	cca_d3[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_cd2[u]	cd2[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_cgly[u]	cgly[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_chol[u]	chol[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_cholate[u]	cholate[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_chsterol[u]	chsterol[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_chtbs[u]	chtbs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_chtn[u]	chtn[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_cit[u]	cit[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_cl[u]	cl[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_clpnd[u]	clpnd[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_cmp[u]	cmp[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_co2[u]	co2[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_co[u]	co[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen

Ex_cobalt2[u]	cobalt2[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_core2[u]	core2[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_core3[u]	core3[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_core4[u]	core4[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_core5[u]	core5[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_core6[u]	core6[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_core7[u]	core7[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_core8[u]	core8[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_coumarin[u]	coumarin[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_cps_bt[u]	cps_bt[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_creat[u]	creat[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_crmp_bs[u]	crmp_bs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_crn[u]	crn[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_crts[u]	crts[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_crtstrn[u]	crtstrn[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_crvnc[u]	crvnc[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_csn[u]	csn[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_cspg_a[u]	cspg_a[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_cspg_a_degr[u]	cspg_a_degr[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_cspg_ab_rest[u]	cspg_ab_rest[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_cspg_b[u]	cspg_b[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_cspg_b_degr[u]	cspg_b_degr[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_cspg_c[u]	cspg_c[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_cspg_c_degr[u]	cspg_c_degr[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_cspg_c_rest[u]	cspg_c_rest[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_cspg_d[u]	cspg_d[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_cspg_e[u]	cspg_e[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_ctbt[u]	ctbt[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_cu2[u]	cu2[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_cyan[u]	cyan[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_cys-L[u]	cys-L[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_cytd[u]	cytd[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_dad-2[u]	dad-2[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_dag_bs[u]	dag_bs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_dcsptn1[u]	dcsptn1[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_dcyt[u]	dcyt[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_debrisoquine[u]	debrisoquine[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_dextran40[u]	dextran40[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_dgchol[u]	dgchol[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_dgsn[u]	dgsn[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_dhdasch[u]	dhdasch[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_dhf[u]	dhf[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_digalsgalside_hs[u]	digalsgalside_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_din[u]	din[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_dlnlcg[u]	dlnlcg[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_dmantipyrine[u]	dmantipyrine[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_dmhptcrn[u]	dmhptcrn[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_dopa[u]	dopa[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_dopas[u]	dopas[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_drib[u]	drib[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_dsT_antigen[u]	dsT_antigen[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_dt5htsu[u]	dt5htsu[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_dur[u]	dur[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_eaflatoxin[u]	eaflatoxin[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_ebastine[u]	ebastine[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_ebastineoh[u]	ebastineoh[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen

Ex_eicoster[u]	eicoster[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_elaid[u]	elaid[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_estradiol[u]	estradiol[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_estradiolglc[u]	estradiolglc[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_estriolglc[u]	estriolglc[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_estronesglc[u]	estronesglc[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_estrones[u]	estrones[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_etha[u]	etha[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_etoh[u]	etoh[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_f1a[u]	f1a[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_fe2[u]	fe2[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_fe3[u]	fe3[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_fe3dcit[u]	fe3dcit[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_fol[u]	fol[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_for[u]	for[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_fru[u]	fru[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_fuc-L[u]	fuc-L[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_fuc13galacglcgal14acglcgalglside_hs[u]	fuc13galacglcgal14acglcgalglside_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_fuc14galacglcgalglside_hs[u]	fuc14galacglcgalglside_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_fucacgallucgalacglcgalglside_hs[u]	fucacgallucgalacglcgalglside_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_fucacngal14acglcgalglside_hs[u]	fucacngal14acglcgalglside_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_fucacngalacglcgalglside_hs[u]	fucacngalacglcgalglside_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_fucfuc12gal14acglcgalglside_hs[u]	fucfuc12gal14acglcgalglside_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_fucfuc132galacglcgal14acglcgalglside_hs[u]	fucfuc132galacglcgal14acglcgalglside_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_fucfucfucgalacglc13galacglcgal14acglcgalglside_hs[u]	fucfucfucgalacglc13galacglcgal14acglcgalglside_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_fucfucfucgalacglcgal14acglcgalglside_hs[u]	fucfucfucgalacglcgal14acglcgalglside_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_fucfucgalacglcgalglside_hs[u]	fucfucgalacglcgalglside_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_fucgal14acglcgalglside_hs[u]	fucgal14acglcgalglside_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_fucgallucgalacglcgalglside_hs[u]	fucgallucgalacglcgalglside_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_fucgalglside_hs[u]	fucgalglside_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_fucneulacnhs[u]	fucneulacnhs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_fum[u]	fum[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_gal[u]	gal[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_galacglcgalglside_hs[u]	galacglcgalglside_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_galam[u]	galam[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_gallfuc12gal14acglcgalglside_hs[u]	gallfuc12gal14acglcgalglside_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_gallfucgalacglcgal14acglcgalglside_hs[u]	gallfucgalacglcgal14acglcgalglside_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_galgalfucfucgalacglcgalacglcgal14acglcgalglside_hs[u]	galgalfucfucgalacglcgalacglcgal14acglcgalglside_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_galgalgalglthcrm_hs[u]	galgalgalglthcrm_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_galur[u]	galur[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_gam26s[u]	gam26s[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_gam[u]	gam[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_glcside_hs[u]	glcside_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_gchola[u]	gchola[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_gd1b2_hs[u]	gd1b2_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_gd1c_hs[u]	gd1c_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_gdchola[u]	gdchola[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_gdp[u]	gdp[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_glc-D[u]	glc-D[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_glcur[u]	glcur[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_glgchlo[u]	glgchlo[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_gln-L[u]	gln-L[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_glrcho[u]	glrcho[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_glutdecho[u]	glutdecho[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_glu-L[u]	glu-L[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_gluala[u]	gluala[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen

Ex_gly[u]	gly[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_glyasn[u]	glyasn[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_glyasp[u]	glyasp[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_glyb[u]	glyb[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_glyc-S[u]	glyc-S[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_glyc[u]	glyc[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_glycogen1500[u]	glycogen1500[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_glygln[u]	glygln[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_glygly[u]	glygly[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_glygly[u]	glygly[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_glygn2[u]	glygn2[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_glygn4[u]	glygn4[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_glygn5[u]	glygn5[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_glyleu[u]	glyleu[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_glymet[u]	glymet[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_glyphe[u]	glyphe[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_glypro[u]	glypro[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_glysar[u]	glysar[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_glytyr[u]	glytyr[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_gmp[u]	gmp[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_gncore1[u]	gncore1[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_gncore2[u]	gncore2[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_gp1c_hs[u]	gp1c_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_gp1calpha_hs[u]	gp1calpha_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_gq1b_hs[u]	gq1b_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_gq1balpha_hs[u]	gq1balpha_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_gsn[u]	gsn[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_gt1a_hs[u]	gt1a_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_gthox[u]	gthox[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_gthrd[u]	gthrd[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_gtp[u]	gtp[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_gua[u]	gua[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_gum[u]	gum[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_gumdchac[u]	gumdchac[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_gumgchol[u]	gumgchol[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_gumtchol[u]	gumtchol[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_h2[u]	h2[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_h2o2[u]	h2o2[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_h2o[u]	h2o[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_h2s[u]	h2s[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_h[u]	h[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_ha[u]	ha[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_ha_deg1[u]	ha_deg1[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_ha_pre1[u]	ha_pre1[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_hco3[u]	hco3[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_hcoumarin[u]	hcoumarin[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_hdca[u]	hdca[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_hdcea[u]	hdcea[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_hestratriol[u]	hestratriol[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_hexc[u]	hexc[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_hg2[u]	hg2[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_his-L[u]	his-L[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_hista[u]	hista[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_hom-L[u]	hom-L[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_homogal[u]	homogal[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_hpdca[u]	hpdca[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen

Ex_hspg[u]	hspg[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_hspg_degr_10[u]	hspg_degr_10[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_hspg_degr_11[u]	hspg_degr_11[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_hspg_degr_12[u]	hspg_degr_12[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_hspg_degr_13[u]	hspg_degr_13[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_hspg_degr_14[u]	hspg_degr_14[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_hspg_degr_15[u]	hspg_degr_15[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_hspg_degr_1[u]	hspg_degr_1[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_hspg_degr_2[u]	hspg_degr_2[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_hspg_degr_3[u]	hspg_degr_3[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_hspg_degr_4[u]	hspg_degr_4[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_hspg_degr_5[u]	hspg_degr_5[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_hspg_degr_6[u]	hspg_degr_6[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_hspg_degr_7[u]	hspg_degr_7[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_hspg_degr_8[u]	hspg_degr_8[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_hspg_degr_9[u]	hspg_degr_9[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_hspg_rest[u]	hspg_rest[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_htaxol[u]	htaxol[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_hxan[u]	hxan[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_i[u]	i[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_idour[u]	idour[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_idp[u]	idp[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_ile-L[u]	ile-L[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_imp[u]	imp[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_inost[u]	inost[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_ins[u]	ins[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_inulin[u]	inulin[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_isobut[u]	isobut[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_isocapr[u]	isocapr[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_isoval[u]	isoval[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_k[u]	k[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_kdo[u]	kdo[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_kesto[u]	kesto[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_kestopt[u]	kestopt[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_kestottr[u]	kestottr[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_ksi[u]	ksi[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_ksi_deg1[u]	ksi_deg1[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_ksii_core2[u]	ksii_core2[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_ksii_core4[u]	ksii_core4[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_l2n2m2mn[u]	l2n2m2mn[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_lac-D[u]	lac-D[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_lac-L[u]	lac-L[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_lacdfluctttr[u]	lacdfluctttr[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_lacndfluchs[u]	lacndfluchs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_lacnfucpt[u]	lacnfucpt[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_lacnnttr[u]	lacnnttr[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_lacnttr[u]	lacnttr[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_lcts[u]	lcts[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_leu-L[u]	leu-L[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_leugly[u]	leugly[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_leuktrA4[u]	leuktrA4[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_leuktrB4[u]	leuktrB4[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_leuktrD4[u]	leuktrD4[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_leuktrE4[u]	leuktrE4[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_leuktrF4[u]	leuktrF4[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_leuleu[u]	leuleu[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen

Ex_levan1000[u]	levan1000[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_levanb[u]	levanb[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_levantr[u]	levantr[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_levantttr[u]	levantttr[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_lgnc[u]	lgnc[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_limnen[u]	limnen[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_lipoate[u]	lipoate[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_lmn2[u]	lmn2[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_lmn30[u]	lmn30[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_lneldc[u]	lneldc[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_lnlc[u]	lnlc[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_lnlnca[u]	lnlnca[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_lnlncg[u]	lnlncg[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_lpchol_hs[u]	lpchol_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_lps_hs[u]	lps_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_lys-L[u]	lys-L[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_m2mn[u]	m2mn[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_mag_hs[u]	mag_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_malt[u]	malt[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_malthp[u]	malthp[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_malths[u]	malths[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_maltpt[u]	maltpt[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_maltrr[u]	maltrr[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_maltttr[u]	maltttr[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_man[u]	man[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_manb[u]	manb[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_manpt[u]	manpt[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_mantr[u]	mantr[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_mantttr[u]	mantttr[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_melib[u]	melib[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_meoh[u]	meoh[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_mepi[u]	mepi[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_mercplaccys[u]	mercplaccys[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_met-L[u]	met-L[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_metala[u]	metala[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_mg2[u]	mg2[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_mn2[u]	mn2[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_mn[u]	mn[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_mqn10[u]	mqn10[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_mqn11[u]	mqn11[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_mqn7[u]	mqn7[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_mqn8[u]	mqn8[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_mqn9[u]	mqn9[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_mthgxl[u]	mthgxl[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_n2m2mn[u]	n2m2mn[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_n2m2mnasn[u]	n2m2mnasn[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_na1[u]	na1[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_nac[u]	nac[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_nad[u]	nad[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_nadp[u]	nadp[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_ncam[u]	ncam[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_neuacntr[u]	neuacntr[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_nh4[u]	nh4[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_nifedipine[u]	nifedipine[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_nmn[u]	nmn[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_no2[u]	no2[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen

Ex_no[u]	no[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_npthl[u]	npthl[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_nrpphr[u]	nrpphr[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_nrpphrs[u]	nrpphrs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_nrvnc[u]	nrvnc[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_o2[u]	o2[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_o2s[u]	o2s[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_oagt3_hs[u]	oagt3_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_oagt3_hs[u]	oagt3_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_ocdca[u]	ocdca[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_ocdcea[u]	ocdcea[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_octa[u]	octa[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_oh1[u]	oh1[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_oligofru4[u]	oligofru4[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_omeprazole[u]	omeprazole[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_onpthl[u]	onpthl[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_orn[u]	orn[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_oxa[u]	oxa[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_pac[u]	pac[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_paf_hs[u]	paf_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_pb[u]	pb[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_pchol_hs[u]	pchol_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_pe_cer1_hs[u]	pe_cer1_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_pe_hs[u]	pe_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_pect[u]	pect[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_pecticgal[u]	pecticgal[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_pectindchac[u]	pectindchac[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_pectingchol[u]	pectingchol[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_pectintchol[u]	pectintchol[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_pephys[u]	pephys[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_perilly[u]	perilly[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_pglyc_hs[u]	pglyc_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_phe-L[u]	phe-L[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_pheacgln[u]	pheacgln[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_phearg[u]	phearg[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_pheme[u]	pheme[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_phyQ[u]	phyQ[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_phyt[u]	phyt[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_pi[u]	pi[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_pnto-R[u]	pnto-R[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_ppa[u]	ppa[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_pregstrn[u]	pregstrn[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_pro-D[u]	pro-D[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_pro-L[u]	pro-L[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_progly[u]	progly[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_prostgf2[u]	prostgf2[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_prostge1[u]	prostge1[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_prostge2[u]	prostge2[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_prostgf2[u]	prostgf2[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_prostgh2[u]	prostgh2[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_prostgi2[u]	prostgi2[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_ps_hs[u]	ps_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_psyl[u]	psyl[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_psylchol[u]	psylchol[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_psyltchol[u]	psyltchol[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_psyltdechol[u]	psyltdechol[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen

Ex_ptdca[u]	ptdca[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_ptrc[u]	ptrc[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_pullulan1200[u]	pullulan1200[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_pydam[u]	pydam[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_pydx[u]	pydx[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_pydxn[u]	pydxn[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_pyr[u]	pyr[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_raffin[u]	raffin[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_rbt[u]	rbt[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_retfa[u]	retfa[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_retinol-9-cis[u]	retinol-9-cis[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_retinol-cis-11[u]	retinol-cis-11[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_retinol[u]	retinol[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_retn[u]	retn[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_retnglc[u]	retnglc[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_rhamnogalurII[u]	rhamnogalurII[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_rhamnogalurI[u]	rhamnogalurI[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_rib-D[u]	rib-D[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_ribflv[u]	ribflv[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_rmn[u]	rmn[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_s2I2fri2m2masn[u]	s2I2fri2m2masn[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_s2I2ri2m2m[u]	s2I2ri2m2m[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_s2I2ri2m2masn[u]	s2I2ri2m2masn[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_s2I2ri2m2mn[u]	s2I2ri2m2mn[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_sT_antigen[u]	sT_antigen[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_sTn_antigen[u]	sTn_antigen[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_sarcs[u]	sarcs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_sbt-D[u]	sbt-D[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_sel[u]	sel[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_ser-D[u]	ser-D[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_ser-L[u]	ser-L[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_sl-L[u]	sl-L[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_so4[u]	so4[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_spc_hs[u]	spc_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_sph1p[u]	sph1p[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_sphmyln_hs[u]	sphmyln_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_sphs1p[u]	sphs1p[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_spmd[u]	spmd[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_srtn[u]	srtn[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_starch1200[u]	starch1200[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_strch1[u]	strch1[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_strch2[u]	strch2[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_strdnc[u]	strdnc[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_stys[u]	stys[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_succ[u]	succ[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_sucr[u]	sucr[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_tag_hs[u]	tag_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_tagat-D[u]	tagat-D[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_taur[u]	taur[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_taxol[u]	taxol[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_tchola[u]	tchola[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_tcynt[u]	tcynt[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_tdchola[u]	tdchola[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_tdechola[u]	tdechola[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_tethex3[u]	tethex3[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_tetpent3[u]	tetpent3[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen

Ex_tetpent6[u]	tetpent6[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_tetter6[u]	tetter6[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_thf[u]	thf[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_thm[u]	thm[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_thmmp[u]	thmmp[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_thmtp[u]	thmtp[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_thr-L[u]	thr-L[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_thym[u]	thym[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_thymd[u]	thymd[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_thyox-L[u]	thyox-L[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_tmndnc[u]	tmndnc[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_tolbutamide[u]	tolbutamide[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_tre[u]	tre[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_triodthy[u]	triodthy[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_triodthysul[u]	triodthysul[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_trp-L[u]	trp-L[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_tststerone[u]	tststerone[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_tststeroneglc[u]	tststeroneglc[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_tststerones[u]	tststerones[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_tsul[u]	tsul[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_ttdca[u]	ttdca[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_txa2[u]	txa2[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_tymsf[u]	tymsf[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_tyr-L[u]	tyr-L[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_udp[u]	udp[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_ump[u]	ump[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_unsdigalur[u]	unsdigalur[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_ura[u]	ura[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_urate[u]	urate[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_urea[u]	urea[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_uri[u]	uri[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_utp[u]	utp[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_vacc[u]	vacc[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_val-L[u]	val-L[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_vitd2[u]	vitd2[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_vitd3[u]	vitd3[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_whddca[u]	whddca[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_whhdca[u]	whhdca[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_whtststerone[u]	whtststerone[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_whtrdca[u]	whtrdca[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_xan[u]	xan[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_xolest2_hs[u]	xolest2_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_xolest_hs[u]	xolest_hs[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_xoltri24[u]	xoltri24[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_xoltri25[u]	xoltri25[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_xoltri27[u]	xoltri27[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_xyl-D[u]	xyl-D[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_xylt[u]	xylt[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_yvite[u]	yvite[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen
Ex_zn2[u]	zn2[u] <=>	-1000	1000		External exchange reaction allowing metabolites to enter the system through the lumen