

Supplemental Table S2A. List of IMC homologs in *S. neurona* SN1 genome.

The 29 IMC proteins identified in *T. gondii* were derived with reference to: Kono, M., Prusty, D., Parkinson, J. and Gilberger, T.W. (2013)

A membranous system in the spotlight: The apicomplexan inner membrane complex and its adaptation to an endoparasitic life style. *Frontiers in Bioscience*. 18. 982-992.

<i>T. gondii</i> gene ID	<i>T. gondii</i> gene name	<i>S. neurona</i> gene ID	Comments
TGME49_019320	TgGAP50	SRCN_2420	
TGME49_023940	TgGAP45	SRCN_4968	
TGME49_049850	TgGAP40	--	Manually refined
TGME49_033030	TgGAP70	--	Absent
TGME49_035470	TgMyoA	--	Manually refined
TGME49_057680	TgMLC1	SRCN_1686	
TGME49_031640	TgALV1	SRCN_2336	
TGME49_216000	TgALV3	SRCN_3639	
TGME49_031630	TgALV4	SRCN_2337	
TGME49_075670	TgALV5	SRCN_3468	
TGME49_026220	TgALV6	--	Absent
TGME49_039770	TgALV7	--	Absent
TGME49_053470	TgALV8	--	Fragments
TGME49_060540	TgALV9	SRCN_3153	
TGME49_024520	TgALV10	SRCN_5144	
TGME49_024530	TgALV11	--	Fragments
TGME49_030210	TgALV12	SRCN_3369	
TGME49_020270	TgIMC6	SRCN_2873	
TGME49_022220	TgIMC7	SRCN_5562	
TGME49_048700	TgIMC12	SRCN_450	
TGME49_110440	TgMORN1	SRCN_2977	
TGME49_058410	TgPhIL1	--	Manually refined
TGME49_009340	TgISP1	SRCN_5775	
TGME49_058540	TgISP2	SRCN_4363	
TGME49_094350	TgISP3	SRCN_3543	
TGME49_063420	TgISP4		Manually refined
TGME49_044470	TgCRMP	SRCN_1290	
TGME49_052880	TgCRMP	SRCN_2572	
TGME49_032940	TgHsp20	SRCN_6477*	

Table S2B. Changes in enzyme:gene assignments for the application of new constraints in *iCS382*

	Previous gene mapping	New gene mapping
1.5.1.34	None	TGME49_285750
3.1.1.32	None	TGME49_313600
2.3.1.41	TGME49_031890 TGME49_094820 TGME49_004560	TGME49_231890
2.7.1.23	TGME49_044700 TGME49_092300	TGME49_244700
2.7.7.13	TGME49_057960 TGME49_072640	TGME49_257960
2.7.7.60	TGME49_016260 TGME49_106260	TGME49_306260
1.10.2.2	TGME49_120220	TGME49_288750 TGME49_320140 TGME49_320220
1.14.16.2	TGME49_012740	TGME49_212740 TGME49_287510
1.2.1.3	TGME49_088450	TGME49_264000 TGME49_288450
1.4.1.1	TGME49_115260	TGME49_203500 TGME49_315260
2.3.1.12	TGME49_006610	TGME49_206610 TGME49_319920
2.3.3.1	TGME49_068890	TGME49_203110 TGME49_268890
2.4.2.1	TGME49_110640	TGME49_307030 TGME49_307040 TGME49_310640
2.6.1.42	TGME49_097850	TGME49_281500 TGME49_297850
2.7.1.137	TGME49_015700	TGME49_215700 TGME49_276170 TGME49_316430
2.7.8.5	TGME49_046530	TGME49_246530 TGME49_254540
3.1.1.5	TGME49_031370	TGME49_226390 TGME49_231370 TGME49_305260 TGME49_306330
3.1.3.4	TGME49_047360	TGME49_230690 TGME49_247360
3.3.1.1	TGME49_025050	TGME49_225050 TGME49_326800
4.4.1.17	TGME49_114040	TGME49_293390 TGME49_314042
6.4.1.2a	TGME49_018560	TGME49_218560 TGME49_284190
6.4.1.2b	TGME49_021320	TGME49_221320 TGME49_284190
1.8.4.9	TGME49_038040	None
2.3.1.168	TGME49_119920	None
2.7.1.32	TGME49_320630	None
2.7.6.3	TGME49_059550	None

Supplemental Table S2C. Predicted impact of single reaction knockouts on parasite growth

Reaction	Description	Subsystem	Relative differences							
			Toxoplasma gondii		Sarcocystis neurona		Differences in carbon source (%)		Differences between Sarco and Toxo (%)	
			With only glucose	With only sucrose	With only glucose	With only sucrose	Toxo: glucose - sucrose	Sarco: glucose - sucrose	Glucose: Toxo - Sarco	Sucrose: Toxo - Sarco
1.1.1.1	alcohol dehydrogenase	Misc	0.999640005	0.999520476	0.999498126	0.999396909	0.011952855	0.010121677	0.014187913	0.012356735
1.1.1.100a	3-oxoacyl-[acp] reductase	Fatty Acid Synthesis	0	0	0	0	0	0	0	0
1.1.1.100b	3-oxoacyl-[acp] reductase	Fatty Acid Synthesis	-1.8753E-17	-3.44621E-17	3.01758E-15	-9.08772E-18	1.57091E-15	3.02667E-13	-3.03633E-13	-2.53743E-15
1.1.1.100c	3-oxoacyl-[acp] reductase	Fatty Acid Synthesis	0	0	0	0	0	0	0	0
1.1.1.100d	3-oxoacyl-[acp] reductase	Fatty Acid Synthesis	-1.8753E-17	-3.44621E-17	3.01758E-15	-9.08772E-18	1.57091E-15	3.02667E-13	-3.03633E-13	-2.53743E-15
1.1.1.100e	3-oxoacyl-[acp] reductase	Fatty Acid Synthesis	-1.8753E-17	-3.44621E-17	3.01758E-15	-9.08772E-18	1.57091E-15	3.02667E-13	-3.03633E-13	-2.53743E-15
1.1.1.100f	3-oxoacyl-[acp] reductase	Fatty Acid Synthesis	0	0	0	0	0	0	0	0
1.1.1.100g	3-oxoacyl-[acp] reductase	Fatty Acid Synthesis	-1.8753E-17	-3.44621E-17	3.01758E-15	-9.08772E-18	1.57091E-15	3.02667E-13	-3.03633E-13	-2.53743E-15
1.1.1.100h	3-oxoacyl-[acp] reductase	Fatty Acid Synthesis	-4.71186E-25	-1.61003E-16	9.74717E-16	1.35057E-16	1.61003E-14	8.3966E-14	-9.74717E-14	-2.9606E-14
1.1.1.102	3-dehydrosphinganine reductase	Phospholipid	0	0	0	0	0	0	0	0
1.1.1.153	sepiapterin reductase	Bioppterin	0	0	-1.03646E-28	0	0	-1.03646E-26	1.03646E-26	0
1.1.1.169	2-dehydropantoate 2-reductase	CoA Synthesis	4.48662E-15	-2.01223E-14	-7.35677E-13	-4.27925E-14	2.46089E-12	-6.92884E-11	7.40164E-11	2.26702E-12
1.1.1.205	IMP dehydrogenase	Purine	-4.85343E-21	-5.93737E-22	4.80379E-26	-4.98388E-27	-4.25967E-19	5.30218E-24	-4.85347E-19	-5.93732E-20
1.1.1.267	1-deoxy-D-xylulose-5-phosphate reductoisomerase	Terpenoid Backbone	0	0	0	0	0	0	0	0
1.1.1.27	L-lactate dehydrogenase	Glycolysis	0.548794889	0.365399255	0.385660047	0.290195542	18.33956337	9.546450591	16.31348411	7.520371338
1.1.1.35a	3-hydroxyacyl-CoA dehydrogenase	Branched Amino Acid	1	1	0.89914251	0.996463615	3.9968E-13	-9.732110504	10.08574896	0.353638453
1.1.1.35b	3-hydroxyacyl-CoA dehydrogenase	Beta Oxidation	1	1	1	1	1	1.4988E-12	-5.9952E-13	8.99281E-13
1.1.1.37	malate dehydrogenase	TCA Cycle	0.760384315	0.909046378	0.427025467	0.992667487	-14.86620629	-56.56420202	33.3358848	-8.362110933
1.1.1.42	isocitrate dehydrogenase (NADP+)	TCA Cycle	0.98592745	0.994576299	0.579376315	0.997577411	-0.864884917	-41.8201096	40.65511352	-0.300111159
1.1.1.44	phosphogluconate dehydrogenase (decarboxylating)	Pentose Phosphate	0.849895296	0.644766931	0	0	20.51283654	0	84.9895296	64.47669307
1.1.1.49	glucose-6-phosphate dehydrogenase	Pentose Phosphate	0.849895296	0.644766931	0	0	20.51283654	0	84.9895296	64.47669307
1.1.1.8	glycerol-3-phosphate dehydrogenase (NAD+)	Phospholipid	4.17692E-28	0	0	-1.98611E-14	4.17692E-26	1.98611E-12	4.17692E-26	1.98611E-12
1.1.1.95	phosphoglycerate dehydrogenase	Serine/Glycine	0.976866879	0.965043468	1	1	1.182341086	9.99201E-13	-2.313312098	-3.495653184
1.10.2.2	ubiquinol-cytochrome-c reductase	Oxidative Phosphorylation	0	0	0	0	0	0	0	0
1.11.1.6	catalase	Misc	4.62452E-13	3.62528E-13	-1.35755E-13	5.64573E-13	9.99237E-12	-7.00328E-11	5.98207E-11	-2.02045E-11
1.14.-.-	sphingolipid delta-4 desaturase	Phospholipid	0	0	0	0	0	0	0	0
1.14.16.2	tyrosine 3-monoxygenase	Bioppterin	1	1	1	1	1	-1.09912E-12	-6.99441E-13	-1.79856E-12
1.14.19.2	acyl-[acyl-carrier-protein] desaturase	Fatty Acid Synthesis	3.17433E-27	-2.93242E-16	3.84044E-16	6.54513E-17	2.93242E-14	3.18593E-14	-3.58693E-14	-3.58693E-14
1.14.19.3	linoleoyl-CoA desaturase	Fatty Acid Synthesis	-4.71186E-25	-1.61003E-16	9.74717E-16	1.35057E-16	1.61003E-14	8.3966E-14	-9.74717E-14	-2.9606E-14
1.14.19.6	Delta12-fatty-acyl desaturase	Fatty Acid Synthesis	6.04204E-27	5.10827E-16	-1.00509E-15	6.54513E-17	-5.10827E-14	-1.07054E-13	1.00509E-13	4.45376E-14
1.15.1.1	superoxide dismutase	Misc	1	1	1	1	1	0	0	0
1.17.1.2a	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	Terpenoid Backbone	0	0	0	0	0	0	0	0
1.17.1.2b	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	Terpenoid Backbone	0	0	0	0	0	0	0	0
1.17.4.1a	ribonucleoside-diphosphate reductase	Purine	1	1	1	1	-1.19904E-12	1.04916E-11	-7.19425E-12	4.4964E-12
1.17.4.1b	ribonucleoside-diphosphate reductase	Pyrimidine	1	1	1	1	4.996E-13	1.03917E-11	-8.29337E-12	1.59872E-12
1.17.4.1c	ribonucleoside-diphosphate reductase	Purine	0	0	0	0	0	0	0	0
1.17.4.1d	ribonucleoside-diphosphate reductase	Pyrimidine	1	1	1	1	-2.9976E-13	4.996E-12	-7.99361E-12	-2.69784E-12
1.17.7.1	(E)-4-hydroxy-3-methylbut-2-enyl-diphosphate synthase	Terpenoid Backbone	0	0	0	0	0	0	0	0
1.2.1.11	aspartate-semialdehyde dehydrogenase	Lysine	0	0	0	0	0	0	0	0
1.2.1.12a	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)	Glycolysis	1	0.722669781	1	1	27.73302188	7.99361E-12	-6.39488E-12	-27.73302188
1.2.1.12b	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)	Glycolysis	1	1	1	1	3.9968E-13	6.19504E-12	-3.9968E-12	1.79856E-12
1.2.1.27	methylmalonate-semialdehyde dehydrogenase (acylating)	Branched Amino Acid	0.948789313	0.981697664	1	1	-3.290835128	0	-5.121068701	-1.830233573
1.2.1.3a	aldehyde dehydrogenase (NAD+)	Glycolysis	0.999640005	0.999520476	0.999498126	0.999396909	0.011952855	0.010121677	0.014187913	0.012356735
1.2.1.3b	aldehyde dehydrogenase (NAD+)	Beta-Alanine	4.48662E-15	-2.01223E-14	-7.35677E-13	-4.27925E-14	2.46089E-12	-6.92884E-11	7.40164E-11	2.26702E-12
1.2.1.3c	aldehyde dehydrogenase (NAD+)	Beta-Alanine	4.48662E-15	-2.01223E-14	-7.35677E-13	-4.27925E-14	2.46089E-12	-6.92884E-11	7.40164E-11	2.26702E-12
1.2.1.41	glutamate-5-semialdehyde dehydrogenase	Arginine/Proline	1	1	1	1	-4.996E-13	9.20375E-12	-2.79776E-12	6.90559E-12
1.2.4.1	pyruvate dehydrogenase (acetyl-transferring)	Glycolysis	2.72596E-15	1.4128E-15	-2.77919E-20	1.47864E-25	1.31316E-13	-2.7792E-18	2.72599E-13	1.4128E-13
1.2.4.2	oxoglutarate dehydrogenase (succinyl-transferring)	TCA Cycle	0.999150613	0.99905425	0.502036447	0.991035437	0.009636247	-48.899899	49.71141657	0.801881324
1.2.4.4a	3-methyl-2-oxobutanoate dehydrogenase	Branched Amino Acid	0.948789313	0.981697664	1	1	-3.290835128	0	-5.121068701	-1.830233573
1.2.4.4b	3-methyl-2-oxobutanoate dehydrogenase	Branched Amino Acid	1	1	1	1	1.69864E-12	0	-9.99201E-14	-1.79856E-12
1.2.4.4c	3-methyl-2-oxobutanoate dehydrogenase	Branched Amino Acid	1	1	0.89914251	0.996463615	3.9968E-13	-9.732110504	10.08574896	0.353638453
1.3.1.26	dihydrodipicolinate reductase	Lysine	0	0	0	0	0	0	0	0
1.3.1.9a	enoyl-[acp] reductase (NADH)	Fatty Acid Synthesis	-1.8753E-17	-3.44621E-17	3.01758E-15	-9.08772E-18	1.57091E-15	3.02667E-13	-3.03633E-13	-2.53743E-15
1.3.1.9b	enoyl-[acp] reductase (NADH)	Fatty Acid Synthesis	0	0	0	0	0	0	0	0
1.3.1.9c	enoyl-[acp] reductase (NADH)	Fatty Acid Synthesis	0	0	0	0	0	0	0	0
1.3.1.9d	enoyl-[acp] reductase (NADH)	Fatty Acid Synthesis	-1.8753E-17	-3.44621E-17	3.01758E-15	-9.08772E-18	1.57091E-15	3.02667E-13	-3.03633E-13	-2.53743E-15
1.3.1.9e	enoyl-[acp] reductase (NADH)	Fatty Acid Synthesis	-1.8753E-17	-3.44621E-17	3.01758E-15	-9.08772E-18	1.57091E-15	3.02667E-13	-3.03633E-13	-2.53743E-15
1.3.1.9f	enoyl-[acp] reductase (NADH)	Fatty Acid Synthesis	-1.8753E-17	-3.44621E-17	3.01758E-15	-9.08772E-18	1.57091E-15	3.02667E-13	-3.03633E-13	-2.53743E-15
1.3.1.9g	enoyl-[acp] reductase (NADH)	Fatty Acid Synthesis	0	0	0	0	0	0	0	0
1.3.1.9h	enoyl-[acp] reductase (NADH)	Fatty Acid Synthesis	-4.71186E-25	-1.61003E-16	9.74717E-16	1.35057E-16	1.61003E-14	8.3966E-14	-9.74717E-14	-2.9606E-14
1.3.3.1	dihydroorotate oxidase	Pyrimidine	-1.12084E-22	-1.76455E-21	-6.84211E-24	5.69964E-22	1.65246E-19	-5.76806E-20	-1.05241E-20	-2.33451E-19
1.3.3.3	coproporphyrinogen oxidase	Porphyrin	0	0	0	0	0	0	0	0
1.3.3.4	protoporphyrinogen oxidase	Porphyrin	0	0	0	0	0	0	0	0
1.3.3.6	acyl-CoA oxidase	Beta Oxidation	1	1	1	1	1	1.4988E-12	-5.9952E-13	8.99281E-13
1.3.5.1	succinate dehydrogenase (ubiquinone)	TCA Cycle	0.760384315	0.909046378	0.427025467	0.992667487	-14.86620629	-56.56420202	33.3358848	-8.362110933
1.3.99.10	isovaleryl-CoA dehydrogenase	Branched Amino Acid	1	1	1	1	1.69864E-12	0	-9.99201E-14	-1.79856E-12

1.3.99.2a	butyryl-CoA dehydrogenase	Branched Amino Acid	0.948789313	0.981697664	1	1	-3.290835128	0	-5.121068701	-1.830233573
1.3.99.2b	butyryl-CoA dehydrogenase	Branched Amino Acid	1	1	0.89914251	0.996463615	3.9968E-13	-9.732110504	10.08574896	0.353638453
1.4.1.1	alanine dehydrogenase	Glutamate/Glutamine	0	0	0	0	0	0	0	0
1.4.1.2	glutamate dehydrogenase	Glutamate/Glutamine	0.864449817	0.906324076	0.8683807	0.960327533	-4.187425978	-9.194683251	-0.393088359	-5.400345632
1.4.1.4	glutamate dehydrogenase (NADP+)	Glutamate/Glutamine	0.999448234	0.999156256	0.994367883	1	0.029197795	-0.563211742	0.508035139	-0.084374399
1.4.3.21	primary-amine oxidase	Beta-Alanine	4.48662E-15	-2.01223E-14	-7.35677E-13	-4.27925E-14	2.46089E-12	-6.92884E-11	7.40164E-11	2.26702E-12
1.4.4.2	glycine dehydrogenase (decarboxylating)	Serine/Glycine	1	1	1	1	0	1.09912E-11	-8.19345E-12	2.79776E-12
1.5.1.12a	1-pyrroline-5-carboxylate dehydrogenase	Arginine/Proline	0	0	0	0	0	0	0	0
1.5.1.12b	1-pyrroline-5-carboxylate dehydrogenase	Arginine/Proline	0.894815379	0.879726105	0.910636622	0.907551908	1.508927435	0.308471409	-1.582124258	-2.782580284
1.5.1.2	pyrroline-5-carboxylate reductase	Arginine/Proline	0	0	0	0	0	0	0	0
1.5.1.3a	dihydrofolate reductase	Folate	1.86129E-13	6.86762E-14	2.16651E-13	1.03878E-15	1.17452E-11	2.15612E-11	-3.0522E-12	6.76374E-12
1.5.1.3b	dihydrofolate reductase	Folate	0.906581551	0.926728226	4.35651E-13	3.63175E-13	-2.01466753	7.24769E-12	90.65815507	92.6728226
1.5.1.34	6,7-dihydropteridine reductase	Bioppterin	1	1	1	1	0	-1.09912E-12	-6.99441E-13	-1.79856E-12
1.5.3.13a	N1-acetylpolyamine oxidase	Polyamines	1	1	1	1	0	0	0	0
1.5.3.13b	N1-acetylpolyamine oxidase	Polyamines	4.48662E-15	-2.01223E-14	-7.35677E-13	-4.27925E-14	2.46089E-12	-6.92884E-11	7.40164E-11	2.26702E-12
1.5.5.1	electron-transferring-flavoprotein dehydrogenase	Oxidative Phosphorylation	0.897758154	0.947473008	0.89914251	0.996463615	-4.97148536	-9.732110504	-0.138435611	-4.899060755
1.5.99.6	spermidine dehydrogenase	Beta-Alanine	4.48662E-15	-2.01223E-14	-7.35677E-13	-4.27925E-14	2.46089E-12	-6.92884E-11	7.40164E-11	2.26702E-12
1.6.2.4	NADPH-hemoprotein reductase	Oxidative Phosphorylation	0.869089507	0.677612809	0	0	19.14766981	0	86.9089507	67.7612809
1.6.5.3	NADH dehydrogenase (ubiquinone)	Oxidative Phosphorylation	0	0	0	0	0	0	0	0
1.8.1.4a	dihydrolipeoyl dehydrogenase	Currency Exchange	2.72596E-15	1.4128E-15	-2.77919E-20	1.47864E-25	1.31316E-13	-2.7792E-18	2.72599E-13	1.4128E-13
1.8.1.4b	dihydrolipeoyl dehydrogenase	Currency Exchange	1.6705E-24	8.304E-13	-2.45993E-27	2.18619E-12	-8.304E-11	-2.18619E-10	1.67296E-22	-1.35579E-10
1.8.1.7	glutathione-disulfide reductase	Currency Exchange	1	1	1	1	0	0	0	0
1.8.1.9	thioredoxin-disulfide reductase	Currency Exchange	-1.36307E-27	4.70842E-25	5.8043E-27	7.52105E-28	-4.72205E-23	5.0522E-25	-7.16737E-25	4.7009E-23
1.8.3.1	sulfite oxidase	Sulfur	1	1	1	1	0	0	0	0
1.8.4.9	adenyllyl-sulfate reductase (glutathione)	Sulfur	1	1	1	1	0	0	0	0
1.9.3.1	cytochrome-c oxidase	Oxidative Phosphorylation	0	0	0	0	0	0	0	0
2.1.1.10	homocysteine S-methyltransferase	Cysteine/Methionine	1	1	1	1	5.9952E-13	6.79456E-12	-1.9984E-12	4.19664E-12
2.1.1.45	thymidylate synthase	Pyrimidine	0	-7.13833E-31	-5.61836E-28	-7.48722E-27	7.13833E-29	6.92539E-25	5.61836E-26	7.48651E-25
2.1.2.1	glycine hydroxymethyltransferase	Serine/Glycine	0	8.26888E-28	0	0	-8.26888E-26	0	0	8.26888E-26
2.1.2.10	aminomethyltransferase	Serine/Glycine	1	1	1	1	0	1.09912E-11	-8.19345E-12	2.79776E-12
2.1.2.11	3-methyl-2-oxobutanoate hydroxymethyltransferase	CoA Synthesis	4.48662E-15	-2.01223E-14	-7.35677E-13	-4.27925E-14	2.46089E-12	-6.92884E-11	7.40164E-11	2.26702E-12
2.1.3.2	aspartate carbamoyltransferase	Pyrimidine	-1.12084E-22	-1.76455E-21	-6.84211E-24	5.69964E-22	1.65246E-19	-5.76806E-20	-1.05241E-20	-2.33451E-19
2.1.3.3	ornithine carbamoyltransferase	Arginine/Proline	0.972219727	0.967916414	0.975155086	0.970208936	0.430331239	0.494614976	-0.293535925	-0.229252188
2.2.1.1a	transketolase	Pentose Phosphate	0.850237067	0.645396232	0	0	20.48408356	0	85.02370672	64.53962316
2.2.1.1b	transketolase	Pentose Phosphate	0.850237067	0.645396232	0	0	20.48408356	0	85.02370672	64.53962316
2.2.1.2	transaldolase	Glycolysis	0.850237067	0.645396232	0	0	20.48408356	0	85.02370672	64.53962316
2.2.1.7	1-deoxy-D-xylulose-5-phosphate synthase	Terpenoid Backbone	0	0	0	0	0	0	0	0
2.3.1.117	2,3,4,5-tetrahydroxyproline-2,6-dicarboxylate N-succinyltransferase	Lysine	0	0	0	0	0	0	0	0
2.3.1.12	dihydrolipeoyllysine-residue acetyltransferase	Glycolysis	2.72596E-15	1.4128E-15	-2.77919E-20	1.47864E-25	1.31316E-13	-2.7792E-18	2.72599E-13	1.4128E-13
2.3.1.15	glycerol-3-phosphate O-acyltransferase	Phospholipid	-1.79849E-28	3.46964E-16	1.83656E-22	-3.27301E-12	-3.46964E-14	3.27301E-10	-1.83656E-20	3.27336E-10
2.3.1.16a	acetyl-CoA C-acyltransferase	Branched Amino Acid	1	1	0.89914251	0.996463615	3.9968E-13	-9.732110504	10.08574896	0.353638453
2.3.1.16b	Acetyl-CoA C-acyltransferase	Beta Oxidation	1	1	1	1	0	1.4988E-12	-5.9952E-13	8.99281E-13
2.3.1.168a	dihydrolipeoyllysine-residue (2-methylpropanoyl)transferase	Branched Amino Acid	0.948789313	0.981697664	1	1	-3.290835128	0	-5.121068701	-1.830233573
2.3.1.168b	dihydrolipeoyllysine-residue (2-methylpropanoyl)transferase	Branched Amino Acid	1	1	0.89914251	0.996463615	3.9968E-13	-9.732110504	10.08574896	0.353638453
2.3.1.168c	dihydrolipeoyllysine-residue (2-methylpropanoyl)transferase	Branched Amino Acid	1	1	1	1	1.69864E-12	0	-9.99201E-14	-1.79856E-12
2.3.1.180	beta-ketoacyl-acyl-carrier-protein synthase III	Fatty Acid Synthesis	0	0	0	0	0	0	0	0
2.3.1.24	sphingosine N-acyltransferase	Phospholipid	0	0	0	0	0	0	0	0
2.3.1.31	homoserine O-acetyltransferase	Cysteine/Methionine	1	1	1	1	0	0	0	0
2.3.1.37	5-aminolevulinatase synthase	Porphyrin	0	0	0	0	0	0	0	0
2.3.1.39	[acp] S-malonyltransferase	Fatty Acid Synthesis	0	0	0	0	0	0	0	0
2.3.1.4	glucosamine-phosphate N-acetyltransferase	Amino Sugar	0	0	0	0	0	0	0	0
2.3.1.41a	beta-ketoacyl-acyl-carrier-protein synthase I	Fatty Acid Synthesis	-1.8753E-17	-3.44621E-17	3.01758E-15	-9.08772E-18	1.57091E-15	3.02667E-13	-3.03633E-13	-2.53743E-15
2.3.1.41b	beta-ketoacyl-acyl-carrier-protein synthase I	Fatty Acid Synthesis	0	0	0	0	0	0	0	0
2.3.1.41c	beta-ketoacyl-acyl-carrier-protein synthase I	Fatty Acid Synthesis	0	0	0	0	0	0	0	0
2.3.1.41d	beta-ketoacyl-acyl-carrier-protein synthase I	Fatty Acid Synthesis	-1.8753E-17	-3.44621E-17	3.01758E-15	-9.08772E-18	1.57091E-15	3.02667E-13	-3.03633E-13	-2.53743E-15
2.3.1.41e	beta-ketoacyl-acyl-carrier-protein synthase I	Fatty Acid Synthesis	-1.8753E-17	-3.44621E-17	3.01758E-15	-9.08772E-18	1.57091E-15	3.02667E-13	-3.03633E-13	-2.53743E-15
2.3.1.41f	beta-ketoacyl-acyl-carrier-protein synthase I	Fatty Acid Synthesis	-1.8753E-17	-3.44621E-17	3.01758E-15	-9.08772E-18	1.57091E-15	3.02667E-13	-3.03633E-13	-2.53743E-15
2.3.1.41g	beta-ketoacyl-acyl-carrier-protein synthase I	Fatty Acid Synthesis	-4.71186E-25	-1.61003E-16	9.74717E-16	1.35057E-16	1.61003E-14	8.3966E-14	-9.74717E-14	-2.9606E-14
2.3.1.50	serine C-palmitoyltransferase	Phospholipid	0	0	0	0	0	0	0	0
2.3.1.51	1-acylglycerol-3-phosphate O-acyltransferase	Phospholipid	-1.79849E-28	3.46964E-16	1.83656E-22	-3.27301E-12	-3.46964E-14	3.27301E-10	-1.83656E-20	3.27336E-10
2.3.1.57a	diamine N-acetyltransferase	Polyamines	4.48662E-15	-2.01223E-14	-7.35677E-13	-4.27925E-14	2.46089E-12	-6.92884E-11	7.40164E-11	2.26702E-12
2.3.1.57b	diamine N-acetyltransferase	Polyamines	1	1	1	1	0	0	0	0
2.3.1.57c	diamine N-acetyltransferase	Polyamines	1	1	1	1	0	0	0	0
2.3.1.61	dihydrolipeoyllysine-residue succinyltransferase	TCA Cycle	0.999150613	0.99905425	0.502036447	0.991035437	0.009636247	-48.899899	49.71141657	0.801881324
2.3.1.8	phosphate acetyltransferase	Misc	0.999640005	1	0.999498126	1	-0.035999496	-0.050187409	0.014187913	6.09512E-12
2.3.1.85	fatty acid synthase I	Fatty Acid Synthesis	7.14357E-17	3.1732E-17	-2.83989E-18	7.8356E-16	3.97037E-15	-7.864E-14	7.42756E-15	-7.51828E-14
2.3.1.9	acetyl-CoA C-acyltransferase	Beta Oxidation	1	1	1	1	1.69864E-12	0	-9.99201E-14	-1.79856E-12
2.3.3.1	citrate (Si)-synthase	TCA Cycle	1	1	0.427025467	0.992667487	-3.9968E-13	-56.56420202	57.29745332	0.733251305
2.3.3.5	2-methylcitrate synthase	MC Cycle	0.912306258	0.981502922	0.89914251	0.996463615	-6.919666435	-9.732110504	1.316374729	-1.49606934

2.3.3.8	ATP citrate synthase	TCA Cycle	2.3982E-28	-3.29691E-28	3.06965E-28	-2.62074E-26	5.69511E-26	2.65143E-24	-6.71453E-27	2.58777E-24
2.4.1.198	phosphatidylinositol N-acetylglucosaminyltransferase	Phospholipid	1	1	1	1	0	0	0	0
2.4.1.83	dolichyl-phosphate beta-D-mannosyltransferase	Amino Sugar	1	1	1	1	0	0	0	0
2.4.2.1a	purine-nucleoside phosphorylase	Purine	1	1	1	1	-9.99201E-13	1.12022E-11	-4.996E-12	7.20535E-12
2.4.2.1b	purine-nucleoside phosphorylase	Purine	1	1	1	1	1.9984E-13	4.89608E-12	-2.29816E-12	2.39808E-12
2.4.2.1c	purine-nucleoside phosphorylase	Purine	1	1	1	1	0	1.21902E-11	-6.99441E-12	5.19584E-12
2.4.2.1d	purine-nucleoside phosphorylase	Purine	1	1	1	1	-8.99281E-13	6.19504E-12	-6.39488E-12	6.99441E-13
2.4.2.1e	purine-nucleoside phosphorylase	Purine	1	1	1	1	0	6.99441E-12	-7.99361E-12	-9.99201E-13
2.4.2.1f	purine-nucleoside phosphorylase	Nicotinate	1	1	1	1	-1.9984E-12	1.45883E-11	-1.09912E-11	5.59552E-12
2.4.2.1g	purine-nucleoside phosphorylase	Nicotinate	1	1	1	1	-6.99441E-13	6.4948E-12	-4.09672E-12	3.09752E-12
2.4.2.1h	purine-nucleoside phosphorylase	Pyrimidine	1	1	1	1	-2.9976E-13	1.0103E-11	-3.29736E-12	7.10543E-12
2.4.2.1i	purine-nucleoside phosphorylase	Purine	1	1	1	1	2.9976E-13	4.09672E-12	-3.39728E-12	3.9968E-13
2.4.2.1j	purine-nucleoside phosphorylase	Purine	1	1	1	1	9.99201E-13	1.03917E-11	-4.996E-12	4.39648E-12
2.4.2.10	orotate phosphoribosyltransferase	Pyrimidine	-1.12084E-22	-1.76455E-21	-6.84211E-24	5.69964E-22	1.65246E-19	-5.76806E-20	-1.05241E-20	-2.33451E-19
2.4.2.11	nicotinate phosphoribosyltransferase	Nicotinate	1	1	1	1	-1.09912E-12	1.13909E-11	-6.39488E-12	6.09512E-12
2.4.2.8a	hypoxanthine phosphoribosyltransferase	Purine	1	1	1	1	-1.09912E-12	1.18017E-11	-4.09672E-12	8.80407E-12
2.4.2.8b	hypoxanthine phosphoribosyltransferase	Purine	1	1	1	1	-9.99201E-13	9.29257E-12	-7.09433E-12	3.19744E-12
2.4.2.8c	hypoxanthine phosphoribosyltransferase	Purine	1	1	1	1	-1.19904E-12	6.39488E-12	-4.19664E-12	3.39728E-12
2.4.2.8d	hypoxanthine phosphoribosyltransferase	Purine	1	1	1	1	-8.99281E-13	6.19504E-12	-6.39488E-12	6.99441E-13
2.4.2.9	uracil phosphoribosyltransferase	Pyrimidine	1	1	1	1	-9.99201E-14	1.0103E-11	-3.29736E-12	6.90559E-12
2.5.1.1	dimethylallyltransferase	Terpenoid Backbone	0	0	0	0	0	0	0	0
2.5.1.10	geranyltransferase	Terpenoid Backbone	0	0	0	0	0	0	0	0
2.5.1.15a	dihydropteroate synthase	Folate	1	1	1	1	9.99201E-14	0	-1.9984E-13	-2.9976E-13
2.5.1.15b	dihydropteroate synthase	Folate	1	1	1	1	9.99201E-14	0	0	-9.99201E-14
2.5.1.19	3-phosphoshikimate 1-carboxyvinyltransferase	Shikimate	1	1	1	1	-1.9984E-13	0	-3.9968E-13	-1.9984E-13
2.5.1.29	farnesyltransferase	Terpenoid Backbone	0	0	0	0	0	0	0	0
2.5.1.31a	di-trans,poly-cis-decaprenylcistransferase	Terpenoid Backbone	0	0	0	0	0	0	0	0
2.5.1.31b	di-trans,poly-cis-decaprenylcistransferase	Terpenoid Backbone	0	0	0	0	0	0	0	0
2.5.1.54	3-deoxy-7-phosphoheptulonate synthase	Shikimate	1	1	1	1	-1.9984E-13	0	-3.9968E-13	-1.9984E-13
2.5.1.6	methionine adenosyltransferase	Cysteine/Methionine	1	1	1	1	5.9952E-13	6.79456E-12	-1.9984E-12	4.19664E-12
2.5.1.61	hydroxymethylbilane synthase	Porphyrin	0	0	0	0	0	0	0	0
2.6.99.2	pyridoxal 5-phosphate synthase	Misc	0	0	0	0	0	0	0	0
2.6.1.1a	aspartate transaminase	Glutamate/Glutamine	4.1122E-28	-2.35636E-28	0	0	6.46856E-26	0	4.1122E-26	-2.35636E-26
2.6.1.1b	aspartate transaminase	Cysteine/Methionine	1	1	1	1	0	0	0	0
2.6.1.13	ornithine aminotransferase	Arginine/Proline	0.894815379	0.879726105	0.910636622	0.907551908	1.508927435	0.308471409	-1.582124258	-2.782580284
2.6.1.16	glutamine-fructose-6-phosphate transaminase (isomerizing)	Amino Sugar	0	0	0	0	0	0	0	0
2.6.1.17	succinyldiaminopimelate transaminase	Lysine	0	0	0	0	0	0	0	0
2.6.1.42a	branched-chain-amino-acid transaminase	Branched Amino Acid	1	1	1	1	1.69864E-12	0	-9.99201E-14	-1.79856E-12
2.6.1.42b	branched-chain-amino-acid transaminase	Branched Amino Acid	7.24182E-14	-7.01904E-14	-7.35677E-13	-4.27925E-14	1.42609E-11	-6.92884E-11	8.08095E-11	-2.73979E-12
2.6.1.42c	branched-chain-amino-acid transaminase	Branched Amino Acid	1	1	0.89914251	0.996463615	3.9968E-13	-9.732110504	10.08574896	0.353638453
2.6.1.52	phosphoserine transaminase	Serine/Glycine	0.976866879	0.965043468	1	1	1.182341086	9.99201E-13	-2.313312098	-3.495653184
2.6.1.85	aminodeoxychorismate synthase	Folate	1	1	1	1	-1.9984E-13	0	-3.9968E-13	-1.9984E-13
2.7.1.1a	hexokinase	Glycolysis	1	5.64243E-17	1	0	100	100	0	5.64243E-15
2.7.1.107	diacylglycerol kinase	Phospholipid	1	1	1	1	-2.9976E-13	5.59552E-12	-1.39888E-12	4.4964E-12
2.7.1.137	phosphatidylinositol 3-kinase	Phospholipid	1	1	1	1	0	0	0	0
2.7.1.148	4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase	Terpenoid Backbone	0	0	0	0	0	0	0	0
2.7.1.15a	ribokinase	Pentose Phosphate	1	1	1	1	0	0	0	0
2.7.1.15b	ribokinase	Pentose Phosphate	1	1	1	1	0	0	0	0
2.7.1.20	adenosine kinase	Purine	0.994618602	0.997468073	0.994522118	0.997794033	-0.284947066	-0.327191532	0.009648411	-0.032596055
2.7.1.23	NAD+ kinase	Nicotinate	1	1	1	1	-3.9968E-13	7.39409E-12	-6.59472E-12	1.19904E-12
2.7.1.24	dephospho-CoA kinase	CoA Synthase	4.48662E-15	-2.01223E-14	-7.35677E-13	-4.27925E-14	2.46089E-12	-6.92884E-11	7.40164E-11	2.26702E-12
2.7.1.25	adenylyl-sulfate kinase	Sulfur	1	1	1	1	0	0	0	0
2.7.1.32	choline kinase	Phospholipid	0	0	0	0	0	0	0	0
2.7.1.33	pantothenate kinase	CoA Synthase	4.48662E-15	-2.01223E-14	-7.35677E-13	-4.27925E-14	2.46089E-12	-6.92884E-11	7.40164E-11	2.26702E-12
2.7.1.39	homoserine kinase	Serine/Glycine	1	1	1	1	0	0	0	0
2.7.1.40a	pyruvate kinase	Glycolysis	0.670137833	0.456466454	0.900813799	0.733913126	21.36713785	16.69006728	-23.06759655	-27.74466712
2.7.1.40b	pyruvate kinase	Glycolysis	0	0	0	0	0	0	0	0
2.7.1.67	1-phosphatidylinositol 4-kinase	Phospholipid	1	1	1	1	0	0	0	0
2.7.1.68	1-phosphatidylinositol-4-phosphate 5-kinase	Phospholipid	1	1	1	1	0	0	0	0
2.7.1.71	shikimate kinase	Shikimate	1	1	1	1	-1.9984E-13	0	-3.9968E-13	-1.9984E-13
2.7.1.90	diphosphate-fructose-6-phosphate 1-phosphotransferase	Glycolysis	0.79556231	0.531160757	0.609323085	0.452122084	26.4401553	15.72010011	18.62392249	7.903867299
2.7.2.11	glutamate 5-kinase	Arginine/Proline	1	1	1	1	-4.996E-13	9.20375E-12	-2.79776E-12	6.90559E-12
2.7.2.2	carbamate kinase	Pyrimidine	0.972876419	0.968686792	0.975809627	0.970890264	0.41896268	0.491936312	-0.293320795	-0.220347163
2.7.2.3a	phosphoglycerate kinase	Glycolysis	1	0.722669781	1	1	27.73302188	7.99361E-12	-6.39488E-12	-27.73302188
2.7.2.3b	phosphoglycerate kinase	Glycolysis	1	1	1	1	3.9968E-13	6.19504E-12	-3.9968E-12	1.79856E-12
2.7.2.4	aspartate kinase	Lysine	0	0	0	0	0	0	0	0
2.7.4.14a	cytidylate kinase	Pyrimidine	0.993880493	0.992764142	-2.48128E-15	-3.83112E-15	0.111635046	1.34984E-13	99.38804928	99.27641424
2.7.4.14b	cytidylate kinase	Pyrimidine	0.999955332	0.999947124	0.999956321	0.999953365	0.000820753	0.000295562	-9.89011E-05	-0.000624092
2.7.4.14c	cytidylate kinase	Pyrimidine	1.6114E-25	4.96196E-25	7.29802E-21	7.11182E-27	-3.35056E-23	7.29801E-19	-7.29786E-19	4.89084E-23

2.7.4.3a	adenylate kinase	Purine	-2.78012E-13	-1.47936E-14	-3.23602E-12	3.24461E-13	-2.63218E-11	-3.56048E-10	2.958E-10	-3.39255E-11
2.7.4.3b	adenylate kinase	Purine	1	1	1	1	0	8.59313E-12	-5.29576E-12	3.29736E-12
2.7.4.6a	nucleoside-diphosphate kinase	Pyrimidine	0	0	0	0	0	0	0	0
2.7.4.6b	nucleoside-diphosphate kinase	Purine	0	0	0	0	0	0	0	0
2.7.4.6c	nucleoside-diphosphate kinase	Pyrimidine	0.994005181	0.992911415	-1.71564E-27	1.11926E-23	0.109376639	-1.11943E-21	99.40051814	99.2911415
2.7.4.6d	nucleoside-diphosphate kinase	Purine	1	1	1	1	-4.996E-13	3.69704E-12	-2.498E-12	1.69864E-12
2.7.4.6e	nucleoside-diphosphate kinase	Pyrimidine	0	0	0	0	0	0	0	0
2.7.4.6f	nucleoside-diphosphate kinase	Purine	0	0	0	0	0	0	0	0
2.7.4.6g	nucleoside-diphosphate kinase	Pyrimidine	0	0	0	0	0	0	0	0
2.7.4.6h	nucleoside-diphosphate kinase	Pyrimidine	0	0	0	0	0	0	0	0
2.7.4.6i	nucleoside-diphosphate kinase	Pyrimidine	1	1	1	1	-3.9968E-13	6.99441E-12	-3.39728E-12	3.9968E-12
2.7.4.8a	guanylate kinase	Purine	-7.00644E-20	-9.27747E-22	7.08152E-23	-2.92078E-20	-6.91367E-18	2.92786E-18	-7.01352E-18	2.828E-18
2.7.4.8b	guanylate kinase	Purine	1	1	1	1	0	6.99441E-12	-7.99361E-12	-9.99201E-13
2.7.4.9a	dTMP kinase	Pyrimidine	0	-2.96039E-29	9.58867E-26	0	2.96039E-27	9.58867E-24	-9.58867E-24	-2.96039E-27
2.7.4.9b	dTMP kinase	Pyrimidine	1	1	1	1	-9.99201E-14	6.09512E-12	-3.79696E-12	2.39808E-12
2.7.6.1	ribose-phosphate diphosphokinase	Pentose Phosphate	-3.21357E-25	3.26838E-15	1.34431E-23	-3.46028E-15	-3.26838E-13	3.46028E-13	-1.37644E-21	6.72866E-13
2.7.6.3	2-amino-4-hydroxy-6-hydroxymethylidihydropteridine diphosphokinase	Folate	1	1	1	1	9.99201E-14	0	-1.9984E-13	-2.9976E-13
2.7.7.13	mannose-1-phosphate guanylyltransferase	Misc	0	0	0	0	0	0	0	0
2.7.7.15	choline-phosphate cytidylyltransferase	Phospholipid	0	0	0	0	0	0	0	0
2.7.7.18	Nicotinate-nucleotide adenyllyltransferase	Nicotinate	1	1	1	1	-3.9968E-13	8.49321E-12	-5.19584E-12	3.69704E-12
2.7.7.23	UDP-N-acetylglucosamine diphosphorylase	Amino Sugar	0	0	0	0	0	0	0	0
2.7.7.27	glucose-1-phosphate adenyllyltransferase	Misc	0	0	0	0	0	0	0	0
2.7.7.3	panthetheine-phosphate adenyllyltransferase	CoA Synthesis	4.48662E-15	-2.01223E-14	-7.35677E-13	-4.27925E-14	2.46089E-12	-6.92884E-11	7.40164E-11	2.26702E-12
2.7.7.4	sulfate adenyllyltransferase	Sulfur	1	1	1	1	0	0	0	0
2.7.7.41	phosphatidate cytidylyltransferase	Phospholipid	0	0	0	0	0	0	0	0
2.7.7.60	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	Terpenoid Backbone	0	0	0	0	0	0	0	0
2.7.8.11	CDP-diacylglycerol-inositol 3-phosphatidyltransferase	Phospholipid	0	0	0	0	0	0	0	0
2.7.8.15	UDP-N-acetylglucosamine-dolichyl-phosphate	Amino Sugar	1	1	1	1	0	0	0	0
2.7.8.2	diacylglycerol cholinephosphotransferase	Phospholipid	0	0	0	0	0	0	0	0
2.7.8.27	sphingomyelin synthase	Phospholipid	0	0	0	0	0	0	0	0
2.7.8.5	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase	Phospholipid	1	1	1	1	0	0	0	0
2.7.8.8	CDP-diacylglycerol-serine O-phosphatidyltransferase	Phospholipid	0	0	0	0	0	0	0	0
2.8.3.8	acetate CoA-transferase	Misc	1	1	1	1	0	0	0	0
3.1.1.31	6-phosphogluconolactonase	Pentose Phosphate	0.849895296	0.644766931	0	0	20.51283654	0	84.9895296	64.47669307
3.1.1.32	phospholipase A1	Phospholipid	1	1	1	1	-1.29896E-12	0	-1.79856E-12	-4.996E-13
3.1.1.4	phospholipase A2	Phospholipid	1	1	1	1	0	7.29417E-12	-2.19824E-12	5.09592E-12
3.1.1.5a	lysophospholipase	Phospholipid	1	1	1	1	0	7.29417E-12	-2.19824E-12	5.09592E-12
3.1.1.5b	lysophospholipase	Phospholipid	1	1	1	1	-1.29896E-12	0	-1.79856E-12	-4.996E-13
3.1.2.14a	oleoyl-[acyl-carrier-protein] hydrolase	Fatty Acid Synthesis	3.17433E-27	-2.93242E-16	3.84044E-16	6.54513E-17	2.93242E-14	3.18593E-14	-3.84044E-14	-3.58693E-14
3.1.2.14b	oleoyl-[acyl-carrier-protein] hydrolase	Fatty Acid Synthesis	1	1	1	1	-5.9952E-13	3.19744E-12	-3.79696E-12	0
3.1.2.14c	oleoyl-[acyl-carrier-protein] hydrolase	Fatty Acid Synthesis	-4.71186E-25	-1.61003E-16	9.74717E-16	1.35057E-16	1.61003E-14	8.3966E-14	-9.74717E-14	-2.9606E-14
3.1.2.14d	oleoyl-[acyl-carrier-protein] hydrolase	Fatty Acid Synthesis	-4.71186E-25	-1.61003E-16	9.74717E-16	1.35057E-16	1.61003E-14	8.3966E-14	-9.74717E-14	-2.9606E-14
3.1.2.14e	oleoyl-[acyl-carrier-protein] hydrolase	Fatty Acid Synthesis	-4.71186E-25	-1.61003E-16	9.74717E-16	1.35057E-16	1.61003E-14	8.3966E-14	-9.74717E-14	-2.9606E-14
3.1.2.2	palmitoyl-CoA hydrolase	Fatty Acid Synthesis	1	1	1	1	-9.99201E-13	7.99361E-12	-4.996E-12	3.9968E-12
3.1.2.4	3-hydroxyisobutyryl-CoA hydrolase	Branched Amino Acid	0.948789313	0.981697664	1	1	-3.290835128	0	-5.121068701	-1.830233573
3.1.2.6	hydroxyacylglutathione hydrolase	Misc	1	1	1	1	0	0	0	0
3.1.3.11	fructose-bisphosphatase	Glycolysis	1	1	1	1	-2.9976E-13	1.21014E-11	-5.4956E-12	6.90559E-12
3.1.3.25	inositol-phosphate phosphatase	Phospholipid	0	0	0	0	0	0	0	0
3.1.3.3	phosphoserine phosphatase	Serine/Glycine	0.976866879	0.965043468	1	1	1.182341086	9.99201E-13	-2.313312098	-3.495653184
3.1.3.37	sedoheptulose-bisphosphatase	Glycolysis	1	1	1	1	0	4.39648E-12	-3.69704E-12	6.99441E-13
3.1.3.4	phosphatidate phosphatase	Phospholipid	1.64372E-25	3.31021E-28	4.377E-29	-5.1165E-28	1.64041E-23	5.5542E-26	1.64329E-23	8.42671E-26
3.1.3.5a	5'-nucleotidase	Purine	1	1	1	1	0	0	0	0
3.1.3.5b	5'-nucleotidase	Pyrimidine	1	1	1	1	-4.996E-13	0	-7.99361E-13	-2.9976E-13
3.1.3.5c	5'-nucleotidase	Pyrimidine	1	1	1	1	-9.99201E-14	0	-4.996E-13	-3.9968E-13
3.1.3.5d	5'-nucleotidase	Purine	1	1	1	1	1.9984E-13	7.39409E-12	-3.29736E-12	3.89688E-12
3.1.3.5e	5'-nucleotidase	Purine	1	1	1	1	0	1.21902E-11	-6.99441E-12	5.19584E-12
3.1.3.5f	5'-nucleotidase	Nicotinate	1	1	1	1	-1.9984E-12	1.45883E-11	-1.09912E-11	5.59552E-12
3.1.3.5g	5'-nucleotidase	Purine	1	1	1	1	-8.99281E-13	6.19504E-12	-6.39488E-12	6.99441E-13
3.1.3.5h	5'-nucleotidase	Nicotinate	1	1	1	1	-6.99441E-13	6.4948E-12	-4.09672E-12	3.09752E-12
3.1.3.5i	5'-nucleotidase	Purine	1	1	1	1	0	6.99441E-12	-7.99361E-12	-9.99201E-13
3.1.3.5j	5'-nucleotidase	Purine	1	1	1	1	0	8.59313E-12	-5.29576E-12	3.29736E-12
3.1.3.5k	2'-Deoxyuridine 5'-monophosphate phosphohydrolase	Pyrimidine	1	1	1	1	-2.9976E-13	1.0103E-11	-3.29736E-12	7.10543E-12
3.1.4.11	phosphoinositide phospholipase C	Phospholipid	1	1	1	1	0	0	0	0
3.1.4.17a	3',5'-cyclic-nucleotide phosphodiesterase	Purine	1	1	1	1	-4.996E-13	1.07914E-11	-6.4948E-12	4.79616E-12
3.1.4.17b	3',5'-cyclic-nucleotide phosphodiesterase	Purine	1	1	1	1	0	1.9984E-12	2.9976E-13	2.29816E-12
3.1.4.46	glycerophosphodiester phosphodiesterase	Phospholipid	1	1	1	1	-8.99281E-13	1.14908E-11	-6.99441E-12	5.39568E-12
3.3.1.1	adenosylhomocysteinease	Cysteine/Methionine	1	1	1	1	5.9952E-13	6.79456E-12	-1.9984E-12	4.19664E-12
3.5.1.18	succinyl-diaminopimelate desuccinylase	Lysine	0	0	0	0	0	0	0	0
3.5.1.19	nicotinamidase	Nicotinate	1	1	1	1	-1.9984E-12	1.45883E-11	-1.09912E-11	5.59552E-12

3.5.1.89	N-acetylglucosaminylphosphatidylinositol deacetylase	Phospholipid	1	1	1	1	0	0	0	0
3.5.2.3	dihydroorotase	Pyrimidine	-1.12084E-22	-1.76455E-21	-6.84211E-24	5.69964E-22	1.65246E-19	-5.76806E-20	-1.05241E-20	-2.33451E-19
3.5.3.6	arginine deiminase	Arginine/Proline	0.972219727	0.967916414	0.975155086	0.970208936	0.430331239	0.494614976	-0.293535925	-0.229252188
3.5.4.12	dCMP aminohydrolase	Pyrimidine	0.999955332	0.999947124	0.999956321	0.999953365	0.000820753	0.000295562	-9.89011E-05	-0.000624092
3.5.4.16	GTP cyclohydrolase I	Folate	0	5.9655E-14	-1.03646E-28	0	-5.9655E-12	-1.03646E-26	1.03646E-26	5.9655E-12
3.5.4.2	adenine deaminase	Purine	1	1	1	1	-1.69864E-12	6.29496E-12	-6.19504E-12	1.79856E-12
3.5.4.4a	adenosine deaminase	Purine	1	1	1	1	-8.99281E-13	5.19584E-12	-3.29736E-12	2.79776E-12
3.5.4.4b	adenosine deaminase	Purine	1	1	1	1	9.99201E-13	1.03917E-11	-4.996E-12	4.39648E-12
3.5.4.6	AMP deaminase	Purine	1	1	1	1	-6.99441E-13	1.10911E-11	-8.09353E-12	3.69704E-12
3.6.1.-	Hydrolases	Folate	1	1	1	1	-9.99201E-14	0	-2.9976E-13	-1.9984E-13
3.6.1.1	inorganic diphosphatase	Misc	1	1	1	1	0	0	0	0
3.6.1.22a	NAD+ diphosphatase	Nicotinate	1	1	1	1	-1.9984E-12	1.45883E-11	-1.09912E-11	5.59552E-12
3.6.1.22b	NAD+ diphosphatase	Nicotinate	1	1	1	1	-9.99201E-14	1.15019E-11	-3.9968E-12	7.60503E-12
3.6.1.23	dUTP diphosphatase	Pyrimidine	1	1	1	1	-3.9968E-13	6.99441E-12	-3.39728E-12	3.9968E-12
3.6.1.29	bis(5'-adenosyl)-triphosphatase	Purine	1	1	1	1	0	0	0	0
3.6.1.5a	apyrase	Purine	1	1	1	1	0	0	0	0
3.6.1.5b	apyrase	Purine	1	1	1	1	-5.9952E-13	0	-8.99281E-13	-2.9976E-13
3.6.1.5c	apyrase	Pyrimidine	1	1	1	1	-1.29896E-12	-8.69305E-12	3.29736E-12	-4.09672E-12
3.6.1.5d	apyrase	Pyrimidine	1	1	1	1	-3.9968E-13	1.09912E-11	-1.14908E-11	-9.99201E-14
3.6.1.5e	apyrase	Purine	1	1	1	1	2.9976E-13	6.79456E-12	-1.4988E-12	4.996E-12
3.6.1.5f	apyrase	Purine	1	1	1	1	0	1.1191E-11	-8.29337E-12	2.89768E-12
3.6.1.5g	apyrase	Pyrimidine	1	1	1	1	3.9968E-13	1.41998E-11	-3.59712E-12	1.02029E-11
3.6.1.5h	apyrase	Pyrimidine	1	1	1	1	-1.9984E-13	1.80966E-11	-8.99281E-12	9.30367E-12
3.6.1.5i	apyrase	Purine	1	1	1	1	-4.996E-13	3.69704E-12	-2.498E-12	1.69864E-12
3.6.1.5j	apyrase	Purine	1	1	1	1	1.9984E-13	0	0	-1.9984E-13
3.6.1.5k	apyrase	Pyrimidine	1	1	1	1	-1.4988E-12	6.09512E-12	-3.59712E-12	3.9968E-12
3.6.1.5l	apyrase	Pyrimidine	1	1	1	1	3.9968E-13	1.05915E-11	-1.03917E-11	-1.9984E-13
3.6.1.7	acylphosphatase	Misc	0.999640005	1	0.999498126	1	-0.035999496	-0.050187409	0.014187913	6.09512E-12
3.6.3.12	K+-transporting ATPase	Extracellular Transport	1	1	1	1	0	0	0	0
3.6.3.14	H+-transporting two-sector ATPase	Oxidative Phosphorylation	0	0	0	0	0	0	0	0
3.6.3.16	arsenite-transporting ATPase	Extracellular Transport	1	1	1	1	0	0	0	0
3.6.3.25	sulfate-transporting ATPase	Extracellular Transport	1	1	1	1	0	0	0	0
3.6.3.4	Cu2+-exporting ATPase	Extracellular Transport	1	1	1	1	0	0	0	0
3.6.3.44	xenobiotic-transporting ATPase	Extracellular Transport	1	1	1	1	0	0	0	0
3.6.3.6	H+-exporting ATPase	Extracellular Transport	1	1	0	0.182691906	-9.99201E-14	-18.26919065	100	81.73080935
3.6.3.8	Ca2+-transporting ATPase	Extracellular Transport	1	1	1	1	0	0	0	0
4.1.1.20	diaminopimelate decarboxylase	Lysine	0	0	0	0	0	0	0	0
4.1.1.23	orotidine-5'-phosphate decarboxylase	Pyrimidine	-1.12084E-22	-1.76455E-21	-6.84211E-24	5.69964E-22	1.65246E-19	-5.76806E-20	-1.05241E-20	-2.33451E-19
4.1.1.36	phosphopantothencysteine decarboxylase	CoA Synthesis	4.48662E-15	-2.01223E-14	-7.35677E-13	-4.27925E-14	2.46089E-12	-6.92884E-11	7.40164E-11	2.26702E-12
4.1.1.37	uroporphyrinogen decarboxylase	Porphyrin	0	0	0	0	0	0	0	0
4.1.1.49	phosphoenolpyruvate carboxylase (ATP)	Glycolysis	1	1	1	1	3.9968E-13	5.29576E-12	-3.09752E-12	1.79856E-12
4.1.1.65	phosphatidylserine decarboxylase	Phospholipid	0	0	0	0	0	0	0	0
4.1.2.13a	fructose-bisphosphate aldolase	Glycolysis	0.79556231	0.531160757	0.609323085	0.452122084	26.4401553	15.72010011	18.62392249	7.903867299
4.1.2.13b	fructose-bisphosphate aldolase	Pentose Phosphate	1	1	1	1	0	6.19504E-12	-5.69544E-12	4.996E-13
4.1.2.25	dihydroneopterin aldolase	Folate	1	1	1	1	-9.99201E-14	0	-2.9976E-13	-1.9984E-13
4.1.2.4	deoxyribose-phosphate aldolase	Pentose Phosphate	1	1	1	1	0	0	0	0
4.1.3.30	methylisocitrate lyase	MC Cycle	0.912306258	0.981502922	0.89914251	0.996463615	-6.919666435	-9.732110504	1.316374729	-1.49606934
4.1.3.38	aminodeoxychorismate lyase	Folate	1	1	1	1	9.99201E-14	0	-3.9968E-13	-4.996E-13
4.2.1.10	3-dehydroquinate dehydratase	Shikimate	1	1	1	1	9.99201E-14	0	-3.9968E-13	-4.996E-13
4.2.1.11	phosphopyruvate hydratase	Glycolysis	1.23067E-15	2.05338E-15	-9.59269E-17	1.25441E-15	-8.22711E-14	-1.35034E-13	1.3266E-13	7.9897E-14
4.2.1.17a	enoyl-CoA hydratase	Beta Oxidation	1	1	1	1	0	1.4988E-12	-5.9952E-13	8.99281E-13
4.2.1.17b	enoyl-CoA hydratase	Branched Amino Acid	1	1	0.89914251	0.996463615	3.9968E-13	-9.732110504	10.08574896	0.353638453
4.2.1.17c	enoyl-CoA hydratase	Branched Amino Acid	0.948789313	0.981697664	1	1	-3.290835128	0	-5.121068701	-1.830233573
4.2.1.18	methylglutaconyl-CoA hydratase	Branched Amino Acid	1	1	1	1	1.69864E-12	0	-9.99201E-14	-1.79856E-12
4.2.1.2	fumarate hydratase	TCA Cycle	0.760384315	0.909046378	0.427025467	0.992667487	-14.86620629	-56.56420202	33.3358848	-8.362110933
4.2.1.22	cystathionine beta-synthase	Cysteine/Methionine	1	1	1	1	0	0	0	0
4.2.1.24	porphobilinogen synthase	Porphyrin	0	0	0	0	0	0	0	0
4.2.1.3	aconitate hydratase	TCA Cycle	0.98592745	0.994576299	0.579376315	0.997577411	-0.864884917	-41.8201096	40.65511352	-0.300111159
4.2.1.52	dihydrodipicolinate synthase	Lysine	0	0	0	0	0	0	0	0
4.2.1.60a	3-hydroxydecanoyl-[acp] dehydratase	Fatty Acid Synthesis	-1.8753E-17	-3.44621E-17	3.01758E-15	-9.08772E-18	1.57091E-15	3.02667E-13	-3.03633E-13	-2.53743E-15
4.2.1.60b	3-hydroxydecanoyl-[acp] dehydratase	Fatty Acid Synthesis	-1.8753E-17	-3.44621E-17	3.01758E-15	-9.08772E-18	1.57091E-15	3.02667E-13	-3.03633E-13	-2.53743E-15
4.2.1.60c	3-hydroxydecanoyl-[acp] dehydratase	Fatty Acid Synthesis	0	0	0	0	0	0	0	0
4.2.1.60d	3-hydroxydecanoyl-[acp] dehydratase	Fatty Acid Synthesis	0	0	0	0	0	0	0	0
4.2.1.60e	3-hydroxydecanoyl-[acp] dehydratase	Fatty Acid Synthesis	0	0	0	0	0	0	0	0
4.2.1.61a	3-hydroxydecanoyl-[acp] dehydratase	Fatty Acid Synthesis	-1.8753E-17	-3.44621E-17	3.01758E-15	-9.08772E-18	1.57091E-15	3.02667E-13	-3.03633E-13	-2.53743E-15
4.2.1.61b	3-hydroxydecanoyl-[acp] dehydratase	Fatty Acid Synthesis	-1.8753E-17	-3.44621E-17	3.01758E-15	-9.08772E-18	1.57091E-15	3.02667E-13	-3.03633E-13	-2.53743E-15
4.2.1.61c	3-hydroxydecanoyl-[acp] dehydratase	Fatty Acid Synthesis	-4.71186E-25	-1.61003E-16	9.74717E-16	1.35057E-16	1.61003E-14	8.3966E-14	-9.74717E-14	-2.9606E-14
4.2.1.75	uroporphyrinogen-III synthase	Porphyrin	0	0	0	0	0	0	0	0
4.2.1.79	2-methylcitrate dehydratase	MC Cycle	0.912306258	0.981502922	0.89914251	0.996463615	-6.919666435	-9.732110504	1.316374729	-1.49606934

O5	phosphate[a]	Organellar Transport	1	1	1	1	-9.99201E-14	6.19504E-12	-5.09592E-12	1.19904E-12
O6	diphosphate[a]	Organellar Transport	-1.30297E-24	-1.11443E-23	-9.33344E-15	6.10553E-16	9.84136E-22	-9.94399E-13	9.33344E-13	-6.10553E-14
O7	NADH[a]	Organellar Transport	1	1	1	1	2.9976E-13	6.09512E-12	-4.4964E-12	1.29896E-12
O8	NAD+[a]	Organellar Transport	1	1	1	1	2.9976E-13	6.09512E-12	-4.4964E-12	1.29896E-12
O9	NADPH[a]	Organellar Transport	1.89016E-15	2.58917E-16	-1.65325E-15	-5.96428E-16	1.63124E-13	-1.05682E-13	3.5434E-13	8.55345E-14
O10	NADP+[a]	Organellar Transport	6.63723E-28	5.22748E-16	7.08811E-16	1.20648E-15	-5.22748E-14	-4.97671E-14	-7.08811E-14	-6.83734E-14
O11	H+[a]	Organellar Transport	1	1	1	1	-9.99201E-14	5.79536E-12	-4.39648E-12	1.4988E-12
O12	Fe2+[m]	Organellar Transport	0	0	0	0	0	0	0	0
O13	O2[a]	Organellar Transport	-4.71186E-25	-1.61003E-16	9.74717E-16	1.35057E-16	1.61003E-14	8.3966E-14	-9.74717E-14	-2.9606E-14
O14	H2O[a]	Organellar Transport	0.979767695	1	0.980206818	1	-2.023230515	-1.979318242	-0.043912273	3.9968E-12
O15	CO2[a]	Organellar Transport	1.47889E-14	1.39398E-15	1.71963E-14	2.15545E-14	1.3395E-12	-4.3582E-13	-2.40739E-13	-2.01606E-12
O16	H2O2[a]	Organellar Transport	1	1	1	1	0	0	0	0
O17	NH3[a]	Organellar Transport	0	0	0	0	0	0	0	0
O18	CoA[a]	Organellar Transport	6.95535E-24	-2.51629E-25	9.51168E-16	3.04616E-12	7.20698E-22	-3.04521E-10	-9.51168E-14	-3.04616E-10
O19	palmitoyl-CoA[a]	Organellar Transport	2.32486E-16	-7.04341E-16	3.24818E-15	4.22005E-17	9.36827E-14	3.20598E-13	-3.01569E-13	-7.46541E-14
O20	glycerone-phosphate[a]	Organellar Transport	1	1	1	1	-1.09912E-12	5.4956E-12	-5.29576E-12	1.29896E-12
O21	phosphoenolpyruvate[a]	Organellar Transport	0	0	0	0	0	0	0	0
O22	3-phospho-D-glycerate[a]	Organellar Transport	1	1	1	1	3.9968E-13	6.19504E-12	-3.9968E-12	1.79856E-12
O23	ATP[er]	Organellar Transport	1	1	1	1	-2.9976E-13	5.59552E-12	-1.39888E-12	4.4964E-12
O24	ADP[er]	Organellar Transport	1	1	1	1	-2.9976E-13	5.59552E-12	-1.39888E-12	4.4964E-12
O25	CTP[er]	Organellar Transport	0	0	0	0	0	0	0	0
O26	CMP[er]	Organellar Transport	0	0	-2.34289E-28	-1.04552E-29	0	-2.23833E-26	2.34289E-26	1.04552E-27
O27	phosphate[er]	Organellar Transport	0	0	0	0	0	0	0	0
O28	NAD+[er]	Organellar Transport	1	1	1	1	0	0	0	0
O29	NADH[er]	Organellar Transport	1	1	1	1	0	0	0	0
O30	NADP+[er]	Organellar Transport	0	0	0	0	0	0	0	0
O31	NADPH[er]	Organellar Transport	0	0	0	0	0	0	0	0
O32	H+[er]	Organellar Transport	0	0	0	0	0	0	0	0
O33	O2[er]	Organellar Transport	0	0	0	0	0	0	0	0
O34	H2O[er]	Organellar Transport	0	0	-6.66072E-27	-9.92225E-28	0	-5.66849E-25	6.66072E-25	9.92225E-26
O35	CO2[er]	Organellar Transport	0	0	0	0	0	0	0	0
O36	L-serine[er]	Organellar Transport	0	0	0	0	0	0	0	0
O37	CoA[er]	Organellar Transport	-1.0518E-14	0	3.4968E-16	2.94505E-16	-1.0518E-12	5.51749E-15	-1.08677E-12	-2.94505E-14
O38	acyl[er]	Organellar Transport	1	1	1	1	-8.99281E-13	1.14908E-11	-6.99441E-12	5.39568E-12
O39	acyl-CoA[er]	Organellar Transport	5.52121E-15	1.52672E-16	3.69321E-16	3.5346E-16	5.36854E-13	1.58614E-15	5.15189E-13	-2.00788E-14
O40	palmitoyl-CoA[er]	Organellar Transport	0	0	0	0	0	0	0	0
O41	1D-myo-inositol-3-phosphate[er]	Organellar Transport	0	0	0	0	0	0	0	0
O42	CDP-choline[er]	Organellar Transport	0	0	0	0	0	0	0	0
O43	sn-glycerol-3-phosphate[er]	Organellar Transport	-1.79849E-28	3.46964E-16	1.83656E-22	-3.27301E-12	-3.46964E-14	3.27301E-10	-1.83656E-20	3.27336E-10
O44	sn-glycero-3-phosphocholine[er]	Organellar Transport	1	1	1	1	-8.99281E-13	1.14908E-11	-6.99441E-12	5.39568E-12
O45	ATP[m]	Organellar Transport	0	0	0	0	0	0	0	0
O46	ADP[m]	Organellar Transport	0	0	0	0	0	0	0	0
O47	AMP[m]	Organellar Transport	1	1	1	1	-1.39888E-12	1.02918E-11	-6.4948E-12	5.19584E-12
O48	CTP[m]	Organellar Transport	4.48662E-15	-2.01223E-14	-7.35677E-13	-4.27925E-14	-2.46089E-12	-6.92884E-11	7.40164E-11	2.26702E-12
O49	phosphate[m]	Organellar Transport	0	0	0	0	0	0	0	0
O50	diphosphate[m]	Organellar Transport	-4.7817E-30	3.4199E-29	0	-2.87355E-12	-3.89807E-27	2.87355E-10	-4.7817E-28	2.87355E-10
O51	NAD+[m]	Organellar Transport	0.977800111	0.930750725	0.995392603	0.900843645	4.704938583	9.454895818	-1.759249175	2.99070806
O52	NADH[m]	Organellar Transport	0.977800111	0.930750725	0.995392603	0.900843645	4.704938583	9.454895818	-1.759249176	2.99070806
O53	NADP+[m]	Organellar Transport	0.866575338	0.673292085	0.119316711	0.161596402	19.32832536	-4.227969104	74.72586269	51.16956823
O54	NADPH[m]	Organellar Transport	0.866575338	0.673292085	0.119316711	0.161596402	19.32832536	-4.227969104	74.72586269	51.16956823
O55	H+[m]	Organellar Transport	0.818367088	0.619066474	0.198555082	0.195957263	19.93006142	0.25978189	61.98120062	42.3109211
O56	H2O2[m]	Organellar Transport	1.84973E-26	8.57786E-13	-6.78311E-13	6.31664E-26	-8.57786E-11	-6.78311E-11	6.78311E-11	8.57786E-11
O57	O2[m]	Organellar Transport	0	0	0	0	0	0	0	0
O58	H2O[m]	Organellar Transport	0	0	0	0	0	0	0	0
O59	CO2[m]	Organellar Transport	0.772264551	0.923249308	0.448626565	0.996872268	-15.09847572	-54.82457034	32.36379854	-7.362296075
O60	NH3[m]	Organellar Transport	0.864449817	0.906324076	0.8683807	0.960327533	-4.187425978	-9.194683251	-0.393088359	-5.400345632
O61	L-aspartate[m]	Organellar Transport	0	0	0	0	0	0	0	0
O62	L-cysteine[m]	Organellar Transport	4.48662E-15	-2.01223E-14	-7.35677E-13	-4.27925E-14	2.46089E-12	-6.92884E-11	7.40164E-11	2.26702E-12
O63	L-isoleucine[m]	Organellar Transport	1	1	0.89914251	0.996463615	3.9968E-13	-9.732110504	10.08574896	0.353638453
O64	L-leucine[m]	Organellar Transport	1	1	1	1	1.69864E-12	0	-9.99201E-14	-1.79856E-12
O65	L-valine[m]	Organellar Transport	7.24182E-14	-7.01904E-14	-7.35677E-13	-4.27925E-14	1.42609E-11	-6.92884E-11	8.08095E-11	-2.73979E-12
O66	L-serine[m]	Organellar Transport	0	8.26888E-28	0	0	0	0	0	8.26888E-26
O67	glycine[m]	Organellar Transport	0	0	0	0	0	0	0	0
O68	L-glutamate[m]	Organellar Transport	0.954756273	0.955623124	0.963177284	0.959732094	-0.086685039	0.344519085	-0.842101131	-0.410897007
O69	CoA[m]	Organellar Transport	1	1	1	1	-1.29896E-12	1.42886E-11	-1.05915E-11	4.996E-12
O70	pyruvate[m]	Organellar Transport	0.918907513	0.984931918	0.904435911	0.997011751	-6.602440543	-9.257584019	1.447160216	-1.20798326
O71	citrate[m]	Organellar Transport	2.3982E-28	-3.29691E-28	3.06965E-28	-2.62074E-26	5.69511E-26	2.65143E-24	-6.71453E-27	2.58777E-24
O72	(S)-dihydroorotate[m]	Organellar Transport	-1.12084E-22	-1.76455E-21	-6.84211E-24	5.69964E-22	1.65246E-19	-5.76806E-20	-1.05241E-20	-2.33451E-19
O73	orotate[m]	Organellar Transport	-1.12084E-22	-1.76455E-21	-6.84211E-24	5.69964E-22	1.65246E-19	-5.76806E-20	-1.05241E-20	-2.33451E-19

O74	(R)-pantoate[m]	Organelar Transport	4.48662E-15	-2.01223E-14	-7.35677E-13	-4.27925E-14	2.46089E-12	-6.92884E-11	7.40164E-11	2.26702E-12
O75	pantothenate[m]	Organelar Transport	4.48662E-15	-2.01223E-14	-7.35677E-13	-4.27925E-14	2.46089E-12	-6.92884E-11	7.40164E-11	2.26702E-12
O76	dimethylallyl-diphosphate[a/m]	Organelar Transport	0	0	0	0	0	0	0	0
O77	isopentenyl-diphosphate[a/m]	Organelar Transport	0	0	0	0	0	0	0	0
O78	N6-(1,2-Dicarboxyethyl)-AMP[m]	Organelar Transport	1	1	1	1	-4.996E-13	1.02918E-11	-5.89528E-12	4.89608E-12
O79	5-aminolevulinate[a/m]	Organelar Transport	0	0	0	0	0	0	0	0
O80	tetrahydrofolate[m]	Organelar Transport	1.3008E-16	1.40728E-13	-2.20075E-13	3.64707E-13	-1.40598E-11	-5.84782E-11	2.20205E-11	-2.2398E-11
O81	5,10-methylenetetrahydrofolate[m]	Organelar Transport	0	-7.13833E-31	-5.61836E-28	-7.48722E-27	7.13833E-29	6.92539E-25	5.61836E-26	7.48651E-25
O82	coproporphyrinogen-III	Organelar Transport	0	0	0	0	0	0	0	0
O83	protoporphyrinogen-IX	Organelar Transport	0	0	0	0	0	0	0	0
O84	heme	Organelar Transport	0	0	0	0	0	0	0	0
O85	ferrocytochrome-c	Organelar Transport	1	1	1	1	1.9984E-13	3.39728E-12	-6.99441E-13	2.498E-12
T1	spermine import	Extracellular Transport	4.48662E-15	-2.01223E-14	-7.35677E-13	-4.27925E-14	2.46089E-12	-6.92884E-11	7.40164E-11	2.26702E-12
T2	arginine transport	Extracellular Transport	0	0	0	0	0	0	0	0
T3	ornithine transport	Extracellular Transport	0.999377281	0.998631242	0.996424789	1	0.074603861	-0.357521054	0.295249137	-0.136875778
T4	glucose transport	Extracellular Transport	7.65506E-17	1	0	1	-100	-100	7.65506E-15	0
T5	folic acid transport	Extracellular Transport	0.906581551	0.926728226	4.35651E-13	3.63175E-13	-2.01466753	7.24769E-12	90.65815507	92.6728226
T6	adenosine transport	Extracellular Transport	0.995417994	0.998380555	0.995518996	0.998570171	-0.29625608	-0.305117543	-0.010100154	-0.018961617
T7	tryptophan transport	Extracellular Transport	0	0	0	0	0	0	0	0
T8	cysteine transport	Extracellular Transport	0	0	-7.15859E-30	0	0	-7.15859E-28	7.15859E-28	0
T9	histidine transport	Extracellular Transport	0	0	0	0	0	0	0	0
T10	threonine transport	Extracellular Transport	0	0	0	0	0	0	0	0
T11	isoleucine transport	Extracellular Transport	0	0	1.80239E-31	0	0	1.80239E-29	-1.80239E-29	0
T12	leucine transport	Extracellular Transport	0	-4.1123E-29	0	0	4.1123E-27	0	0	-4.1123E-27
T13	methionine transport	Extracellular Transport	0	0	0	0	0	0	0	0
T14	phenylalanine transport	Extracellular Transport	0	0	0	0	0	0	0	0
T15	tyrosine transport	Extracellular Transport	0	0	0	0	0	0	0	0
T16	valine transport	Extracellular Transport	4.49316E-15	-2.30703E-15	-1.42802E-32	0	6.80019E-13	-1.42802E-30	4.49316E-13	-2.30703E-13
T17	cholesterol transport	Extracellular Transport	0	0	0	0	0	0	0	0
T18	choline transport	Extracellular Transport	9.70979E-43	-1.91626E-28	1.44923E-45	1.13793E-28	1.91626E-26	-1.13793E-26	9.69529E-41	-3.0542E-26
T19	adenine transport	Extracellular Transport	1	1	1	1	7.99361E-13	9.10383E-12	-1.09912E-12	7.20535E-12
T20	serine transport	Extracellular Transport	1	1	1	1	-1.19904E-12	7.69385E-12	-4.39648E-12	4.4964E-12
T21	Iron (II) ion transport	Extracellular Transport	0	0	0	0	0	0	0	0
T22	(S)-lactate transport	Extracellular Transport	0.548794889	0.365399255	0.385660047	0.290195542	18.33965337	9.546450591	16.31348411	7.520371338
X1	oxidative stress	Stress	1	1	1	1	0	0	0	0
D1	water	Diffusion	0.986123569	0.88771845	0.934298806	0.996772524	9.840511915	-6.247371827	5.182476297	-10.90540744
D2	oxygen import	Diffusion	0	0	0	0	0	0	0	0
D3	CO2 export	Diffusion	0	0	0	0	0	0	0	0
D4	NH3 import	Diffusion	0.900095002	0.942046245	0.884293839	0.970922374	-4.195124207	-8.662853429	1.580116314	-2.887612908
D5	diphosphate	Diffusion	0.898765729	0.662465977	0.728872861	0.606656791	23.62997518	12.22160696	16.98928686	5.580918629
D6	phosphate	Diffusion	0.673014687	0.665758983	0.494175477	0.60933143	0.725570451	-11.51559532	17.88392104	5.642755267
D7	ethanol	Diffusion	0.999640005	0.999520476	0.999498126	0.999396909	0.011952855	0.010121677	0.014187913	0.012356735
Demand	acyl carrier protein	Demand	-3.20318E-27	-6.44494E-27	1.50644E-24	-2.38004E-22	3.24175E-25	2.3951E-20	-1.50964E-22	2.37998E-20
Sink1	4-aminobutanoate	Sink	4.48662E-15	-2.01223E-14	-7.35677E-13	-4.27925E-14	2.46089E-12	-6.92884E-11	7.40164E-11	2.26702E-12
Sink2	formate	Sink	0	5.9655E-14	-1.03646E-28	0	-5.9655E-12	-1.03646E-26	1.03646E-26	5.9655E-12
Sink3	3-acetamidopropanal	Sink	4.48662E-15	-2.01223E-14	-7.35677E-13	-4.27925E-14	2.46089E-12	-6.92884E-11	7.40164E-11	2.26702E-12
Sink4	5,10-methylenetetrahydrofolate[m]	Sink	1.8907E-13	1.3936E-13	8.7226E-16	3.67628E-13	4.97095E-12	-3.66756E-11	1.88198E-11	-2.28268E-11
Sink5	glycolaldehyde	Sink	1	1	1	1	-9.99201E-14	0	-2.9976E-13	-1.9984E-13
Sink6	3,4-dihydroxy-L-phenylalanine	Sink	1	1	1	1	0	-1.09912E-12	-6.99441E-13	-1.79856E-12
3.2.1.20	alpha-glucosidase	Misc	1	5.64243E-17	1	0	100	100	0	5.64243E-15
T23	Sucrose transport	Extracellular Transport	1	5.64243E-17	1	0	100	100	0	5.64243E-15
2.7.1.1b	hexokinase	Misc	1	5.64243E-17	1	0	100	100	0	5.64243E-15
T24	Fructose transport	Extracellular Transport	1	1	1	1	0	0	0	0
4.3.1.19a	L-threonine ammonia-lyase (2-oxobutanoate-forming)	Misc	#N/A	#N/A	1	1	#N/A	6.59472E-12	#N/A	#N/A
4.3.1.19b	L-serine ammonia-lyase	Misc	#N/A	#N/A	0.994234223	1	#N/A	-0.576577721	#N/A	#N/A
T25	2-oxobutanoate	Extracellular Transport	1	1	1	1	0	6.59472E-12	-3.9968E-12	2.59792E-12
1.1.1.25	shikimate dehydrogenase	Shikimate	1	1	#N/A	#N/A	9.99201E-14	#N/A	#N/A	#N/A
1.1.1.31	3-hydroxyisobutyrate dehydrogenase	Branched Amino Acid	0.948789313	0.981697664	#N/A	#N/A	-3.290835128	#N/A	#N/A	#N/A
2.4.1.117	dolichyl-phosphate beta-glucosyltransferase	Amino Sugar	1	1	#N/A	#N/A	0	#N/A	#N/A	#N/A
2.4.1.142	chitobiosyldiphosphodolichol beta-mannosyltransferase	Amino Sugar	1	1	#N/A	#N/A	0	#N/A	#N/A	#N/A
2.4.2.3	uridine phosphorylase	Pyrimidine	1	1	#N/A	#N/A	-1.29896E-12	#N/A	#N/A	#N/A
2.8.1.2	3-mercaptopyruvate sulfurtransferase	Cysteine/Methionine	1	1	#N/A	#N/A	0	#N/A	#N/A	#N/A
3.5.4.5	cytidine deaminase	Pyrimidine	1	1	#N/A	#N/A	-4.996E-13	#N/A	#N/A	#N/A
4.1.3.4	hydroxymethylglutaryl-CoA lyase	Branched Amino Acid	1	1	#N/A	#N/A	1.69864E-12	#N/A	#N/A	#N/A
6.2.1.16	acetoacetate-CoA ligase	Misc	1	1	#N/A	#N/A	1.69864E-12	#N/A	#N/A	#N/A