

0 Enzyme	Abrev	EC Number	Location	Pathway	Reaction	Lower Bound	Upper Bound	Thermodynamics
1 ATP Objective Flux	Obj_atp			Objective	atp -->	0	999999	
2 Insulin Availability	Ex_ins			Signaling/Hormone	insulin[e] <==>	-999999	0	
3 Glucose Exchange	Ex_gluc			Exchange	gluc[e] <==>	-999999	999999	
4 Lactate Exchange	Ex_lac			Exchange	lac[e] <==>	-999999	999999	
5 Pyruvate Exchange	Ex_pyr			Exchange	pyr[e] <==>	0	0	
6 Palmitate Exchange	Ex_pal			Exchange	pal[e] <==>	-999999	999999	
7 Propanoate Input	Ex_prop			Exchange	prop[e] <==>	0	0	
8 Butanoate Input	Ex_but			Exchange	but[e] <==>	0	0	
9 Pentanoate Input	Ex_5c			Exchange	5c-fa[e] <==>	0	0	
10 Hexanoate Input	Ex_6c			Exchange	6c-fa[e] <==>	0	0	
11 Octanoate Input	Ex_8c			Exchange	8c-fa[e] <==>	0	0	
12 Nonanoate Input	Ex_9c			Exchange	9c-fa[e] <==>	0	0	
13 Decanoate Input	Ex_10c			Exchange	10c-fa[e] <==>	0	0	
14 Dodecanoate Input	Ex_12c			Exchange	12c-fa[e] <==>	0	0	
15 Tetradecanoate Input	Ex_14c			Exchange	14c-fa[e] <==>	0	0	
16 Octadecanoate Input	Ex_18c			Exchange	18c-fa[e] <==>	0	0	
17 Glycerol Input	Ex_glyc			Exchange	glyc[e] <==>	0	0	
18 Triacylglycerol Exchange	Ex_tag			Exchange	tag[e] <==>	0	0	
19 Diacylglycerol Exchange	Ex_dag			Exchange	12dag[e] <==>	0	0	
20 Monoacylglycerol Exchange	Ex_mag			Exchange	1mag[e] <==>	0	0	
21 Alpha-ketoglutarate Exchange	Ex_akg			Exchange	akg[e] -->	-999999	999999	
22 Oxaloacetate Exchange	Ex_oaa			Exchange	oaa[e] -->	-999999	999999	
23 Ribose Nutrient	Ex_rib		Extracellular	Exchange	rib[e] <==>	0	0	
24 Oxygen Input	Nut_o2			Nutrient	o2 <==>	-999999	999999	
25 Carbon Dioxide Input	Nut_co2			Nutrient	co2 <==>	-999999	999999	
26 Water Nutrient	Nut_h2o			Nutrient	h2o <==>	-999999	999999	
27 Phosphate Nutrient	Nut_p			Nutrient	p <==>	-999999	999999	
28 Bicarbonate	Nut_hco3			Nutrient	hco3 <==>	-999999	999999	
29 Coenzyme A	Nut_coa			Nutrient	coa[e] <==>	-999999	999999	
30 Carnitine	Nut_carn			Nutrient	carn[e] <==>	0	999999	
31 Folate Nutrient	Nut_dhf			Nutrient	dhf[c] <==>	-999999	999999	
32 lipoprotein lipase	LPL	3.1.1.34	extracellular	mer Fatty Acid	tag[e] + h2o --> pal[e] + 12dag[e]	0	999999	
33 diacylglycerol lipase	DAGL	3.1.1.-	extracellular	mer Fatty Acid	12dag[e] + h2o --> 2mag[e] + pal[e]	0	999999	
34 triacylglycerol degradation	12DAG		extracellular	mer Fatty Acid	2mag[e] <==> 1mag[e]	0	999999	
35 monoacylglycerol lipase	MAGL	3.1.1.23	extracellular	mer Fatty Acid	1mag[e] + h2o --> glyc[e] + pal[e]	0	999999	
36 Glucose Input	GLUT4			Cellular Uptake	insulin[e] + gluc[e] --> gluc[c]	0	999999	
37 Lactate Input	MCT4			Cellular Uptake	lac[e] <==> lac[c]	0	999999	
38 Pyruvate Uptake	MCT_pyr			Cellular Uptake	pyr[e] --> pyr[c]	0	999999	
39 Palmitate Input (hexadecanoate)	FAT-CD36			Cellular Uptake	pal[e] --> pal[c]	0	999999	
40 Propanoate Input	FATprop			Cellular Uptake	prop[e] <==> prop[c]	0	0	
41 Butanoate Input	FATbut			Cellular Uptake	but[e] <==> but[c]	0	0	
42 Pentanoate Input	FAT5c			Cellular Uptake	5c-fa[e] <==> 5c-fa[c]	0	0	
43 Hexanoate Input	FAT6c			Cellular Uptake	6c-fa[e] <==> 6c-fa[c]	0	0	
44 Octanoate Input	FAT8c			Cellular Uptake	8c-fa[e] <==> 8c-fa[c]	0	0	
45 Nonanoate Input	FAT9c			Cellular Uptake	9c-fa[e] <==> 9c-fa[c]	0	0	
46 Decanoate Input	FAT10c			Cellular Uptake	10c-fa[e] <==> 10c-fa[c]	0	0	
47 Dodecanoate Input	FAT12c			Cellular Uptake	12c-fa[e] <==> 12c-fa[c]	0	0	
48 Tetradecanoate Input	FAT14c			Cellular Uptake	14c-fa[e] <==> 14c-fa[c]	0	0	
49 Octadecanoate Input	FAT18c			Cellular Uptake	18c-fa[e] <==> 18c-fa[c]	0	0	
50 Glycerol Input	Alc_glyc			Cellular Uptake	glyc[e] <==> glyc[c]	0	0	
51 Coenzyme A Transport	COA			Cellular Uptake	coa[e] --> coa[c]	0	999999	
52 Solute Carrier family 22 member 5	SLC22A5-OCTN2	transport	Outer membranc	Cellular Uptake	carn[e] <==> carn[c]	0	999999	
53 Ribose Membrane Transport	Xport_rib		Membrane	Cellular Uptake	rib[e] --> rib[c]	0	999999	
54 alpha-ketoglutarate drain	Dr_akg			Cellular Export	akg[c] --> akge[e]	0	999999	
55 Oxaloacetate drain	Dr_oaa			Cellular Export	oaa[c] --> oaa[e]	0	999999	
56 Hexokinase	Hex	2.7.1.2	Cytosolic	Glycolysis	atp + gluc[c] --> adp + p + g6p[c]	0	999999	IR
57 Phosphoglucisomerase	PGI	5.3.1.9	Cytosolic	Glycolysis	g6p[c] <==> f6p[c]	-999999	999999	
58 Phosphofructokinase	PFK	2.7.1.11	Cytosolic	Glycolysis	atp + f6p[c] --> adp + fbp[c]	0	999999	IR
59 Fructosebisphosphatase	FBP	3.1.3.13	Cytosolic	Glycolysis	fbp[c] + h2o --> f6p[c] + p	0	999999	IR
60 Aldolase	Ald	4.1.2.13	Cytosolic	Glycolysis	fbp[c] <==> dhap[c] + g3p[c]	-999999	999999	
61 Triose-P-isomerase	TPI	5.3.1.1	Cytosolic	Glycolysis	g3p[c] <==> dhap[c]	0	999999	IR
62 Glyceraldehyde-3-phosphate dehydrogenase	D3PDeh	1.2.1.12	Cytosolic	Glycolysis	g3p[c] + nad[c] <==> dpg[c] + nadh[c]	-999999	999999	
63 Phosphoglycerate kinase	PGK	2.7.2.3	Cytosolic	Glycolysis	dpg[c] + adp <==> 3pg[c] + atp	0	999999	IR
64 Phosphoglycerate mutase	PGM	5.4.2.1	Cytosolic	Glycolysis	3pg[c] <==> 2pg[c]	-999999	999999	
65 Enolase	Eno	4.2.1.11	Cytosolic	Glycolysis	2pg[c] <==> pep[c] + h2o	-999999	999999	
66 Pyruvate kinase	PyrK	2.7.1.40	Cytosolic	Glycolysis	pep[c] + adp --> pyr[c] + atp	0	999999	IR
67 PEP synthase	PEPSynth	2.7.9.2	Cytosolic	Glycolysis	pyr[c] + atp + h2o --> pep[c] + amp + p	0	999999	IR

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68 PEP carboxy kinase	PEPCarbK	4.1.1.49	Cytosolic	Glycolysis	oaa[c] + atp --> co2 + pep[c] + adp	0	999999	IR
69 PEP carboxylase	PEPCarbI	4.1.1.31	Cytosolic	Glycolysis	oaa[c] + p --> pep[c] + h2o + co2	0	999999	IR
70 Lactate dehydrogenase	LacDeh	1.1.2.4	Cytosolic	Glycolysis	lac[c] + nad[c] <=> pyr[c] + nadh[c]	-999999	999999	
71 Malatate dehydrogenase (isozyme)	MalDehC		Cytosolic	Shuttle Cytosolic	oaa[c] + nadh[c] <=> mal[c] + nad[c]	-999999	999999	
72 Aspartate aminotransferase	ASTC		Cytosolic	Shuttle Cytosolic	asp[c] + akgl[c] <=> glu[c] + oaa[c]	-999999	999999	
73 Cytosolic glycerol-3-P-dehydrogenase	G3PDehC	1.1.1.8	Cytosolic	Shuttle Cytosolic	dhap[c] + nadh[c] <=> gly3p[c] + nad[c]	-999999	999999	
74 Malate-alpha-ketoglutarate exchange	Mal-AKGEX		Mitochondrion T1	Shuttle Mitochondrial	mal[c] + akgl[m] <=> mal[m] + akgl[c]	-999999	999999	
75 Glutamate-aspartate exchange	Glu-AspEx		Mitochondrion T1	Shuttle Mitochondrial	asp[m] + glu[c] <=> asp[c] + glu[m]	-999999	999999	
76 Pyruvate Transport (MCT)	MCT		Mitochondrion T1	TCA	pyr[c] --> pyr[m]	-999999	999999	
77 Aspartate aminotransferase	ASTM	2.6.1.1	Mitochondrion	Shuttle Mitochondrial	glu[m] + oaa[m] <=> asp[m] + akgl[m]	-999999	999999	
78 Mitochondrial glycerol-3-P-dehydrogenase	G3PDehM	1.1.95.5	Mitochondrion	Shuttle Mitochondrial	glyc3p[m] + fad[m] <=> dhap[m] + fadh2[m]	-999999	999999	
79 Pyruvate synthase	PyrSynth	1.2.4.1	Mitochondrion	TCA	pyr[m] + coa[m] + nad[m] --> acetyl-coa[m] + nadh[m] + co2	0	999999	IR
80 Citrate synthase	CitSynth	2.3.3.1	Mitochondrion	TCA	oaa[m] + acetyl-coa[m] + h2o <=> cit[m] + coa[m]	-999999	999999	R
81 Aconitase	Acon	4.2.1.3	Mitochondrion	TCA	cit[m] <=> iso[m]	-999999	999999	R
82 Isocitrate dehydrogenase	IsoDeh	1.1.1.41	Mitochondrion	TCA	iso[m] + nad[m] --> akgl[m] + co2 + nadh[m]	0	999999	IR
83 Isocitrate dehydrogenase	IsoDehnadph	1.1.1.42	Mitochondrion	TCA	iso[m] + nadp[m] --> akgl[m] + co2 + nadph[m]	0	999999	IR
84 alpha-Ketoglutarate dehydrogenase	AKGDeh	1.2.4.2	Mitochondrion	TCA	akgl[m] + coa[m] + nad[m] --> suc-coa[m] + co2 + nadh[m]	0	999999	IR
85 Succinyl-CoA synthetase	SunCoaSynth	6.2.1.5	Mitochondrion	TCA	suc-coa[m] + adp + p <=> suc[m] + coa[m] + atp	-999999	999999	R
86 Succinate dehydrogenase (complex II)	SucDeh-II	1.3.99.1	Mitochondrion	TCA	suc[c] + fad[m] <=> fum[m] + fadh2[m]	-999999	999999	R
87 Fumarase	Fum	4.2.1.2	Mitochondrion	TCA	fum[m] <=> mal[m] + h2o	-999999	999999	R
88 Malatate dehydrogenase (isozyme)	MalDehM	1.1.1.37	Mitochondrion	TCA	mal[m] + nad[m] <=> oaa[m] + nadh[m]	-999999	999999	R
89 NADH dehydrogenase (complex I)	NADHDeh-I	1.6.5.3	Mitochondrion	Electron Transport Chain	nadh[m] + uq[m] --> nad[m] + uqh2[m] + 4 h[out]	0	999999	IR
90 Electron transfer flavoprotein-ubiquinone oxidoreductase	ETFUO	1.5.5.1	Mitochondrion	Electron Transport Chain	fadh2[m] + uq[m] --> fad[m] + uqh2[m]	0	999999	IR
91 Ubiquinone cytochrome c-oxidoreductase (complex III)	UCytC-III	1.10.2.2	Mitochondrion	Electron Transport Chain	2 rcytC[m] + uqh2[m] --> 2 rcytC[m] + uq[m] + 4 h[out]	0	999999	IR
92 Cytochrome c-oxidase (complex IV)	CytCO-IV	1.9.3.1	Mitochondrion	Electron Transport Chain	o2 + 4 rcytC[m] --> 2 h2o + 4 rcytC[m] + 8 h[out]	0	999999	IR
93 ATP synthase (complex V)	ATPSynth-V	3.6.3.14	Mitochondrion	Electron Transport Chain	adp + p + 4 h[out] <=> atp + h2o	0	999999	IR
94 Convert Amp to Adp	AMP_ADPSupply		Mitochondrion	Electron Transport Chain	amp + p <=> adp	-999999	999999	R
95 Palmitate thio kinase	PalTK	6.2.1.3	Cytosolic	Mitochondrial Transport	pal[c] + coa[c] + atp --> 234pal-coa[c] + 2 p + amp	0	999999	
96 Carnitine palmitoyltransferase mitochondrial muscle isoform	CPT1B-CHKL	2.3.1.21	outer mitochond	Mitochondrial Transport	carn[c] + 234pal-coa[c] <=> pal-carn[c] + coa[c]	0	999999	
97 Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20-CACT	transport		Mitochondrial Transport	pal-carn[c] + carn[m] --> carn[c] + pal-carn[m]	0	999999	
98	CPT2	2.3.1.21		Fatty Acid	pal-carn[m] + coa[m] --> 234pal-coa[m] + carn[m]	0	999999	
99 Acyl-CoA dehydrogenase	AcylCoADeh	1.3.99.3	Mitochondrion	Fatty Acid	234pal-coa[m] + fad[m] --> fadh2[m] + 23pal-coa[m]	0	999999	
100 Enoyl-CoA hydratase	EnoCoADeh	4.2.1.17	Mitochondrion	Fatty Acid	23pal-coa[m] + h2o <=> 3ohpal-coa[m]	-999999	999999	
101 3-Hydroxyacyl-CoA dehydrogenase	3HA-CoADeh	1.1.1.35	Mitochondrion	Fatty Acid	3ohpal-coa[m] + nad[m] <=> 3ketopal-coa[m] + nadh[m]	-999999	999999	
102 Acyl-CoA acetyltransferase	AcylCoAAT	2.3.1.16	Mitochondrion	Fatty Acid	3ketopal-coa[m] + coa[m] --> 14c-234acyl-coa[m] + acetyl-coa[m]	0	999999	
103 Acyl-CoA dehydrogenase	AcylCoADeh-18-c	1.3.99.3	Mitochondrion	Fatty Acid	18c-234acyl-coa[m] + fad[m] --> 18c-t2enoyl-coa[m] + fadh2[m]	0	999999	
104 Enoyl-CoA hydratase	EnoCoADeh-18c	4.2.1.17	Mitochondrion	Fatty Acid	18c-t2enoyl-coa[m] + h2o <=> 18c-3ohacyl-coa[m]	-999999	999999	
105 3-Hydroxyacyl-CoA dehydrogenase	3HA-CoADeh-18c	1.1.1.35	Mitochondrion	Fatty Acid	18c-3ohacyl-coa[m] + nad[m] <=> 18c-3ketoacyl-coa[m] + nadh[m]	-999999	999999	
106 Acyl-CoA acetyltransferase	AcylCoAAT-18c	2.3.1.16	Mitochondrion	Fatty Acid	18c-3ketoacyl-coa[m] + coa[m] --> 234pal-coa[m] + acetyl-coa[m]	0	999999	
107 Acyl-CoA dehydrogenase	AcylCoADeh-14c	1.3.99.3	Mitochondrion	Fatty Acid	14c-234acyl-coa[m] + fad[m] --> 14c-t2enoyl-coa[m] + fadh2[m]	0	999999	
108 Enoyl-CoA hydratase	EnoCoADeh-14c	4.2.1.17	Mitochondrion	Fatty Acid	14c-t2enoyl-coa[m] + h2o <=> 14c-3ohacyl-coa[m]	-999999	999999	
109 3-Hydroxyacyl-CoA dehydrogenase	3HA-CoADeh-14c	1.1.1.35	Mitochondrion	Fatty Acid	14c-3ohacyl-coa[m] + nad[m] <=> 14c-3ketoacyl-coa[m] + nadh[m]	-999999	999999	
110 Acyl-CoA acetyltransferase	AcylCoAAT-14c	2.3.1.16	Mitochondrion	Fatty Acid	14c-3ketoacyl-coa[m] + coa[m] --> 12c-234acyl-coa[m] + acetyl-coa[m]	0	999999	
111 Acyl-CoA dehydrogenase	AcylCoADeh-12-c	1.3.99.3	Mitochondrion	Fatty Acid	12c-234acyl-coa[m] + fad[m] --> 12c-t2enoyl-coa[m] + fadh2[m]	0	999999	
112 Enoyl-CoA hydratase	EnoCoADeh-12c	4.2.1.17	Mitochondrion	Fatty Acid	12c-t2enoyl-coa[m] + h2o <=> 12c-3ohacyl-coa[m]	-999999	999999	
113 3-Hydroxyacyl-CoA dehydrogenase	3HA-CoADeh-12c	1.1.1.35	Mitochondrion	Fatty Acid	12c-3ohacyl-coa[m] + nad[m] <=> 12c-3ketoacyl-coa[m] + nadh[m]	-999999	999999	
114 Acyl-CoA acetyltransferase	AcylCoAAT-12c	2.3.1.16	Mitochondrion	Fatty Acid	12c-3ketoacyl-coa[m] + coa[m] --> 10c-234acyl-coa[m] + acetyl-coa[m]	0	999999	
115 Acyl-CoA dehydrogenase	AcylCoADeh-10-c	1.3.99.3	Mitochondrion	Fatty Acid	10c-234acyl-coa[m] + fad[m] --> 10c-t2enoyl-coa[m] + fadh2[m]	0	999999	
116 Enoyl-CoA hydratase	EnoCoADeh-10c	4.2.1.17	Mitochondrion	Fatty Acid	10c-t2enoyl-coa[m] + h2o <=> 10c-3ohacyl-coa[m]	-999999	999999	
117 3-Hydroxyacyl-CoA dehydrogenase	3HA-CoADeh-10c	1.1.1.35	Mitochondrion	Fatty Acid	10c-3ohacyl-coa[m] + nad[m] <=> 10c-3ketoacyl-coa[m] + nadh[m]	-999999	999999	
118 Acyl-CoA acetyltransferase	AcylCoAAT-10c	2.3.1.16	Mitochondrion	Fatty Acid	10c-3ketoacyl-coa[m] + coa[m] --> 8c-234acyl-coa[m] + acetyl-coa[m]	0	999999	
119 Acyl-CoA dehydrogenase	AcylCoADeh-8-c	1.3.99.3	Mitochondrion	Fatty Acid	8c-234acyl-coa[m] + fad[m] --> 8c-t2enoyl-coa[m] + fadh2[m]	0	999999	
120 Enoyl-CoA hydratase	EnoCoADeh-8c	4.2.1.17	Mitochondrion	Fatty Acid	8c-t2enoyl-coa[m] + h2o <=> 8c-3ohacyl-coa[m]	-999999	999999	
121 3-Hydroxyacyl-CoA dehydrogenase	3HA-CoADeh-8c	1.1.1.35	Mitochondrion	Fatty Acid	8c-3ohacyl-coa[m] + nad[m] <=> 8c-3ketoacyl-coa[m] + nadh[m]	-999999	999999	
122 Acyl-CoA acetyltransferase	AcylCoAAT-8c	2.3.1.16	Mitochondrion	Fatty Acid	8c-3ketoacyl-coa[m] + coa[m] --> 6c-234acyl-coa[m] + acetyl-coa[m]	0	999999	
123 Acyl-CoA dehydrogenase	AcylCoADeh-6-c	1.3.99.3	Mitochondrion	Fatty Acid	6c-234acyl-coa[m] + fad[m] --> 6c-t2enoyl-coa[m] + fadh2[m]	0	999999	
124 Enoyl-CoA hydratase	EnoCoADeh-6c	4.2.1.17	Mitochondrion	Fatty Acid	6c-t2enoyl-coa[m] + h2o <=> 6c-3ohacyl-coa[m]	-999999	999999	
125 3-Hydroxyacyl-CoA dehydrogenase	3HA-CoADeh-6c	1.1.1.35	Mitochondrion	Fatty Acid	6c-3ohacyl-coa[m] + nad[m] <=> 6c-3ketoacyl-coa[m] + nadh[m]	-999999	999999	
126 Acyl-CoA acetyltransferase	AcylCoAAT-6c	2.3.1.16	Mitochondrion	Fatty Acid	6c-3ketoacyl-coa[m] + coa[m] --> butyryl-coa[m] + acetyl-coa[m]	0	999999	
127 Butyryl-coa Dehydrogenase	ButyrylCoADeh	1.3.99.2	Mitochondrion	Fatty Acid	butyryl-coa[m] + fad[m] --> tbut2enoyl-coa[m] + fadh2[m]	0	999999	
128 Enoyl-CoA hydratase	EnoCoADeh-But	4.2.1.17	Mitochondrion	Fatty Acid	tbut2enoyl-coa[m] + h2o <=> 3ohbutyryl-coa[m]	-999999	999999	
129 3-Hydroxyacyl-CoA dehydrogenase	3HA-CoADeh-But	1.1.1.35	Mitochondrion	Fatty Acid	3ohbutyryl-coa[m] + coa[m] <=> acetoacetyl-coa[m]	-999999	999999	
130 Acyl-CoA acetyltransferase	AcylCoAAT-But	2.3.1.9	Mitochondrion	Fatty Acid	acetoacetyl-coa[m] --> 2 acetyl-coa[m]	0	999999	
131 Glycerol Kinase	GK	2.7.1.30		TAG	glyc[c] + atp <=> gly3p[c] + adp	0	999999	IR
132 Glycerol-3-phosphate acyltransferase 4	GPAT4	2.3.1.15		TAG	glyc3p[c] + 234pal-coa[c] <=> 1acyl-g3p[c] + coa[c]	-999999	999999	R
133 1-acylglycerol-3-phosphate O-acyltransferase	ABHD5	2.3.1.51		TAG	1acyl-g3p[c] + 234pal-coa[c] <=> 12dacyl-g3p[c] + coa[c]	-999999	999999	R
134 Diacylglycerol Kinase zeta	DAGZ-DAGK6	2.7.1.107		TAG	12dacyl-g3p[c] + adp <=> 12dag[c] + atp	-999999	999999	R

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135 diacylglycerol acyl transferase	DGAT1	2.3.1.20		TAG	12dag[c] + 234pal-coa[c] <==> tag[c] + coa[c]	-999999	999999	R
136 Store TAG	St_TAG			TAG	tag[c] -->	0	999999	IR
137 Acyl-coenzyme A synthetase	ACAS2	6.2.1.1/6.2.1	Cellular	Fatty Acid	prop[c] + atp + coa[c] --> prop-coa[c] + adp + p	0	999999	
138 Acyl-coenzyme A synthetase	ACSM-But	6.2.1.2	Cellular	Fatty Acid	but[c] + atp + coa[c] --> butyryl-coa[c] + adp + p	0	999999	
139 Acyl-coenzyme A synthetase	ASCM-5c	6.2.1.2	Cellular	Fatty Acid	5c-fa[c] + atp + coa[c] --> 5c-234acyl-coa[c] + adp + p	0	999999	
140 Acyl-coenzyme A synthetase	ASCM-6c	6.2.1.3	Cellular	Fatty Acid	6c-fa[c] + atp + coa[c] --> 6c-234acyl-coa[c] + adp + p	0	999999	
141 Acyl-coenzyme A synthetase	ACSM-8c	6.2.1.4	Cellular	Fatty Acid	8c-fa[c] + atp + coa[c] --> 8c-234acyl-coa[c] + adp + p	0	999999	
142 Acyl-coenzyme A synthetase	ACSM-9c	6.2.1.5	Cellular	Fatty Acid	9c-fa[c] + atp + coa[c] --> 9c-234acyl-coa[c] + adp + p	0	999999	
143 Acyl-coenzyme A synthetase	ACSM-10c	6.2.1.6	Cellular	Fatty Acid	10c-fa[c] + atp + coa[c] --> 10c-234acyl-coa[c] + adp + p	0	999999	
144 Acyl-coenzyme A synthetase	ACSM-12c	6.2.1.7	Cellular	Fatty Acid	12c-fa[c] + atp + coa[c] --> 12c-234acyl-coa[c] + adp + p	0	999999	
145 Acyl-coenzyme A synthetase	ACSM-14c	6.2.1.8	Cellular	Fatty Acid	14c-fa[c] + atp + coa[c] --> 14c-234acyl-coa[c] + adp + p	0	999999	
146 Acyl-coenzyme A synthetase	ACSM-18c	6.2.1.8	Cellular	Fatty Acid	18c-fa[c] + atp + coa[c] --> 18c-234acyl-coa[c] + adp + p	0	999999	
147 Carnitine palmitoyltransferase mitochondrial muscle isoform	CPT1B-CHKL	2.3.1.21	outer mitochond	Mitochondrial Transport	prop-coa[c] + carn[c] --> prop-carn[c] + coa[c]	0	999999	
148 Carnitine palmitoyltransferase mitochondrial muscle isoform	CPT1B-CHKL	2.3.1.21	outer mitochond	Mitochondrial Transport	butyryl-coa[c] + carn[c] --> butyryl-carn[c] + coa[c]	0	999999	
149 Carnitine palmitoyltransferase mitochondrial muscle isoform	CPT1B-CHKL	2.3.1.21	outer mitochond	Mitochondrial Transport	5c-234acyl-coa[c] + carn[c] --> 5c-234acyl-carn[c] + coa[c]	0	999999	
150 Carnitine palmitoyltransferase mitochondrial muscle isoform	CPT1B-CHKL	2.3.1.21	outer mitochond	Mitochondrial Transport	6c-234acyl-coa[c] + carn[c] --> 6c-234acyl-carn[c] + coa[c]	0	999999	
151 Carnitine palmitoyltransferase mitochondrial muscle isoform	CPT1B-CHKL	2.3.1.21	outer mitochond	Mitochondrial Transport	8c-234acyl-coa[c] + carn[c] --> 8c-234acyl-carn[c] + coa[c]	0	999999	
152 Carnitine palmitoyltransferase mitochondrial muscle isoform	CPT1B-CHKL	2.3.1.21	outer mitochond	Mitochondrial Transport	9c-234acyl-coa[c] + carn[c] --> 9c-234acyl-carn[c] + coa[c]	0	999999	
153 Carnitine palmitoyltransferase mitochondrial muscle isoform	CPT1B-CHKL	2.3.1.21	outer mitochond	Mitochondrial Transport	10c-234acyl-coa[c] + carn[c] --> 10c-234acyl-carn[c] + coa[c]	0	999999	
154 Carnitine palmitoyltransferase mitochondrial muscle isoform	CPT1B-CHKL	2.3.1.21	outer mitochond	Mitochondrial Transport	12c-234acyl-coa[c] + carn[c] --> 12c-234acyl-carn[c] + coa[c]	0	999999	
155 Carnitine palmitoyltransferase mitochondrial muscle isoform	CPT1B-CHKL	2.3.1.21	outer mitochond	Mitochondrial Transport	14c-234acyl-coa[c] + carn[c] --> 14c-234acyl-carn[c] + coa[c]	0	999999	
156 Carnitine palmitoyltransferase mitochondrial muscle isoform	CPT1B-CHKL	2.3.1.21	outer mitochond	Mitochondrial Transport	18c-234acyl-coa[c] + carn[c] --> 18c-234acyl-carn[c] + coa[c]	0	999999	
157 Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20-CACT	transport	Mitochondrial M	Mitochondrial Transport	prop-carn[c] + carn[m] --> prop-carn[m] + carn[c]	0	999999	
158 Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20-CACT	transport	Mitochondrial M	Mitochondrial Transport	butyryl-carn[c] + carn[m] --> butyryl-carn[m] + carn[c]	0	999999	
159 Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20-CACT	transport	Mitochondrial M	Mitochondrial Transport	5c-234acyl-carn[c] + carn[m] --> 5c-234acyl-carn[m] + carn[c]	0	999999	
160 Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20-CACT	transport	Mitochondrial M	Mitochondrial Transport	6c-234acyl-carn[c] + carn[m] --> 6c-234acyl-carn[m] + carn[c]	0	999999	
161 Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20-CACT	transport	Mitochondrial M	Mitochondrial Transport	8c-234acyl-carn[c] + carn[m] --> 8c-234acyl-carn[m] + carn[c]	0	999999	
162 Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20-CACT	transport	Mitochondrial M	Mitochondrial Transport	9c-234acyl-carn[c] + carn[m] --> 9c-234acyl-carn[m] + carn[c]	0	999999	
163 Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20-CACT	transport	Mitochondrial M	Mitochondrial Transport	10c-234acyl-carn[c] + carn[m] --> 10c-234acyl-carn[m] + carn[c]	0	999999	
164 Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20-CACT	transport	Mitochondrial M	Mitochondrial Transport	12c-234acyl-carn[c] + carn[m] --> 12c-234acyl-carn[m] + carn[c]	0	999999	
165 Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20-CACT	transport	Mitochondrial M	Mitochondrial Transport	14c-234acyl-carn[c] + carn[m] --> 14c-234acyl-carn[m] + carn[c]	0	999999	
166 Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20-CACT	transport	Mitochondrial M	Mitochondrial Transport	18c-234acyl-carn[c] + carn[m] --> 18c-234acyl-carn[m] + carn[c]	0	999999	
167	CPT2	2.3.1.21		Mitochondrial Transport	prop-carn[m] + coa[m] --> prop-coa[m] + carn[m]	0	999999	
168	CPT2	2.3.1.21		Mitochondrial Transport	butyryl-carn[m] + coa[m] --> butyryl-coa[m] + carn[m]	0	999999	
169	CPT2	2.3.1.21		Mitochondrial Transport	5c-234acyl-carn[m] + coa[m] --> 5c-234acyl-coa[m] + carn[m]	0	999999	
170	CPT2	2.3.1.21		Mitochondrial Transport	6c-234acyl-carn[m] + coa[m] --> 6c-234acyl-coa[m] + carn[m]	0	999999	
171	CPT2	2.3.1.21		Mitochondrial Transport	8c-234acyl-carn[m] + coa[m] --> 8c-234acyl-coa[m] + carn[m]	0	999999	
172	CPT2	2.3.1.21		Mitochondrial Transport	9c-234acyl-carn[m] + coa[m] --> 9c-234acyl-coa[m] + carn[m]	0	999999	
173	CPT2	2.3.1.21		Mitochondrial Transport	10c-234acyl-carn[m] + coa[m] --> 10c-234acyl-coa[m] + carn[m]	0	999999	
174	CPT2	2.3.1.21		Mitochondrial Transport	12c-234acyl-carn[m] + coa[m] --> 12c-234acyl-coa[m] + carn[m]	0	999999	
175	CPT2	2.3.1.21		Mitochondrial Transport	14c-234acyl-carn[m] + coa[m] --> 14c-234acyl-coa[m] + carn[m]	0	999999	
176	CPT2	2.3.1.21		Mitochondrial Transport	18c-234acyl-carn[m] + coa[m] --> 18c-234acyl-coa[m] + carn[m]	0	999999	
177 Acyl-CoA dehydrogenase	AcylCoADeh-9c	1.3.99.3	Mitochondrion	Fatty Acid	9c-234acyl-coa[m] + fad[m] --> 9c-t2enoyl-coa[m] + fadh2[m]	0	999999	
178 Enoyl-CoA hydratase	EnoCoADeh-9c	4.2.1.17	Mitochondrion	Fatty Acid	9c-t2enoyl-coa[m] + h2o <==> 9c-3ohacyl-coa[m]	-999999	999999	
179 3-Hydroxyacyl-CoA dehydrogenase	3HA-CoADeh-9c	1.1.1.35	Mitochondrion	Fatty Acid	9c-3ohacyl-coa[m] + nad[m] <==> 9c-3ketoacyl-coa[m] + nadh[m]	-999999	999999	
180 Acyl-CoA acetyltransferase	AcylCoAAT-9c	2.3.1.16	Mitochondrion	Fatty Acid	9c-3ketoacyl-coa[m] + coa[m] --> 7c-234acyl-coa[m] + acetyl-coa[m]	0	999999	
181 Acyl-CoA dehydrogenase	AcylCoADeh-7c	1.3.99.3	Mitochondrion	Fatty Acid	7c-234acyl-coa[m] + fad[m] --> 7c-t2enoyl-coa[m] + fadh2[m]	0	999999	
182 Enoyl-CoA hydratase	EnoCoADeh-7c	4.2.1.17	Mitochondrion	Fatty Acid	7c-t2enoyl-coa[m] + h2o <==> 7c-3ohacyl-coa[m]	-999999	999999	
183 3-Hydroxyacyl-CoA dehydrogenase	3HA-CoADeh-7c	1.1.1.35	Mitochondrion	Fatty Acid	7c-3ohacyl-coa[m] + nad[m] <==> 7c-3ketoacyl-coa[m] + nadh[m]	-999999	999999	
184 Acyl-CoA acetyltransferase	AcylCoAAT-7c	2.3.1.16	Mitochondrion	Fatty Acid	7c-3ketoacyl-coa[m] + coa[m] --> 5c-234acyl-coa[m] + acetyl-coa[m]	0	999999	
185 Acyl-CoA dehydrogenase	AcylCoADeh-5c	1.3.99.3	Mitochondrion	Fatty Acid	5c-234acyl-coa[m] + fad[m] --> 5c-t2enoyl-coa[m] + fadh2[m]	0	999999	
186 Enoyl-CoA hydratase	EnoCoADeh-5c	4.2.1.17	Mitochondrion	Fatty Acid	5c-t2enoyl-coa[m] + h2o <==> 5c-3ohacyl-coa[m]	-999999	999999	
187 3-Hydroxyacyl-CoA dehydrogenase	3HA-CoADeh-5c	1.1.1.35	Mitochondrion	Fatty Acid	5c-3ohacyl-coa[m] + nad[m] <==> 5c-3ketoacyl-coa[m] + nadh[m]	-999999	999999	
188 Acyl-CoA acetyltransferase	AcylCoAAT-5c	2.3.1.16	Mitochondrion	Fatty Acid	5c-3ketoacyl-coa[m] + coa[m] --> acetyl-coa[m] + prop-coa[m]	0	999999	
189 Alcohol Dehydrogenase (NADP)	AKR1A1	1.1.1.2	Cytosolic	Fatty Alcohol	glyc[c] + nadp[c] --> glyc-ald[c] + nadph[c]	0	999999	
190 Fatty aldehyde dehydrogenase	ALDH3A2	1.2.1.3	Cytosolic	Fatty Alcohol	glyc-ald[c] + nad[c] + h2o --> glyc-ate[c] + nadh[c]	0	999999	
191 Glycerate Kinase	GLYCK	2.7.1.31	Cytosolic	Fatty Alcohol	glyc-ate[c] + atp --> 3pg[c] + adp + p	0	999999	
192	EAA_arg			Exchange	arg[c] <==>	-999999	0	
193	EAA_his			Exchange	his[c] <==>	-999999	0	
194	EAA_ile			Exchange	ile[c] <==>	-999999	0	
195	EAA_leu			Exchange	leu[c] <==>	-999999	0	
196	EAA_lys			Exchange	lys[c] <==>	-999999	0	
197	EAA_met			Exchange	met[c] <==>	-999999	0	
198	EAA_phe			Exchange	phe[c] <==>	-999999	0	
199	EAA_thr			Exchange	thr[c] <==>	-999999	0	
200	EAA_trp			Exchange	trp[c] <==>	-999999	0	
201	EAA_val			Exchange	val[c] <==>	-999999	0	

0 Enzyme	Abrev	EC Number	Location	Pathway	Reaction	Lower Bound	Upper Bound	Thermodynamics
202	NEAA_ala			Exchange	ala[c] <=>	-999999	0	
203	NEAA_asn			Exchange	asn[c] <=>	-999999	0	
204	NEAA_asp			Exchange	asp[c] <=>	-999999	0	
205	NEAA_cys			Exchange	cys[c] <=>	-999999	0	
206	NEAA_glu			Exchange	glu[c] <=>	-999999	0	
207	NEAA_gln			Exchange	gln[c] <=>	-999999	0	
208	NEAA_gly			Exchange	gly[c] <=>	-999999	0	
209	NEAA_pro			Exchange	pro[c] <=>	-999999	0	
210	NEAA_ser			Exchange	ser[c] <=>	-999999	0	
211	NEAA_tyr			Exchange	tyr[c] <=>	-999999	0	
212	Dihydropolyl dehydrogenase, mitochondrial	DLDH 1.8.1.4	Mitochondrion	Amino Acid Catabolism	laN6dhpl[m] + nad[m] <=> laN6ll[m] + nadh[m]	-999999	999999	
213	Valine mitochondrial transport	MT_val		Mitochondrial Transport	val[c] --> val[m]	0	999999	
214	Branched-chain amino acid aminotransferase, mitochondrial precursor	BCAT2-val 2.6.1.42	Mitochondrion	Amino Acid Catabolism	val[m] + akg[m] --> akisov[m] + glu[m]	0	999999	
215	Oxoisovalerate dehydrogenase	BCKDHB-val 1.2.4.4	Mitochondrion	Amino Acid Catabolism	akisov[m] + laN6ll[m] --> laN6S2mpdhpl[m] + co2	0	999999	
216	Lipoamide acyltransferase component of branched-chain alpha-ke	BCKADE2-val 2.3.1.168	Mitochondrion	Amino Acid Catabolism	laN6S2mpdhpl[m] + coa[m] --> laN6dhpl[m] + isob-coa[m]	0	999999	
217	Acyl-coa dehydrogenase, mitochondrial precursor	ACADSB 1.3.99.12	Mitochondrion	Amino Acid Catabolism	isob-coa[m] + fad[m] --> methacr1-coa[m] + fadh2[m]	0	999999	
218	Enoyl-coa hydratase, mitochondrial precursor	ECHS1 4.2.1.17	Mitochondrion	Amino Acid Catabolism	methacr1-coa[m] + h2o --> 3hisob-coa[m]	0	999999	
219	3-hydroxyisobutyryl-coenzyme A hydrolase	HIBCH 3.1.2.4	Mitochondrion	Amino Acid Catabolism	3hisob-coa[m] + h2o --> 3hisob[m] + coa[m]	0	999999	
220	3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor	HIBADH 1.1.1.31	Mitochondrion	Amino Acid Catabolism	3hisob[m] + nad[m] --> methalmesemald[m] + nadh[m]	0	999999	
221	Methylmalonate-semialdehyde dehydrogenase (acylating), mitochondrial precursor	ALDH6A1 1.2.1.27	Mitochondrion	Amino Acid Catabolism	methalmesemald[m] + nad[m] + coa[m] + h2o --> prop-coa[m] + hco3 + nadh[m]	0	999999	
222	Propionyl-coa carboxylase	PCCB 6.4.1.3	Mitochondrion	Amino Acid Catabolism	prop-coa[m] + atp + hco3 --> Smethmal-coa[m] + adp + p	0	999999	
223	Methylmalonyl-coa epimerase	MCEE 5.1.99.1	Mitochondrion	Amino Acid Catabolism	Smethmal-coa[m] --> Rmethmal-coa[m]	0	999999	
224	Methylmalonyl-coa mutase, mitochondrial precursor	MUT 5.4.99.2	Mitochondrion	Amino Acid Catabolism	Rmethmal-coa[m] --> suc-coa[m]	0	999999	
225	Isoleucine mitochondrial transport	MT_ile		Mitochondrial Transport	ile[c] --> ile[m]	0	999999	
226	Branched-chain amino acid aminotransferase, mitochondrial precursor	BCAT-ile 2.3.1.42	Mitochondrion	Amino Acid Catabolism	ile[m] + akg[m] --> ak3mvalt[m] + glu[m]	0	999999	
227	Oxoisovalerate dehydrogenase	BCKDHB-ile 1.2.4.4	Mitochondrion	Amino Acid Catabolism	ak3mvalt[m] + laN6ll[m] --> eN6S2mbdhp[m] + co2	0	999999	
228	Lipoamide acyltransferase component of branched-chain alpha-ke	BCKADE2-ile 2.3.1.168	Mitochondrion	Amino Acid Catabolism	eN6S2mbdhp[m] + coa[m] --> laN6dhpl[m] + t2metbut2en-coa[m]	0	999999	
229	Enoyl Coa hydratase	ECHS1 4.2.1.17	Mitochondrion	Amino Acid Catabolism	t2metbut2en-coa[m] + h2o --> 3oh2metbut-coa[m]	0	999999	
230	Hydroxysteroid dehydrogenase 10	HSD17B10_ 1.1.1.178	Mitochondrion	Amino Acid Catabolism	3oh2metbut-coa[m] + nad[m] --> 2met-acetoacetyl-coa[m] + nadh[m]	0	999999	
231	Acetyl-coa acetyltransferase, mitochondrial	ACAT1 2.3.1.9	Mitochondrion	Amino Acid Catabolism	2met-acetoacetyl-coa[m] + coa[m] --> prop-coa[m] + acetyl-coa[m]	0	999999	
232	Isoleucine mitochondrial transport	MT_leu		Mitochondrial Transport	leu[c] --> leu[m]	0	999999	
233	Branched-chain amino acid aminotransferase, mitochondrial precursor	BCAT2-leu 2.6.1.42	Mitochondrion	Amino Acid Catabolism	leu[m] + akg[m] --> akiso[m] + glu[m]	0	999999	
234	Oxoisovalerate dehydrogenase	BCKDHB-leu 1.2.4.4	Mitochondrion	Amino Acid Catabolism	akiso[m] + laN6ll[m] --> eN6S3mbdhp[m] + co2	0	999999	
235	Lipoamide acyltransferase component of branched-chain alpha-ke	BCKADE2-leu 2.3.1.168	Mitochondrion	Amino Acid Catabolism	eN6S3mbdhp[m] + coa[m] --> laN6dhpl[m] + isov-coa[m]	0	999999	
236	Isovaleryl-coa dehydrogenase, mitochondrial precursor	IVD 1.3.99.10	Mitochondrion	Amino Acid Catabolism	isov-coa[m] + fad[m] --> 3mc-coa[m] + fadh2[m]	0	999999	
237	Methylcrotonyl-coa carboxylase	MCC1-MCC2 6.4.1.4	Mitochondrion	Amino Acid Catabolism	3mc-coa[m] + atp + hco3 --> 3mg-coa[m] + adp + p	0	999999	
238	Methylglutaconyl-CoA hydratase, mitochondrial	MGCA 4.2.1.18	Mitochondrion	Amino Acid Catabolism	3mg-coa[m] + h2o --> 3h3mg-coa[m]	0	999999	
239	Hydroxymethylglutaryl-coa lyase, mitochondrial precursor	HMGCL 4.1.3.4	Mitochondrion	Amino Acid Catabolism	3h3mg-coa[m] --> acetacet[m] + acetyl-coa[m]	0	999999	
240	Succinyl-coa: 3-keoacid-coanezyme A transferase, mitochondrial precursor	HOXA10 2.8.3.5	Mitochondrion	Amino Acid Catabolism	acetacet[m] + suc-coa[m] --> suc[m] + acetoacetyl-coa[m]	0	999999	
241	Hydroxymethylglutaryl-coa synthase, mitochondrial precursor	HMGCS2 2.3.3.10	Mitochondrion	Amino Acid Catabolism	acetoacetyl-coa[m] + acetyl-coa[m] + h2o --> 3h3mg-coa[m] + coa[m]	0	999999	
242	Glutamate Dehydrogenase	GLUDH 1.4.1.3	Mitochondrion	Amino Acid Catabolism	glu[m] + nadp[m] + h2o <=> akg[m] + nadph[m] + nh3	-999999	999999	R
243	Glutamine Synthetase	GlnSynth 6.3.1.2	Cytosolic	Amino Acid Biosynthesis	nh3 + glu[c] + atp --> gln[c] + adp + p	0	999999	IR
244	Glutamin (nitrogen) elimination in muscle	GLN_Elim	Cytosolic	Cellular Export	gln[c] -->	0	999999	IR
245	Alanine amino transferase 2	ALT 2.6.1.2	Cytosolic	Amino Acid Biosynthesis	glu[c] + pyr[c] <=> akg[c] + ala[c]	-999999	999999	R
246	Alanine nitrogen elimination in muscle	ALA_Elim	Cytosolic	Cellular Export	ala[c] -->	0	999999	IR
247	Serine Dehydratase	SDS 4.3.1.17	Cytosolic	Amino Acid Catabolism	ser[c] --> pyr[c] + nh3	0	999999	
248	Cystathionine beta-synthase	CBS 4.2.1.22	Cytosolic	Amino Acid Catabolism	ser[c] + hcys[c] --> cyst[c] + h2o	0	999999	
249	Cystathionine gamma-lyase	CTH 4.4.1.1	Cytosolic	Amino Acid Catabolism	cyst[c] + h2o --> nh3 + cys[c] + 2ob[c]	0	999999	
250	ILVB	ILVBL 2.2.1.6	Cytosolic	Amino Acid Catabolism	pyr[c] + 2ob[c] --> 2a2hbut[c] + co2	0	999999	
251	2-aceto-2-hydroxybutyrate Leak	2a2hButLeak		Cellular Export	2a2hbut[c] -->	0	999999	
252	Lysine mitochondrial transport	MT_lys		Amino Acid Mit Transport	lys[c] --> lys[m]	0	999999	
253	Lysine-ketoglutarate reductase/saccharopine dehydrogenase	AASS 1.5.1.7	Mitochondrion	Amino Acid Catabolism	lys[m] + akg[m] + nadh[m] <=> sacpn[m] + nad[m] + h2o	0	999999	
254	Lysine-ketoglutarate reductase/saccharopine dehydrogenase	AASS 1.5.1.9	Mitochondrion	Amino Acid Catabolism	sacpn[m] + nad[m] + h2o <=> 2aap6semald[m] + glu[m] + nadh[m]	0	999999	
255	Lysine-ketoglutarate reductase/saccharopine dehydrogenase	aAASADeh 1.2.1.31	Mitochondrion	Amino Acid Catabolism	2aap6semald[m] + nad[m] + h2o <=> aaap[m] + nadh[m]	0	999999	
256	L-kynurenine/alpha-aminoadipate aminotransferase	KATII 2.6.1.39	Mitochondrion	Amino Acid Catabolism	aaap[m] + akg[m] <=> glu[m] + akap[m]	0	999999	
257	lysdeg	lysdeg	Mitochondrion	Amino Acid Catabolism	akap[m] + nad[m] + coa[m] <=> glut-coa[m] + nadh[m] + co2	0	999999	
258	Glutaryl-coa Dehydrogenase, mitochondrial precursor	IVD 1.3.99.7	Mitochondrion	Amino Acid Catabolism	glut-coa[m] + fad[m] <=> tbut2enoyl-coa[m] + fadh2[m]	0	999999	
259	Poline oxidase, mitochondrial precursor	MT_pro		Amino Acid Mit Transport	pro[c] --> pro[m]	0	999999	
260	Aldehyde dehydrogenase 4A1 precursor	PRODH 1.5.99.8	Mitochondrion	Amino Acid Catabolism	pro[m] + fad[m] --> 1pyrr5carb[m] + fadh2[m]	0	999999	
261	Aldehyde dehydrogenase 4A1 precursor	ALDH4a1 1.5.1.12	Mitochondrion	Amino Acid Catabolism	1pyrr5carb[m] + nad[m] + 2 h2o --> glu[m] + nadh[m]	0	999999	IR
262	glycine amidinotransferase, Mitochondrial Precursor	GATM 2.1.4.1	Mitochondrion	Amino Acid Catabolism	gly[c] + arg[c] --> guan[c] + orn[m]	0	999999	committed step
263	ornithine leak	Dr_orn		Cellular Export	orn[m] -->	0	999999	
264	Guanidinoacetate N-methyltransferase	GAMT 2.1.1.2	Cytosolic	Amino Acid Catabolism	guan[c] + sal-met[c] --> cr + sal-hcys[c]	0	999999	
265	Adenosylhomocysteinase	Dr_cr		Cellular Export	cr -->	0	999999	
266	Adenosylhomocysteinase	AdoHcyase 3.3.1.1		Amino Acid Biosynthesis	sal-hcys[c] + h2o --> hcys[c] + amp	0	999999	
267	5-methyltetrahydrofolate-homocysteine-methyltransferase	MTR 2.1.1.13	Cytosolic	Amino Acid Biosynthesis	hcys[c] + 5meth-thf[c] <=> met[c] + thf[c]	-999999	999999	
268	S-adenosylmethionine synthetase	AdoMet 2.5.1.6		Amino Acid Biosynthesis	atp + met[c] + h2o --> sal-met[c] + 2 p	0	999999	

0 Enzyme	Abrev	EC Number	Location	Pathway	Reaction	Lower Bound	Upper Bound	Thermodynamics
269 Serine hydroxymethyltransferase	SHMT	2.1.2.1	Cytosolic	Amino Acid Biosynthesis	ser[c] + thf[c] <=> gly[c] + 5methyln-thf[c]	-999999	999999	R
270 Methylenetetrahydrofolate reductase	MTHFR	1.5.1.20	Cytosolic	Vitamin Metabolism	5methyln-thf[c] + nadph[c] --> 5meth-thf[c] + nadp[c]	0	999999	R
271 Dihydrofolate Reductase	DHFR	1.5.1.3	Cytosolic	Vitamin Metabolism	dhf[c] + nadph[c] --> thf[c] + nadp[c]	0	999999	IR
272 Histidine Ammonia-lyase	HAL	4.3.1.3	Cytosolic	Amino Acid Catabolism	his[c] --> uro[c] + nh3	0	999999	IR
273 Probable urocanate hydratase	FLI31300	4.2.1.49	Cytosolic	Amino Acid Catabolism	uro[c] + h2o --> 4im5prop[c]	0	999999	IR
274 Unknown	MGC35366	3.5.2.7	Cytosolic	Amino Acid Catabolism	4im5prop[c] + h2o --> form-glu[c]	0	999999	IR
275 Formimidoyltransferase-cyclodeaminase, pt 1	FTCD1	2.1.2.5	Cytosolic	Amino Acid Catabolism	form-glu[c] + thf[c] --> glu[c] + form-thf[c]	0	999999	IR
276 Formimidoyltransferase-cyclodeaminase, pt 2	FTCD2	4.3.1.4	Cytosolic	Vitamin Metabolism	form-thf[c] <=> 5methn-thf[c] + nh3	-999999	999999	R
277 Folate Transformation	FT	1.5.1.15	Cytosolic	Vitamin Metabolism	5methn-thf[c] + nadh[c] <=> 5methyln-thf[c] + nad[c]	-999999	999999	R
278 Asparaginase (asparagine amidohydrolase)	ASNase	3.5.1.1	Cytosolic	Amino Acid Biosynthesis	asn[c] + h2o --> asp[c] + nh3	0	999999	IR
279 Asparagine synthetase (glutamine-hydrolyzing)	ASNSynth	6.3.5.4	Cytosolic	Amino Acid Biosynthesis	gln[c] + asp[c] + atp + h2o --> glu[c] + asn[c] + amp + 2 p	0	999999	R
280 Phosphoglycerate dehydrogenase	PHGDH	1.1.1.95	Cytosolic	Amino Acid Biosynthesis	3pg[c] + nad[c] --> 3phdpyr[c] + nadh[c]	0	999999	IR
281 Phosphoserine aminotransferase	PSA	2.6.1.52	Cytosolic	Amino Acid Biosynthesis	3phdpyr[c] + glu[c] --> 3pser[c] + akgl[c]	0	999999	IR
282 Phosphoserine phosphatase	PSPH	3.1.3.3	Cytosolic	Amino Acid Biosynthesis	3pser[c] + h2o --> ser[c] + p	0	999999	IR
283 Glutamate 5-kinase	P5CS	2.7.2.11	Mitochondrion	Amino Acid Biosynthesis	glu[m] + atp --> glu-5-p[m] + adp + p	0	999999	
284 Gamma-glutamyl phosphate reductase	PYCS	1.2.1.41	Mitochondrion	Amino Acid Biosynthesis	glu-5-p[m] + nadph[m] --> glu-5-semald[m] + nadp[m]	0	999999	
285 Spontaneous	Spont_Glu		Mitochondrion	Amino Acid Biosynthesis	glu-5-semald[m] --> 1pyrr5carb[m] + h2o	0	999999	
286 Pyrroline 5-carboxylate reductase	PYRCR1	1.5.1.2	Mitochondrion	Amino Acid Biosynthesis	1pyrr5carb[m] + nadph[m] --> pro[m] + nadp[m]	0	999999	IR
287 Phenylalanine-4-hydroxylase	PAG	1.14.16.1	Cytosolic	Amino Acid Biosynthesis	phe[c] + thb[c] --> tyr[c] + 4ah-thb[c]	0	999999	IR
288 Pterin-4-alpha-carinolamine dehydratase	PCBD	4.2.1.96	Cytosolic	Amino Acid Biosynthesis	4ah-thb[c] --> dhb[c] + h2o	0	999999	IR
289 Dihydropterin Reductase	QDPR	1.5.1.34	Cytosolic	Amino Acid Biosynthesis	dhb[c] + nadh[c] --> thb[c] + nad[c]	0	999999	IR
290	MT_glu			Mitochondrial Transport	glu[m] <=> glu[c]	-999999	999999	
291	tRNA			Nutrient	trna[c] <=>	-999999	999999	
292 Tyrosyl-tRNA synthetase	YARS	6.1.1.1		Translation	trna[c] + tyr[c] + atp <=> trna-tyr[c] + amp + 2 p	-999999	999999	R
293 Tryptophanyl-tRNA synthetase	WARS	6.1.1.2		Translation	trna[c] + trp[c] + atp <=> trna-trp[c] + amp + 2 p	-999999	999999	R
294 Threonyl-tRNA Synthetase	TARS	6.1.1.3		Translation	trna[c] + thr[c] + atp <=> trna-thr[c] + amp + 2 p	-999999	999999	R
295 Leucyl-tRNA Synthetase	LARS	6.1.1.4		Translation	trna[c] + leu[c] + atp <=> trna-leu[c] + amp + 2 p	-999999	999999	R
296 Isoleucyl-tRNA Synthetase	IARS	6.1.1.5		Translation	trna[c] + ile[c] + atp <=> trna-ile[c] + amp + 2 p	-999999	999999	R
297 Lysyl-tRNA Synthetase	KARS	6.1.1.6		Translation	trna[c] + lys[c] + atp <=> trna-lys[c] + amp + 2 p	-999999	999999	R
298 Alanyl-tRNA Synthetase	AARS	6.1.1.7		Translation	trna[c] + ala[c] + atp <=> trna-ala[c] + amp + 2 p	-999999	999999	R
299 Valyl-tRNA Synthetase	VARS	6.1.1.9		Translation	trna[c] + val[c] + atp <=> trna-val[c] + amp + 2 p	-999999	999999	R
300 Methionyl-tRNA Synthetase	MARS	6.1.1.10		Translation	trna[c] + met[c] + atp <=> trna-met[c] + amp + 2 p	-999999	999999	R
301 Seryl-tRNA Synthetase	SARS	6.1.1.11		Translation	trna[c] + ser[c] + atp <=> trna-ser[c] + amp + 2 p	-999999	999999	R
302 Aspartyl-tRNA Synthetase	DARS	6.1.1.12		Translation	trna[c] + asp[c] + atp <=> trna-asp[c] + amp + 2 p	-999999	999999	R
303 Glycyl-tRNA Synthetase	GARS	6.1.1.14		Translation	trna[c] + gly[c] + atp <=> trna-gly[c] + amp + 2 p	-999999	999999	R
304 Prolyl-tRNA Synthetase	PARS	6.1.1.15		Translation	trna[c] + pro[c] + atp <=> trna-pro[c] + amp + 2 p	-999999	999999	R
305 Cysteinyl-tRNA Synthetase	CARS	6.1.1.16		Translation	trna[c] + cys[c] + atp <=> trna-cys[c] + amp + 2 p	-999999	999999	R
306 Glutamyl-tRNA Synthetase	EPRS	6.1.1.17		Translation	trna[c] + glu[c] + atp <=> trna-glu[c] + amp + 2 p	-999999	999999	R
307 Glutaminyl-tRNA Synthetase	QARS	6.1.1.18		Translation	trna[c] + gln[c] + atp <=> trna-gln[c] + amp + 2 p	-999999	999999	R
308 Arginyl-tRNA Synthetase	RARS	6.1.1.19		Translation	trna[c] + arg[c] + atp <=> trna-arg[c] + amp + 2 p	-999999	999999	R
309 Phenylalanyl-tRNA Synthetase	FARS	6.1.1.20		Translation	trna[c] + phe[c] + atp <=> trna-phe[c] + amp + 2 p	-999999	999999	R
310 Histidyl-tRNA Synthetase	HARS	6.1.1.21		Translation	trna[c] + his[c] + atp <=> trna-his[c] + amp + 2 p	-999999	999999	R
311 Asparaginyl-tRNA Synthetase	NARS	6.1.1.22		Translation	trna[c] + asn[c] + atp <=> trna-asn[c] + amp + 2 p	-999999	999999	R
312 Actin Synthesis	ACT	4501881		Protein Synthesis	29 trna-ala[c] + 6 trna-cys[c] + 22 trna-asp[c] + 28 trna-glu[c] + 12 trna-phe[c]	0	999999	IR
313 Myosin Heavy Chain type 1 and 2x muscle fiber	MYOHC1-2x	115527082		Protein Synthesis	171 trna-ala[c] + 17 trna-cys[c] + 98 trna-asp[c] + 261 trna-glu[c] + 56 trna-pf	0	999999	IR
314 Myosin Heavy Chain type 2a muscle fiber	MYOHC2a	153792663		Protein Synthesis	172 trna-ala[c] + 18 trna-cys[c] + 93 trna-asp[c] + 265 trna-glu[c] + 58 trna-pf	0	999999	IR
315 Myosin Heavy Chain type 2b muscle fiber	MYOHC2b	110611903		Protein Synthesis	168 trna-ala[c] + 17 trna-cys[c] + 94 trna-asp[c] + 263 trna-glu[c] + 61 trna-pf	0	999999	IR
316 Myosin Light Chain Kinase	MYOLCK	14993776		Protein Synthesis	56 trna-ala[c] + 10 trna-cys[c] + 30 trna-asp[c] + 48 trna-glu[c] + 20 trna-phe	0	999999	IR
317 Myosin Light Chain Phosphorylated	MYOLCp	28372499		Protein Synthesis	12 trna-ala[c] + 2 trna-cys[c] + 15 trna-asp[c] + 15 trna-glu[c] + 12 trna-phe	0	999999	IR
318 Myosin type 1 muscle fiber	MYO1-2x			Polymerizatin	2 myoHC1-2x[c] + 2 myoLCK[c] + 2 myoLCP[c] --> myo1[c]	0	999999	IR
319 Myosin type 2a muscle fiber	MYO2a			Polymerizatin	2 myoHC2a[c] + 2 myoLCK[c] + 2 myoLCP[c] --> myo2a[c]	0	999999	IR
320 Myosin type 2x muscle fiber	MYO2x			Polymerizatin	2 myoHC1-2x[c] + 2 myoLCK[c] + 2 myoLCP[c] --> myo2x[c]	0	999999	IR
321 Myosin type 2b muscle fiber	MYO2b			Polymerizatin	2 myoHC2b[c] + 2 myoLCK[c] + 2 myoLCP[c] --> myo2b[c]	0	999999	IR
322 Tropomyosin type 1 muscle fiber	TMN1	114155140		Protein Synthesis	38 trna-ala[c] + 1 trna-cys[c] + 19 trna-asp[c] + 61 trna-glu[c] + 1 trna-phe	0	999999	IR
323 Tropomyosin type 2 muscle fiber	TMN2	114155144		Protein Synthesis	28 trna-ala[c] + 3 trna-cys[c] + 14 trna-asp[c] + 54 trna-glu[c] + 1 trna-phe	0	999999	IR
324 Tropomyosin complex for type 1 muscle fibers	DIM-TMN1			Polymerizatin	2 tmn1[c] --> dim-tmn1[c]	0	999999	IR
325 Tropomyosin complex for type 2 muscle fibers	DIM-TMN2			Polymerizatin	2 tmn2[c] --> dim-tmn2[c]	0	999999	IR
326 Troponin c for type 1 muscle fibers	TPNC1	4507615		Protein Synthesis	7 trna-ala[c] + 2 trna-cys[c] + 23 trna-asp[c] + 23 trna-glu[c] + 9 trna-phe	0	999999	IR
327 Troponin c for type 2 muscle fibers	TPNC2	4507617		Protein Synthesis	12 trna-ala[c] + 1 trna-cys[c] + 19 trna-asp[c] + 26 trna-glu[c] + 10 trna-phe	0	999999	IR
328 Troponin I for type 1 muscle fibers	TPNI1	56682969		Protein Synthesis	15 trna-ala[c] + 3 trna-cys[c] + 10 trna-asp[c] + 22 trna-glu[c] + 2 trna-phe	0	999999	IR
329 Troponin I for type 2 muscle fibers	TPNI2	4507621		Protein Synthesis	13 trna-ala[c] + 3 trna-cys[c] + 11 trna-asp[c] + 25 trna-glu[c] + 3 trna-phe	0	999999	IR
330 Troponin T for type 1 muscle fibers	TPNT1	187173288		Protein Synthesis	20 trna-ala[c] + 1 trna-cys[c] + 12 trna-asp[c] + 54 trna-glu[c] + 6 trna-phe	0	999999	IR
331 Troponin T for type 2 muscle fibers	TPNT2	5803203		Protein Synthesis	24 trna-ala[c] + 18 trna-asp[c] + 49 trna-glu[c] + 4 trna-phe[c] + 9 trna-gly	0	999999	IR
332 Troponin for type 1 muscle fibers	TPN1			Polymerizatin	tpnc1[c] + tpni1[c] + tpnt1[c] --> tpn1[c]	0	999999	IR
333 Troponin for type 2 muscle fibers	TPN2			Polymerizatin	tpnc2[c] + tpni2[c] + tpnt2[c] --> tpn2[c]	0	999999	IR
334 Contractile complex for type 1 muscle fibers	CONTR-COMP1			Polymerizatin	7 act[c] + 7 myo1[c] + dim-tmn1[c] + tpn1[c] --> contr-comp1[c]	0	999999	IR
335 Contractile complex for type 2a muscle fibers	CONTR-COMP2a			Polymerizatin	7 act[c] + 7 myo2a[c] + dim-tmn2[c] + tpn2[c] --> contr-comp2a[c]	0	999999	IR

0 Enzyme	Abrev	EC Number	Location	Pathway	Reaction	Lower Bound	Upper Bound	Thermodynamics
336 Contractile complex for type 2x muscle fibers	CONTR-COMP2x			Polymerizatin	7 act[c] + 7 myo2x[c] + dim-tmn2[c] + tpn2[c] --> contr-comp2x[c]	0	999999	IR
337 Contractile complex for type 2b muscle fibers	CONTR-COMP2b			Polymerizatin	7 act[c] + 7 myo2b[c] + dim-tmn2[c] + tpn2[c] --> contr-comp2b[c]	0	999999	IR
338 Storage Contractile complex type 1 muscle fibers	Str_CONTR-COMP1			Muscle	contr-comp1[c] -->	0	999999	IR
339 Storage Contractile complex type 2a muscle fibers	Str_CONTR-COMP2a			Muscle	contr-comp2a[c] -->	0	999999	IR
340 Storage Contractile complex type 2x muscle fibers	Str_CONTR-COMP2x			Muscle	contr-comp2x[c] -->	0	999999	IR
341 Storage Contractile complex type 2b muscle fibers	Str_CONTR-COMP2b			Muscle	contr-comp2b[c] -->	0	999999	IR
342 Creatine Kinase, M Chain	CKM	2.7.3.2		Creatine	cr-p + adp <=> cr + atp	-999999	999999	R
343 Creatine Supply	Spont_CrP			Creatine	cr-p <=> cr + p	-999999	999999	R
344	Nut_cr			Creatine	cr <=>	0	999999	IR
345 Fake Transfer	ATP2UTP			Glycogen Synthesis 2	atp --> utp	0	999999	
346 Fake Transfer	UDP2ADP			Glycogen Synthesis	udp --> adp	0	999999	
347 Phosphoglucomutase	PGM1	5.4.2.2		Glycogen Synthesis	g6p[c] <=> g1p[c]	-999999	999999	IR
348 UTP-glucose--1-phosphate uridylyltransferase	UGP2	2.7.7.9		Glycogen Synthesis 2	g1p[c] + utp --> udp-g1p[c] + (2) p	-999999	999999	
349 Modified Glycogenin-1 and 2 for model	mGYG	2.4.1.186/2.4.1.11		Glycogen Synthesis	udp-g1p[c] <=> glycogen[c] + udp	-999999	999999	
350 Modified Glycogen Synthase - muscle for the model	mGYS1			Glycogen Synthesis	glycogen[c] -->	0	999999	
351 glucose-6-phosphate 1-dehydrogenase	G6PD	1.1.1.49	cytosol	Pentose Phosphate Pathway	g6p[c] + nadp[c] <=> gluc-lac-6p[c] + nadph[c]	-999999	999999	
352 6-phosphogluconalactonase	PGLS	3.1.1.31	cytosol	Pentose Phosphate Pathway	gluc-lac-6p[c] + h2o <=> 6pgluconate[c]	-999999	999999	
353 6-phosphogluconate dehydrogenase	PGD	1.1.1.44	cytosol	Pentose Phosphate Pathway	6pgluconate[c] + nadp[c] <=> ru5p[c] + co2 + nadph[c]	-999999	0	
354 6-phosphogluconate dehydrogenase	PGD	1.1.1.44	cytosol	Pentose Phosphate Pathway	6pgluconate[c] + nad[c] <=> ru5p[c] + co2 + nadh[c]	0	999999	
355 ribulose-5-phosphate-3-epimerase	RPE	5.1.3.1	cytosol	Pentose Phosphate Pathway	ru5p[c] <=> x5p[c]	-999999	999999	
356 ribose-5-phosphate isomerase	RPIA	5.3.1.6	cytosol	Pentose Phosphate Pathway	ru5p[c] <=> r5p[c]	-999999	999999	
357 transketolase	TKT1	2.2.1.1	cytosol	Pentose Phosphate Pathway	e4p[c] + x5p[c] <=> f6p[c] + g3p[c]	-999999	999999	
358 transketolase	TKT2	2.2.1.1	cytosol	Pentose Phosphate Pathway	s7p[c] + g3p[c] <=> r5p[c] + x5p[c]	-999999	999999	
359 transaldolase	TALDO	2.2.1.2	cytosol	Pentose Phosphate Pathway	s7p[c] + g3p[c] <=> e4p[c] + f6p[c]	-999999	999999	
360 Ribokinase	RBSK	2.7.1.15	cytosol	Pentose Phosphate Pathway	rib[c] + atp <=> r5p[c] + adp + p	-999999	999999	
361 Glutamate-cystein Ligase	GCL	6.3.2.2	Cytosol	Glutathione biosynthesis	cys[c] + glu[c] + atp --> glu-cys[c] + p + adp	0	999999	
362 Glutathione synthetase	GSS	6.3.2.3	Cytosol	Glutathione biosynthesis	glu-cys[c] + gly[c] + atp --> glutath[c] + adp + p	0	999999	
363 Glutathione transport	glutathport			Mitochondrial Transport	glutath[c] <=> glutath[m]	-999999	999999	
364 Glutathione reductase, cellular	GSR	1.8.1.7	Cytosol	Glutathione Redox	2 glutath[c] + nadp[c] --> gssg[c] + nadph[c]	0	999999	
365 Glutathione reductase	GSR	1.8.1.7	Mitochondria	Glutathione Redox	2 glutath[m] + nadp[m] --> gssg[m] + nadph[m]	0	999999	
366 Gluathione leak	GlutathLeak			Cellular Export	gssg[c] -->	0	999999	
367 Gluathione leak	GlutathLeak			Cellular Export	gssg[m] -->	0	999999	
368	Acetyl-coaLeak			Cellular Export	acetyl-coa[m] -->	0	999999	