Supplemental data S1: Reactions in the mitochondrial metabolic network

Conf: confidence level
Prot: proteomic data
[c]: cytosolic compartment; [m]: mitochondrial compartment; [e]: extracellular compartment
[c] or [m] at the beginning of each equation denotes the compartment where the reaction takes place
[c], [e] or [m] following a metabolite localizes that metabolite to one of the three compartment.
References refer to biochemical evidence for a reaction in additional to, or in place of, proteomic data

	Abbreviation	Official Name	Equation	Conf	Subsystem	EC	Prot	References
1	HEX1	hexokinase (D-glucose:AT	[c] : atp + glc-D --> adp + g6p + h	4	Glycolysis	2.7.1.1	yes	(Voet, Voet et al. 1999)
2	G6PI	Glucose-6-phosphate isom	[c] : g6p <==> g6p-B	4	Glycolysis	5.3.1.9	yes	(Voet, Voet et al. 1999)
3	G6PI2	Glucose-6-phosphate isom	[c] : g6p-B <==> f6p-B	4	Glycolysis	5.3.1.9	yes	(Voet, Voet et al. 1999)
4	PGI	glucose-6-phosphate isom	[c] : g6p <==> f6p	4	Glycolysis	5.3.1.9	yes	(Voet, Voet et al. 1999)
5	PFK	phosphofructokinase	[c] : atp + f6p --> adp + fdp + h	4	Glycolysis	2.7.1.11	yes	(Voet, Voet et al. 1999)
6	FBA	fructose-bisphosphate aldo	[c] : fdp <==> dhap + g3p	4	Glycolysis	4.1.2.13	yes	(Voet, Voet et al. 1999)
7	TPI	triose-phosphate isomeras	[c] : dhap <==> g3p	4	Glycolysis	5.3.1.1	yes	(Voet, Voet et al. 1999)
8	GAPD	glyceraldehyde-3-phospha	[c] : g3p + nad + pi <==> 13dpg + h + nadh	4	Glycolysis	1.2.1.12	yes	(Voet, Voet et al. 1999)
9	PGK	phosphoglycerate kinase	[c] : 3pg + atp <==> 13dpg + adp	4	Glycolysis	2.7.2.3	yes	(Voet, Voet et al. 1999)
10	PGM	phosphoglycerate mutase	[c] : 2pg <==> 3pg	4	Glycolysis	5.4.2.1		(Voet, Voet et al. 1999)
11	ENO	enolase	[c] : 2pg <==> h2o + pep	4	Glycolysis	4.2.1.11		(Voet, Voet et al. 1999)
12	PYK	pyruvate kinase	[c] : adp + h + pep --> atp + pyr	4	Glycolysis	2.7.1.40	yes	(Voet, Voet et al. 1999)
13	PDHm	pyruvate dehydrogenase	[m] : coa + nad + pyr --> accoa + co2 + nadh	3	TCA cycle	1.2.4.1	yes	(Voet, Voet et al. 1999)
14	CSm	citrate synthase	[m] : accoa + h2o + oaa --> cit + coa + h	4	TCA cycle	4.1.3.7	yes	(Voet, Voet et al. 1999)
15	ACONTm	Aconitate hydratase	[m] : cit <==> icit	4	TCA cycle	4.2.1.3	yes	(Voet, Voet et al. 1999)
16	ICDHxm	Isocitrate dehydrogenase (	[m] : icit + nad --> akg + co2 + nadh	4	TCA cycle	1.1.1.41	yes	(Voet, Voet et al. 1999)
17	ICDHym	Isocitrate dehydrogenase (	[m] : icit + nadp --> akg + co2 + nadph	4	TCA cycle	1.1.1.42	yes	(Voet, Voet et al. 1999)
18	AKGDm	2-oxoglutarate dehydroger	[m] : akg + coa + nad --> co2 + nadh + succoa	4	TCA cycle	1.2.4.2	yes	(Voet, Voet et al. 1999)
19	SUCOASm	succinyl-CoA synthetase ((	[m] : coa + gtp + succ <==> gdp + pi + succoa	4	TCA cycle	6.2.1.4	yes	(Voet, Voet et al. 1999)
20	SUCD1m	succinate dehydrogenase	[m] : fad + succ <==> fadh2 + fum	4	TCA cycle	1.3.99.1	yes	(Voet, Voet et al. 1999)
21	FUMm	fumarase, mitochondrial	[m] : fum + h2o <==> mal-L	4	TCA cycle	4.2.1.2	yes	(Voet, Voet et al. 1999)
22	MDHm	malate dehydrogenase, mi	[m] : mal-L + nad <==> h + nadh + oaa	4	TCA cycle	1.1.1.37	yes	(Voet, Voet et al. 1999)
23	NADH2-u10m	NADH dehydrogenase, mit	(5) h[m] + nadh[m] + q10[m] --> (4) h[c] + nad[m] + q10h2[m]	4	OxPhos	1.6.99.3	yes	(Voet, Voet et al. 1999)
24	SUCD3-u10m	succinate dehydrogenase	[m] : fadh2 + q10 <==> fad + q10h2	4	OxPhos	1.3.5.1	yes	(Voet, Voet et al. 1999)
25	CYOR-u10m	ubiquinol-6 cytochrome c r	(2) ficytC[m] + (2) h[m] + q10h2[m] --> (2) focytC[m] + (4) h[c] + q10[m]	4	OxPhos	1.10.2.2	yes	(Voet, Voet et al. 1999)
26	CYOOm3	cytochrome c oxidase, mito	(4) focytC[m] + (7.92) h[m] + o2[m] --> (4) ficytC[m] + (4) h[c] + (1.96) h2o[m] + (0.02) o2-[m]	3	OxPhos	1.9.3.1	yes	(Voet, Voet et al. 1999)
27	ATPS4m	ATP synthase (four proton:	adp[m] + (4) h[c] + pi[m] --> atp[m] + (3) h[m] + h2o[m]	4	OxPhos	3.6.3.14	yes	(Voet, Voet et al. 1999)
28	GLUCYS	gamma-glutamylcysteine s	[c] : atp + cys-L + glu-L --> adp + glucys + h + pi	4	ROS detoxification	6.3.2.2		(Meister 1995)
29	GTHDHm	Glutathione dehydrogenas	[m] : dhdascb + (2) gthrd --> ascb-L + gthox	2	ROS detoxification	1.8.5.1		(Meister 1995)

30	GTHOm	glutathione oxidoreductase	[m] : gthox + h + nadph --> (2) gthrd + nadp	4	ROS detoxification	1.8.1.7	yes	
31	GTHPm	glutathione peroxidase, mit	[m] : (2) gthrd + h2o2 <==> gthox + (2) h2o	4	ROS detoxification	1.11.1.9	yes	(Shlafer, Myers et al. 1987)
32	GTHRDt	Glutathione transport into r	atp[c] + gthrd[c] + h2o[c] <==> adp[c] + gthrd[m] + h[c] + pi[c]	2	ROS detoxification			(Kurosawa, Hayashi et al. 1990)
33	GTHS	glutathione synthetase	[c] : atp + glucys + gly --> adp + gthrd + h + pi	4	ROS detoxification	6.3.2.3		(Meister 1995)
34	SPODMm	superoxide dismutase	[m] : (2) h + (2) o2- --> h2o2 + o2	3	ROS detoxification	1.15.1.1	yes	(Shlafer, Myers et al. 1987)
35	THD1m	NAD(P) transhydrogenase	h[c] + nadh[m] + nadp[m] <==> h[m] + nad[m] + nadph[m]	4	ROS detoxification	1.6.1.1	yes	(Jackson, Peake et al. 1999; Peake, Jackson et al. 2000; White, Peake et al. 2000)
36	CATm	catalase	[m] : (2) h2o2 --> (2) h2o + o2	3	ROS detoxification	1.11.1.6	yes	(Nohl and Hegner 1978; Radi, Turrens et al. 1991; Antunes, Han et al. 2002)
37	ASPGLUm	aspartate-glutamate mitoch	asp-L[m] + glu-L[c] + h[c] <==> asp-L[c] + glu-L[m] + h[m]	4	Mal-Asp Shuttle			(Kaplan 2001; Palmieri, Pardo et al. 2001)
38	ASPTA	aspartate transaminase	[c] : akg + asp-L <==> glu-L + oaa	4	Mal-Asp Shuttle	2.6.1.1		(Voet, Voet et al. 1999)
39	MDH	malate dehydrogenase	[c] : mal-L + nad <==> h + nadh + oaa	4	Mal-Asp Shuttle	1.1.1.37	yes	(Voet, Voet et al. 1999)
40	AKGMALtm	alpha-ketoglutarate/malate	akg[m] + mal-L[c] <==> akg[c] + mal-L[m]	4	Mal-Asp Shuttle		yes	(Kaplan 2001; Palmieri 2004)
41	ASPTAm	aspartate transaminase	[m] : akg + asp-L <==> glu-L + oaa	4	Mal-Asp Shuttle	2.6.1.1	yes	
42	ALASm	5-aminolevulinate synthase	[m] : gly + h + succoa --> 5aop + co2 + coa	3	Heme biosynthesis	2.3.1.37	yes	(Voet, Voet et al. 1999)
43	5AOPtm	5-Aminolevulinate mitocho	5aop[c] <==> 5aop[m]	2	Heme biosynthesis			(Voet, Voet et al. 1999)
44	PPBNGS	porphobilinogen synthase	[c] : (2) 5aop --> h + (2) h2o + ppbng	2	Heme biosynthesis	4.2.1.24		(Voet, Voet et al. 1999)
45	HMBS	hydroxymethylbilane synth	[c] : h2o + (4) ppbng --> hmbil + (4) nh4	2	Heme biosynthesis	4.3.1.8		(Voet, Voet et al. 1999)
46	UPP3S	uroporphyrinogen-III synth	[c] : hmbil --> h2o + uppg3	3	Heme biosynthesis	4.2.1.75	yes	(Voet, Voet et al. 1999)
47	UPPDC1	uroporphyrinogen decarbo	[c] : (4) h + uppg3 --> (4) co2 + cpppg3	4	Heme biosynthesis	4.1.1.37		(Voet, Voet et al. 1999)
48	CPPPGO	coproporphyrinogen oxidas	[c] : cpppg3 + (2) h + o2 --> (2) co2 + (2) h2o + pppg9	3	Heme biosynthesis	1.3.3.3	yes	(Voet, Voet et al. 1999)
49	PPPG9tm	protoporphyrinogen IX mitc	pppg9[c] <==> pppg9[m]	2	Heme biosynthesis			(Voet, Voet et al. 1999)
50	PPPGOm	protoporphyrinogen oxidas	[m] : (3) o2 + (2) pppg9 --> (6) h2o + (2) ppp9	3	Heme biosynthesis	1.3.3.4	yes	(Voet, Voet et al. 1999)
51	FCLTm	Ferrochelatase, mitochond	[m] : fe2 + ppp9 --> (2) h + pheme	3	Heme biosynthesis	4.99.1.1	yes	(Voet, Voet et al. 1999)
52	FAOXC160	Beta oxidation of long chai	[m] : (7) coa + (7) fad + (7) h2o + (7) nad + pmtcoa --> (8) accoa + (7) fadh2 + (7) h + (7) nadh	4	Fatty acid oxidation	1.3.99.3		(Voet, Voet et al. 1999)
53	FAOXC180	Beta oxidation of long chai	[m] : coa + fad + h2o + nad + stcoa --> accoa + fadh2 + h + nadh + pmtcoa	4	Fatty acid oxidation	1.3.99.3		(Voet, Voet et al. 1999)
54	FAOXC181	Beta oxidation of long chai	[m] : coa + h2o + nad + odecoa --> accoa + h + nadh + pmtcoa	4	Fatty acid oxidation	1.3.99.3		(Voet, Voet et al. 1999)
55	FAOXC182	Beta oxidation of long chai	[m] : (8) coa + (6) fad + (8) h2o + (8) nad + ocdycacoa --> (9) accoa + (6) fadh2 + (8) h + (8) nadh	4	Fatty acid oxidation	1.3.99.3		(Voet, Voet et al. 1999)
56	FAOXC204	Beta oxidation of long chai	[m] : c204coa + (9) coa + (5) fad + (9) h2o + (9) nad --> (10) accoa + (5) fadh2 + (9) h + (9) nadh	4	Fatty acid oxidation	1.3.99.3		(Voet, Voet et al. 1999)
57	FAOXC226	Beta oxidation of long chai	[m] : c226coa + (10) coa + (4) fad + (10) h2o + (10) nad --> (11) accoa + (4) fadh2 + (10) h + (10) nadh	4	Fatty acid oxidation	1.3.99.3		(Voet, Voet et al. 1999)
58	C160	C160 fatty acid activation	[c] : atp + coa + hdca --> amp + pmtcoa + ppi	4	Fatty acid transport	6.2.1.3	yes	(Indiveri, Tonazzi et al. 1991; Indiveri, Tonazzi et al. 1991; Indiveri, Tonazzi et al. 1994; Voet, Voet et al.
59	C160CPT1	carnitine O-palmitoyltransfe	[c] : crn + pmtcoa --> coa + pmtcrn	4	Fatty acid transport	2.3.1.21	yes	
60	C160CPT2	C160 transport into the mit	[m] : coa + pmtcrn --> crn + pmtcoa	4	Fatty acid transport		yes	
61	C160CRN	C160 transport into the mit	pmtcrn[c] --> pmtcrn[m]	4	Fatty acid transport		yes	
62	C180	C180 fatty acid activation	[c] : atp + coa + ocdca --> amp + ppi + stcoa	4	Fatty acid transport	6.2.1.3	yes	
63	C180CPT1	carnitine O-stearoyl transfe	[c] : crn + stcoa --> coa + stcrn	4	Fatty acid transport	2.3.1.21	yes	
64	C180CPT2	carnitine O-stearoyl transfe	[m] : coa + stcrn --> crn + stcoa	4	Fatty acid transport			
65	C180CRN	C180 transport into the mit	stcrn[c] --> stcrn[m]	4	Fatty acid transport			
66	C181	C181 fatty acid activation	[c] : atp + coa + ocdcea --> amp + odecoa + ppi	4	Fatty acid transport	6.2.1.3	yes	

67	C181CRN1	carnitine octadecenoyl trar	[c] : crn + odecoa --> coa + odecrn	4	Fatty acid transport	2.3.1.21	yes	
68	C181CRN2	C181 transport into the mit	odecrn[c] --> odecrn[m]	4	Fatty acid transport			
69	C181CRN3	carnitine octadecenoyl trar	[m] : coa + odecrn --> crn + odecoa	4	Fatty acid transport			
70	C182	C182 fatty acid activation	[c] : atp + coa + ocdcya --> amp + ocdycacoa + ppi	4	Fatty acid transport	6.2.1.3	yes	
71	C182CRN1	carnitine octadecynoyl tran	[c] : crn + ocdycacoa --> coa + ocdycrn	4	Fatty acid transport	2.3.1.21	yes	
72	C182CRN2	C182 transport into the mit	ocdycrn[c] --> ocdycrn[m]	4	Fatty acid transport			
73	C182CRN3	carnitine octadecynol trans	[m] : coa + ocdycrn --> crn + ocdycacoa	4	Fatty acid transport			
74	C204	C204 fatty acid activation	[c] : atp + c204 + coa --> amp + c204coa + ppi	4	Fatty acid transport	6.2.1.3	yes	
75	C204CRN1	carnitine C20:4 transferase	[c] : c204coa + crn --> c204crn + coa	4	Fatty acid transport	2.3.1.21	yes	
76	C204CRN2	C204 transport into the mit	c204crn[c] --> c204crn[m]	4	Fatty acid transport			
77	C204CRN3	C204 transport into the mit	[m] : c204crn + coa --> c204coa + crn	4	Fatty acid transport			
78	C226	C226 fatty acid activation	[c] : atp + c226 + coa --> amp + c226coa + ppi	4	Fatty acid transport	6.2.1.3	yes	
79	C226CRN1	carnitine C22:6 transferase	[c] : c226coa + crn --> c226crn + coa	4	Fatty acid transport	2.3.1.21	yes	
80	C226CRN2	C226 transport into the mit	c226crn[c] --> c226crn[m]	4	Fatty acid transport			
81	C226CRN3	C226 transport into the mit	[m] : c226crn + coa --> c226coa + crn	4	Fatty acid transport			
82	CRNtim	L-carnitine transport out of	crn[m] --> crn[c]	4	Fatty acid transport			(Murthy and Pande 1984; Indiveri, Tonazzi et al. 1991; Indiveri, Tonazzi et al. 1991; Indiveri, Tonazzi et al. 1992; Indiveri, Tonazzi et al. 1994)
83	CHLPCTD	choline phosphate cytididy	[c] : cholp + ctp + h --> cdpchol + ppi	2	Lipid	2.7.7.15		(Zelinski, Savard et al. 1980; Choy, Tran et al. 1997)
84	DAGCPTm	diacylglycerol cholinephos	[c] : 12dgr_m + cdpchol --> cmp + h + pc_m	4	Lipid	2.7.8.2		(Henneberry, Wright et al. 2002; Wright and McMaster 2002)
85	PCtm	Phosphatidylcholine transp	pc_m[c] --> pc_m[m]	2	Lipid			
86	PSDm	Phosphatidylserine decarb	[m] : h + ps_m --> co2 + pe_m	4	Lipid	4.1.1.65		(Shiao and Vance 1995)
87	PStm	Phosphatidylserine transpo	ps_m[c] --> ps_m[m]	2	Lipid			(Shiao, Lupo et al. 1995)
88	G3PDm	glycerol-3-phosphate dehy	[m] : fad + glyc3p --> dhap + fadh2	3	Lipid	1.1.99.5	yes	
89	CLPNSm	Cardiolipin Synthase, mito	[m] : (2) pg_m <==> clpn_m + glyc	4	Lipid			(Daum 1985)
90	PAPAm	Phosphatidate phosphatas	[m] : h2o + pa_m --> 12dgr_m + pi	2	Lipid	3.1.3.4		(Sumikawa, Saeki et al. 1987)
91	DAGKm	Diacylglycerol kinase, mito	[m] : 12dgr_m + atp --> adp + h + pa_m	2	Lipid	2.7.1.107		(Hart, Zhou et al. 1994)
92	ETHAPTm	Ethanolaminephosphotran	[m] : 12dgr_m + cdpea <==> cmp + h + pe_m	2	Lipid	2.7.8.1		(Wright and McMaster 2002)
93	HMGLm	hydroxymethylglutaryl-CoA	[m] : hmgcoa --> acac + accoa	3	Lipid	4.1.3.4	yes	
94	OCOAT1m	3-oxoacid CoA-transferase	[m] : acac + succoa <==> aacoa + succ	3	Lipid	2.8.3.5	yes	
95	ACACT1m	acetyl-CoA C-acetyltransfe	[m] : (2) accoa --> aacoa + coa	2	Lipid	2.3.1.9		(Schwerdt and Huth 1993)
96	MMSAD1m	methylmalonate-semialdeh	[m] : 2mop + coa + nad --> co2 + nadh + ppcoa	3	Lipid	1.2.1.27	yes	
97	PPCOACm	Propionyl-CoA carboxylase	[m] : atp + hco3 + ppcoa --> adp + h + mmcoa-S + pi	3	Lipid	6.4.1.3	yes	
98	HACDm	3-hydroxyacyl-CoA dehydr	[m] : 3hacoa + nad <==> 3oacoa + h + nadh	3	Lipid	1.1.1.35	yes	
99	GLYKm	glycerol kinase	[m] : atp + glyc --> adp + glyc3p + h	3	Lipid	2.7.1.30	yes	
100	FASYNm	Average fatty acid of heart	[m] : (0.25) c204coa + (0.05) c226coa + (0.2) ocdycacoa + (0.1) odecoa + (0.2) pmtcoa + (0.2) stcoa --> facoa_m	1	Lipid			Modeling purpose
101	G3PATm	glycerol 3-phosphate acylt	[m] : facoa_m + glyc3p --> aglyc3p_m + coa	3	Lipid	2.3.1.15	yes	(Lewin, Schwerbrock et al. 2004)
102	AGATm	1-Acyl-glycerol-3-phosphat	[m] : aglyc3p_m + facoa_m --> coa + pa_m	2	Lipid	2.3.1.51		(Haldar, Kelker et al. 1983)
103	DASYNm	CDP-Diacylglycerol synthe	[m] : ctp + h + pa_m <==> cdpdag_m + ppi	2	Lipid	2.7.7.41		(Monaco and Feldman 1997)
104	PCHOLPm	choline phosphatase	[m] : h2o + pc_m --> chol + h + pa_m	2	Lipid	3.1.4.4		(Monaco and Feldman 1997)
105	PGSAm	Phosphatidylglycerol synth	[m] : cdpdag_m + glyc3p <==> cmp + h + pgp_m	2	Lipid	2.7.8.5		(Ohtsuka, Nishijima et al. 1993)
106	PGPPm	Phosphatidylglycerol phos	[m] : h2o + pgp_m --> pg_m + pi	2	Lipid	3.1.3.27		(MacDonald and McMurray 1980)

107	NH4tm	NH3 mitochondrial transpo	nh4[c] <==> nh4[m]	2	Urea cycle			Physiological data
108	UREAt	Urea transport via facilitate	urea[e] <==> urea[c]	1	Urea cycle			Physiological data
109	CBMKm	Carbamate kinase	[m] : atp + co2 + nh4 --> adp + cbp + (2) h	2	Urea cycle	2.7.2.2		(Voet, Voet et al. 1999)
110	OCBTm	ornithine carbamoyltransfe	[m] : cbp + orn --> citr-L + h + pi	3	Urea cycle	2.1.3.3	yes	(Indiveri, Tonazzi et al. 1999)
111	ARGSS	argininosuccinate synthase	[c] : asp-L + atp + citr-L --> amp + argsuc + h + ppi	2	Urea cycle	6.3.4.5		(Voet, Voet et al. 1999)
112	ARGSL	argininosuccinate lyase	[c] : argsuc <==> arg-L + fum	2	Urea cycle	4.3.2.1		(Voet, Voet et al. 1999)
113	ARGN	arginase	[c] : arg-L + h2o --> orn + urea	3	Urea cycle	3.5.3.1	yes	(Voet, Voet et al. 1999)
114	ORNt4m	ornithine mitochondrial tran	citr-L[c] + h[c] + orn[m] <==> citr-L[m] + h[m] + orn[c]	4	Urea cycle			(Indiveri, Tonazzi et al. 1997; Fiermonte, Dolce et al. 2003; Palmieri 2004)
115	GLYAMDTR	glycine amidinotransferase	[m] : arg-L + gly <==> gudac + orn	3	Urea cycle	2.1.4.1	yes	(Voet, Voet et al. 1999)
116	GACMTR	guanidinoacetate N-methyl	[m] : amet + gudac <==> ahcys + creat + h	2	Urea cycle	2.1.1.2		(Voet, Voet et al. 1999)
117	CK	ATP Creatine kinase	[m] : atp + creat <==> adp + pcreat	3	Urea cycle	2.7.3.2	yes	
118	ADK1	adenylate kinase	[c] : amp + atp <==> (2) adp	3	Nucleotide	2.7.4.3	yes	
119	ADK1m	adenylate kinase, mitochon	[m] : amp + atp <==> (2) adp	3	Nucleotide	2.7.4.3	yes	(Salway 1999)
120	ADK4m	adentylate kinase (ITP), mi	[m] : amp + itp <==> adp + idp	3	Nucleotide	2.7.4.3	yes	
121	DGNSKm	deoxyguanosine kinase	[m] : atp + dgsn --> adp + dgmp + h	3	Nucleotide	2.7.1.113	yes	
122	DHORDm	dihydoorotic acid dehydrog	[m] : dhor-S + o2 <==> h2o2 + orot	3	Nucleotide	1.3.3.1	yes	
123	DUTPDPm	dUTP diphosphatase	[m] : dutp + h2o --> dump + h + ppi	3	Nucleotide	3.6.1.23	yes	
124	NDPK1	nucleoside-diphosphate kin	[c] : atp + gdp <==> adp + gtp	2	Nucleotide	2.7.4.6		(Salway 1999)
125	TMDK1m	thymidine kinase (ATP:thym	[m] : atp + thymd --> adp + dtmp + h	3	Nucleotide	2.7.1.21	yes	
126	GLUDx	glutamate dehydrogenase	[c] : glu-L + h2o + nad <==> akg + h + nadh + nh4	3	Others	1.4.1.2	yes	
127	GLUDy	glutamate dehydrogenase	[c] : glu-L + h2o + nadp <==> akg + h + nadph + nh4	2	Others	1.4.1.4		(Delabar, Martin et al. 1982)
128	TYRTAm	tyrosine transaminase, mito	[m] : akg + tyr-L <==> 34hpp + glu-L	3	Others	2.6.1.5	yes	
129	LDH_L	L-lactate dehydrogenase	[c] : lac-L + nad <==> h + nadh + pyr	3	Others	1.1.1.27	yes	(Kline, Brandt et al. 1986; Brandt, Laux et al. 1987)
130	ME2m	malic enzyme (NADP), mit	[m] : mal-L + nadp --> co2 + nadph + pyr	3	Others	1.1.1.40	yes	
131	PCm	pyruvate carboxylase	[m] : atp + hco3 + pyr --> adp + h + oaa + pi	3	Others	6.4.1.1	yes	
132	PEPCKm	Phosphoenolpyruvate carb	[m] : gtp + oaa --> co2 + gdp + pep	3	Others	4.1.1.32	yes	
133	FTHFLm	formate-tetrahydrofolate lig	[m] : atp + for + thf <==> 10fthf + adp + pi	2	Others	6.3.4.3		(Prasannan, Pike et al. 2003)
134	GHMT2rm	glycine hydroxymethyltrans	[m] : ser-L + thf <==> gly + h2o + mlthf	4	Others	2.1.2.1	yes	(Lin, Huang et al. 1993)
135	HMGCOASm	Hydroxymethylglutaryl CoA	[m] : coa + h + hmgcoa <==> aacoa + accoa + h2o	3	Others	4.1.3.5	yes	
136	THFATm	tetrahydrofolate aminometh	[m] : h2o + methf --> 5fthf + h	3	Others	2.1.2.10	yes	
137	H2CO3Dm	carboxylic acid dissociation	[m] : co2 + h2o <==> h2co3	3	Others	4.2.1.1	yes	
138	H2OD	Water dissociation	[c] : h2o <==> h + oh1	2	Others			Physiological data
139	HCO3Em	HCO3 equilibration reactio	[m] : co2 + h2o <==> h + hco3	1	Others			Physiological data
140	PPA	inorganic diphosphatase	[c] : h2o + ppi --> h + (2) pi	3	Others	3.6.1.1	yes	
141	PPAm	inorganic diphosphatase	[m] : h2o + ppi --> h + (2) pi	3	Others	3.6.1.1	yes	
142	ARGtm	arginine mitochondrial tran	arg-L[c] + h[m] <==> arg-L[m] + h[c]	4	Transport			(Fiermonte, Dolce et al. 2003)
143	ATPtm	ADP/ATP transporter, mito	adp[c] + atp[m] --> adp[m] + atp[c]	4	Transport			(De Marcos Lousa, Trezeguet et al. 2002)
144	CITRtm	citrulline mitochondrial tran	citr-L[m] <==> citr-L[c]	4	Transport			(Fiermonte, Dolce et al. 2003)
145	CITtam	citrate transport, mitochond	cit[c] + mal-L[m] <==> cit[m] + mal-L[c]	4	Transport			(Bisaccia, De Palma et al. 1990; Kaplan 2001; De Palma, Scalera et al. 2003; Palmieri 2004)
146	CITtbm	citrate transport, mitochond	cit[c] + pep[m] <==> cit[m] + pep[c]	4	Transport			(Bisaccia, De Palma et al. 1990; Kaplan 2001; De Palma, Scalera et al. 2003; Palmieri 2004)
147	CO2tm	CO2 transport (diffusion), m	co2[c] <==> co2[m]	1	Transport			Modeling purpose

148	COAtm	CoA transporter	coa[c] <==> coa[m]	1	Transport			Modeling purpose
149	DNC1C	Deoxynucleotide carrier	atp[m] + cdp[c] <==> atp[c] + cdp[m]	4	Transport			(Dolce, Fiermonte et al. 2001; Palmieri 2004)
150	DNC1G	Deoxynucleotide carrier	atp[m] + gdp[c] <==> atp[c] + gdp[m]	4	Transport			(Dolce, Fiermonte et al. 2001; Palmieri 2004)
151	DNC1U	Deoxynucleotide carrier	atp[m] + udp[c] <==> atp[c] + udp[m]	4	Transport			(Dolce, Fiermonte et al. 2001; Palmieri 2004)
152	FE2tm	iron (II) transport	fe2[c] + h[c] --> fe2[m] + h[m]	2	Transport			(Lange, Kispal et al. 1999)
153	FRDcm	fumarate reductase, cytoso	fadh2[m] + fum[c] --> fad[m] + succ[c]	3	Transport	1.3.99.1	yes	
154	GLUt2m	L-glutamate reversible tran	glu-L[c] + h[c] <==> glu-L[m] + h[m]	4	Transport			(Fiermonte, Palmieri et al. 2002)
155	GLYC3Ptm	glycerol-3-phosphate shutt	glyc3p[c] --> glyc3p[m]	2	Transport			(Xu and Hatch 1997)
156	GLYCtm	glycerol transport	glyc[c] <==> glyc[m]	1	Transport			Modeling purpose
157	GLYtm	glycine passive transport to	gly[c] <==> gly[m]	4	Transport			(Benavides, Garcia et al. 1980)
158	GTPtm	GTP/GDP translocase, mit	gdp[c] + gtp[m] --> gdp[m] + gtp[c]	2	Transport			(Salway 1999)
159	H2Otm	H2O transport, mitochondr	h2o[c] <==> h2o[m]	1	Transport			Modeling purpose
160	Htm	Uncoupling proteins	h[c] --> h[e]	4	Transport			(Kaplan 2001; Palmieri 2004)
161	LYStm	Lysine mitochondrial trans	h[m] + lys-L[c] <==> h[c] + lys-L[m]	4	Transport			(Fiermonte, Dolce et al. 2003; Palmieri 2004)
162	MALtm	malate transport, mitochon	mal-L[c] + pi[m] <==> mal-L[m] + pi[c]	4	Transport			(Palmieri 2004)
163	O2tm	O2 transport (diffusion)	o2[c] <==> o2[m]	1	Transport			Modeling purpose
164	ORNt3m	ornithine mitochondrial trar	h[c] + orn[m] <==> h[m] + orn[c]	4	Transport			(Indiveri, Tonazzi et al. 1997; Indiveri, Tonazzi et al. 1999; Fiermonte, Dolce et al. 2003; Palmieri 2004)
165	PIt2m	phosphate transporter, mit	h[c] + pi[c] <==> h[m] + pi[m]	4	Transport			(Dolce, Fiermonte et al. 1996)
166	PYRt2m	pyruvate mitochondrial trar	h[c] + pyr[c] <==> h[m] + pyr[m]	2	Transport			(Palmieri 2004)
167	SUCCt2m	succinate transport, mitoch	pi[m] + succ[c] <==> pi[c] + succ[m]	4	Transport			(Palmieri 2004)
168	12DGRt1	1,2 diacylglycerol transport	12dgr_m[e] --> 12dgr_m[c]	1	Transport to cytosol			Modeling purpose
169	C204t	(n-C20:4) transport in via u	c204[e] --> c204[c]	1	Transport to cytosol			Modeling purpose
170	C226t	(n-C22:6) transport in via u	c226[e] --> c226[c]	1	Transport to cytosol			Modeling purpose
171	CO2t	CO2 transporter via diffusi	co2[e] <==> co2[c]	1	Transport to cytosol			Modeling purpose
172	COAt	CoA transporter	coa[e] <==> coa[c]	1	Transport to cytosol			Modeling purpose
173	CYSt2r	L-cysteine reversible trans	cys-L[e] + h[e] <==> cys-L[c] + h[c]	1	Transport to cytosol			Modeling purpose
174	FE2t1	iron (II) transport	fe2[e] --> fe2[c]	1	Transport to cytosol			Modeling purpose
175	GLCt1	glucose transport (uniport)	glc-D[e] --> glc-D[c]	1	Transport to cytosol			Modeling purpose
176	GLUt2r	L-glutamate transport via p	glu-L[e] + h[e] <==> glu-L[c] + h[c]	1	Transport to cytosol			Modeling purpose
177	GLYC3Pt1	glycerol-3-phosphate trans	glyc3p[e] --> glyc3p[c]	1	Transport to cytosol			Modeling purpose
178	GLYCt1	glycerol transport via unipo	glyc[e] --> glyc[c]	1	Transport to cytosol			Modeling purpose
179	GLYt2r	glycine reversible transpor	gly[e] + h[e] <==> gly[c] + h[c]	1	Transport to cytosol			Modeling purpose
180	H2Ot	H2O transport via diffusion	h2o[e] <==> h2o[c]	1	Transport to cytosol			Modeling purpose
181	HDCAt	Hexadecanoate (n-C16:0)	hdca[e] --> hdca[c]	1	Transport to cytosol			Modeling purpose
182	Ht	proton diffusion	h[c] <==> h[e]	1	Transport to cytosol			Modeling purpose
183	L-LACt2r	L-lactate reversible transpo	h[e] + lac-L[e] <==> h[c] + lac-L[c]	1	Transport to cytosol			Modeling purpose
184	O2t	o2 transport (diffusion)	o2[e] <==> o2[c]	1	Transport to cytosol			Modeling purpose
185	OCDCAt	Octadecanoate (n-C18:0) t	ocdca[e] --> ocdca[c]	1	Transport to cytosol			Modeling purpose
186	OCDCEAt	Octadecenoate (n-C18:1) t	ocdcea[e] --> ocdcea[c]	1	Transport to cytosol			Modeling purpose
187	OCDCYAt	Octadecynoate (n-C18:2) t	ocdcya[e] --> ocdcya[c]	1	Transport to cytosol			Modeling purpose
188	PIt2r	phosphate reversible trans	h[e] + pi[e] <==> h[c] + pi[c]	1	Transport to cytosol			Modeling purpose
189	PSt	phosphatidylserine transpo	ps_m[e] <==> ps_m[c]	1	Transport to cytosol			Modeling purpose