

Sheet1

Principal Flux modes (lambda1) for aLL samples

Reactions	1 st SPMF ⁽¹²⁾	2 nd SPMF ⁽¹²⁾	ID
AKG transporter, mitochondrial	0.26	0.04	r_1112
malate transport	0.26	0.08	r_1226
succinate transport	0.25	-	r_1264
glutamyl-tRNA synthetase	0.24	-	r_0480
L-lactate transport	0.23	-0.04	r_1206
ADP/ATP transporter	0.22	-0.08	r_1110
succinyl-CoA:acetate CoA transferase	-0.20	-	r_4039
pyruvate transport	0.19	0.00	r_2034
NADH dehydrogenase, cytosolic/mitochondrial	0.19	0.00	r_0770
acetolactate synthase	0.17	0.00	r_0097
malic enzyme (NADP)	0.17	0.00	r_0719
glycine-cleavage complex (lipoamide)	0.14	0.08	r_0505
methionyl-tRNA formyltransferase	0.11	0.08	r_0728
ferrocytochrome-c: oxygen oxidoreductase	-	0.08	r_0438
oxoglutarate dehydrogenase (dihydrolipoamide S-succinyltransferase)	0.13	0.08	r_0831
methylenetetrahydrofolate dehydrogenase (NADP)	-0.06	0.08	r_0733
oxoglutarate dehydrogenase (lipoamide)	0.12	0.08	r_0832
aldehyde dehydrogenase (acetaldehyde, NADP)	-	0.08	r_0175
succinate dehydrogenase (ubiquinone-6)	0.05	0.08	r_1021
citrate to cis-aconitate(3-)	0.03	0.08	r_0302
ATP synthase	-	0.08	r_0226
ubiquinol:ferricytochrome c reductase	-	0.08	r_0439
adenylate kinase (GTP)	0.03	0.08	r_0150
oxoglutarate/malate exchange	0.10	0.08	r_2132
L-glutamate transport	-	0.08	r_1194
carnitine O-acetyltransferase	-	0.08	r_0254
aspartate-glutamate transporter	-	0.08	r_1118
acetyl-CoA synthetase	-	0.08	r_0113
phosphate transport	0.12	0.08	r_1245
glycine-cleavage complex (lipoylprotein)	-	0.08	r_0508
(S)-lactate:ferricytochrome-c 2-oxidoreductase	-	0.08	r_0004
malate dehydrogenase	0.07	0.08	r_0713
citrate transport	0.05	0.08	r_1126
2-aceto-2-hydroxybutanoate synthase	0.16	-	r_0016
cis-aconitate(3-) to isocitrate	-	0.08	r_0280
nicotinate-nucleotide diphosphorylase (carboxylating)	0.15	-	r_0787
acetyl-CoA C-acetyltransferase	0.14	-	r_0104
2-deoxy-D-arabino-heptulosonate 7-phosphate synthetase	0.14	-	r_0020
malic enzyme (NAD)	0.14	-	r_0718
aldehyde dehydrogenase (indole-3-acetaldehyde, NADP)	-	0.07	r_0178
methylenetetrahydrofolic acid cyclohydrolase	-0.03	0.07	r_0724
thioredoxin reductase (NADPH)	0.14	0.06	r_1039
glycine-cleavage complex (lipoylprotein)	-	0.07	r_0507
thiamine diphosphate transport	0.13	-	r_1269
succinate-fumarate transport	-	0.07	r_1265
2-methylcitrate dehydratase	0.13	-	r_0027
glycine hydroxymethyltransferase	-0.03	0.07	r_0503
glycine-cleavage complex (lipoylprotein)	-	0.07	r_0506
L-4-hydroxyglutamate semialdehyde dehydrogenase	0.13	-	r_0673

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riboflavin kinase	-	0.06	r_0966
GTP/GDP translocase	0.03	0.06	r_1175
homoacontinate hydratase	0.12	-0.01	r_0542
1-pyrroline-5-carboxylate dehydrogenase	0.11	-0.03	r_0012
L-1-pyrroline-3-hydroxy-5-carboxylate dehydrogenase	0.10	-0.05	r_0672
inorganic diphosphatase	0.08	0.05	r_0569
hydroxymethylglutaryl CoA synthase	-	0.05	r_0560
fadH2 transport	0.10	0.02	r_1151
citrate transport	0.05	0.05	r_1128
phenylalanyl-tRNA synthetase	0.10	-	r_0853
2-isopropylmalate synthase	-	0.04	r_0025
aldehyde dehydrogenase (2-methylbutanol, NAD)	0.04	0.04	r_0167
aldehyde dehydrogenase (isobutyl alcohol, NAD)	0.04	0.04	r_0183
aldehyde dehydrogenase (isoamyl alcohol, NAD)	0.04	0.04	r_0180
aldehyde dehydrogenase (2-phenylethanol, NAD)	0.04	0.04	r_0170
ornithine transport	-	0.04	r_1237
leucyl-tRNA synthetase	0.08	-	r_0702
dihydropteroate synthase	-	0.04	r_0350
coenzyme A transport	-	0.04	r_1129
proline oxidase (NAD)	0.08	-	r_0940
S-adenosyl-L-methionine transport	-0.05	0.04	r_1256
asparaginyl-tRNA synthetase, miotochondrial	0.08	-	r_0213
3-methyl-2-oxobutanoate hydroxymethyltransferase	0.08	0.02	r_0063
dihydroneopterin aldolase	-	0.04	r_0347
histidyl-tRNA synthetase	0.08	-	r_0540
2-oxoadipate and AKG transport	0.07	-	r_1099
guanosine phosphorylase	0.07	-	r_0950
oxaloacetate transport	0.07	-	r_1239
ornithine transacetylase	-	0.04	r_0818
NAD kinase	-	0.04	r_0766
hydrogen peroxide reductase (thioredoxin)	0.07	0.03	r_0551
itaconate-CoA ligase (ADP-forming)	0.06	-0.03	r_0668
acetylglutamate kinase	0.06	-	r_0115
dihydrofolate reductase	-	0.03	r_0345
NADH:ubiquinone oxidoreductase	0.06	-	r_0773
adenylate kinase	0.06	0.02	r_0149
aconitase	-0.06	-	r_0117
N-acetyl-g-glutamyl-phosphate reductase	0.06	0.02	r_0759
formate-tetrahydrofolate ligase	-	-0.03	r_0447
glycerol-3-phosphate dehydrogenase (NAD)	0.06	-	r_0492
ketol-acid reductoisomerase (2-aceto-2-hydroxybutanoate)	-	0.03	r_0669
Aminobutyraldehyde dehydrogenase	-	0.03	r_0201
aldehyde dehydrogenase (tryptophol, NAD)	0.04	0.03	r_0187
malonyl-CoA-ACP transacylase	0.05	0.02	r_0721
acetohydroxy acid isomeroeductase	-	0.03	r_0096
acetyl-CoA ACP transacylase	0.05	-	r_0099
mitochondrial alcohol dehydrogenase	0.04	0.02	r_0165
glycerol-3-phosphate dehydrogenase (fad)	0.05	-	r_0490
methylisocitrate lyase	0.05	-	r_0734
acetyl-CoA carboxylase	-	0.02	r_0108
tetrahydrofolate aminomethyltransferase	-	0.02	r_1030
2-methylcitrate synthase	-	0.02	r_0028
hexaprenyldihydroxybenzoate methyltransferase	-	0.02	r_0532

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threonyl-tRNA synthetase	0.04	-	r_1043
2-hexaprenyl-6-methoxy-1,4-benzoquinone methyltransferase	-	0.02	r_0021
UTP/UMP antiport	0.03	-	r_1276
CTP/CMP antiport	0.03	-	r_1131
citrate transport	0.03	-0.02	r_1127
protoporphyrinogen oxidase	0.03	-	r_0942
fumarase	-	0.02	r_0451
CTP transport	-	0.02	r_1130
2-hexaprenyl-6-methoxyphenol monooxygenase	-	0.02	r_0022
arginyl-tRNA synthetase	0.03	0.02	r_0210
quinone oxidoreductase	-	0.02	r_0963
UTP transport	-	0.02	r_1275
succinate-CoA ligase (ADP-forming)	0.03	-	r_1022
Heme O synthase	-	-	r_0531
glutathione oxidoreductase	0.03	-	r_0482
Aspartyl-tRNA synthetase	0.03	-	r_0221
aldehyde dehydrogenase (acetaldehyde, NAD)	-	-	r_0174
glutathione peroxidase, mitochondria	-0.03	-	r_0484
citrate synthase	-	-	r_0300
S-adenosyl-L-methionine:3-hexaprenyl-4,5-dihydroxylate O-methyltransferase	-	-	r_0985
L-erythro-4-hydroxyglutamate:2-oxoglutarate aminotransferase	-	-	r_0682
isocitrate dehydrogenase (NAD+)	-	-	r_0658
heme O monooxygenase	-	-	r_0530
hydroxybenzoate octaprenyltransferase	-	-	r_0555
glycine-cleavage system (lipoamide)	-	-	r_0509
tryptophanyl-tRNA synthetase	-	-	r_1058
tyrosyl-tRNA synthetase	-	-	r_1067
isoleucyl-tRNA synthetase	-	-	r_0666
NAD transport	-	-	r_1232
fumarate reductase	-	-	r_0454
NAD transport	-	-	r_1230
(R)-lactate:ferricytochrome-c 2-oxidoreductase	-	-	r_0001
carnithine-acetylcarnithine carrier	-	-	r_1120
dihydropteroate synthase	-	-	r_0351
homoisocitrate dehydrogenase	-	-	r_0545
(R)-lactate:ferricytochrome-c 2-oxidoreductase	-	-	r_0002
NAD transport	-	-	r_1229
N-acetylglutamate synthase	-	-	r_0761
hydroxyacylglutathione hydrolase	-	-	r_0554
2-oxo-4-methyl-3-carboxypentanoate decarboxylation	-	-	r_0030
NAD transport	-	-	r_1231
L-threonine deaminase	-	-	r_0693
homocitrate synthase	-	-	r_1838
acetyl-CoA hydrolase	-	-	r_0111
dephospho-CoA kinase	-	-	r_0334
trans-pentaprenyltransferase	-	-	r_1047
glycine cleavage system	-	-	r_0501
aldehyde dehydrogenase (indole-3-acetaldehyde, NAD)	-	-	r_0176
pyruvate dehydrogenase	-	-	r_0961
NADH kinase mitochondrial	-	-	r_0772
deoxyhypusine synthase, cytosolic/mitochondrial	-	-	r_0331
ferricytochrome-c:hydrogen-peroxide oxidoreductase	-	-	r_0437

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acyl carrier protein synthase	-	-	r_0119
ferrochelatase	-	-	r_0436
NAPRTase	-	-	r_0775
dihydroxy-acid dehydratase (2,3-dihydroxy-3-methylpentanoate)	-	-	r_0353
2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase	-	-	r_0017
dihydroxy-acid dehydratase (2,3-dihydroxy-3-methylbutanoate)	-	-	r_0352
5-aminolevulinate synthase	-	-	r_0081
lysyl-tRNA synthetase	-	-	r_0712
glycine-cleavage complex (lipoamide)	-	-	r_0504
isocitrate dehydrogenase	-	-	r_2131
methionyl-tRNA synthetase	-	-	r_0730
valyl-tRNA synthetase	-	-	r_1090