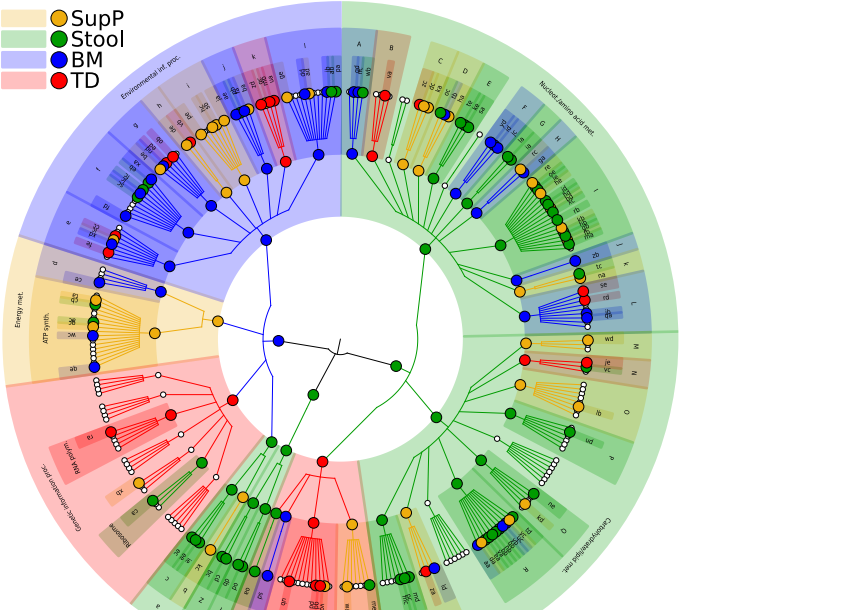

A:Cysteine and methionine metabolism
B:Lysine metabolism
C:Polyamine biosynthesis
D:Pyrimidine metabolism
E:Arginine and proline metabolism
F:Purine metabolism
G:Histidine metabolism
H:Branched chain amino acid metabolism
I:Cofactor and vitamin biosynthesis
J:Serine and threonine metabolism
K:Aromatic amino acid metabolism
M:Other terpenoid biosynthesis
N:Lipopolysaccharide metabolism
O:Lipid metabolism
P:Fatty acid metabolism
Q:Other carbohydrate metabolism
R:Central carbohydrate metabolism
S:Tetrapyrrole biosynthesis
T:Glycosaminoglycan metabolism
U:Methane metabolism
V:Carbon fixation
W:Nitrogen fixation
X:Sulfur metabolism
Y:Aminoacyl tRNA
Z:Nucleotide sugar
a:Carbohydrate and lipid metabolism
aa:M00004 Pentose phosphate pathway Pentose phosphate cycle
ab:M00222 Phosphate transport system
ac:M00149 Complex II succinate dehydrogenase fumarate reductase
ad:M00233 Glutamate transport system
ae:M00239 Peptides nickel transport system
b:Glycan metabolism
ba:M00349 Microcin C transport system
bb:M00008 Entner Doudoroff pathway glucose 6P glyceraldehyde 3P pyruvate
bc:M00362 Nucleotide sugar biosynthesis prokaryotes
bd:M00122 Cobalamin biosynthesis cobinamide cobalamin
be:M00270 PTS system trehalose specific II component
c:Carbohydrate metabolism
ca:M00178 Ribosome bacteria
cb:M00159 V type ATPase prokaryotes
cc:M00193 Putative spermidine putrescine transport system
cd:M00361 Nucleotide sugar biosynthesis eukaryotes
ce:M00164 ATP synthase
d:Energy met.
da:M00011 Citrate cycle second carbon oxidation
db:M00359 Aminoacyl tRNA biosynthesis eukaryotes
dc:M00133 Polyamine biosynthesis arginine agmatine putrescine spermidine
dd:M00237 Branched chain amino acid transport system
de:M00219 Al 2 transport system
e:Mineral and organic ion transport system
ea:M00002 Glycolysis core module involving three carbon compounds
eb:M00199 Lactose L arabinose transport system
ec:M00311 2 oxoglutarate ferredoxin oxidoreductase
ed:M00287 PTS system galactosamine specific II component
ee:M00310 Pyruvate ferredoxin oxidoreductase
f:Oligosaccharide and polyol transport system
fa:M00324 Dipeptide transport system
fb:M00129 Ascorbate biosynthesis animals glucose 1P ascorbate
fc:M00198 sn Glycerol 3 phosphate transport system
fd:M00207 Multiple sugar transport system
fe:M00189 Molybdate transport system
g:Phosphotransferase system PTS
ga:M00019 Leucine biosynthesis pyruvate 2 oxoisovalerate leucine
gb:M00123 Biotin biosynthesis pimeloyl CoA biotin
gc:M00317 Manganese iron transport system
gd:M00021 Cysteine biosynthesis serine cysteine
ge:M00232 General L amino acid transport system
h:Monosaccharide transport system
ha:M00053 Pyrimidine deoxyribonucleotide biosynthesis CDP CTP dCDP dCTP dTDP dTTP
hb:M00126 Tetrahydrofolate biosynthesis GTP THF
hc:M00335 Sec secretion system
hd:M00115 NAD biosynthesis aspartate NAD
he:M00118 Glutathione biosynthesis glutamate glutathione
i:Bacterial secretion system
ia:M00045 Histidine degradation histidine N formiminoglutamate glutamate
ib:M00023 Tryptophan biosynthesis chorismate tryptophan
ic:M00185 Sulfate transport system
id:M00048 Inosine monophosphate biosynthesis PRPP glutamine IMP
ie:M00312 2 oxoisovalerate ferredoxin oxidoreductase
j:Peptide and nickel transport system
ja:M00334 Type VI secretion system
jb:M00229 Arginine transport system
jc:M00049 Adenine nucleotide biosynthesis IMP ADP dADP ATP dATP
jd:M00127 Thiamine biosynthesis AIR thiamine P thiamine 2P
je:M00064 ADP L glycero D manno heptose biosynthesis
k:Metallic cation iron siderophore and vitamin B12 transport system
k:Other amino acid metabolism
ka:M00135 GABA biosynthesis eukaryotes putrescine GABA
kb:M00121 Heme biosynthesis glutamate protoheme siroheme
kc:M00072 Oligosaccharyltransferase
kd:M00012 Glyoxylate cycle
ke:M00029 Urea cycle
l:Phosphate and amino acid transport system
la:M00026 Histidine biosynthesis PRPP histidine
lb:M00098 Acylglycerol degradation
lc:M00194 Maltose maltodextrin transport system
ld:M00364 C10 C20 isoprenoid biosynthesis bacteria
le:M00125 Riboflavin biosynthesis GTP riboflavin FMN FAD
ma:M00119 Pantothenate biosynthesis valine L aspartate pantothenate
mb:M00319 Manganese zinc iron transport system
mc:M00079 Keratan sulfate degradation
md:M00076 Dermatan sulfate degradation
me:M00345 Formaldehyde assimilation ribulose monophosphate pathway
na:M00027 GABA gamma Aminobutyrate shunt
nb:M00007 Pentose phosphate pathway non oxidative phase fructose 6P ribose 5P
nc:M00017 Methionine biosynthesis aspartate homoserine methionine
nd:M00274 PTS system mannose specific I component
ne:M00061 Uronic acid metabolism
oa:M00176 Sulfur reduction sulfate H2S
ob:M00277 PTS system N acetylglalactosamine specific II component
oc:M00051 Uridine monophosphate biosynthesis glutamine PRPP UMP
od:M00360 Aminoacyl tRNA biosynthesis prokaryotes
oe:M00120 Coenzyme A biosynthesis pantothenate CoA
of:M00230 Glutamate aspartate transport system
pb:M00348 Glutathione transport system
pc:M00077 Chondroitin sulfate degradation
pd:M00172 C4 dicarboxylic acid cycle NADP malic enzyme type
pe:M00333 Type IV secretion system
qa:M00022 Shikimate pathway phosphoenolpyruvate erythrose 4P chorismate
qb:M00001 Glycolysis Embden Meyerhof pathway glucose pyruvate
qc:M00156 Complex IV Cytochrome c oxidase cytochrome c oxidase cob3 type
qd:M00170 C4 dicarboxylic acid cycle phosphoenolpyruvate carboxykinase type
qe:M00157 F type ATPase bacteria
ra:M00183 RNA polymerase bacteria
rb:M00124 Pyridoxal biosynthesis erythrose 4P pyridoxal 5P
rc:M00036 Leucine degradation leucine acetoacetate acetyl CoA
rd:M00025 Tyrosine biosynthesis chorismate tyrosine
re:M00117 Ubiquinone biosynthesis prokaryotes chorismate ubiquinone
sa:M00028 Ornithine biosynthesis glutamate ornithine
sb:M00336 Twin arginine translocation Tat system
sc:M00202 Oligogalacturonide transport system
sd:M00175 Nitrogen fixation N2 ammonia
se:M00024 Phenylalanine biosynthesis chorismate phenylalanine
ta:M00151 Complex III Cytochrome bc1 complex
tb:M00052 Pyrimidine ribonucleotide biosynthesis UMP UDP UTP CDP CTP
tc:M00046 beta Alanine biosynthesis cytosine uracil beta alanine
td:M00010 Citrate cycle first carbon oxidation
te:M00015 Proline biosynthesis glutamate proline
ua:M00246 Nickel transport system
ub:M00173 Reductive citric acid cycle Arnon Buchanan cycle
uc:M00006 Pentose phosphate pathway oxidative phase glucose 6P ribulose 5P
ud:M00083 Fatty acid biosynthesis elongation
ue:M00016 Lysine biosynthesis aspartate lysine
va:M00220 Rhamnose transport system
vc:M00060 Lipopolysaccharide biosynthesis KDO2 lipid A
vd:M00168 CAM Crassulacean acid metabolism dark
wa:M00174 Methane oxidation methylotroph methane CO2
wb:M00035 Methionine degradation
wc:M00150 Complex II succinate dehydrogenase fumarate reductase fumarate reductase
wd:M00045 beta Carotene biosynthesis GGAP beta carotene
xa:M00197 Putative sugar transport system
xb:M00295 BRCA1 associated genome surveillance complex BASC
xc:M00141 C1 unit interconversion eukaryotes
xd:M00299 Spermidine putrescine transport system
ya:M00003 Gluconeogenesis oxaloacetate fructose 6P
yb:M00307 Pyruvate oxidation pyruvate acetyl CoA
yc:M00009 Citrate cycle TCA cycle Krebs cycle
yd:M00050 Guanine nucleotide biosynthesis IMP GDP dGDP GTP dGTP
za:M00096 C5 isoprenoid biosynthesis non mevalonate pathway
zb:M00018 Threonine biosynthesis aspartate homoserine threonine
zc:M00136 GABA biosynthesis prokaryotes putrescine GABA
zd:M00245 Cobalt transport system