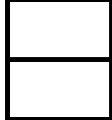# Node types

gene
(protein/enzyme)

group
(complex)

compound
(metabolite/glycan)

map
(pathway)

Pathway name

C15972

DLST

C15973

2-(alpha-Hydrox\
yethyl)thiamine\
diphosphate

PDHA1

Thiamin diphosp\
hate

PDHA1

D-Glutamine
and
D-glutamate
metabolism

DLD

DLD

C15973

alpha-Ketogluta\
ric acid

Ascorbate and
aldarate
metabolism

IDH1

C16255

Arginine
biosynthesis

C15972

3-Carboxy-1-hyd\
roxypropyl-ThPP

C16254

Oxalosuccinate

Alanine,
aspartate and
glutamate
metabolism

OGDH

Thiamin diphosp\
hate

IDH1

1-Hydroxypropan\
e-1,2,3-tricarb\
oxylic acid

OGDH

ACO1

cis-Aconitic acid

K17753

IDH3A

ACO1

DLAT

Pyroracemic acid

Fatty acid
elongation

Acetyl-CoA

Fatty acid
degradation

Phosphoenolpyru\
vate

Glycolysis /
Gluconeogenesis

2-Hydroxytricar\
ballylic acid

Valine,
leucine and
isoleucine
degradation

ACLY

K05942

CS

PC

Oxosuccinic acid

Alanine,
aspartate and
glutamate
metabolism

MDH1

PCK2

L-2-Hydroxybuta\
nedioic acid

Arginine
biosynthesis

Fumaric acid

Tyrosine
metabolism

FH

Succinyl-CoA

SUCLG2

K00244

SDHA

Ethylenesuccinic
acid

SUCLG2

Valine,
leucine and
isoleucine

Data with KEGG pathway–
–Rendered by Pathview–

-2.3   0.0   2.3