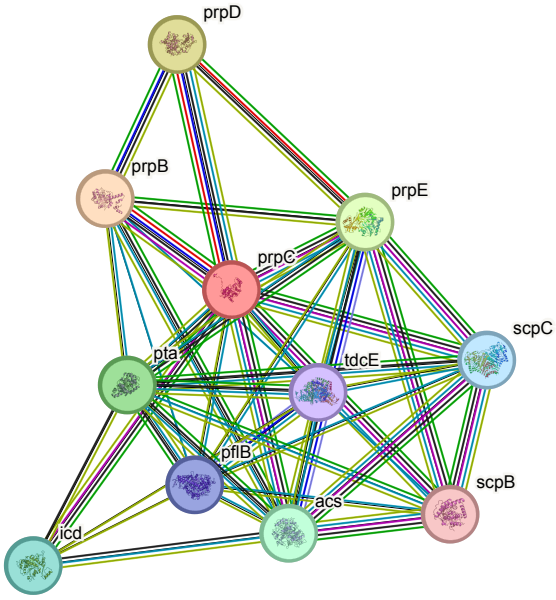
prpD
prpB
prpE
prpC
scpC
pta
tdcE
pflB
scpB
acs
icd

Nodes:

Network nodes represent proteins

splice isoforms or post-translational modifications are collapsed, i.e. each node represents all the proteins produced by a single, protein-coding gene locus.

Node Color

colored nodes:
query proteins and first shell of interactors

white nodes:
second shell of interactors

Node Content

empty nodes:
proteins of unknown 3D structure

filled nodes:
a 3D structure is known or predicted

Edges:

Edges represent protein-protein associations

associations are meant to be specific and meaningful, i.e. proteins jointly contribute to a shared function; this does not necessarily mean they are physically binding to each other.

Known Interactions

from curated databases

experimentally determined

Predicted Interactions

gene neighborhood

gene fusions

gene co-occurrence

Others

textmining

co-expression

protein homology

Your Input:

		Neighborhood	*Gene Fusion*	*Cooccurence*	*Coexpression*	*Experiments*	*Databases*	*Textmining*	*[Homology]*	***Score***
prpC	*2-methylcitrate synthase; Involved in the catabolism of short chain fatty acids (SCFA) via the tricarboxylic acid (TCA)(acetyl degradation route) and via the 2-methylcitrate cycle I (propionate degradation route). Catalyzes the Claisen condensation of propionyl-CoA and oxaloacetate (OAA) to yield 2-methylcitrate (2-MC) and CoA. Also catalyzes the condensation of oxaloacetate with acetyl-CoA to yield citrate but with a lower specificity. (389 aa)*									

Predicted Functional Partners:

prpB	*2-methylisocitrate lyase; Involved in the catabolism of short chain fatty acids (SCFA) via the 2-methylcitrate cycle I (propionate de...*	0.999
prpD	*2-methylcitrate dehydratase; Involved in the catabolism of short chain fatty acids (SCFA) via the tricarboxylic acid (TCA)(acetyl de...*	0.999
prpE	*propionate--CoA ligase; Catalyzes the synthesis of propionyl-CoA from propionate and CoA. Also converts acetate to acetyl-CoA b...*	0.996
pta	*Phosphate acetyltransferase; Involved in acetate metabolism. Catalyzes the reversible interconversion of acetyl-CoA and acetyl p...*	0.977
acs	*acetyl-CoA synthetase; Catalyzes the conversion of acetate into acetyl-CoA (AcCoA), an essential intermediate at the junction of a...*	0.969
icd	*Isocitrate dehydrogenase, specific for NADP+; Protein involved in tricarboxylic acid cycle and anaerobic respiration; Belongs to th...*	0.959
scpC	*propionyl-CoA:succinate CoA transferase; Catalyzes the transfer of coenzyme A from propionyl-CoA to succinate. Could be part o...*	0.956
pflB	*Formate acetyltransferase 1; Protein involved in anaerobic respiration and cellular amino acid catabolic process.*	0.950
tdcE	*Pyruvate formate-lyase 4/2-ketobutyrate formate-lyase; Catalyzes the cleavage of 2-ketobutyrate to propionyl-CoA and formate. It ...*	0.948
scpB	*methylmalonyl-CoA decarboxylase, biotin-independent; Catalyzes the decarboxylation of (R)-methylmalonyl-CoA to propionyl-CoA....*	0.938

Your Current Organism:

Escherichia coli K12

NCBI taxonomy Id: 511145
Other names: E. coli str. K-12 substr. MG1655, Escherichia coli MG1655, Escherichia coli str. K-12 substr. MG1655, Escherichia coli str. K12 substr. MG1655, Escherichia coli str. MG1655, Escherichia coli strain MG1655

Server load: low (20%) [HD]

Permalink

SIB - Swiss Institute of Bioinformatics

CPR - Novo Nordisk Foundation Center Protein Research

EMBL - European Molecular Biology Laboratory

STRING is a Core Data Resource as designated by Global Biodata Coalition and ELIXIR.