



Viewers

Legend

Settings

Analysis

Exports

Clusters

More

Less

Network Stats

number of nodes: 76

number of edges: 55

average node degree: 1.45

avg. local clustering coefficient: 0.381

expected number of edges: 29

PPI enrichment p-value: 1.31e-05

your network has significantly more interactions than expected (what does that mean?)

Functional enrichments in your network

Biological Process (GO)			
GO-term	description	count in gene set	false discovery rate
GO:0055114	oxidation-reduction process	15 of 923	0.0049
GO:0051593	response to folic acid	3 of 11	0.0049
GO:0046395	carboxylic acid catabolic process	8 of 237	0.0049
GO:0044282	small molecule catabolic process	10 of 388	0.0049
GO:0043603	cellular amide metabolic process	12 of 732	0.0049
GO:0043436	oxoacid metabolic process	15 of 943	0.0049
GO:0034032	purine nucleoside bisphosphate metabolic process	6 of 123	0.0049
GO:0033875	ribonucleoside bisphosphate metabolic process	6 of 123	0.0049
GO:0033540	fatty acid beta-oxidation using acyl-CoA oxidase	3 of 15	0.0049
GO:0032787	monocarboxylic acid metabolic process	11 of 477	0.0049
GO:0019752	carboxylic acid metabolic process	14 of 854	0.0049
GO:0019395	fatty acid oxidation	5 of 75	0.0049
GO:0009062	fatty acid catabolic process	5 of 84	0.0049
GO:0006790	sulfur compound metabolic process	9 of 343	0.0049
GO:0006625	protein targeting to peroxisome	5 of 68	0.0049
GO:0006635	fatty acid beta-oxidation	4 of 56	0.0066
GO:0051186	cofactor metabolic process	9 of 467	0.0067
GO:0001544	nontransmembrane compound metabolic process	36 of 5281	0.0086

GO:0006717	organonitrogen compound metabolic process	30 of 3201	0.0000
GO:0044281	small molecule metabolic process	18 of 1779	0.0092
GO:2000259	positive regulation of protein activation cascade	2 of 3	0.0097
GO:0045917	positive regulation of complement activation	2 of 3	0.0097
GO:0010954	positive regulation of protein processing	3 of 25	0.0102
GO:0006732	coenzyme metabolic process	7 of 297	0.0102
GO:0006631	fatty acid metabolic process	7 of 294	0.0102
GO:0106077	histone succinylation	2 of 4	0.0119
GO:0006084	acetyl-CoA metabolic process	3 of 27	0.0119
GO:0006552	leucine catabolic process	2 of 5	0.0155
GO:0033036	macromolecule localization	20 of 2268	0.0163
GO:0009259	ribonucleotide metabolic process	8 of 440	0.0163
GO:0006637	acyl-CoA metabolic process	4 of 88	0.0205
GO:0006768	biotin metabolic process	2 of 7	0.0229
GO:0006551	leucine metabolic process	2 of 7	0.0229
GO:0016042	lipid catabolic process	6 of 265	0.0261
GO:0042398	cellular modified amino acid biosynthetic process	3 of 41	0.0264
GO:0017144	drug metabolic process	9 of 622	0.0283
GO:0034613	cellular protein localization	14 of 1367	0.0290
GO:1901566	organonitrogen compound biosynthetic process	14 of 1370	0.0291
GO:0071840	cellular component organization or biogenesis	34 of 5342	0.0310
GO:0046907	intracellular transport	14 of 1390	0.0310
GO:0006575	cellular modified amino acid metabolic process	5 of 185	0.0310
GO:0072594	establishment of protein localization to organelle	7 of 396	0.0324
GO:0033365	protein localization to organelle	9 of 649	0.0327
GO:0008152	metabolic process	51 of 9569	0.0350
GO:0044237	cellular metabolic process	48 of 8797	0.0384
GO:0072330	monocarboxylic acid biosynthetic process	5 of 200	0.0384
GO:1901575	organic substance catabolic process	15 of 1609	0.0391
GO:0009987	cellular process	68 of 14652	0.0391
GO:0009260	ribonucleotide biosynthetic process	5 of 202	0.0391
GO:0008104	protein localization	17 of 1966	0.0391
GO:2000257	regulation of protein activation cascade	3 of 54	0.0409
GO:0009150	purine ribonucleotide metabolic process	7 of 425	0.0409
GO:1901605	alpha-amino acid metabolic process	5 of 209	0.0410
GO:0051641	cellular localization	18 of 2180	0.0419
GO:0044248	cellular catabolic process	15 of 1646	0.0419
GO:0009437	carnitine metabolic process	2 of 13	0.0419
GO:0006886	intracellular protein transport	10 of 836	0.0419
GO:0006605	protein targeting	6 of 318	0.0421
GO:0043173	nucleotide salvage	2 of 14	0.0446
GO:0006977	DNA damage response, signal transduction by p53 class m...	3 of 59	0.0453
GO:0090407	organophosphate biosynthetic process	8 of 577	0.0465
GO:0009056	catabolic process	16 of 1859	0.0465
GO:0061024	membrane organization	9 of 729	0.0473
GO:0016043	cellular component organization	32 of 5163	0.0476
GO:0032507	maintenance of protein location in cell	3 of 64	0.0483
(less ...)			

Molecular Function (GO)				
GO-term	description	count in gene set	false discovery rate	
GO:0019166	trans-2-enoyl-CoA reductase (NADPH) activity	2 of 3	0.0315	
GO:0016628	oxidoreductase activity, acting on the CH-CH group of dono...	3 of 26	0.0315	
GO:0016491	oxidoreductase activity	11 of 716	0.0315	
GO:0016406	carnitine O-acyltransferase activity	2 of 6	0.0315	
GO:0004485	methylcrotonoyl-CoA carboxylase activity	2 of 2	0.0315	

Cellular Component (GO)				
GO-term	description	count in gene set	false discovery rate	
GO:0005829	cytosol	44 of 4958	7.01e-07	
GO:0044444	cytoplasmic part	61 of 9377	1.27e-06	
GO:0005737	cytoplasm	65 of 11238	1.70e-05	
GO:0005622	intracellular	71 of 14286	0.00060	
GO:0044424	intracellular part	70 of 13996	0.00071	
GO:0005777	peroxisome	6 of 127	0.00076	
GO:0070013	intracellular organelle lumen	37 of 5162	0.0012	
GO:0044446	intracellular organelle part	52 of 8882	0.0014	
GO:0044439	peroxisomal part	5 of 96	0.0014	
GO:0002169	3-methylcrotonyl-CoA carboxylase complex, mitochondrial	2 of 2	0.0023	
GO:0045252	oxoglutarate dehydrogenase complex	2 of 6	0.0086	
GO:0031967	organelle envelope	13 of 1146	0.0092	
GO:0044464	cell part	73 of 16244	0.0097	
GO:0044452	nucleolar part	5 of 180	0.0122	
GO:0005739	mitochondrion	15 of 1531	0.0122	
GO:0043231	intracellular membrane-bounded organelle	54 of 10365	0.0145	
GO:0005778	peroxisomal membrane	3 of 51	0.0165	
GO:0005782	peroxisomal matrix	3 of 53	0.0167	
GO:0044429	mitochondrial part	11 of 1015	0.0219	
GO:0043227	membrane-bounded organelle	56 of 11244	0.0286	
GO:0012505	endomembrane system	28 of 4347	0.0298	
(less ...)				

Reference publications				
publication	(year) title	count in gene set	false discovery rate	
PMID:22758915	(2012) An inventory of peroxisomal proteins and pathways ...	5 of 32	0.0210	
PMID:28431015	(2017) Large-scale collection of full-length cDNA and trans...	4 of 15	0.0268	

KEGG Pathways				
pathway	description	count in gene set	false discovery rate	
hsa04146	Peroxisome	5 of 81	0.0017	
hsa00280	Valine, leucine and isoleucine degradation	4 of 48	0.0020	
hsa01100	Metabolic pathways	15 of 1250	0.0024	
hsa00380	Tryptophan metabolism	3 of 40	0.0129	
hsa00330	Arginine and proline metabolism	3 of 48	0.0170	
hsa00120	Primary bile acid biosynthesis	2 of 17	0.0339	
(less ...)				

Reactome Pathways				
pathway	description	count in gene set	false discovery rate	
HSA-1430728	Metabolism	25 of 2032	3.56e-05	
HSA-70895	Branched-chain amino acid catabolism	4 of 23	0.00057	
HSA-390918	Peroxisomal lipid metabolism	4 of 23	0.00057	
HSA-71291	Metabolism of amino acids and derivatives	9 of 354	0.00092	
HSA-600044	Protein transport to lysosome	4 of 50	0.0022	

HSA-9033241	Peroxisomal protein import	4 of 38	0.0000
HSA-8978868	Fatty acid metabolism	5 of 171	0.0280
HSA-6788656	Histidine, lysine, phenylalanine, tyrosine, proline and tryptop...	3 of 46	0.0280
HSA-556833	Metabolism of lipids	10 of 721	0.0280
HSA-389887	Beta-oxidation of pristanoyl-CoA	2 of 8	0.0280
HSA-3371599	Defective HLC8 causes multiple carboxylase deficiency	2 of 7	0.0280
HSA-196780	Biotin transport and metabolism	2 of 11	0.0316
HSA-71064	Lysine catabolism	2 of 12	0.0339
HSA-193775	Synthesis of bile acids and bile salts via 24-hydroxycholest...	2 of 14	0.0386
(less ...)			

UniProt Keywords			
keyword	description	count in gene set	false discovery rate
KW-0576	Peroxisome	6 of 101	0.00075
KW-0560	Oxidoreductase	11 of 557	0.0010
KW-0007	Acetylation	29 of 3335	0.0010
KW-0225	Disease mutation	24 of 2951	0.0123
KW-1067	Emery-Dreifuss muscular dystrophy	2 of 6	0.0169
KW-0597	Phosphoprotein	46 of 8066	0.0190
KW-9995	Disease	27 of 3799	0.0224
KW-0276	Fatty acid metabolism	4 of 123	0.0386
KW-0443	Lipid metabolism	7 of 442	0.0403
(less ...)			

Statistical background

For the above enrichment analysis,
the following statistical background
is assumed:

Whole Genome

UPDATE

Save / Export

Biological Process (GO)	download	64 GO-terms significantly enriched; file-format: tab-delimited
Molecular Function (GO)	download	5 GO-terms significantly enriched; file-format: tab-delimited
Cellular Component (GO)	download	21 GO-terms significantly enriched; file-format: tab-delimited
Reference publications	download	2 publications significantly enriched; file-format: tab-delimited
KEGG Pathways	download	6 pathways significantly enriched; file-format: tab-delimited
Reactome Pathways	download	13 pathways significantly enriched; file-format: tab-delimited
UniProt Keywords	download	9 keywords significantly enriched; file-format: tab-delimited

there were no significant pathway enrichments observed in the following categories:
PFAM Protein Domains, INTERPRO Protein Domains and Features, SMART Protein Domains.