





76 items (human) - STRING interaction network

00.1901304	organoniu ogen compound metabolic process	30 01 320 1 18 of 1779	0.0000
G0:0044281 G0:2000259	small molecule metabolic process positive regulation of protein activation cascade	2 of 3	0.0092
GO:0045917	positive regulation of complement activation	2 of 3	0.0097
G0:0010954	positive regulation of protein processing	3 of 25	0.0102
G0:0006732	coenzyme metabolic process	7 of 297	0.0102
G0:0006631 G0:0106077	fatty acid metabolic process histone succinylation	7 of 294 2 of 4	0.0102 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
G0:0009259 G0:0006637	ribonucleotide metabolic process acyl-CoA metabolic process	8 of 440 4 of 88	0.0163 0.0205
GO:0006768	biotin metabolic process	2 of 7	0.0203
GO:0006551	leucine metabolic process	2 of 7	0.0229
G0:0016042	lipid catabolic process	6 of 265	0.0261
G0:0042398 G0:0017144	cellular modified amino acid biosynthetic process	3 of 41 9 of 622	0.0264 0.0283
G0:0017144 G0:0034613	drug metabolic process cellular protein localization	9 of 622	0.0283
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
G0:0006575 G0:0072594	cellular modified amino acid metabolic process establishment of protein localization to organelle	5 of 185 7 of 396	0.0310 0.0324
GO:0072394 GO:0033365	protein localization to organelle	9 of 649	0.0324
GO:0008152	metabolic process	51 of 9569	0.0350
G0:0044237	cellular metabolic process	48 of 8797	0.0358
G0:0072330	monocarboxylic acid biosynthetic process	5 of 200	0.0384
G0:1901575 G0:0009987	organic substance catabolic process cellular process	15 of 1609 68 of 14652	0.0391 0.0391
G0:0009987	ribonucleotide biosynthetic process	5 of 202	0.0391
GO:0008104	protein localization	17 of 1966	0.0391
G0:2000257	regulation of protein activation cascade	3 of 54	0.0409
G0:0009150 G0:1901605	purine ribonucleotide metabolic process alpha-amino acid metabolic process	7 of 425 5 of 209	0.0409 0.0410
GO:1901605 GO:0051641	cellular localization	18 of 2180	0.0410
GO:0044248	cellular catabolic process	15 of 1646	0.0419
GO:0009437	carnitine metabolic process	2 of 13	0.0419
GO:0006886 GO:0006605	intracellular protein transport	10 of 836 6 of 318	0.0419 0.0421
G0:0006605 G0:0043173	protein targeting nucleotide salvage	6 of 318 2 of 14	0.0421
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
G0:0061024 G0:0016043	membrane organization	9 of 729 32 of 5163	0.0473
GO:0016043 GO:0032507	cellular component organization maintenance of protein location in cell	32 01 5103 3 of 64	0.0483
00.0002007	mantenance of protein location in cen	0 01 04	(less)
	Molecular Function (G0)		
GO-term	description		false discovery rate
G0:0019166	trans-2-enoyl-CoA reductase (NADPH) activity	2 of 3	0.0315
G0:0016628 G0:0016491	oxidoreductase activity, acting on the CH-CH group of dono oxidoreductase activity	3 of 26 11 of 716	0.0315 0.0315
G0:0016406	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	description cytosol	44 of 4958	7.01e-07
G0:0005829 G0:0044444	description cytosol cytoplasmic part	44 of 4958 61 of 9377	7.01e-07 1.27e-06
GO:0005829	description cytosol	44 of 4958	7.01e-07
G0:0005829 G0:0044444 G0:0005737 G0:0005622 G0:0044424	description cytosol cytoplasmic part cytoplasm intracellular intracellular	44 of 4958 61 of 9377 65 of 11238 71 of 14286 70 of 13996	7.01e-07 1.27e-06 1.70e-05 0.00060 0.00071
G0:0005829 G0:0044444 G0:0005737 G0:0005622 G0:0044424 G0:0005777	description cytosol cytosol cytoplasmic part cytoplasmic intracellular intracellular printracellular preproxisome	44 of 4958 61 of 9377 65 of 11238 71 of 14286 70 of 13996 6 of 127	7.01e-07 1.27e-06 1.70e-05 0.00060 0.00071 0.00076
G0:0005829 G0:0044444 G0:0005737 G0:0005622 G0:0044424 G0:0005777 G0:0070013	description cytosol cytosol cytoplasmic part cytoplasm intracellular intracellular intracellular peroxisome intracellular organelle lumen	44 of 4958 61 of 9377 65 of 11238 71 of 14286 70 of 13996 6 of 127 37 of 5162	7.01e-07 1.27e-06 1.70e-05 0.00060 0.00071 0.00076
G0:0005829 G0:0044444 G0:0005737 G0:0005622 G0:0044424 G0:0005777	description cytosol cytosol cytoplasmic part cytoplasmic intracellular intracellular printracellular preproxisome	44 of 4958 61 of 9377 65 of 11238 71 of 14286 70 of 13996 6 of 127	7.01e-07 1.27e-06 1.70e-05 0.00060 0.00071 0.00076
G0:0005829 G0:0044444 G0:0005737 G0:0005622 G0:0044424 G0:0005777 G0:0070013 G0:0044449 G0:00044439 G0:0002169	description cytosol cytosol cytoplasmic part cytoplasmic intracellular intracellular intracellular part peroxisome intracellular organelle lumen intracellular organelle part peroxisomal part arethylcrotonyl-CoA carboxylase complex, mitochondrial	44 of 4958 61 of 9377 65 of 11238 71 of 14286 70 of 13996 6 of 127 37 of 5162 52 of 8882 5 of 96 2 of 2	7.01e-07 1.27e-06 1.70e-05 0.00060 0.00071 0.00076 0.0012 0.0014 0.0014 0.0023
G0:0005829 G0:0044444 G0:0005737 G0:0005622 G0:0044424 G0:0005777 G0:0070013 G0:0044446 G0:0044439 G0:0002169 G0:0045252	description cytosol cytosol cytoplasmic part cytoplasmic intracellular intracellular peroxisome intracellular part peroxisome intracellular organelle lumen intracellular organelle part peroxisoma peroxisomal peroxisomal peroxisomal part a-methylicrotonyl-CoA carboxylase complex, mitochondrial oxoglutarate delydrogenase complex	44 of 4958 61 of 9377 65 of 11238 71 of 14286 70 of 13996 6 of 127 37 of 5162 52 of 8882 5 of 96 2 of 2 2 of 6	7.01e-07 1.27e-06 1.70e-05 0.00060 0.00071 0.00076 0.0012 0.0014 0.0014 0.0023 0.0086
G0:0005829 G0:00044444 G0:0005737 G0:0005622 G0:00044424 G0:0005777 G0:0070013 G0:0044446 G0:0044439 G0:0002169 G0:0045252 G0:0031967	description cytosio cytosio cytoplasmic part cytoplasmic intracellular intracellular intracellular part peroxisome intracellular organelle lumen intracellular organelle part peroxisomal part aretnylcrotnyl-CoA carboxylase complex, mitochondrial oxoglutarate dehydrogenase complex organelle envelope	44 of 4958 61 of 9377 65 of 11238 71 of 14286 70 of 13996 6 of 127 37 of 5162 52 of 8882 5 of 96 2 of 2 2 of 6 13 of 1146	7.01e-07 1.27e-06 1.70e-05 0.00060 0.00071 0.00076 0.0012 0.0014 0.0023 0.0086 0.0092
G0:0005829 G0:0044444 G0:0005737 G0:0005622 G0:0044424 G0:0005777 G0:0070013 G0:0044446 G0:0044439 G0:0002169 G0:0045252	description cytosol cytosol cytoplasmic part cytoplasmic intracellular intracellular peroxisome intracellular part peroxisome intracellular organelle lumen intracellular organelle part peroxisoma peroxisomal peroxisomal peroxisomal part a-methylicrotonyl-CoA carboxylase complex, mitochondrial oxoglutarate delydrogenase complex	44 of 4958 61 of 9377 65 of 11238 71 of 14286 70 of 13996 6 of 127 37 of 5162 52 of 8882 5 of 96 2 of 2 2 of 6 13 of 1146 73 of 16244 5 of 180	7.01e-07 1.27e-06 1.70e-05 0.00060 0.00071 0.00076 0.0014 0.0014 0.0023 0.0086 0.0092 0.0097 0.0122
GC:0005829 GC:0044444 GC:0005737 GC:0005622 GC:0044424 GC:0005777 GC:0070013 GC:0044444 GC:0044449 GC:00045252 GC:00031967 GC:0044464 GC:0044462 GC:00045739	description cytopals cytopalsamic part cytoplasmic part cytoplasmic intracellular intracellular organelle lumen intracellular organelle lumen intracellular organelle part peroxisoma peroxisoma peroxisomal part peroxisomal peroxisomal part peroxisomal peroxisomal part peroxisomal peroxisomal part peroxisomal peroxisomal peroxisomal peroxisomal per untracellular organelle part peroxisomal peroxisomal peroxisomal peroxisomal per untracellular organelle envelope cell part unucleolar part mutochondrion	44 of 4958 61 of 9377 65 of 11238 71 of 14286 70 of 13996 6 of 127 37 of 5162 52 of 8882 2 of 2 2 of 6 13 of 1146 73 of 16244 5 of 180	7.01e-07 1.27e-06 1.70e-05 0.00060 0.00071 0.00076 0.0012 0.0014 0.0014 0.0023 0.0086 0.0092 0.0097 0.0122
GO.0005829 GO.0044444 GO.0005737 GO.0005622 GO.0044424 GO.0005777 GO.0070013 GO.0044434 GO.0002169 GO.0044439 GO.0002169 GO.00445252 GO.0031967 GO.0044454 GO.0004452 GO.0005739 GO.0005739 GO.0005739 GO.0005739	description cytosio cytosio cytosio cytoplasmic part cytoplasm intracellular intracellular part peroxisome intracellular organelle lumen intracellular organelle part peroxisomal part amethycrotonyt-CoA carboxylase complex, mitochondrial oxoglutarate dehydrogenase complex organelle envelope cell part nucleolar part mitochondrion intracellular membrane-bounded organelle	44 of 4958 61 of 9377 65 of 11238 71 of 14286 70 of 1396 6 of 127 37 of 5162 52 of 8882 5 of 96 2 of 2 2 of 6 13 of 1146 73 of 16244 5 of 180 15 of 180	7.01e-07 1.27e-06 1.70e-05 0.00060 0.00071 0.00076 0.0012 0.0014 0.0023 0.0092 0.0097 0.0122 0.0122 0.0122 0.0124
GC.0005829 GC.0044444 GC.0005737 GC.0005622 GC.0044424 GC.0005777 GC.0070013 GC.00044446 GC.0002169 GC.004252 GC.0044464 GC.0044462 GC.000439 GC.0005739 GC.00043231 GC.0005778	description cytopals cytoplasmic part cytoplasmic part cytoplasmic intracellular intracellular organelle lumen intracellular organelle lumen intracellular organelle part peroxisoma part 3-methylcrotonyl-CoA carboxylase complex, mitochondrial oxogluratare delydrogenase complex organelle envelope cell part nucleolar part mitochondrion intracellular membrane-bounded organelle peroxisomal permembrane	44 of 4958 61 of 9377 65 of 11238 71 of 14286 70 of 13996 6 of 127 37 of 5162 52 of 8882 5 of 96 2 of 2 2 of 6 13 of 1146 73 of 16244 5 of 180 15 of 1353 54 of 10365 3 of 51	7.01e-07 1.27e-06 1.70e-05 0.0005 0.00077 0.00076 0.0012 0.0014 0.0014 0.0023 0.0086 0.0092 0.0097 0.0122 0.0142 0.0142 0.0145
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GO.0005829 GO.0005737 GO.0005622 GO.00044424 GO.0005777 GO.00005777 GO.0070013 GO.0044446 GO.0002169 GO.0044459 GO.00044525 GO.0004459 GO.004459 GO.004459 GO.004459 GO.004459 GO.004578 GO.0005778 GO.005778 GO.005778 GO.005778 GO.005778 GO.005778 GO.004429	description cytosio cytosio cytosio cytoplasmic part cytoplasmic intracellular intracellular part peroxisome intracellular organelle lumen intracellular organelle part peroxisomal part peroxisomal part amethylcrotonyt-CoA carboxylase complex, mitochondrial oxoglutarate dehydrogenase complex organelle envelope cell part mutochondrion intracellular membrane-bounded organelle peroxisomal membrane	44 of 4958 61 of 9977 65 of 11228 71 of 14286 70 of 13996 6 of 127 37 of 5162 52 of 882 5 of 96 2 of 2 2 of 6 13 of 1146 73 of 16244 5 of 180 15 of 153 3 of 51 3 of 51 3 of 53 11 of 1015 5 6 of 11244	7.01e-07 1.27e-06 1.70e-05 1.70e-05 1.70e-05 0.00006 0.00071 0.00076 0.0012 0.0014 0.0014 0.0023 0.0086 0.0092 0.0097 0.0122 0.0122 0.0125 0.0165 0.0165 0.0167 0.0219 0.0226
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G.0006829 G.0004444 G.0006737 G.0005622 G.0005622 G.0006822 G.000673 G.0006	description cytosol cytosol cytoplasmic part cytoplasmic intracellular part peroxisome intracellular part peroxisome intracellular organelle lumen intracellular organelle part peroxisomal part amethylorotomyloro Acaboxylase complex, mitochondrial oxoglutarate delydrogenase complex oxoganelle emethylorogenase complex mitochondrinon intracellular membrane bounded organelle emotosmal matrix mitochondrial part membrane-bounded organelle endomembrane bystem Reference publications	44 of 4958 fol of 9377 65 of 11238 71 of 14286 70 of 13996 6 of 127 37 of 5162 2 5 of 98 2 of 2 2 of 6 13 of 1146 73 of 15244 5 of 189 15 of 153 1 of 1015 5 of 1124 28 of 4347	7.01e-07 1.27e-06 1.70e-05 1.70e-05 0.00060 0.00076 0.0017 0.00076 0.0014 0.0014 0.0023 0.0086 0.0092 0.0097 0.0122 0.0122 0.0122 0.0125 0.0165 0.0165 0.0165 0.0219 0.0298 (less)
G.0006829 G.0004444 G.0006737 G.0005622 G.0005622 G.0006822 G.000673 G.0006	description Cytosia Cytosia Cytosia Cytosiamic part Cytoplasmic part Cytop	44 of 4958 61 of 9377 65 of 11238 71 of 14286 70 of 13298 66 of 127 37 of 5162 52 of 8882 5 of 96 2 of 2 2 of 6 13 of 1146 73 of 1624 5 of 180 15 of 153 1 of 10365 3 of 51 3 of 51 3 of 51 3 of 51 3 of 53 1 of 104 20 of 4347	7.01e-07 1.27e-06 1.70e-05 1.70e-05 0.00006 0.00076 0.0012 0.0014 0.0014 0.0023 0.0086 0.0092 0.0097 0.0122 0.0122 0.0122 0.0125 0.0165 0.0216 0.0298 (less)
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76 items (human) - STRING interaction network

HSA-9033241 Peroxisomai protein import 4	FOT 58	U UUbb
HOAF9033241 Peroxisornal protein import		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 1	0 of 721	0.0280
HSA-389887 Beta-oxidation of pristanoyl-CoA 2	2 of 8	0.0280
HSA-3371599 Defective HLCS causes multiple carboxylase deficiency 2	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
			(1000)

Statistical background

the following statistical background

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Biological Process (GO) download 64 GO-terms significantly enriched; file-format: tab-delimited Molecular Function (G0) 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

Server load: low (11%) [HD]

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