


While parsing you click empty space and and drag to zoom

interpretation of the coordinate axes?




Could not parse GO ID from line: 'Term'. Line will be skipped.
Go term 1904831 was not found in the current version of the GeneOntology, dated 26:06:2015 07:17. GO term will be skipped.
Go term 102337 was not found in the current version of the GeneOntology, dated 26:06:2015 07:17. GO term will be skipped.
Go term 102338 was not found in the current version of the GeneOntology, dated 26:06:2015 07:17. GO term will be skipped.
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Go term 102391 was not found in the current version of the GeneOntology, dated 26:06:2015 07:17. GO term will be skipped.

Tip: your resulting list of GO terms seems to be quite long. If you want to reduce it further, press the Back button in your browser and choose a different setting for the "allowed similarity" parameter.

 Hide/show dispensable GO terms

 Export results to text table (CSV)

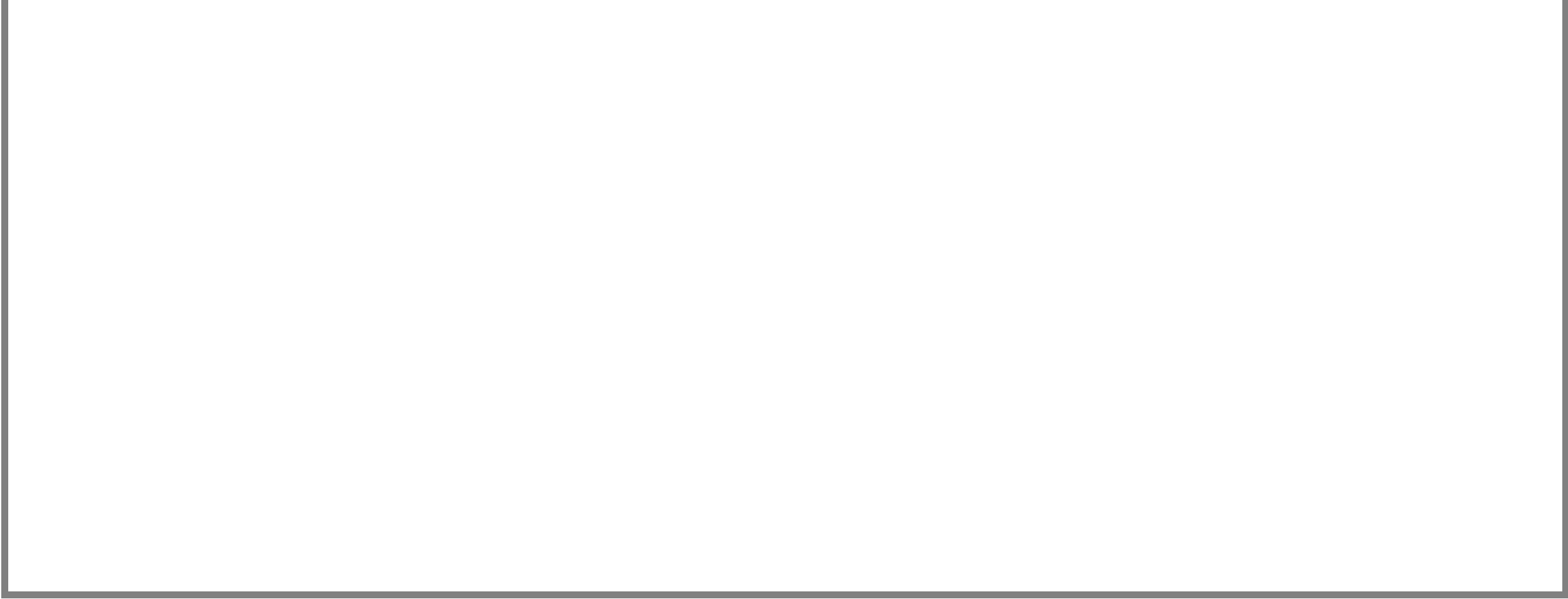
 Make R script for plotting

term ID	description	frequency	pin?	uniqueness	dispensability
GO:0007568	aging	0.013 %		0.92	0.00
... GO:0031175	neuron projection development	0.043 %		0.82	0.86
... GO:0021762	substantia nigra development	0.003 %		0.90	1.10
... GO:0032964	collagen biosynthetic process	0.001 %		0.85	0.51
... GO:0007420	brain development	0.041 %		0.89	0.51
GO:0008152	metabolic process	82.183 %		1.00	0.00
GO:0019835	cytolysis	0.185 %		0.96	0.00
GO:0031639	plasminogen activation	0.009 %		0.93	0.00
GO:0048678	response to axon injury	0.002 %		0.91	0.00
GO:0051170	nuclear import	0.098 %		0.94	0.00
GO:0051881	regulation of mitochondrial membrane potential	0.002 %		0.93	0.00

GO:0009058	biosynthetic process	30.325 %		0.98	0.01
GO:0051289	protein homotetramerization	0.004 %		0.91	0.02
GO:0006091	generation of precursor metabolites and energy	3.224 %		0.93	0.03
GO:0000281	mitotic cytokinesis	0.011 %		0.91	0.03
GO:0006104	succinyl-CoA metabolic process	0.000 %		0.88	0.03
GO:0001771	immunological synapse formation	0.000 %		0.91	0.05
GO:0046651	<i>lymphocyte proliferation</i>	0.014 %		0.88	0.75
GO:0006629	lipid metabolic process	3.094 %		0.87	0.05
GO:0000050	urea cycle	0.001 %		0.83	0.07
GO:0042426	choline catabolic process	0.000 %		0.81	0.10
GO:0008202	steroid metabolic process	0.040 %		0.83	0.10
GO:0006102	isocitrate metabolic process	0.013 %		0.77	0.12
GO:0006099	<i>tricarboxylic acid cycle</i>	0.483 %		0.69	1.10
GO:0022904	respiratory electron transport chain	0.881 %		0.82	0.14
GO:0006122	<i>mitochondrial electron transport, ubiquinol to cytochrome c</i>	0.004 %		0.79	0.59
GO:0006120	<i>mitochondrial electron transport, NADH to ubiquinone</i>	0.107 %		0.75	0.80
GO:0009060	<i>aerobic respiration</i>	1.366 %		0.82	0.82
GO:0006096	<i>glycolytic process</i>	0.522 %		0.62	0.67
GO:0032781	positive regulation of ATPase activity	0.003 %		0.92	0.15
GO:0001937	negative regulation of endothelial cell proliferation	0.002 %		0.86	0.16
GO:0044524	protein sulfhydration	0.000 %		0.93	0.16
GO:0033344	cholesterol efflux	0.002 %		0.90	0.16
GO:0045332	<i>phospholipid translocation</i>	0.012 %		0.77	0.72
GO:0015908	<i>fatty acid transport</i>	0.003 %		0.89	0.67
GO:0042159	lipoprotein catabolic process	0.001 %		0.88	0.17
GO:0008380	RNA splicing	0.097 %		0.88	0.18
GO:0006579	amino-acid betaine catabolic process	0.002 %		0.87	0.19
GO:0050966	detection of mechanical stimulus involved in sensory perception of pain	0.000 %		0.87	0.19
GO:0006094	gluconeogenesis	0.274 %		0.83	0.21
GO:0046038	GMP catabolic process	0.000 %		0.81	0.21
GO:0055114	oxidation-reduction process	15.044 %		0.86	0.21
GO:0045471	response to ethanol	0.003 %		0.87	0.21
GO:0048545	<i>response to steroid hormone</i>	0.034 %		0.85	0.89
GO:0009725	<i>response to hormone</i>	0.077 %		0.85	0.80
GO:0071392	<i>cellular response to estradiol stimulus</i>	0.001 %		0.85	0.79
GO:0014070	<i>response to organic cyclic compound</i>	0.061 %		0.85	0.66
GO:0006144	purine nucleobase metabolic process	0.215 %		0.79	0.23
GO:0046034	<i>ATP metabolic process</i>	5.374 %		0.72	0.51
GO:0006103	2-oxoglutarate metabolic process	0.010 %		0.75	0.24
GO:0018272	protein-pyridoxal-5-phosphate linkage via peptidyl-N6-pyridoxal phosphate-L-lysine	0.000 %		0.93	0.24
GO:0002357	defense response to tumor cell	0.000 %		0.91	0.25
GO:0002418	<i>immune response to tumor cell</i>	0.001 %		0.90	0.92
GO:0015992	proton transport	1.974 %		0.86	0.27
GO:0015991	<i>ATP hydrolysis coupled proton transport</i>	0.196 %		0.84	0.76
GO:0006810	<i>transport</i>	17.382 %		0.94	0.51
GO:0015986	<i>ATP synthesis coupled proton transport</i>	0.450 %		0.69	0.82
GO:0006734	NADH metabolic process	0.000 %		0.83	0.27
GO:0036109	alpha-linolenic acid metabolic process	0.000 %		0.79	0.29
GO:0006636	<i>unsaturated fatty acid biosynthetic process</i>	0.007 %		0.71	0.76
GO:0019346	transsulfuration	0.000 %		0.78	0.29
GO:0071266	<i>'de novo' L-methionine biosynthetic process</i>	0.059 %		0.67	0.60
GO:0019343	<i>cysteine biosynthetic process via cystathionine</i>	0.005 %		0.72	0.50
GO:0019344	<i>cysteine biosynthetic process</i>	0.189 %		0.66	0.76
GO:0031396	regulation of protein ubiquitination	0.009 %		0.87	0.29
GO:0009072	aromatic amino acid family metabolic process	0.683 %		0.71	0.31
GO:0006520	<i>cellular amino acid metabolic process</i>	6.437 %		0.68	0.57
GO:0019628	urate catabolic process	0.001 %		0.74	0.32
GO:0071071	regulation of phospholipid biosynthetic process	0.001 %		0.78	0.34
GO:0060696	<i>regulation of phospholipid catabolic process</i>	0.000 %		0.76	0.63
GO:0055088	lipid homeostasis	0.006 %		0.92	0.35
GO:0042632	<i>cholesterol homeostasis</i>	0.004 %		0.92	0.60
GO:0000038	very long-chain fatty acid metabolic process	0.002 %		0.76	0.36
GO:0097237	cellular response to toxic substance	0.001 %		0.87	0.37
GO:0006979	response to oxidative stress	0.539 %		0.88	0.38
GO:0070814	hydrogen sulfide biosynthetic process	0.072 %		0.87	0.39
GO:0035999	<i>tetrahydrofolate interconversion</i>	0.102 %		0.70	0.69
GO:0006749	<i>glutathione metabolic process</i>	0.123 %		0.81	0.58
GO:0034392	negative regulation of smooth muscle cell apoptotic process	0.000 %		0.83	0.39
GO:1902254	<i>negative regulation of intrinsic apoptotic signaling pathway by p53 class mediator</i>	0.001 %		0.77	0.88
GO:2001234	<i>negative regulation of apoptotic signaling pathway</i>	0.011 %		0.74	0.74
GO:2001243	<i>negative regulation of intrinsic apoptotic signaling pathway</i>	0.004 %		0.75	0.88
GO:0033033	<i>negative regulation of myeloid cell apoptotic process</i>	0.001 %		0.83	0.68
GO:0006572	tyrosine catabolic process	0.002 %		0.72	0.39
GO:0006559	<i>L-phenylalanine catabolic process</i>	0.011 %		0.70	0.76

GO:0006532	aspartate biosynthetic process	0.000 %		0.75	0.39
GO:0006533	<i>aspartate catabolic process</i>	0.000 %	🔒	0.72	0.66
GO:0019550	<i>glutamate catabolic process to aspartate</i>	0.000 %	🔒	0.72	0.65
GO:0019551	<i>glutamate catabolic process to 2-oxoglutarate</i>	0.010 %	🔒	0.67	0.78
GO:0033512	<i>L-lysine catabolic process to acetyl-CoA via saccharopine</i>	0.019 %	🔒	0.65	0.67
GO:0034626	fatty acid elongation, polyunsaturated fatty acid	0.000 %		0.75	0.40
GO:0019367	<i>fatty acid elongation, saturated fatty acid</i>	0.000 %	🔒	0.74	0.88
GO:1904049	negative regulation of spontaneous neurotransmitter secretion	0.000 %		0.82	0.41
GO:0042761	very long-chain fatty acid biosynthetic process	0.001 %		0.75	0.41
GO:0031508	pericentric heterochromatin assembly	0.000 %		0.90	0.42
GO:0006694	steroid biosynthetic process	0.030 %		0.80	0.42
GO:0008203	<i>cholesterol metabolic process</i>	0.007 %	🔒	0.79	0.88
GO:0006695	<i>cholesterol biosynthetic process</i>	0.002 %	🔒	0.78	0.89
GO:0035338	long-chain fatty-acyl-CoA biosynthetic process	0.000 %		0.88	0.43
GO:0007005	mitochondrion organization	0.046 %		0.88	0.44
GO:0009395	phospholipid catabolic process	0.023 %		0.75	0.45
GO:0033539	<i>fatty acid beta-oxidation using acyl-CoA dehydrogenase</i>	0.013 %	🔒	0.66	0.91
GO:0006635	<i>fatty acid beta-oxidation</i>	0.053 %	🔒	0.64	0.83
GO:0052695	cellular glucuronidation	0.000 %		0.80	0.46
GO:1900407	regulation of cellular response to oxidative stress	0.002 %		0.81	0.46
GO:1903202	<i>negative regulation of oxidative stress-induced cell death</i>	0.000 %	🔒	0.75	0.88
GO:0000398	mRNA splicing, via spliceosome	0.036 %		0.89	0.47
GO:0051497	negative regulation of stress fiber assembly	0.001 %		0.80	0.47
GO:1900740	<i>positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway</i>	0.000 %	🔒	0.68	0.80
GO:0032212	<i>positive regulation of telomere maintenance via telomerase</i>	0.000 %	🔒	0.76	0.56
GO:0098779	<i>activation of mitophagy in response to mitochondrial depolarization</i>	0.000 %	🔒	0.70	0.63
GO:0006097	glyoxylate cycle	0.055 %		0.74	0.48
GO:0042776	mitochondrial ATP synthesis coupled proton transport	0.000 %		0.78	0.48
GO:0000413	protein peptidyl-prolyl isomerization	0.268 %		0.90	0.48
GO:0032981	mitochondrial respiratory chain complex I assembly	0.001 %		0.87	0.49
GO:0042407	<i>cristae formation</i>	0.000 %	🔒	0.84	0.65
GO:0008637	<i>apoptotic mitochondrial changes</i>	0.006 %	🔒	0.78	0.73
GO:0070125	<i>mitochondrial translational elongation</i>	0.001 %	🔒	0.78	0.72
GO:0070124	<i>mitochondrial translational initiation</i>	0.000 %	🔒	0.81	0.57
GO:0009083	branched-chain amino acid catabolic process	0.010 %		0.71	0.49
GO:0006527	<i>arginine catabolic process</i>	0.105 %	🔒	0.66	0.68
GO:0006574	<i>valine catabolic process</i>	0.005 %	🔒	0.71	0.56
GO:0009074	<i>aromatic amino acid family catabolic process</i>	0.055 %	🔒	0.68	0.58
GO:0060828	regulation of canonical Wnt signaling pathway	0.011 %		0.79	0.49
GO:0006547	histidine metabolic process	0.448 %		0.69	0.49
GO:0019556	<i>histidine catabolic process to glutamate and formamide</i>	0.065 %	🔒	0.63	0.84
GO:0019557	<i>histidine catabolic process to glutamate and formate</i>	0.055 %	🔒	0.63	0.97
GO:0042493	response to drug	0.207 %		0.86	0.49
GO:0006855	<i>drug transmembrane transport</i>	0.162 %	🔒	0.75	0.65
GO:0009636	<i>response to toxic substance</i>	0.341 %	🔒	0.85	0.69
GO:0015893	<i>drug transport</i>	0.194 %	🔒	0.78	0.97
GO:0006107	oxaloacetate metabolic process	0.017 %		0.75	0.50
GO:0006536	<i>glutamate metabolic process</i>	0.272 %	🔒	0.68	0.69
GO:0006531	<i>aspartate metabolic process</i>	0.016 %	🔒	0.72	0.51
GO:0006108	<i>malate metabolic process</i>	0.093 %	🔒	0.72	0.60
GO:0006105	<i>succinate metabolic process</i>	0.041 %	🔒	0.73	0.54

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[Make R script for plotting treemaps](#)

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GO:0016020	membrane	51.720 %		0.98	0.00
GO:0034362	low-density lipoprotein particle	0.001 %		0.66	0.00
GO:0042627	chylomicron	0.002 %		0.65	1.18
GO:0034364	high-density lipoprotein particle	0.003 %		0.64	1.28
GO:0034361	very-low-density lipoprotein particle	0.002 %		0.65	1.24
GO:0043209	myelin sheath	0.005 %		0.93	0.00
GO:0070469	respiratory chain	2.726 %		0.90	0.00
GO:0044194	cytolytic granule	0.000 %		0.66	0.01
GO:0000922	spindle pole	0.028 %		0.58	0.15
GO:0005829	cytosol	0.807 %		0.66	0.20
GO:0034709	methylosome	0.003 %		0.62	0.23
GO:0005763	mitochondrial small ribosomal subunit	0.004 %		0.44	0.61
GO:0045244	succinate-CoA ligase complex (GDP-forming)	0.000 %		0.44	0.60
GO:0045252	oxoglutarate dehydrogenase complex	0.056 %		0.54	0.55
GO:0031904	endosome lumen	0.000 %		0.56	0.24
GO:0005788	endoplasmic reticulum lumen	0.007 %		0.48	0.64
GO:0005783	endoplasmic reticulum	0.299 %		0.50	0.50
GO:0005833	hemoglobin complex	0.014 %		0.61	0.25

GO:0000243	commitment complex	0.002 %		0.51	0.28
GO:0016023	cytoplasmic membrane-bounded vesicle	0.132 %		0.54	0.30
GO:0070062	extracellular exosome	0.300 %		0.51	0.88
GO:0005777	peroxisome	0.063 %		0.53	0.32
GO:0005778	peroxisomal membrane	0.027 %		0.46	0.95
GO:0005782	peroxisomal matrix	0.003 %		0.48	0.83
GO:0045263	proton-transporting ATP synthase complex, coupling factor F(o)	0.411 %		0.51	0.32
GO:0005643	nuclear pore	0.036 %		0.31	0.84
GO:0005753	mitochondrial proton-transporting ATP synthase complex	0.058 %		0.31	1.04
GO:0005751	mitochondrial respiratory chain complex IV	0.005 %		0.37	0.77
GO:0005750	mitochondrial respiratory chain complex III	0.006 %		0.36	0.84
GO:0005747	mitochondrial respiratory chain complex I	0.011 %		0.34	0.87
GO:0045261	proton-transporting ATP synthase complex, catalytic core F(1)	0.470 %		0.50	1.04
GO:0000276	mitochondrial proton-transporting ATP synthase complex, coupling factor F(o)	0.053 %		0.31	0.94
GO:0000275	mitochondrial proton-transporting ATP synthase complex, catalytic core F(1)	0.003 %		0.38	0.71
GO:0005741	mitochondrial outer membrane	0.043 %		0.47	0.33
GO:0000786	nucleosome	0.143 %		0.47	0.38
GO:0030529	ribonucleoprotein complex	6.088 %		0.63	0.40
GO:0005739	mitochondrion	3.808 %		0.46	0.45
GO:0008180	COP9 signalosome	0.006 %		0.47	0.49
GO:0031966	mitochondrial membrane	2.312 %		0.35	0.97
GO:0097526	spliceosomal tri-snRNP complex	0.007 %		0.47	0.52
GO:0005685	U1 snRNP	0.009 %		0.46	1.02
GO:0005759	mitochondrial matrix	0.055 %		0.42	0.64
GO:0005758	mitochondrial intermembrane space	0.013 %		0.45	0.57
GO:0005681	spliceosomal complex	0.053 %		0.43	0.59
GO:0005743	mitochondrial inner membrane	2.192 %		0.35	0.64
GO:0016363	nuclear matrix	0.008 %		0.47	0.53
GO:0005654	nucleoplasm	0.221 %		0.38	0.77

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















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GO:0003824	catalytic activity	69.295 %		1.00	0.00
GO:0005344	oxygen transporter activity	0.039 %		0.96	0.00
GO:0005536	glucose binding	0.001 %		0.98	0.00
GO:0009055	electron carrier activity	2.493 %		0.99	0.00
GO:0016853	isomerase activity	3.154 %		0.96	0.00
GO:0060230	lipoprotein lipase activator activity	0.000 %		0.99	0.00
GO:0008480	sarcosine dehydrogenase activity	0.000 %		0.93	0.01
GO:0080146	L-cysteine desulfhydrase activity	0.002 %		0.94	0.02
GO:0004123	<i>cystathionine gamma-lyase activity</i>	0.002 %		0.94	0.61
GO:0044540	<i>L-cystine L-cysteine-lyase (deaminating)</i>	0.002 %		0.94	0.60
GO:0004658	propionyl-CoA carboxylase activity	0.003 %		0.95	0.02
GO:0004334	fumarylacetoacetase activity	0.006 %		0.95	0.02
GO:0003962	cystathionine gamma-synthase activity	0.010 %		0.87	0.02
GO:1990446	U1 snRNP binding	0.000 %		0.98	0.02
GO:0019825	oxygen binding	0.074 %		0.97	0.03
GO:0017091	AU-rich element binding	0.002 %		0.97	0.03

GO:0008013	beta-catenin binding	0.006 %		0.95	0.03
GO:0016829	lyase activity	4.488 %		0.96	0.03
GO:0005543	phospholipid binding	0.064 %		0.96	0.04
GO:0008289	lipid binding	0.237 %		0.97	0.04
GO:0042277	peptide binding	0.093 %		0.96	0.04
GO:0005542	<i>folic acid binding</i>	0.011 %		0.95	0.68
GO:0002060	purine nucleobase binding	0.000 %		0.97	0.04
GO:0008144	drug binding	0.260 %		0.97	0.04
GO:0016491	oxidoreductase activity	14.657 %		0.95	0.04
GO:0051536	iron-sulfur cluster binding	2.612 %		0.97	0.05
GO:0016787	hydrolase activity	21.764 %		0.95	0.07
GO:0016740	transferase activity	22.118 %		0.95	0.07
GO:0048037	cofactor binding	6.702 %		0.97	0.08
GO:0008951	palmitoleoyl [acyl-carrier-protein]-dependent acyltransferase activity	0.000 %		0.80	0.09
GO:0034930	1-hydroxypyrene sulfotransferase activity	0.000 %		0.82	0.09
GO:0008327	methyl-CpG binding	0.001 %		0.96	0.11
GO:0051990	(R)-2-hydroxyglutarate dehydrogenase activity	0.000 %		0.93	0.12
GO:0004053	arginase activity	0.014 %		0.95	0.13
GO:0052745	inositol phosphate phosphatase activity	0.020 %		0.95	0.14
GO:0000062	fatty-acyl-CoA binding	0.016 %		0.96	0.15
GO:0008483	transaminase activity	0.805 %		0.81	0.17
GO:0080130	<i>L-phenylalanine:2-oxoglutarate aminotransferase activity</i>	0.070 %		0.84	0.79
GO:0004069	<i>L-aspartate:2-oxoglutarate aminotransferase activity</i>	0.020 %		0.85	0.71
GO:0004838	<i>L-tyrosine:2-oxoglutarate aminotransferase activity</i>	0.001 %		0.87	0.57
GO:0016627	oxidoreductase activity, acting on the CH-CH group of donors	1.092 %		0.90	0.18
GO:0016401	palmitoyl-CoA oxidase activity	0.000 %		0.92	0.18
GO:0000166	nucleotide binding	20.353 %		0.94	0.19
GO:0019186	acyl-CoA N-acyltransferase activity	0.000 %		0.79	0.20
GO:0034738	lanosterol O-acyltransferase activity	0.000 %		0.77	0.20
GO:0034737	<i>ergosterol O-acyltransferase activity</i>	0.000 %		0.76	0.78
GO:0016752	sinapoyltransferase activity	0.000 %		0.78	0.22
GO:0046941	azetidine-2-carboxylic acid acetyltransferase activity	0.000 %		0.79	0.25
GO:0070404	NADH binding	0.000 %		0.95	0.25
GO:0022829	wide pore channel activity	0.137 %		0.95	0.26
GO:0009922	fatty acid elongase activity	0.000 %		0.76	0.26
GO:0000253	3-keto sterol reductase activity	0.000 %		0.92	0.26
GO:0043849	Ras palmitoyltransferase activity	0.000 %		0.75	0.27
GO:0019105	<i>N-palmitoyltransferase activity</i>	0.060 %		0.66	0.98
GO:0018031	<i>peptidyl-lysine N6-palmitoyltransferase activity</i>	0.026 %		0.68	1.05
GO:0016416	<i>O-palmitoyltransferase activity</i>	0.008 %		0.68	0.79
GO:0016454	<i>C-palmitoyltransferase activity</i>	0.001 %		0.73	0.64
GO:0019948	SUMO activating enzyme activity	0.000 %		0.94	0.27
GO:0004467	<i>long-chain fatty acid-CoA ligase activity</i>	0.016 %		0.94	0.57
GO:0004775	<i>succinate-CoA ligase (ADP-forming) activity</i>	0.072 %		0.93	0.78
GO:0004147	dihydrolipoamide branched chain acyltransferase activity	0.000 %		0.74	0.28
GO:0030523	<i>dihydrolipoamide S-acyltransferase activity</i>	0.020 %		0.68	0.79
GO:0019707	<i>protein-cysteine S-acyltransferase activity</i>	0.017 %		0.68	0.61
GO:0016418	<i>S-acetyltransferase activity</i>	0.020 %		0.68	0.80
GO:0016419	<i>S-malonyltransferase activity</i>	0.041 %		0.67	0.84
GO:0052858	peptidyl-lysine N-acetyltransferase activity, acting on acetyl phosphate as donor	0.000 %		0.76	0.28
GO:0044822	poly(A) RNA binding	0.135 %		0.96	0.30
GO:0018030	peptidyl-lysine N6-myristoyltransferase activity	0.006 %		0.72	0.32
GO:0019705	<i>protein-cysteine S-myristoyltransferase activity</i>	0.009 %		0.68	1.13
GO:0004361	glutaryl-CoA dehydrogenase activity	0.000 %		0.92	0.34
GO:0008137	NADH dehydrogenase (ubiquinone) activity	0.693 %		0.89	0.35
GO:0003954	<i>NADH dehydrogenase activity</i>	0.792 %		0.89	0.87
GO:0019107	myristoyltransferase activity	0.002 %		0.74	0.35
GO:0016620	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	0.788 %		0.88	0.35
GO:0034604	<i>pyruvate dehydrogenase (NAD+) activity</i>	0.012 %		0.90	0.66
GO:0004029	<i>aldehyde dehydrogenase (NAD) activity</i>	0.042 %		0.89	0.72
GO:0019145	<i>aminobutyraldehyde dehydrogenase activity</i>	0.008 %		0.90	0.64
GO:0071949	FAD binding	0.034 %		0.94	0.35
GO:0032216	glucosaminyl-phosphotidylinositol O-acyltransferase activity	0.000 %		0.76	0.36
GO:0031492	nucleosomal DNA binding	0.003 %		0.94	0.36
GO:0030060	L-malate dehydrogenase activity	0.038 %		0.90	0.36
GO:0004448	<i>isocitrate dehydrogenase activity</i>	0.053 %		0.90	0.51
GO:0004450	<i>isocitrate dehydrogenase (NADP+) activity</i>	0.050 %		0.90	0.50
GO:0030351	inositol-1,3,4,5,6-pentakisphosphate 3-phosphatase activity	0.000 %		0.96	0.37
GO:0016651	oxidoreductase activity, acting on NAD(P)H	1.351 %		0.90	0.37
GO:0043741	L-2-aminoadipate N-acetyltransferase activity	0.007 %		0.72	0.38
GO:0016831	carboxy-lyase activity	0.915 %		0.94	0.38
GO:0004163	<i>diphosphomevalonate decarboxylase activity</i>	0.015 %		0.95	0.61
GO:0016753	O-sinapoyltransferase activity	0.000 %		0.76	0.39
GO:0052890	oxidoreductase activity, acting on the CH-CH group of donors, with a flavin as acceptor	0.003 %		0.91	0.39

GO:0003995	<i>acyl-CoA dehydrogenase activity</i>	0.368 %		0.89	0.56
GO:0016414	O-octanoyltransferase activity	0.000 %		0.75	0.41
GO:0016420	malonyltransferase activity	0.041 %		0.70	0.41
GO:0030170	pyridoxal phosphate binding	1.703 %		0.93	0.42
GO:0050660	<i>flavin adenine dinucleotide binding</i>	1.624 %		0.92	0.68
GO:0051287	<i>NAD binding</i>	1.108 %		0.93	0.59
GO:0015078	hydrogen ion transmembrane transporter activity	1.909 %		0.93	0.43
GO:0004129	<i>cytochrome-c oxidase activity</i>	1.070 %		0.85	0.84
GO:0046961	<i>proton-transporting ATPase activity, rotational mechanism</i>	0.159 %		0.90	0.75
GO:0046933	<i>proton-transporting ATP synthase activity, rotational mechanism</i>	0.362 %		0.89	0.92
GO:0042626	<i>ATPase activity, coupled to transmembrane movement of substances</i>	1.903 %		0.90	0.58
GO:0016887	<i>ATPase activity</i>	5.234 %		0.92	0.71
GO:0042803	protein homodimerization activity	0.122 %		0.95	0.44
GO:0005102	<i>receptor binding</i>	0.416 %		0.94	0.62
GO:0019899	<i>enzyme binding</i>	0.221 %		0.95	0.56
GO:0004772	sterol O-acyltransferase activity	0.000 %		0.74	0.44
GO:0047105	4-trimethylammoniobutyraldehyde dehydrogenase activity	0.000 %		0.92	0.46
GO:0080131	hydroxyjasmonate sulfotransferase activity	0.000 %		0.81	0.46
GO:0016406	carnitine O-acyltransferase activity	0.000 %		0.73	0.47
GO:0016411	<i>acylglycerol O-acyltransferase activity</i>	0.074 %		0.66	0.80
GO:0016412	<i>serine O-acyltransferase activity</i>	0.051 %		0.67	0.60
GO:0034915	2-methylhexanoyl-CoA C-acetyltransferase activity	0.058 %		0.70	0.47
GO:0090595	acetyl-CoA:L-lysine N6-acetyltransferase	0.010 %		0.71	0.47
GO:0004149	<i>dihydrolipoyllysine-residue succinyltransferase activity</i>	0.030 %		0.67	0.89
GO:0016751	<i>S-succinyltransferase activity</i>	0.030 %		0.67	0.89
GO:0016750	<i>O-succinyltransferase activity</i>	0.016 %		0.67	0.85
GO:0016749	<i>N-succinyltransferase activity</i>	0.040 %		0.68	0.51
GO:0004776	succinate-CoA ligase (GDP-forming) activity	0.000 %		0.94	0.48
GO:0018711	benzoyl acetate-CoA thiolase activity	0.058 %		0.70	0.48
GO:0018712	3-hydroxybutyryl-CoA thiolase activity	0.058 %		0.70	0.48
GO:0018713	3-ketopimelyl-CoA thiolase activity	0.058 %		0.70	0.48
GO:0034848	naphthyl-2-oxomethyl-succinyl-CoA succinyl transferase activity	0.058 %		0.70	0.48
GO:0034851	2,4,4-trimethyl-3-oxopentanoyl-CoA 2-C-propanoyl transferase activity	0.058 %		0.70	0.48
GO:0034919	butyryl-CoA 2-C-propionyltransferase activity	0.058 %		0.70	0.48
GO:0034945	2,6-dimethyl-5-methylene-3-oxo-heptanoyl-CoA C-acetyltransferase activity	0.058 %		0.70	0.48
GO:0043806	keto acid formate lyase activity	0.058 %		0.70	0.48
GO:0016748	succinyltransferase activity	0.086 %		0.69	0.49
GO:0016408	<i>C-acyltransferase activity</i>	0.096 %		0.69	0.51
GO:0016417	<i>S-acyltransferase activity</i>	0.107 %		0.69	0.52
GO:0016232	HNK-1 sulfotransferase activity	0.000 %		0.80	0.49
GO:0018727	<i>2-phenanthrol sulfotransferase activity</i>	0.033 %		0.71	1.53
GO:0018726	<i>9-phenanthrol sulfotransferase activity</i>	0.033 %		0.71	1.53
GO:0018725	<i>trans-3,4-dihydrodiolphenanthrene sulfotransferase activity</i>	0.000 %		0.78	0.65
GO:0018723	<i>3-phenanthrol sulfotransferase activity</i>	0.033 %		0.71	0.84
GO:0018724	<i>4-phenanthrol sulfotransferase activity</i>	0.033 %		0.71	1.53
GO:0018721	<i>trans-9R,10R-dihydrodiolphenanthrene sulfotransferase activity</i>	0.000 %		0.78	0.65
GO:0018722	<i>1-phenanthrol sulfotransferase activity</i>	0.033 %		0.71	1.53
GO:0004394	<i>heparan sulfate 2-O-sulfotransferase activity</i>	0.000 %		0.79	0.54
GO:0019111	<i>phenanthrol sulfotransferase activity</i>	0.000 %		0.78	0.64
GO:0050694	<i>galactose 3-O-sulfotransferase activity</i>	0.001 %		0.77	0.68
GO:0050698	<i>proteoglycan sulfotransferase activity</i>	0.000 %		0.79	0.57
GO:0051922	<i>cholesterol sulfotransferase activity</i>	0.000 %		0.78	0.59

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metabolic deteriorating organic biopolymer electrochemical sulfotransferase definition 2-aminobutanedioic atom non-encoded waxes coash
momp phospholipids substance rotational fats phosphate-containing 2fe-2s s-acyltransferase myristoyl acids proton-motive chemical gradually
permeabilization mitochondrial mitochondrion h2s molecules purine tca succinate-coa protons simply **localizer** esterified mitophagy
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