



While parsing you can 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 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.
Go term 102336 was not found in the current version of the GeneOntology, dated 26:06:2015 07:17. GO term will be skipped.
Go term 102391 was not found in the current version of the GeneOntology, dated 26:06:2015 07:17. GO term 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.

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.

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term ID	description	frequency	pin?	uniqueness	dispensability
GO:0008152	metabolic process	82.183 %		1.00	0.00
GO:0016192	vesicle-mediated transport	0.381 %		0.94	0.00
GO:0019835	cytolysis	0.185 %		0.96	0.00
GO:0030212	hyaluronan metabolic process	0.003 %		0.93	0.00
GO:0034616	response to laminar fluid shear stress	0.001 %		0.91	0.00
GO:0040008	regulation of growth	0.042 %		0.87	0.00
GO:0090245	<i>axis elongation involved in somitogenesis</i>	0.000 %		0.86	0.70
GO:0030308	<i>negative regulation of cell growth</i>	0.008 %		0.75	0.83
GO:0070988	demethylation	0.007 %		0.92	0.00
GO:0060155	platelet dense granule organization	0.000 %		0.93	0.01
GO:0035338	long-chain fatty-acyl-CoA biosynthetic process	0.000 %		0.91	0.02

GO:0071266	<i>'de novo' L-methionine biosynthetic process</i>	0.059 %		0.77	0.58
GO:0006084	<i>acetyl-CoA metabolic process</i>	0.146 %		0.89	0.57
GO:0045445	myoblast differentiation	0.004 %		0.89	0.03
GO:0036155	acylglycerol acyl-chain remodeling	0.000 %		0.84	0.04
GO:0006641	<i>triglyceride metabolic process</i>	0.005 %		0.80	0.75
GO:0001771	immunological synapse formation	0.000 %		0.88	0.04
GO:0006068	ethanol catabolic process	0.000 %		0.85	0.05
GO:0006071	<i>glycerol metabolic process</i>	0.254 %		0.80	0.54
GO:0044524	protein sulfhydration	0.000 %		0.92	0.06
GO:0019748	secondary metabolic process	0.177 %		0.91	0.07
GO:0052695	cellular glucuronidation	0.000 %		0.85	0.09
GO:0090305	nucleic acid phosphodiester bond hydrolysis	2.508 %		0.90	0.11
GO:0006629	lipid metabolic process	3.094 %		0.88	0.11
GO:0006725	cellular aromatic compound metabolic process	33.051 %		0.94	0.12
GO:0060356	leucine import	0.000 %		0.90	0.14
GO:0046166	glyceraldehyde-3-phosphate biosynthetic process	0.000 %		0.87	0.16
GO:0010666	positive regulation of cardiac muscle cell apoptotic process	0.000 %		0.82	0.16
GO:2001234	<i>negative regulation of apoptotic signaling pathway</i>	0.011 %		0.72	0.61
GO:0010664	<i>negative regulation of striated muscle cell apoptotic process</i>	0.001 %		0.81	0.94
GO:0042157	lipoprotein metabolic process	0.098 %		0.91	0.17
GO:0070672	response to interleukin-15	0.000 %		0.90	0.18
GO:0044268	multicellular organismal protein metabolic process	0.000 %		0.85	0.18
GO:1902807	negative regulation of cell cycle G1/S phase transition	0.004 %		0.81	0.18
GO:0010951	<i>negative regulation of endopeptidase activity</i>	0.083 %		0.76	0.54
GO:0055088	lipid homeostasis	0.006 %		0.86	0.19
GO:0055091	<i>phospholipid homeostasis</i>	0.001 %		0.85	0.55
GO:0035356	<i>cellular triglyceride homeostasis</i>	0.000 %		0.83	0.91
GO:0042632	<i>cholesterol homeostasis</i>	0.004 %		0.84	0.92
GO:0070328	<i>triglyceride homeostasis</i>	0.002 %		0.85	0.84
GO:0050746	regulation of lipoprotein metabolic process	0.001 %		0.86	0.19
GO:0030521	androgen receptor signaling pathway	0.003 %		0.81	0.20
GO:0006888	ER to Golgi vesicle-mediated transport	0.019 %		0.88	0.20
GO:0050766	<i>positive regulation of phagocytosis</i>	0.002 %		0.75	0.82
GO:0006911	<i>phagocytosis, engulfment</i>	0.001 %		0.85	0.56
GO:0055114	oxidation-reduction process	15.044 %		0.88	0.21
GO:0018272	protein-pyridoxal-5-phosphate linkage via peptidyl-N6-pyridoxal phosphate-L-lysine	0.000 %		0.92	0.24
GO:0051289	protein homotetramerization	0.004 %		0.93	0.26
GO:0015917	aminophospholipid transport	0.000 %		0.88	0.26
GO:0032307	<i>negative regulation of prostaglandin secretion</i>	0.000 %		0.77	0.56
GO:0045332	<i>phospholipid translocation</i>	0.012 %		0.72	0.72
GO:0033344	<i>cholesterol efflux</i>	0.002 %		0.86	0.50
GO:0032367	<i>intracellular cholesterol transport</i>	0.001 %		0.86	0.88
GO:0015908	<i>fatty acid transport</i>	0.003 %		0.86	0.67
GO:0043314	<i>negative regulation of neutrophil degranulation</i>	0.000 %		0.70	0.66
GO:0016062	adaptation of rhodopsin mediated signaling	0.000 %		0.80	0.26
GO:0006953	acute-phase response	0.002 %		0.89	0.27
GO:0019346	transsulfuration	0.000 %		0.84	0.28
GO:0006544	<i>glycine metabolic process</i>	0.250 %		0.80	0.50
GO:0009070	<i>serine family amino acid biosynthetic process</i>	0.413 %		0.76	0.87
GO:0008202	steroid metabolic process	0.040 %		0.80	0.28
GO:0008299	<i>isoprenoid biosynthetic process</i>	0.463 %		0.74	0.73
GO:0006631	<i>fatty acid metabolic process</i>	0.867 %		0.71	0.79
GO:0006633	<i>fatty acid biosynthetic process</i>	0.629 %		0.69	0.76
GO:0008610	<i>lipid biosynthetic process</i>	2.206 %		0.74	0.58
GO:0015827	tryptophan transport	0.000 %		0.90	0.32
GO:0006743	ubiquinone metabolic process	0.140 %		0.84	0.33
GO:0035999	<i>tetrahydrofolate interconversion</i>	0.102 %		0.79	0.52
GO:0002790	peptide secretion	0.010 %		0.88	0.33
GO:0042761	very long-chain fatty acid biosynthetic process	0.001 %		0.78	0.34
GO:0000717	nucleotide-excision repair, DNA duplex unwinding	0.000 %		0.81	0.34
GO:0060313	negative regulation of blood vessel remodeling	0.000 %		0.81	0.34
GO:0045908	<i>negative regulation of vasodilation</i>	0.000 %		0.79	0.58
GO:0006508	proteolysis	3.705 %		0.89	0.36
GO:0007584	response to nutrient	0.004 %		0.89	0.37
GO:0042493	<i>response to drug</i>	0.207 %		0.88	0.50
GO:0009083	branched-chain amino acid catabolic process	0.010 %		0.83	0.38
GO:0006548	<i>histidine catabolic process</i>	0.076 %		0.81	0.59
GO:0061045	negative regulation of wound healing	0.000 %		0.79	0.38
GO:0060136	embryonic process involved in female pregnancy	0.000 %		0.88	0.38
GO:0048702	<i>embryonic neurocranium morphogenesis</i>	0.000 %		0.88	0.63
GO:0090527	actin filament reorganization	0.000 %		0.89	0.39
GO:0002692	negative regulation of cellular extravasation	0.000 %		0.77	0.39
GO:0007040	lysosome organization	0.003 %		0.92	0.39
GO:0034625	fatty acid elongation, monounsaturated fatty acid	0.000 %		0.77	0.40

GO:0034626	<i>fatty acid elongation, polyunsaturated fatty acid</i>	0.000 %		0.77	0.95
GO:0019367	<i>fatty acid elongation, saturated fatty acid</i>	0.000 %		0.77	0.86
GO:0042574	retinal metabolic process	0.001 %		0.81	0.42
GO:0042572	<i>retinol metabolic process</i>	0.001 %		0.70	0.91
GO:0002357	defense response to tumor cell	0.000 %		0.89	0.42
GO:0002418	<i>immune response to tumor cell</i>	0.001 %		0.86	0.92
GO:0006694	steroid biosynthetic process	0.030 %		0.76	0.42
GO:0008203	<i>cholesterol metabolic process</i>	0.007 %		0.75	0.88
GO:0016126	<i>sterol biosynthetic process</i>	0.006 %		0.74	0.93
GO:0006695	<i>cholesterol biosynthetic process</i>	0.002 %		0.75	0.89
GO:0033488	<i>cholesterol biosynthetic process via 24,25-dihydrolanosterol</i>	0.000 %		0.80	0.64
GO:0032489	regulation of Cdc42 protein signal transduction	0.001 %		0.79	0.45
GO:0006936	muscle contraction	0.018 %		0.88	0.46
GO:0007275	<i>multicellular organismal development</i>	0.460 %		0.86	0.69
GO:0006636	unsaturated fatty acid biosynthetic process	0.007 %		0.76	0.47
GO:0030819	positive regulation of cAMP biosynthetic process	0.003 %		0.75	0.47
GO:0001970	<i>positive regulation of activation of membrane attack complex</i>	0.000 %		0.72	0.68
GO:0006957	<i>complement activation, alternative pathway</i>	0.000 %		0.74	0.70
GO:0006958	<i>complement activation, classical pathway</i>	0.001 %		0.73	0.76
GO:0006956	<i>complement activation</i>	0.069 %		0.68	0.56
GO:0055098	response to low-density lipoprotein particle	0.001 %		0.90	0.48
GO:0045471	<i>response to ethanol</i>	0.003 %		0.89	0.52

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Go term 1904831 was not found in the current version of the GeneOntology, dated 26:06:2015 07:17. GO term will be skipped.

term ID	description	frequency	pin?	uniqueness	dispensability
GO:0005576	extracellular region	4.572 %		0.93	0.00
GO:0005615	extracellular space	0.249 %		0.86	0.00
GO:0016020	membrane	51.720 %		0.97	0.00
GO:0045121	membrane raft	0.025 %		0.83	0.00
GO:0016324	apical plasma membrane	0.024 %		0.79	0.75
GO:0097447	dendritic tree	0.006 %		0.85	0.00
GO:0043025	neuronal cell body	0.028 %		0.85	0.78
GO:0005811	lipid particle	0.010 %		0.70	0.02
GO:0005579	membrane attack complex	0.002 %		0.80	0.07
GO:0030118	clathrin coat	0.051 %		0.66	0.62
GO:0016021	integral component of membrane	35.230 %		0.89	0.14
GO:0044194	cytolytic granule	0.000 %		0.66	0.15
GO:0005764	lysosome	0.049 %		0.59	0.76
GO:0031904	endosome lumen	0.000 %		0.61	0.17
GO:0030176	integral component of endoplasmic reticulum membrane	0.034 %		0.50	0.90
GO:0005783	endoplasmic reticulum	0.299 %		0.52	0.50
GO:0005789	endoplasmic reticulum membrane	0.136 %		0.47	0.80
GO:0031410	cytoplasmic vesicle	0.167 %		0.61	0.20

GO:0070062	<i>extracellular exosome</i>	0.300 %		0.53	0.88
GO:0008274	gamma-tubulin ring complex	0.001 %		0.66	0.22
GO:0005833	hemoglobin complex	0.014 %		0.71	0.23
GO:0031430	M band	0.002 %		0.66	0.24
GO:0005856	cytoskeleton	0.714 %		0.64	0.34
GO:0005778	peroxisomal membrane	0.027 %		0.52	0.37
GO:0005739	mitochondrion	3.808 %		0.51	0.39
 GO:0043231	<i>intracellular membrane-bounded organelle</i>	8.847 %		0.52	0.77
GO:0072562	blood microparticle	0.012 %		0.87	0.46
GO:0005759	mitochondrial matrix	0.055 %		0.56	0.49
 GO:0005654	<i>nucleoplasm</i>	0.221 %		0.55	0.77

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GO:0003713	transcription coactivator activity	0.025 %		0.94	0.00
GO:0001105	<i>RNA polymerase II transcription coactivator activity</i>	0.002 %		0.94	0.77
GO:0003824	catalytic activity	69.295 %		0.99	0.00
GO:0005044	scavenger receptor activity	0.013 %		0.95	0.00
GO:0016874	ligase activity	3.868 %		0.95	0.00
GO:0022829	wide pore channel activity	0.137 %		0.93	0.00
GO:0030247	polysaccharide binding	0.035 %		0.94	0.00
GO:0030294	receptor signaling protein tyrosine kinase inhibitor activity	0.000 %		0.91	0.00
GO:0004866	<i>endopeptidase inhibitor activity</i>	0.084 %		0.89	0.61
GO:0004867	<i>serine-type endopeptidase inhibitor activity</i>	0.030 %		0.89	0.93
GO:0004869	<i>cysteine-type endopeptidase inhibitor activity</i>	0.025 %		0.89	0.92
GO:0009922	fatty acid elongase activity	0.000 %		0.94	0.01
GO:0008398	sterol 14-demethylase activity	0.001 %		0.92	0.01
GO:0004506	<i>squalene monooxygenase activity</i>	0.002 %		0.92	0.62
GO:0080146	L-cysteine desulhydrase activity	0.002 %		0.92	0.02
GO:0004123	<i>cystathionine gamma-lyase activity</i>	0.002 %		0.92	0.61
GO:0044540	<i>L-cystine L-cysteine-lyase (deaminating)</i>	0.002 %		0.92	0.60
GO:0004075	biotin carboxylase activity	0.108 %		0.88	0.02

GO:0008234	cysteine-type peptidase activity	0.221 %		0.90	0.02
GO:0004252	<i>serine-type endopeptidase activity</i>	0.675 %	🔒	0.89	0.94
GO:0008236	<i>serine-type peptidase activity</i>	1.044 %	🔒	0.89	0.64
GO:0034186	apolipoprotein A-I binding	0.000 %		0.90	0.02
GO:0019825	oxygen binding	0.074 %		0.94	0.03
GO:0005543	phospholipid binding	0.064 %		0.92	0.04
GO:0044822	poly(A) RNA binding	0.135 %		0.94	0.04
GO:0016491	oxidoreductase activity	14.657 %		0.95	0.04
GO:0005515	protein binding	2.482 %		0.93	0.05
GO:0048037	cofactor binding	6.702 %		0.93	0.08
GO:0000234	phosphoethanolamine N-methyltransferase activity	0.000 %		0.94	0.09
GO:0015020	glucuronosyltransferase activity	0.003 %		0.94	0.10
GO:0005509	calcium ion binding	0.365 %		0.92	0.11
GO:0003962	cystathionine gamma-synthase activity	0.010 %		0.94	0.12
GO:0052650	NADP-retinol dehydrogenase activity	0.000 %		0.92	0.13
GO:0008201	heparin binding	0.013 %		0.91	0.15
GO:0070402	NADPH binding	0.068 %		0.90	0.17
GO:0005344	oxygen transporter activity	0.039 %		0.93	0.26
GO:0050733	RS domain binding	0.000 %		0.90	0.28
GO:0000166	nucleotide binding	20.353 %		0.91	0.29
GO:0005548	phospholipid transporter activity	0.019 %		0.90	0.30
GO:0090556	<i>phosphatidylserine-translocating ATPase activity</i>	0.012 %	🔒	0.87	0.80
GO:0090554	<i>phosphatidylcholine-translocating ATPase activity</i>	0.012 %	🔒	0.85	1.00
GO:0047676	arachidonate-CoA ligase activity	0.000 %		0.88	0.30
GO:0004745	retinol dehydrogenase activity	0.001 %		0.91	0.31
GO:0051117	ATPase binding	0.002 %		0.89	0.31
GO:0004372	glycine hydroxymethyltransferase activity	0.056 %		0.93	0.33
GO:0005506	iron ion binding	2.467 %		0.91	0.34
GO:0042282	hydroxymethylglutaryl-CoA reductase activity	0.002 %		0.91	0.35
GO:0034188	apolipoprotein A-I receptor activity	0.000 %		0.95	0.35
GO:0004658	propionyl-CoA carboxylase activity	0.003 %		0.88	0.36
GO:0003989	<i>acetyl-CoA carboxylase activity</i>	0.129 %	🔒	0.87	0.78
GO:0001848	complement binding	0.018 %		0.88	0.37
GO:0016901	oxidoreductase activity, acting on the CH-OH group of donors, quinone or similar compound as acceptor	0.136 %		0.90	0.42
GO:0030170	pyridoxal phosphate binding	1.703 %		0.89	0.44
GO:0009374	biotin binding	0.000 %		0.90	0.45
GO:0031177	<i>phosphopantetheine binding</i>	0.062 %	🔒	0.90	0.52
GO:0031957	very long-chain fatty acid-CoA ligase activity	0.001 %		0.87	0.48
GO:0030729	<i>acetoacetate-CoA ligase activity</i>	0.005 %	🔒	0.87	0.57
GO:0004467	<i>long-chain fatty acid-CoA ligase activity</i>	0.016 %	🔒	0.86	0.80
GO:0042802	identical protein binding	0.154 %		0.87	0.48
GO:0005102	<i>receptor binding</i>	0.416 %	🔒	0.87	0.60

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metabolism multicellular morphology activitory heterocycle single-organism subcellular coo- trigger transform aged compound oils
dismantle microbody culminates non-living similarly lipids very-long-chain individual reactions metabolic deteriorating cease organic attack inherited
renovation non-encoded flippase proteinase saturated fatty-acid immunological skeleton peptidolysis organonitrogen glyceride vacuoles acids proteolytic
caspases chemical gradually leucocyte tcc encapsulating biochemical net organismal mac simply actions abiotic non-membrane-bounded
organism-specific halting substances peptidase immune subcomponent monocarboxylic immunogenic organelle pathways process bounded cellular
macromolecules

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