



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.  
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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.

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

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

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

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


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

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

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



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

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Frequent keywords within your set of GO terms:

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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