

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 61752 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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term ID	description	frequency	pin?	uniqueness	dispensability
<a href="#">GO:0006950</a>	response to stress	4.119 %		0.80	0.00
<a href="#">GO:0008152</a>	metabolic process	82.183 %		0.99	0.00
<a href="#">GO:0016192</a>	vesicle-mediated transport	0.381 %		0.88	0.00
<a href="#">GO:0016311</a>	dephosphorylation	0.777 %		0.90	0.00
<a href="#">GO:0042157</a>	lipoprotein metabolic process	0.098 %		0.85	0.01
<a href="#">GO:0031247</a>	actin rod assembly	0.000 %		0.83	0.02
<a href="#">GO:0007050</a>	cell cycle arrest	0.011 %		0.71	0.04
<a href="#">GO:0043066</a>	negative regulation of apoptotic process	0.047 %		0.69	0.55
<a href="#">GO:2001238</a>	positive regulation of extrinsic apoptotic signaling pathway	0.004 %		0.61	0.75
<a href="#">GO:0040020</a>	regulation of meiotic nuclear division	0.003 %		0.71	0.66
<a href="#">GO:0008380</a>	RNA splicing	0.097 %		0.82	0.11
<a href="#">GO:0006397</a>	mRNA processing	0.373 %		0.80	0.56
<a href="#">GO:0000380</a>	alternative mRNA splicing, via spliceosome	0.003 %		0.83	0.65
<a href="#">GO:0043666</a>	regulation of phosphoprotein phosphatase activity	0.004 %		0.79	0.20
<a href="#">GO:0051028</a>	mRNA transport	0.053 %		0.86	0.22
<a href="#">GO:0000209</a>	protein polyubiquitination	0.010 %		0.83	0.23
<a href="#">GO:0019217</a>	regulation of fatty acid metabolic process	0.029 %		0.77	0.23

<a href="#">GO:0006898</a>	receptor-mediated endocytosis	0.166 %		0.88	0.24
<a href="#">GO:0006465</a>	signal peptide processing	0.023 %		0.81	0.25
<a href="#">GO:1900034</a>	regulation of cellular response to heat	0.000 %		0.70	0.27
<a href="#">GO:0071318</a>	cellular response to ATP	0.000 %		0.77	0.28
<a href="#">GO:0090398</a>	cellular senescence	0.002 %		0.73	0.32
<a href="#">GO:0006457</a>	protein folding	0.863 %		0.80	0.34
<a href="#">GO:0002502</a>	peptide antigen assembly with MHC class I protein complex	0.000 %		0.82	0.34
<a href="#">GO:0045727</a>	positive regulation of translation	0.047 %		0.62	0.36
<small>GO</small> <a href="#">GO:2000510</a>	<i>positive regulation of dendritic cell chemotaxis</i>	0.000 %		0.57	0.53
<a href="#">GO:0002244</a>	hematopoietic progenitor cell differentiation	0.010 %		0.77	0.43
<small>GO</small> <a href="#">GO:1900026</a>	<i>positive regulation of substrate adhesion-dependent cell spreading</i>	0.001 %		0.63	0.72
<small>GO</small> <a href="#">GO:0045665</a>	<i>negative regulation of neuron differentiation</i>	0.004 %		0.67	0.60
<a href="#">GO:0032211</a>	negative regulation of telomere maintenance via telomerase	0.000 %		0.63	0.43
<small>GO</small> <a href="#">GO:0032212</a>	<i>positive regulation of telomere maintenance via telomerase</i>	0.000 %		0.63	0.96
<a href="#">GO:0048387</a>	negative regulation of retinoic acid receptor signaling pathway	0.001 %		0.64	0.45
<small>GO</small> <a href="#">GO:0033144</a>	<i>negative regulation of intracellular steroid hormone receptor signaling pathway</i>	0.002 %		0.64	0.60
<a href="#">GO:0006957</a>	complement activation, alternative pathway	0.000 %		0.61	0.47
<a href="#">GO:0036498</a>	IRE1-mediated unfolded protein response	0.000 %		0.67	0.48
<small>GO</small> <a href="#">GO:0030970</a>	<i>retrograde protein transport, ER to cytosol</i>	0.000 %		0.59	0.79
<small>GO</small> <a href="#">GO:0030433</a>	<i>ER-associated ubiquitin-dependent protein catabolic process</i>	0.003 %		0.65	0.78
<a href="#">GO:0034504</a>	protein localization to nucleus	0.025 %		0.83	0.49
<small>GO</small> <a href="#">GO:0051168</a>	<i>nuclear export</i>	0.078 %		0.82	0.52
<small>GO</small> <a href="#">GO:0051170</a>	<i>nuclear import</i>	0.098 %		0.81	0.90

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<a href="#">GO:0005576</a>	extracellular region	4.572 %		0.91	0.00
<a href="#">GO:0005615</a>	extracellular space	0.249 %		0.82	0.00
<a href="#">GO:0005925</a>	focal adhesion	0.016 %		0.91	0.00
<a href="#">GO:0016020</a>	membrane	51.720 %		0.95	0.00
<a href="#">GO:0019013</a>	viral nucleocapsid	0.446 %		0.91	0.00
<a href="#">GO:0030496</a>	midbody	0.014 %		0.89	0.00
<a href="#">GO:0031012</a>	extracellular matrix	0.156 %		0.91	0.00
<a href="#">GO:0016235</a>	aggresome	0.003 %		0.85	0.02
<a href="#">GO:0005844</a>	polysome	0.004 %		0.82	0.05
<a href="#">GO:0048471</a>	perinuclear region of cytoplasm	0.050 %		0.73	0.05
<a href="#">GO:0033018</a>	sarcoplasmic reticulum lumen	0.000 %		0.57	0.16
<a href="#">GO:0042824</a>	MHC class I peptide loading complex	0.000 %		0.53	0.54
<a href="#">GO:0043231</a>	intracellular membrane-bounded organelle	8.847 %		0.60	0.53
<a href="#">GO:0034663</a>	endoplasmic reticulum chaperone complex	0.000 %		0.54	0.54
<a href="#">GO:0005788</a>	endoplasmic reticulum lumen	0.007 %		0.52	0.64
<a href="#">GO:0005783</a>	endoplasmic reticulum	0.299 %		0.50	0.52
<a href="#">GO:0005789</a>	endoplasmic reticulum membrane	0.136 %		0.44	0.81
<a href="#">GO:0042470</a>	melanosome	0.004 %		0.61	0.20
<a href="#">GO:0030669</a>	clathrin-coated endocytic vesicle membrane	0.004 %		0.55	0.66
<a href="#">GO:0070062</a>	extracellular exosome	0.300 %		0.54	0.69
<a href="#">GO:0005829</a>	cytosol	0.807 %		0.70	0.28
<a href="#">GO:0034361</a>	very-low-density lipoprotein particle	0.002 %		0.77	0.41

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<a href="#">GO:0005044</a>	scavenger receptor activity	0.013 %		0.89	0.00
<a href="#">GO:0016901</a>	oxidoreductase activity, acting on the CH-OH group of donors, quinone or similar compound as acceptor	0.136 %		0.89	0.00
<a href="#">GO:0046790</a>	virion binding	0.000 %		0.85	0.00
<a href="#">GO:0098505</a>	G-rich strand telomeric DNA binding	0.000 %		0.83	0.02
<a href="#">GO:0003924</a>	GTPase activity	0.935 %		0.87	0.02
<a href="#">GO:0005537</a>	mannose binding	0.001 %		0.85	0.02
<a href="#">GO:0050750</a>	low-density lipoprotein particle receptor binding	0.001 %		0.81	0.02
<a href="#">GO:0042277</a>	peptide binding	0.093 %		0.84	0.03
<a href="#">GO:0008201</a>	heparin binding	0.013 %		0.82	0.03
<a href="#">GO:0030246</a>	carbohydrate binding	0.825 %		0.83	0.04
<a href="#">GO:0036002</a>	pre-mRNA binding	0.001 %		0.79	0.08
<a href="#">GO:0005509</a>	calcium ion binding	0.365 %		0.78	0.10
<a href="#">GO:0016208</a>	AMP binding	0.024 %		0.76	0.22
<a href="#">GO:0004252</a>	serine-type endopeptidase activity	0.675 %		0.86	0.25
<a href="#">GO:0000166</a>	nucleotide binding	20.353 %		0.79	0.26
<a href="#">GO:0044822</a>	poly(A) RNA binding	0.135 %		0.76	0.29
<a href="#">GO:0005506</a>	iron ion binding	2.467 %		0.77	0.34
<a href="#">GO:0003729</a>	mRNA binding	0.070 %		0.76	0.39
<a href="#">GO:0051082</a>	unfolded protein binding	0.451 %		0.79	0.43



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Frequent keywords within your set of GO terms:

membrane-bounded multicellular erad modifications **single-organism** oxoacid subcellular macromolecular transform history aged non-  
apoptotic cell-substrate exons membrane-enclosed anhydride **culminates** topologically plastids individual **repetition**  
deteriorating cease **biopolymer** telomeric reticulum adhesion-dependent young unfolded markedly vital later  
telomere tagging monitors internally organonitrogen vacuoles ribosomes **gradually** multiple surroundings rar molecules level  
encapsulating lectin anhydrides responses organismal low endoplasmic **simply neurogenesis** protein-coding infectious triad  
**halting** substances phosphorus regularly **macromolecule** organelle humidity nucleobase-containing clathrin-coated  
**lengthening** cellular macromolecules inactions

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