

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 61738 was not found in the current version of the GeneOntology, dated 26:06:2015 07:17. GO term will be skipped.
Go term 1904468 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:0002376	immune system process	0.625 %		0.98	0.00
GO:0006913	nucleocytoplasmic transport	0.181 %		0.90	0.00
... GO:0050663	<i>cytokine secretion</i>	0.010 %		0.77	0.53
... GO:0071638	<i>negative regulation of monocyte chemotactic protein-1 production</i>	0.000 %		0.74	0.58
... GO:0072615	<i>interleukin-17 secretion</i>	0.001 %		0.79	0.65
... GO:0032692	<i>negative regulation of interleukin-1 production</i>	0.001 %		0.73	0.75
... GO:1902714	<i>negative regulation of interferon-gamma secretion</i>	0.000 %		0.72	0.61
... GO:0032715	<i>negative regulation of interleukin-6 production</i>	0.001 %		0.72	0.83
... GO:0050714	<i>positive regulation of protein secretion</i>	0.006 %		0.69	0.62
... GO:0032720	<i>negative regulation of tumor necrosis factor production</i>	0.002 %		0.72	0.86
... GO:2000778	<i>positive regulation of interleukin-6 secretion</i>	0.000 %		0.67	0.80
GO:0007159	leukocyte cell-cell adhesion	0.003 %		0.95	0.00
GO:0033622	integrin activation	0.001 %		0.92	0.00

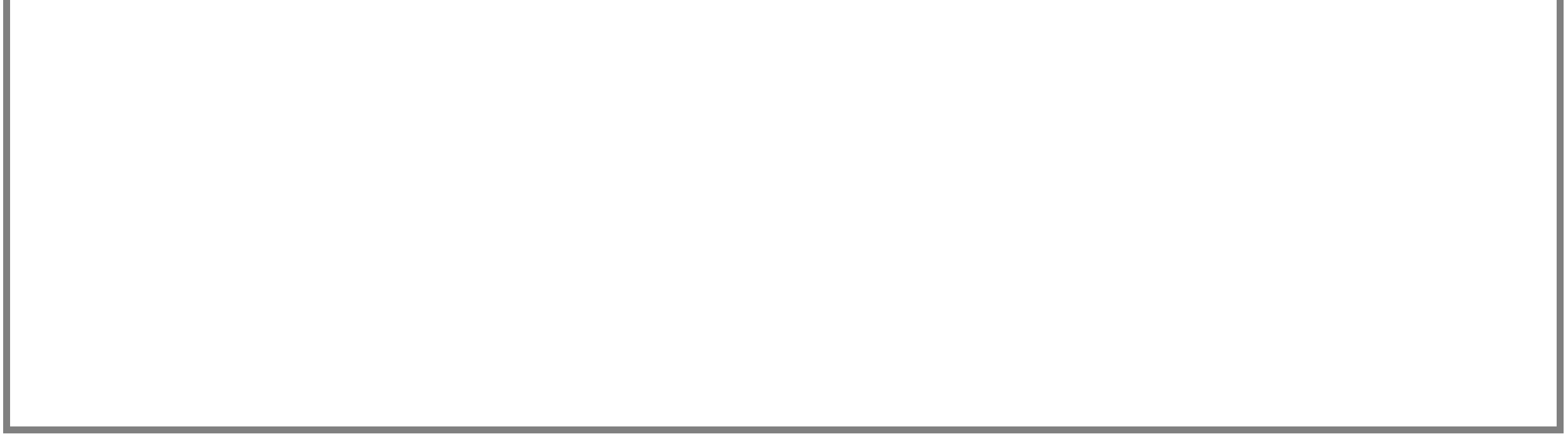
GO:0055089	fatty acid homeostasis	0.001 %		0.84	0.00
GO:0042593	glucose homeostasis	0.010 %	📊	0.82	0.55
GO:0006879	cellular iron ion homeostasis	0.130 %	📊	0.76	0.75
GO:0035356	cellular triglyceride homeostasis	0.000 %	📊	0.82	0.76
GO:0071333	cellular response to glucose stimulus	0.003 %	📊	0.57	0.94
GO:0035606	peptidyl-cysteine S-trans-nitrosylation	0.000 %		0.92	0.01
GO:0071499	cellular response to laminar fluid shear stress	0.000 %		0.80	0.01
GO:0007568	aging	0.013 %		0.93	0.03
GO:0006006	glucose metabolic process	0.741 %		0.91	0.04
GO:0006776	vitamin A metabolic process	0.000 %		0.88	0.06
GO:0042572	retinol metabolic process	0.001 %	📊	0.77	0.85
GO:0008380	RNA splicing	0.097 %		0.91	0.08
GO:0006103	2-oxoglutarate metabolic process	0.010 %		0.87	0.11
GO:0034255	regulation of urea metabolic process	0.000 %		0.83	0.12
GO:0006147	guanine catabolic process	0.013 %		0.87	0.13
GO:0046098	guanine metabolic process	0.013 %	📊	0.87	0.68
GO:0042985	negative regulation of amyloid precursor protein biosynthetic process	0.000 %		0.78	0.16
GO:0006910	phagocytosis, recognition	0.001 %		0.88	0.16
GO:0006911	phagocytosis, engulfment	0.001 %	📊	0.86	0.78
GO:0050892	intestinal absorption	0.001 %		0.84	0.16
GO:0055114	oxidation-reduction process	15.044 %		0.91	0.17
GO:0050900	leukocyte migration	0.014 %		0.74	0.19
GO:0050921	positive regulation of chemotaxis	0.005 %	📊	0.57	0.93
GO:0034142	toll-like receptor 4 signaling pathway	0.003 %	📊	0.57	0.64
GO:0072679	thymocyte migration	0.000 %	📊	0.77	0.85
GO:0072678	T cell migration	0.002 %	📊	0.75	0.73
GO:0030335	positive regulation of cell migration	0.017 %	📊	0.63	0.83
GO:1904179	positive regulation of adipose tissue development	0.002 %	📊	0.71	0.65
GO:0030097	hemopoiesis	0.047 %	📊	0.73	0.61
GO:0048247	lymphocyte chemotaxis	0.001 %	📊	0.58	0.94
GO:0050871	positive regulation of B cell activation	0.004 %	📊	0.68	0.53
GO:0050861	positive regulation of B cell receptor signaling pathway	0.000 %	📊	0.60	0.82
GO:0002548	monocyte chemotaxis	0.002 %	📊	0.58	0.81
GO:0050853	B cell receptor signaling pathway	0.003 %	📊	0.58	0.57
GO:0045087	innate immune response	0.137 %	📊	0.67	0.83
GO:0002523	leukocyte migration involved in inflammatory response	0.000 %	📊	0.65	0.77
GO:0051607	defense response to virus	0.321 %	📊	0.63	0.89
GO:0060326	cell chemotaxis	0.016 %	📊	0.58	0.83
GO:0006955	immune response	0.380 %	📊	0.68	0.76
GO:0030593	neutrophil chemotaxis	0.004 %	📊	0.56	0.90
GO:0051085	chaperone mediated protein folding requiring cofactor	0.013 %		0.91	0.19
GO:0071332	cellular response to fructose stimulus	0.000 %		0.72	0.20
GO:0042908	xenobiotic transport	0.021 %		0.90	0.20
GO:0038183	bile acid signaling pathway	0.000 %		0.73	0.20
GO:0034354	'de novo' NAD biosynthetic process from tryptophan	0.008 %		0.86	0.22
GO:0019805	quinolinate biosynthetic process	0.031 %	📊	0.84	0.60
GO:0038185	intracellular bile acid receptor signaling pathway	0.000 %		0.74	0.23
GO:0043420	anthranilate metabolic process	0.008 %		0.85	0.23
GO:0097053	L-kynurenine catabolic process	0.004 %	📊	0.84	0.67
GO:0006569	tryptophan catabolic process	0.044 %	📊	0.82	0.58
GO:0019441	tryptophan catabolic process to kynurenine	0.029 %	📊	0.81	0.97
GO:0019442	tryptophan catabolic process to acetyl-CoA	0.000 %	📊	0.85	0.69
GO:0070534	protein K63-linked ubiquitination	0.002 %		0.91	0.27
GO:0097192	extrinsic apoptotic signaling pathway in absence of ligand	0.005 %		0.68	0.27
GO:0007186	G-protein coupled receptor signaling pathway	0.368 %	📊	0.61	0.65
GO:0070327	thyroid hormone transport	0.000 %		0.81	0.27
GO:0034435	cholesterol esterification	0.001 %		0.88	0.28
GO:0008206	bile acid metabolic process	0.001 %	📊	0.85	0.68
GO:0070858	negative regulation of bile acid biosynthetic process	0.000 %	📊	0.71	0.63
GO:0042060	wound healing	0.025 %		0.77	0.29
GO:0007596	blood coagulation	0.015 %	📊	0.61	0.79
GO:0050728	negative regulation of inflammatory response	0.005 %	📊	0.60	0.75
GO:0046327	glycerol biosynthetic process from pyruvate	0.000 %		0.86	0.34
GO:0006656	phosphatidylcholine biosynthetic process	0.002 %	📊	0.82	0.63
GO:1902904	negative regulation of fibril organization	0.000 %		0.77	0.34
GO:0031647	regulation of protein stability	0.033 %		0.83	0.35
GO:0032392	DNA geometric change	0.428 %		0.90	0.35
GO:0034971	histone H3-R17 methylation	0.000 %	📊	0.85	0.58
GO:0043981	histone H4-K5 acetylation	0.001 %	📊	0.83	0.67
GO:0043982	histone H4-K8 acetylation	0.001 %	📊	0.83	0.86
GO:0046777	protein autophosphorylation	0.022 %		0.89	0.36
GO:2001250	positive regulation of ammonia assimilation cycle	0.000 %		0.72	0.38
GO:2000213	positive regulation of glutamate metabolic process	0.000 %	📊	0.72	0.95

GO:0007043	cell-cell junction assembly	0.004 %		0.88	0.39
GO:0006954	inflammatory response	0.099 %		0.74	0.40
GO:0071222	cellular response to lipopolysaccharide	0.009 %		0.64	0.95
GO:0001867	complement activation, lectin pathway	0.000 %		0.60	0.54
GO:0006953	acute-phase response	0.002 %		0.78	0.58
GO:0042742	defense response to bacterium	0.075 %		0.70	0.73
GO:0032496	response to lipopolysaccharide	0.014 %		0.66	0.87
GO:0010988	regulation of low-density lipoprotein particle clearance	0.000 %		0.78	0.40
GO:0090107	regulation of high-density lipoprotein particle assembly	0.000 %		0.74	0.78
GO:0061402	positive regulation of transcription from RNA polymerase II promoter in response to acidic pH	0.000 %		0.69	0.40
GO:0042493	response to drug	0.207 %		0.70	0.41
GO:0006805	xenobiotic metabolic process	0.067 %		0.66	0.60
GO:0006935	chemotaxis	0.336 %		0.63	0.69
GO:0042594	response to starvation	0.058 %		0.73	0.43
GO:0034516	response to vitamin B6	0.000 %		0.72	0.68
GO:0051365	cellular response to potassium ion starvation	0.000 %		0.75	0.67
GO:0006644	phospholipid metabolic process	1.014 %		0.84	0.43
GO:0001558	regulation of cell growth	0.021 %		0.78	0.43
GO:0008285	negative regulation of cell proliferation	0.034 %		0.76	0.44
GO:0010951	negative regulation of endopeptidase activity	0.083 %		0.71	0.65
GO:0008156	negative regulation of DNA replication	0.032 %		0.74	0.58
GO:0072318	clathrin coat disassembly	0.000 %		0.85	0.45
GO:0002576	platelet degranulation	0.001 %		0.86	0.46
GO:0016480	negative regulation of transcription from RNA polymerase III promoter	0.002 %		0.76	0.48
GO:0006357	regulation of transcription from RNA polymerase II promoter	0.211 %		0.76	0.56
GO:0032088	negative regulation of NF-kappaB transcription factor activity	0.004 %		0.74	0.59
GO:0006990	positive regulation of transcription from RNA polymerase II promoter involved in unfolded protein response	0.000 %		0.57	0.60
GO:0006195	purine nucleotide catabolic process	4.797 %		0.81	0.49
GO:0032967	positive regulation of collagen biosynthetic process	0.001 %		0.69	0.49
GO:0043124	negative regulation of I-kappaB kinase/NF-kappaB signaling	0.002 %		0.63	0.50
GO:0007257	activation of JUN kinase activity	0.001 %		0.58	0.54
GO:0070374	positive regulation of ERK1 and ERK2 cascade	0.007 %		0.57	0.80
GO:0051384	response to glucocorticoid	0.004 %		0.69	0.50
GO:0034097	response to cytokine	0.100 %		0.66	0.68
GO:0043401	steroid hormone mediated signaling pathway	0.024 %		0.55	0.88
GO:0032868	response to insulin	0.010 %		0.68	0.74
GO:0071356	cellular response to tumor necrosis factor	0.005 %		0.67	0.70
GO:0035924	cellular response to vascular endothelial growth factor stimulus	0.003 %		0.69	0.57
GO:0043627	response to estrogen	0.006 %		0.69	0.80
GO:0071417	cellular response to organonitrogen compound	0.019 %		0.64	0.90
GO:0070098	chemokine-mediated signaling pathway	0.009 %		0.57	0.73
GO:2001275	positive regulation of glucose import in response to insulin stimulus	0.000 %		0.54	0.82
GO:0010804	negative regulation of tumor necrosis factor-mediated signaling pathway	0.000 %		0.56	0.87
GO:0071320	cellular response to cAMP	0.002 %		0.67	0.80
GO:0071347	cellular response to interleukin-1	0.004 %		0.68	0.69

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term ID	description	frequency	pin?	uniqueness	dispensability
GO:0000974	Prp19 complex	0.001 %		0.85	0.00
GO:0005576	extracellular region	4.572 %		0.94	0.00
GO:0005615	extracellular space	0.249 %		0.84	0.00
 GO:0070062	<i>extracellular exosome</i>	0.300 %		0.57	0.58
GO:0005623	cell	64.133 %		0.98	0.00
GO:0005925	focal adhesion	0.016 %		0.93	0.00
GO:0016020	membrane	51.720 %		0.97	0.00
GO:0031012	extracellular matrix	0.156 %		0.93	0.00
GO:0043209	myelin sheath	0.005 %		0.91	0.00
GO:0009897	external side of plasma membrane	0.032 %		0.91	0.02
GO:0030175	filopodium	0.007 %		0.89	0.02
GO:0048471	perinuclear region of cytoplasm	0.050 %		0.81	0.02
GO:0000151	ubiquitin ligase complex	0.066 %		0.77	0.24
GO:0002102	podosome	0.002 %		0.67	0.25
GO:0022625	cytosolic large ribosomal subunit	0.008 %		0.64	0.26
GO:0005719	nuclear euchromatin	0.003 %		0.57	0.27
 GO:0000123	<i>histone acetyltransferase complex</i>	0.035 %		0.53	0.77
 GO:0005681	<i>spliceosomal complex</i>	0.053 %		0.54	0.61
 GO:0016607	<i>nuclear speck</i>	0.012 %		0.56	0.56
 GO:0005654	<i>nucleoplasm</i>	0.221 %		0.51	0.73
GO:0005829	cytosol	0.807 %		0.79	0.28

GO:0005768	endosome	0.077 %		0.62	0.29
GO:0032580	<i>Golgi cisterna membrane</i>	0.012 %	+	0.61	0.61
GO:0005777	peroxisome	0.063 %		0.61	0.30
GO:0005782	<i>peroxisomal matrix</i>	0.003 %	+	0.57	0.83
GO:0097542	ciliary tip	0.000 %		0.70	0.38
GO:0005634	nucleus	2.809 %		0.58	0.41
GO:0031090	<i>organelle membrane</i>	2.751 %	+	0.55	0.61
GO:0043231	<i>intracellular membrane-bounded organelle</i>	8.847 %	+	0.55	0.73
GO:0072562	blood microparticle	0.012 %		0.84	0.46
GO:0034364	<i>high-density lipoprotein particle</i>	0.003 %	+	0.75	0.62

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term ID	description	frequency	pin?	uniqueness	dispensability
GO:0001540	beta-amyloid binding	0.002 %		0.93	0.00
GO:0003824	catalytic activity	69.295 %		0.99	0.00
GO:0004867	serine-type endopeptidase inhibitor activity	0.030 %		0.93	0.00
GO:0016176	<i>superoxide-generating NADPH oxidase activator activity</i>	0.000 %		0.93	0.52
GO:0004887	thyroid hormone receptor activity	0.002 %		0.94	0.00
GO:0005215	transporter activity	12.041 %		0.96	0.00
GO:0015349	thyroid hormone transmembrane transporter activity	0.000 %		0.95	0.00
GO:0035605	peptidyl-cysteine S-nitrosylase activity	0.000 %		0.94	0.00
GO:0030429	kynureninase activity	0.006 %		0.94	0.01
GO:0004833	tryptophan 2,3-dioxygenase activity	0.004 %		0.90	0.01
GO:0016491	oxidoreductase activity	14.657 %		0.95	0.02
GO:0055131	C3HC4-type RING finger domain binding	0.000 %		0.81	0.02
GO:0008301	DNA binding, bending	0.001 %		0.91	0.02
GO:0003823	antigen binding	0.064 %		0.92	0.03
GO:0008201	heparin binding	0.013 %		0.91	0.03
GO:0008144	drug binding	0.260 %		0.92	0.04
GO:0005515	protein binding	2.482 %		0.91	0.05
GO:0020037	heme binding	1.765 %		0.91	0.07
GO:0004607	phosphatidylcholine-sterol O-acyltransferase activity	0.000 %		0.94	0.09
GO:0003831	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase activity	0.000 %		0.94	0.09
GO:0008892	guanine deaminase activity	0.015 %		0.91	0.13

GO:0004000	<i>adenosine deaminase activity</i>	0.061 %		0.91	0.71
GO:0044822	poly(A) RNA binding	0.135 %		0.91	0.13
GO:0008392	arachidonic acid epoxxygenase activity	0.000 %		0.88	0.14
GO:0035091	phosphatidylinositol binding	0.046 %		0.87	0.15
GO:1902122	<i>chenodeoxycholic acid binding</i>	0.000 %		0.87	0.69
GO:0032052	<i>bile acid binding</i>	0.000 %		0.87	0.59
GO:0000977	RNA polymerase II regulatory region sequence-specific DNA binding	0.021 %		0.91	0.17
GO:0004448	isocitrate dehydrogenase activity	0.053 %		0.90	0.19
GO:0051213	dioxygenase activity	0.413 %		0.89	0.25
GO:0005070	SH3/SH2 adaptor activity	0.001 %		0.79	0.28
GO:0034987	immunoglobulin receptor binding	0.000 %		0.77	0.30
GO:0051219	phosphoprotein binding	0.004 %		0.78	0.33
GO:0038181	bile acid receptor activity	0.000 %		0.94	0.35
GO:0008395	steroid hydroxylase activity	0.001 %		0.87	0.38
GO:0031625	ubiquitin protein ligase binding	0.019 %		0.77	0.39
GO:0046983	<i>protein dimerization activity</i>	0.735 %		0.73	0.53
GO:0042803	<i>protein homodimerization activity</i>	0.122 %		0.75	0.62
GO:0046965	retinoid X receptor binding	0.001 %		0.77	0.45
GO:0005178	<i>integrin binding</i>	0.004 %		0.75	0.50
GO:0048020	CCR chemokine receptor binding	0.001 %		0.75	0.46
GO:0008009	<i>chemokine activity</i>	0.006 %		0.73	0.88
GO:0016712	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen	0.029 %		0.86	0.49
GO:0070330	<i>aromatase activity</i>	0.004 %		0.86	0.53

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Frequent keywords within your set of GO terms:

metabolism multicellular results single-organism enzyme state compounds occasionally **stress-activated** macromolecular coo- expression secretion
polyhydric **transform** production -cooh compound ifng living cascade lipids plastids stimulus individual reactions cell steady **repetition** metabolic
organic response biopolymer **non-encoded** tertiary keto **shear** kynurenine assisting **organonitrogen** fairly vacuoles acidity chemical change **non-**
protein organism glycose level encapsulating organismal external **tensile** noncovalent substances result tn timer **macromolecule** organelle nucleobase-
containing nucleic elemental movement pathways process **sapk** bounded **cellular** macromolecules internal

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