

While parsing you can click empty space and and drag to zoom

interpretation of the coordinate axes?

Go term 1904628 was not found in the current version of the GeneOntology, dated 26:06:2015 07:17. GO term will be skipped.
Go term 1904582 was not found in the current version of the GeneOntology, dated 26:06:2015 07:17. GO term will be skipped.
Go term 1904640 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.



Hide/show dispensable GO terms

































Export results to text table (CSV)



Make R script for plotting

term ID	description	frequency	pin?	log ₁₀ p-value	uniqueness	dispensability
GO:0002376	immune system process	0.625 %		-3.4202	0.99	0.00
GO:0006957	complement activation, alternative pathway	0.000 %		-17.8928	0.61	0.00
GO:0007160	cell-matrix adhesion	0.015 %		-2.4539	0.97	0.00
GO:0008152	metabolic process	82.183 %		-4.6517	1.00	0.00
GO:0032981	mitochondrial respiratory chain complex I assembly	0.001 %		-4.4168	0.92	0.00
GO:0008637	<i>apoptotic mitochondrial changes</i>	0.006 %		-1.0525	0.83	0.73
GO:0019835	cytolysis	0.185 %		-3.3307	0.97	0.02
GO:0032920	putrescine acetylation	0.000 %		-1.1866	0.92	0.02
GO:0032918	<i>spermidine acetylation</i>	0.000 %		-1.1866	0.92	0.99
GO:0032919	<i>spermine acetylation</i>	0.000 %		-1.1866	0.92	0.98
GO:0007568	aging	0.013 %		-3.5884	0.92	0.03
GO:0008283	cell proliferation	0.105 %		-2.4571	0.95	0.04
GO:0031086	nuclear-transcribed mRNA catabolic process, deadenylation-independent decay	0.000 %		-2.7309	0.92	0.06

GO:000288	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	0.003 %		-1.2318	0.91	0.75
GO:0006099	tricarboxylic acid cycle	0.483 %		-6.0545	0.81	0.06
GO:0009060	aerobic respiration	1.366 %		-2.9631	0.87	0.77
GO:0006102	isocitrate metabolic process	0.013 %		-1.3550	0.87	1.10
GO:0022904	respiratory electron transport chain	0.881 %		-2.4270	0.87	0.82
GO:0006629	lipid metabolic process	3.094 %		-2.8044	0.91	0.13
GO:0010866	regulation of triglyceride biosynthetic process	0.001 %		-5.9957	0.80	0.13
GO:0046327	glycerol biosynthetic process from pyruvate	0.000 %		-3.2668	0.87	0.83
GO:0055088	lipid homeostasis	0.006 %		-3.5452	0.84	0.15
GO:0006475	internal protein amino acid acetylation	0.018 %		-2.9918	0.91	0.17
GO:0043066	negative regulation of apoptotic process	0.047 %		-3.3449	0.73	0.19
GO:2001243	negative regulation of intrinsic apoptotic signaling pathway	0.004 %		-1.8222	0.62	0.86
GO:0008630	intrinsic apoptotic signaling pathway in response to DNA damage	0.007 %		-1.1258	0.66	0.89
GO:1902172	regulation of keratinocyte apoptotic process	0.000 %		-1.4235	0.81	0.74
GO:0051402	neuron apoptotic process	0.013 %		-1.7586	0.87	0.72
GO:2000811	negative regulation of anoikis	0.001 %		-1.3328	0.77	0.79
GO:0043524	negative regulation of neuron apoptotic process	0.008 %		-1.0064	0.75	0.96
GO:0006915	apoptotic process	0.247 %		-1.8961	0.86	0.86
GO:0043434	response to peptide hormone	0.013 %		-4.2226	0.71	0.20
GO:0043200	response to amino acid	0.005 %		-2.1890	0.73	0.85
GO:0032869	cellular response to insulin stimulus	0.008 %		-1.2809	0.69	0.97
GO:0032868	response to insulin	0.010 %		-1.2996	0.72	0.98
GO:0071375	cellular response to peptide hormone stimulus	0.010 %		-1.2508	0.69	0.98
GO:0071377	cellular response to glucagon stimulus	0.000 %		-1.3328	0.73	0.83
GO:0071320	cellular response to cAMP	0.002 %		-2.1411	0.71	0.82
GO:0009725	response to hormone	0.077 %		-1.5439	0.70	0.84
GO:0070389	chaperone cofactor-dependent protein refolding	0.000 %		-1.0816	0.93	0.21
GO:0055114	oxidation-reduction process	15.044 %		-10.4353	0.90	0.21
GO:0051365	cellular response to potassium ion starvation	0.000 %		-2.3237	0.79	0.22
GO:0014823	response to activity	0.001 %		-1.6781	0.84	0.22
GO:0015986	ATP synthesis coupled proton transport	0.450 %		-2.9644	0.80	0.22
GO:0019346	transsulfuration	0.000 %		-3.9788	0.87	0.23
GO:0070493	thrombin receptor signaling pathway	0.001 %		-1.5625	0.72	0.23
GO:0010506	regulation of autophagy	0.078 %		-2.4593	0.79	0.23
GO:0007529	establishment of synaptic specificity at neuromuscular junction	0.000 %		-1.1307	0.90	0.25
GO:0051823	regulation of synapse structural plasticity	0.000 %		-1.0816	0.80	0.71
GO:0046038	GMP catabolic process	0.000 %		-1.1307	0.88	0.27
GO:0006104	succinyl-CoA metabolic process	0.000 %		-2.1133	0.93	0.29
GO:0014065	phosphatidylinositol 3-kinase signaling	0.005 %		-1.5591	0.71	0.29
GO:0006103	2-oxoglutarate metabolic process	0.010 %		-5.2557	0.86	0.30
GO:0044524	protein sulfhydration	0.000 %		-1.2515	0.93	0.30
GO:0018272	protein-pyridoxal-5-phosphate linkage via peptidyl-N6-pyridoxal phosphate-L-lysine	0.000 %		-1.2515	0.93	0.30
GO:0006979	response to oxidative stress	0.539 %		-3.2733	0.77	0.33
GO:0033539	fatty acid beta-oxidation using acyl-CoA dehydrogenase	0.013 %		-4.0975	0.83	0.35
GO:0006635	fatty acid beta-oxidation	0.053 %		-2.3372	0.82	0.91
GO:0043491	protein kinase B signaling	0.009 %		-1.2550	0.70	0.37
GO:2000427	positive regulation of apoptotic cell clearance	0.000 %		-9.3063	0.69	0.37
GO:0060100	positive regulation of phagocytosis, engulfment	0.000 %		-1.8530	0.69	0.84
GO:0048259	regulation of receptor-mediated endocytosis	0.003 %		-1.2515	0.76	0.80
GO:0045807	positive regulation of endocytosis	0.005 %		-1.0384	0.67	0.91
GO:0006910	phagocytosis, recognition	0.001 %		-2.0373	0.88	0.73
GO:0006911	phagocytosis, engulfment	0.001 %		-1.5428	0.88	0.92
GO:0036109	alpha-linolenic acid metabolic process	0.000 %		-1.0816	0.89	0.39
GO:0070814	hydrogen sulfide biosynthetic process	0.072 %		-1.6817	0.93	0.39
GO:0019550	glutamate catabolic process to aspartate	0.000 %		-1.0816	0.86	0.39
GO:0007260	tyrosine phosphorylation of STAT protein	0.003 %		-1.0379	0.69	0.40
GO:0006144	purine nucleobase metabolic process	0.215 %		-1.3328	0.86	0.40
GO:0008202	steroid metabolic process	0.040 %		-1.3747	0.90	0.40
GO:0010575	positive regulation of vascular endothelial growth factor production	0.001 %		-2.8703	0.69	0.41
GO:0009607	response to biotic stimulus	0.465 %		-2.4937	0.79	0.42
GO:0009069	serine family amino acid metabolic process	0.643 %		-1.3286	0.82	0.42
GO:0002507	tolerance induction	0.001 %		-1.3286	0.76	0.42
GO:0061158	3'-UTR-mediated mRNA destabilization	0.000 %		-1.4775	0.78	0.43
GO:0001666	response to hypoxia	0.019 %		-2.5565	0.80	0.44
GO:0071456	cellular response to hypoxia	0.004 %		-1.7537	0.72	0.92
GO:0006097	glyoxylate cycle	0.055 %		-1.6450	0.85	0.45
GO:0003342	proepicardium development	0.000 %		-1.1307	0.86	0.45
GO:0045600	positive regulation of fat cell differentiation	0.002 %		-4.1965	0.69	0.46
GO:0001525	angiogenesis	0.026 %		-1.0680	0.83	0.89
GO:0045766	positive regulation of angiogenesis	0.006 %		-3.0259	0.66	0.73
GO:0048008	platelet-derived growth factor receptor signaling pathway	0.003 %		-1.4955	0.71	0.46
GO:0045742	positive regulation of epidermal growth factor receptor signaling pathway	0.001 %		-1.2508	0.62	0.72
GO:0001659	temperature homeostasis	0.004 %		-1.1953	0.76	0.46
	positive regulation of transcription from RNA polymerase II promoter in response to acidic					

GO:0061402	pH	0.000 %		-2.4081	0.69	0.46
GO:0050726	positive regulation of interleukin-1 alpha biosynthetic process	0.000 %		-1.7203	0.72	0.47
GO:0032651	regulation of interleukin-1 beta production	0.002 %		-1.3286	0.77	0.75
GO:0000038	very long-chain fatty acid metabolic process	0.002 %		-1.1778	0.87	0.48
GO:0046204	nor-spermidine metabolic process	0.000 %		-1.1866	0.93	0.48
GO:0006094	gluconeogenesis	0.274 %		-1.2870	0.90	0.48
GO:0006006	glucose metabolic process	0.741 %		-1.1478	0.90	0.85
GO:0051289	protein homotetramerization	0.004 %		-1.6228	0.93	0.48
GO:0006977	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	0.001 %		-1.9123	0.59	0.49
GO:1901991	negative regulation of mitotic cell cycle phase transition	0.013 %		-1.3286	0.77	1.04
GO:0000082	G1/S transition of mitotic cell cycle	0.010 %		-1.4926	0.92	0.88
GO:0007050	cell cycle arrest	0.011 %		-1.1398	0.78	0.81
GO:0010884	positive regulation of lipid storage	0.001 %		-5.0353	0.72	0.49
GO:0051209	release of sequestered calcium ion into cytosol	0.004 %		-1.9550	0.72	0.76
GO:0051281	positive regulation of release of sequestered calcium ion into cytosol	0.001 %		-1.6632	0.65	1.03
GO:0007204	positive regulation of cytosolic calcium ion concentration	0.009 %		-1.0851	0.80	0.96
GO:0019343	cysteine biosynthetic process via cystathionine	0.005 %		-2.8736	0.84	0.50
GO:0019344	cysteine biosynthetic process	0.189 %		-1.8008	0.80	0.74
GO:0006563	L-serine metabolic process	0.264 %		-1.4014	0.82	0.82
GO:0006954	inflammatory response	0.099 %		-6.3820	0.78	0.51
GO:1903898	negative regulation of PERK-mediated unfolded protein response	0.000 %		-1.1866	0.63	0.51
GO:0030890	positive regulation of B cell proliferation	0.002 %		-2.8836	0.62	0.51
GO:0001935	endothelial cell proliferation	0.006 %		-1.2508	0.91	0.77
GO:0001937	negative regulation of endothelial cell proliferation	0.002 %		-1.0668	0.78	0.83
GO:0050871	positive regulation of B cell activation	0.004 %		-1.3550	0.63	0.93
GO:0042127	regulation of cell proliferation	0.080 %		-1.0280	0.78	0.92
GO:0042102	positive regulation of T cell proliferation	0.005 %		-2.1128	0.59	0.93
GO:0008284	positive regulation of cell proliferation	0.044 %		-1.1908	0.67	0.91
GO:0008285	negative regulation of cell proliferation	0.034 %		-2.5184	0.75	0.76
GO:0045577	regulation of B cell differentiation	0.001 %		-2.0539	0.65	0.89
GO:0045579	positive regulation of B cell differentiation	0.001 %		-1.2133	0.60	0.90
GO:0043372	positive regulation of CD4-positive, alpha-beta T cell differentiation	0.001 %		-1.3286	0.58	1.55
GO:0048146	positive regulation of fibroblast proliferation	0.003 %		-1.0063	0.71	0.77
GO:0070527	platelet aggregation	0.002 %		-1.3408	0.61	0.99
GO:0071332	cellular response to fructose stimulus	0.000 %		-2.1133	0.75	0.51
GO:0097403	cellular response to raffinose	0.001 %		-1.5463	0.73	0.77
GO:2001034	positive regulation of double-strand break repair via nonhomologous end joining	0.000 %		-1.0379	0.65	0.52
GO:0006105	succinate metabolic process	0.041 %		-3.7878	0.85	0.52
GO:0046655	folic acid metabolic process	0.011 %		-1.6938	0.83	0.53
GO:0006950	response to stress	4.119 %		-2.5176	0.76	0.53
GO:0001970	positive regulation of activation of membrane attack complex	0.000 %		-5.9957	0.58	0.53
GO:0050667	homocysteine metabolic process	0.009 %		-1.2906	0.84	0.53
GO:0031638	zymogen activation	0.014 %		-1.4512	0.91	0.53
GO:0007166	cell surface receptor signaling pathway	0.621 %		-1.2924	0.63	0.54
GO:0006531	aspartate metabolic process	0.016 %		-1.6588	0.84	0.54
GO:0006107	oxaloacetate metabolic process	0.017 %		-2.5252	0.86	0.54
GO:0030308	negative regulation of cell growth	0.008 %		-2.3964	0.75	0.54
GO:0001558	regulation of cell growth	0.021 %		-1.1109	0.78	0.89
GO:0032911	negative regulation of transforming growth factor beta1 production	0.000 %		-1.0379	0.76	0.55
GO:0033512	L-lysine catabolic process to acetyl-CoA via saccharopine	0.019 %		-1.8530	0.81	0.55
GO:0006935	chemotaxis	0.336 %		-3.3696	0.69	0.56
GO:0030335	positive regulation of cell migration	0.017 %		-1.9881	0.64	0.83
GO:0050900	leukocyte migration	0.014 %		-1.4559	0.76	0.82
GO:0002548	monocyte chemotaxis	0.002 %		-1.6632	0.62	0.90
GO:0090023	positive regulation of neutrophil chemotaxis	0.001 %		-2.0111	0.52	0.93
GO:0072679	thymocyte migration	0.000 %		-1.4235	0.80	0.74
GO:0048247	lymphocyte chemotaxis	0.001 %		-2.1202	0.63	0.87
GO:0060326	cell chemotaxis	0.016 %		-2.1128	0.65	0.78
GO:0030593	neutrophil chemotaxis	0.004 %		-2.4417	0.61	0.71
GO:0010759	positive regulation of macrophage chemotaxis	0.000 %		-1.4014	0.54	0.87
GO:0050853	B cell receptor signaling pathway	0.003 %		-2.7937	0.57	0.56
GO:1900182	positive regulation of protein localization to nucleus	0.005 %		-1.7800	0.70	0.56
GO:0042776	mitochondrial ATP synthesis coupled proton transport	0.000 %		-1.8530	0.86	0.57
GO:0006547	histidine metabolic process	0.448 %		-1.0816	0.82	0.58
GO:0070374	positive regulation of ERK1 and ERK2 cascade	0.007 %		-4.6990	0.55	0.58
GO:0001934	positive regulation of protein phosphorylation	0.039 %		-1.9074	0.65	0.88
GO:0045860	positive regulation of protein kinase activity	0.026 %		-1.4247	0.65	0.95
GO:1900153	positive regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	0.001 %		-1.3328	0.70	0.81
GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB signaling	0.011 %		-1.9753	0.58	0.82
GO:0070371	ERK1 and ERK2 cascade	0.010 %		-2.8381	0.66	0.80
GO:0051603	proteolysis involved in cellular protein catabolic process	0.218 %		-1.1275	0.87	0.72
GO:0000186	activation of MAPKK activity	0.004 %		-1.2207	0.56	0.84

GO:0045732	positive regulation of protein catabolic process	0.007 %		-1.4044	0.68	0.71
GO:0006958	complement activation, classical pathway	0.001 %		-17.7352	0.59	0.58
GO:0030449	regulation of complement activation	0.067 %		-8.1512	0.46	1.00
GO:0001798	positive regulation of type IIa hypersensitivity	0.000 %		-5.1141	0.62	0.76
GO:0050776	regulation of immune response	0.265 %		-1.5439	0.59	0.89
GO:0045087	innate immune response	0.137 %		-8.8268	0.68	0.80
GO:0002250	adaptive immune response	0.073 %		-1.0064	0.71	0.80
GO:0006955	immune response	0.380 %		-5.8928	0.68	0.83
GO:0006956	complement activation	0.069 %		-14.8570	0.51	0.76
GO:0032967	positive regulation of collagen biosynthetic process	0.001 %		-1.9605	0.66	0.58
GO:0019882	antigen processing and presentation	0.131 %		-2.4035	0.84	0.59
GO:0002474	antigen processing and presentation of peptide antigen via MHC class I	0.060 %		-1.1607	0.84	0.72
GO:0042590	antigen processing and presentation of exogenous peptide antigen via MHC class I	0.001 %		-1.1866	0.87	0.76
GO:0006749	glutathione metabolic process	0.123 %		-1.3944	0.89	0.59
GO:0007596	blood coagulation	0.015 %		-3.0026	0.63	0.59
GO:0002248	connective tissue replacement involved in inflammatory response wound healing	0.000 %		-1.0816	0.73	0.76
GO:0030168	platelet activation	0.007 %		-1.2132	0.61	0.95
GO:0030193	regulation of blood coagulation	0.005 %		-2.4540	0.59	0.93
GO:0007205	protein kinase C-activating G-protein coupled receptor signaling pathway	0.068 %		-1.4803	0.66	0.59
GO:0007186	G-protein coupled receptor signaling pathway	0.368 %		-1.0871	0.63	0.78
GO:0042632	cholesterol homeostasis	0.004 %		-1.2299	0.84	0.60
GO:0006631	fatty acid metabolic process	0.867 %		-1.4687	0.82	0.60
GO:0006120	mitochondrial electron transport, NADH to ubiquinone	0.107 %		-2.9544	0.83	0.61
GO:0006122	mitochondrial electron transport, ubiquinol to cytochrome c	0.004 %		-1.6450	0.86	0.80
GO:0051258	protein polymerization	0.107 %		-1.2906	0.92	0.62
GO:0006461	protein complex assembly	0.564 %		-1.0334	0.91	0.86
GO:0002367	cytokine production involved in immune response	0.004 %		-1.1307	0.65	0.62
GO:0071356	cellular response to tumor necrosis factor	0.005 %		-4.1618	0.71	0.62
GO:0070098	chemokine-mediated signaling pathway	0.009 %		-2.8157	0.60	0.73
GO:0007155	cell adhesion	0.564 %		-1.5846	0.97	0.62
GO:0032620	interleukin-17 production	0.002 %		-1.0816	0.86	0.62
GO:0010951	negative regulation of endopeptidase activity	0.083 %		-4.9066	0.71	0.63
GO:0008635	activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c	0.000 %		-2.0539	0.67	0.88
GO:0043547	positive regulation of GTPase activity	0.130 %		-2.5247	0.70	0.84
GO:0031639	plasminogen activation	0.009 %		-2.5349	0.91	0.92
GO:0006919	activation of cysteine-type endopeptidase activity involved in apoptotic process	0.005 %		-2.9799	0.63	0.82
GO:1900134	negative regulation of renin secretion into blood stream	0.000 %		-1.5463	0.70	0.63
GO:0045907	positive regulation of vasoconstriction	0.001 %		-1.3280	0.68	0.78
GO:0003105	negative regulation of glomerular filtration	0.000 %		-1.2515	0.75	0.83
GO:0060696	regulation of phospholipid catabolic process	0.000 %		-1.4235	0.79	0.63
GO:0046034	ATP metabolic process	5.374 %		-1.6150	0.82	0.63
GO:0031175	neuron projection development	0.043 %		-1.8705	0.76	0.64
GO:0008038	neuron recognition	0.002 %		-1.2515	0.81	0.81
GO:0021762	substantia nigra development	0.003 %		-1.5756	0.85	0.74
GO:0008631	intrinsic apoptotic signaling pathway in response to oxidative stress	0.002 %		-1.3778	0.62	0.64
GO:0016477	cell migration	0.069 %		-3.1192	0.86	0.64
GO:0006536	glutamate metabolic process	0.272 %		-3.5544	0.81	0.65
GO:0006560	proline metabolic process	0.180 %		-1.0816	0.83	0.70
GO:0042407	cristae formation	0.000 %		-1.1607	0.89	0.65
GO:0045987	positive regulation of smooth muscle contraction	0.001 %		-1.1778	0.69	0.65
GO:0051930	regulation of sensory perception of pain	0.001 %		-1.0668	0.78	0.71
GO:0032496	response to lipopolysaccharide	0.014 %		-4.1831	0.71	0.66
GO:0071223	cellular response to lipoteichoic acid	0.001 %		-1.7306	0.73	0.82
GO:0071222	cellular response to lipopolysaccharide	0.009 %		-1.0064	0.68	0.95
GO:0097305	response to alcohol	0.019 %		-1.2515	0.72	0.73
GO:0032355	response to estradiol	0.003 %		-3.3675	0.73	0.77
GO:0071385	cellular response to glucocorticoid stimulus	0.002 %		-1.1279	0.71	0.96
GO:0051384	response to glucocorticoid	0.004 %		-1.7556	0.73	0.78
GO:0071549	cellular response to dexamethasone stimulus	0.001 %		-1.0384	0.72	0.96
GO:0032570	response to progesterone	0.001 %		-3.7352	0.74	0.72
GO:0034097	response to cytokine	0.100 %		-1.2996	0.70	0.82
GO:0042742	defense response to bacterium	0.075 %		-2.1349	0.75	0.87
GO:0070561	vitamin D receptor signaling pathway	0.001 %		-2.7309	0.64	0.71
GO:0014070	response to organic cyclic compound	0.061 %		-2.4415	0.71	0.72
GO:0010828	positive regulation of glucose transport	0.002 %		-4.9830	0.71	0.66
GO:0070741	response to interleukin-6	0.001 %		-1.0379	0.75	0.66
GO:0009447	putrescine catabolic process	0.013 %		-1.1307	0.90	0.67
GO:2000778	positive regulation of interleukin-6 secretion	0.000 %		-1.3328	0.65	0.67
GO:0006855	drug transmembrane transport	0.162 %		-1.7586	0.66	0.67
GO:0015893	drug transport	0.194 %		-1.7693	0.68	0.97
GO:0071346	cellular response to interferon-gamma	0.003 %		-1.2096	0.64	0.68
GO:0070125	mitochondrial translational elongation	0.001 %		-1.0411	0.84	0.68
GO:0042493	response to drug	0.207 %		-1.4857	0.73	0.69

GO:0034341	response to interferon-gamma	0.004 %	-2.0919	0.65	0.69
GO:0006108	malate metabolic process	0.093 %	-1.0668	0.84	0.69
GO:0035999	tetrahydrofolate interconversion	0.102 %	-1.3271	0.83	0.69
GO:0001771	immunological synapse formation	0.000 %	-1.8100	0.80	0.69
GO:0045745	positive regulation of G-protein coupled receptor protein signaling pathway	0.001 %	-4.4486	0.62	0.70
GO:0071347	cellular response to interleukin-1	0.004 %	-2.3636	0.71	0.70

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








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While parsing your data, warning(s) were encountered:
Go term 1904628 was not found in the current version of the GeneOntology, dated 26:06:2015 07:17. GO term will be skipped.
Go term 1904582 was not found in the current version of the GeneOntology, dated 26:06:2015 07:17. GO term will be skipped.
Go term 1904640 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.

term ID	description	frequency	pin?	log ₁₀ p-value	uniqueness	dispensability
GO:0005576	extracellular region	4.572 %		-5.8601	0.96	0.00
GO:0005623	cell	64.133 %		-2.3132	0.99	0.00
GO:0005925	focal adhesion	0.016 %		-1.1781	0.96	0.00
GO:0016020	membrane	51.720 %		-2.5213	0.98	0.00
GO:0043209	myelin sheath	0.005 %		-12.5171	0.94	0.00
GO:0070062	extracellular exosome	0.300 %		-33.4377	0.53	0.00
GO:0016023	cytoplasmic membrane-bounded vesicle	0.132 %		-1.6784	0.57	0.88
GO:0031410	cytoplasmic vesicle	0.167 %		-1.9536	0.63	0.88
GO:0009897	external side of plasma membrane	0.032 %		-6.5607	0.86	0.02
GO:0005833	hemoglobin complex	0.014 %		-3.9666	0.68	0.02
GO:0043025	neuronal cell body	0.028 %		-1.4658	0.93	0.02
GO:0009986	cell surface	0.186 %		-4.3233	0.93	0.02
GO:0045177	apical part of cell	0.035 %		-1.4806	0.93	0.02
GO:0005938	cell cortex	0.094 %		-1.1678	0.71	0.22
GO:0097136	Bcl-2 family protein complex	0.001 %		-1.0257	0.83	0.22
GO:0002102	podosome	0.002 %		-1.4789	0.65	0.23
GO:0031094	platelet dense tubular network	0.001 %		-1.0694	0.73	0.25
GO:0005581	collagen trimer	0.057 %		-1.3125	0.80	0.28
GO:0005886	plasma membrane	13.934 %		-1.1910	0.86	0.32
GO:0005764	lysosome	0.049 %		-2.0371	0.62	0.33

GO:0005765	lysosomal membrane	0.024 %		-1.0519	0.54	0.94
GO:0005759	mitochondrial matrix	0.055 %		-13.3391	0.54	0.33
GO:0005654	nucleoplasm	0.221 %		-1.5706	0.55	0.77
GO:0005777	peroxisome	0.063 %		-2.2963	0.63	0.33
GO:0005778	peroxisomal membrane	0.027 %		-1.0066	0.55	0.95
GO:0031301	integral component of organelle membrane	0.076 %		-1.4281	0.59	0.35
GO:0005747	mitochondrial respiratory chain complex I	0.011 %		-3.7932	0.43	0.44
GO:0000276	mitochondrial proton-transporting ATP synthase complex, coupling factor F(o)	0.053 %		-1.9513	0.40	1.04
GO:0000275	mitochondrial proton-transporting ATP synthase complex, catalytic core F(1)	0.003 %		-2.0888	0.47	0.80
GO:0005753	mitochondrial proton-transporting ATP synthase complex	0.058 %		-3.5302	0.40	0.94
GO:0005751	mitochondrial respiratory chain complex IV	0.005 %		-1.5097	0.46	0.87
GO:0005750	mitochondrial respiratory chain complex III	0.006 %		-2.5417	0.45	0.87
GO:0072562	blood microparticle	0.012 %		-9.9747	0.87	0.46
GO:0005741	mitochondrial outer membrane	0.043 %		-1.3886	0.54	0.48
GO:0005739	mitochondrion	3.808 %		-13.9586	0.55	0.48
GO:0043231	intracellular membrane-bounded organelle	8.847 %		-1.4150	0.55	0.77
GO:0031904	endosome lumen	0.000 %		-2.0295	0.63	0.49
GO:0031902	late endosome membrane	0.006 %		-1.5746	0.56	0.72
GO:0005770	late endosome	0.019 %		-1.1501	0.62	0.78
GO:0042571	immunoglobulin complex, circulating	0.000 %		-1.6351	0.75	0.54
GO:0019815	B cell receptor complex	0.001 %		-1.0257	0.67	0.94
GO:0035631	CD40 receptor complex	0.001 %		-2.8373	0.69	0.55
GO:0042612	MHC class I protein complex	0.126 %		-1.5697	0.62	0.77
GO:0045252	oxoglutarate dehydrogenase complex	0.056 %		-1.6351	0.63	0.56
GO:0005615	extracellular space	0.249 %		-10.0783	0.88	0.58
GO:0005763	mitochondrial small ribosomal subunit	0.004 %		-1.1578	0.54	0.60
GO:0005577	fibrinogen complex	0.002 %		-1.4281	0.75	0.60
GO:0034361	very-low-density lipoprotein particle	0.002 %		-2.0030	0.78	0.60
GO:0005788	endoplasmic reticulum lumen	0.007 %		-1.5426	0.58	0.62
GO:0005758	mitochondrial intermembrane space	0.013 %		-1.5264	0.57	0.64
GO:0045244	succinate-CoA ligase complex (GDP-forming)	0.000 %		-1.4109	0.54	0.64
GO:0005743	mitochondrial inner membrane	2.192 %		-10.6108	0.46	0.64
GO:0043159	acrosomal matrix	0.000 %		-1.0257	0.60	0.67
GO:0042470	melanosome	0.004 %		-1.1744	0.64	0.69

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













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Go term 1904582 was not found in the current version of the GeneOntology, dated 26:06:2015 07:17. GO term will be skipped.
Go term 1904640 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.

term ID	description	frequency	pin?	log ₁₀ p-value	uniqueness	dispensability
GO:0003824	catalytic activity	69.295 %		-1.4412	1.00	0.00
GO:0004866	endopeptidase inhibitor activity	0.084 %		-7.6576	0.97	0.00
GO:0004867	<i>serine-type endopeptidase inhibitor activity</i>	0.030 %		-1.0922	0.97	0.93
GO:0005344	oxygen transporter activity	0.039 %		-2.3940	0.98	0.00
GO:0009055	electron carrier activity	2.493 %		-1.8926	0.99	0.00
GO:0016620	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	0.788 %		-5.5513	0.90	0.00
GO:0004029	<i>aldehyde dehydrogenase (NAD) activity</i>	0.042 %		-5.9747	0.92	0.72
GO:0031715	C5L2 anaphylatoxin chemotactic receptor binding	0.000 %		-6.9355	0.87	0.00
GO:0008009	<i>chemokine activity</i>	0.006 %		-3.5129	0.85	0.73
GO:0048020	<i>CCR chemokine receptor binding</i>	0.001 %		-2.2570	0.86	0.88
GO:0005172	<i>vascular endothelial growth factor receptor binding</i>	0.001 %		-1.0431	0.87	0.75
GO:0031731	<i>CCR6 chemokine receptor binding</i>	0.000 %		-1.4289	0.87	0.82
GO:0032216	glucosaminyl-phosphotidylinositol O-acyltransferase activity	0.000 %		-2.3344	0.76	0.01
GO:0004776	succinate-CoA ligase (GDP-forming) activity	0.000 %		-3.8827	0.96	0.01
GO:0004775	<i>succinate-CoA ligase (ADP-forming) activity</i>	0.072 %		-1.7796	0.95	0.71
GO:0004613	phosphoenolpyruvate carboxykinase (GTP) activity	0.010 %		-1.7041	0.95	0.02

GO:0004053	arginase activity	0.014 %		-2.5131	0.96	0.02
GO:0005542	folic acid binding	0.011 %		-3.4855	0.95	0.02
GO:0070026	nitric oxide binding	0.000 %		-1.4289	0.97	0.02
GO:0016829	lyase activity	4.488 %		-1.2259	0.96	0.03
GO:0003823	antigen binding	0.064 %		-2.9727	0.97	0.03
GO:0019825	oxygen binding	0.074 %		-2.6974	0.97	0.04
GO:0016491	oxidoreductase activity	14.657 %		-7.9508	0.96	0.04
GO:0005515	protein binding	2.482 %		-2.6122	0.96	0.05
GO:0008289	lipid binding	0.237 %		-1.2249	0.97	0.05
GO:0008144	drug binding	0.260 %		-1.9804	0.96	0.05
GO:0070025	carbon monoxide binding	0.000 %		-1.5518	0.97	0.06
GO:0044822	poly(A) RNA binding	0.135 %		-3.3372	0.96	0.06
GO:0034930	1-hydroxypyrene sulfotransferase activity	0.000 %		-1.0869	0.83	0.07
GO:0048037	cofactor binding	6.702 %		-3.8761	0.96	0.08
GO:0030351	inositol-1,3,4,5,6-pentakisphosphate 3-phosphatase activity	0.000 %		-1.0431	0.97	0.09
GO:0020037	heme binding	1.765 %		-1.4483	0.96	0.09
GO:0019809	spermidine binding	0.000 %		-1.1920	0.97	0.10
GO:0002060	purine nucleobase binding	0.000 %		-1.0869	0.96	0.11
GO:0000062	fatty-acyl-CoA binding	0.016 %		-2.9913	0.95	0.14
GO:0004252	serine-type endopeptidase activity	0.675 %		-2.1144	0.96	0.17
GO:0008403	25-hydroxycholecalciferol-24-hydroxylase activity	0.000 %		-1.5518	0.93	0.17
GO:0030342	<i>1-alpha,25-dihydroxyvitamin D3 24-hydroxylase activity</i>	0.000 %		-1.5518	0.93	0.95
GO:0008480	sarcosine dehydrogenase activity	0.000 %		-1.5518	0.94	0.18
GO:0004623	phospholipase A2 activity	0.011 %		-1.0205	0.96	0.21
GO:0008951	palmitoleoyl [acyl-carrier-protein]-dependent acyltransferase activity	0.000 %		-1.2569	0.80	0.21
GO:0019186	acyl-CoA N-acyltransferase activity	0.000 %		-1.2569	0.79	0.21
GO:0052890	oxidoreductase activity, acting on the CH-CH group of donors, with a flavin as acceptor	0.003 %		-3.5129	0.93	0.22
GO:0050421	nitrite reductase (NO-forming) activity	0.005 %		-1.5518	0.93	0.22
GO:0046941	azetidine-2-carboxylic acid acetyltransferase activity	0.000 %		-1.2569	0.79	0.25
GO:0004450	isocitrate dehydrogenase (NADP+) activity	0.050 %		-2.9470	0.92	0.26
GO:0004658	propionyl-CoA carboxylase activity	0.003 %		-2.7417	0.96	0.27
GO:0035925	mRNA 3'-UTR AU-rich region binding	0.000 %		-1.4875	0.96	0.28
GO:0044540	L-cystine L-cysteine-lyase (deaminating)	0.002 %		-1.1920	0.95	0.30
GO:0016751	S-succinyltransferase activity	0.030 %		-1.2569	0.67	0.30
GO:0030523	<i>dihydrolipoamide S-acyltransferase activity</i>	0.020 %		-1.2569	0.68	0.82
GO:0019705	<i>protein-cysteine S-myristoyltransferase activity</i>	0.007 %		-1.2569	0.69	0.77
GO:0019707	<i>protein-cysteine S-acyltransferase activity</i>	0.017 %		-1.1920	0.69	0.81
GO:0018030	<i>peptidyl-lysine N6-myristoyltransferase activity</i>	0.002 %		-1.2569	0.73	1.06
GO:0016418	<i>S-acetyltransferase activity</i>	0.020 %		-1.2569	0.68	0.82
GO:0016419	<i>S-malonyltransferase activity</i>	0.041 %		-1.2569	0.67	0.86
GO:0016750	<i>O-succinyltransferase activity</i>	0.016 %		-1.2569	0.68	0.84
GO:0016749	<i>N-succinyltransferase activity</i>	0.040 %		-1.2569	0.68	0.89
GO:0017091	AU-rich element binding	0.002 %		-1.1703	0.96	0.30
GO:0016752	sinapoyltransferase activity	0.000 %		-1.1920	0.78	0.31
GO:0004122	cystathionine beta-synthase activity	0.006 %		-1.3340	0.95	0.31
GO:0052858	peptidyl-lysine N-acetyltransferase activity, acting on acetyl phosphate as donor	0.000 %		-1.1920	0.76	0.32
GO:0051990	(R)-2-hydroxyglutarate dehydrogenase activity	0.000 %		-1.0869	0.94	0.34
GO:0016627	oxidoreductase activity, acting on the CH-CH group of donors	1.092 %		-2.3548	0.91	0.35
GO:0003954	NADH dehydrogenase activity	0.792 %		-1.6355	0.92	0.35
GO:0034738	lanosterol O-acyltransferase activity	0.000 %		-1.1920	0.77	0.36
GO:0034737	<i>ergosterol O-acyltransferase activity</i>	0.000 %		-1.0869	0.76	0.78
GO:0016454	C-palmitoyltransferase activity	0.001 %		-1.2569	0.73	0.36
GO:0019105	<i>N-palmitoyltransferase activity</i>	0.060 %		-1.2569	0.66	0.87
GO:0018031	<i>peptidyl-lysine N6-palmitoyltransferase activity</i>	0.026 %		-1.2569	0.68	1.05
GO:0016416	<i>O-palmitoyltransferase activity</i>	0.008 %		-1.1920	0.67	0.98
GO:0005102	receptor binding	0.416 %		-5.9914	0.85	0.37
GO:0016651	oxidoreductase activity, acting on NAD(P)H	1.351 %		-1.7796	0.91	0.37
GO:0019107	myristoyltransferase activity	0.002 %		-1.0431	0.74	0.38
GO:0016753	O-sinapoyltransferase activity	0.000 %		-1.2569	0.76	0.39
GO:0004361	glutaryl-CoA dehydrogenase activity	0.000 %		-1.5518	0.93	0.39
GO:0043741	L-2-aminoadipate N-acetyltransferase activity	0.007 %		-1.2569	0.72	0.41
GO:0034987	immunoglobulin receptor binding	0.000 %		-1.3877	0.88	0.41
GO:0015078	hydrogen ion transmembrane transporter activity	1.909 %		-1.3915	0.98	0.41
GO:0001965	G-protein alpha-subunit binding	0.001 %		-1.0477	0.89	0.41
GO:0016414	O-octanoyltransferase activity	0.000 %		-1.2569	0.75	0.41
GO:0045296	cadherin binding	0.003 %		-2.5449	0.87	0.45
GO:0005178	<i>integrin binding</i>	0.004 %		-1.7346	0.85	0.90
GO:0004145	diamine N-acetyltransferase activity	0.005 %		-1.1360	0.72	0.45
GO:0016406	carnitine O-acyltransferase activity	0.000 %		-1.2569	0.73	0.46
GO:0050660	flavin adenine dinucleotide binding	1.624 %		-1.4406	0.93	0.46
GO:0034915	2-methylhexanoyl-CoA C-acetyltransferase activity	0.058 %		-1.2569	0.70	0.46
GO:0051219	phosphoprotein binding	0.004 %		-1.3940	0.88	0.46
GO:0004772	sterol O-acyltransferase activity	0.000 %		-1.0038	0.74	0.47
GO:0016420	malonyltransferase activity	0.041 %		-1.2569	0.70	0.47
GO:0090595	acetyl-CoA:L-lysine N6-acetyltransferase	0.010 %		-1.2569	0.71	0.47

GO:0019955	cytokine binding	0.006 %		-1.2230	0.88	0.47
GO:0001948	glycoprotein binding	0.006 %		-1.2545	0.87	0.47
GO:0016748	succinyltransferase activity	0.086 %		-1.2569	0.69	0.49
GO:0018711	benzoyl acetate-CoA thiolase activity	0.058 %		-1.2569	0.70	0.49
GO:0018712	3-hydroxybutyryl-CoA thiolase activity	0.058 %		-1.2569	0.70	0.49
GO:0018713	3-ketopimelyl-CoA thiolase activity	0.058 %		-1.2569	0.70	0.49
GO:0034848	naphthyl-2-oxomethyl-succinyl-CoA succinyl transferase activity	0.058 %		-1.2569	0.70	0.49
GO:0034851	2,4,4-trimethyl-3-oxopentanoyl-CoA 2-C-propanoyl transferase activity	0.058 %		-1.2569	0.70	0.49
GO:0034919	butyryl-CoA 2-C-propionyltransferase activity	0.058 %		-1.2569	0.70	0.49
GO:0034945	2,6-dimethyl-5-methylene-3-oxo-heptanoyl-CoA C-acetyltransferase activity	0.058 %		-1.2569	0.70	0.49
GO:0043806	keto acid formate lyase activity	0.058 %		-1.2569	0.70	0.49
GO:0005518	collagen binding	0.014 %		-1.5273	0.87	0.50
GO:0001848	complement binding	0.018 %		-1.9091	0.87	0.51
GO:0004448	isocitrate dehydrogenase activity	0.053 %		-1.1360	0.92	0.51
GO:0016417	S-acyltransferase activity	0.107 %		-1.2569	0.69	0.52
GO:0016408	C-acyltransferase activity	0.096 %		-1.2569	0.69	0.52
GO:0043395	heparan sulfate proteoglycan binding	0.002 %		-1.0762	0.86	0.52
GO:0051922	cholesterol sulfotransferase activity	0.000 %		-1.0869	0.80	0.52
GO:0080131	hydroxyjasmonate sulfotransferase activity	0.000 %		-1.0038	0.83	0.54
GO:0003995	acyl-CoA dehydrogenase activity	0.368 %		-2.3328	0.91	0.56
GO:0016232	HNK-1 sulfotransferase activity	0.000 %		-1.0038	0.82	0.56
GO:0008201	heparin binding	0.013 %		-1.0235	0.95	0.57
GO:0016831	carboxy-lyase activity	0.915 %		-1.4942	0.94	0.59
GO:0042803	protein homodimerization activity	0.122 %		-1.8985	0.86	0.59
GO:0046982	<i>protein heterodimerization activity</i>	0.108 %		-1.3052	0.86	0.72
GO:0050698	proteoglycan sulfotransferase activity	0.000 %		-1.0431	0.81	0.59
GO:0016412	serine O-acyltransferase activity	0.051 %		-1.1920	0.67	0.60
GO:0016411	<i>acylglycerol O-acyltransferase activity</i>	0.074 %		-1.0431	0.66	0.80
GO:0032403	protein complex binding	0.146 %		-2.7098	0.86	0.60
GO:0042802	identical protein binding	0.154 %		-1.2577	0.86	0.60
GO:0080146	L-cysteine desulfhydrase activity	0.002 %		-1.0869	0.95	0.60
GO:0004147	dihydrolipoamide branched chain acyltransferase activity	0.000 %		-1.1920	0.74	0.63
GO:0016410	N-acyltransferase activity	1.192 %		-1.1215	0.64	0.64
GO:0018723	3-phenanthrol sulfotransferase activity	0.000 %		-1.0869	0.78	0.64
GO:0018727	<i>2-phenanthrol sulfotransferase activity</i>	0.000 %		-1.0869	0.78	1.00
GO:0018726	<i>9-phenanthrol sulfotransferase activity</i>	0.000 %		-1.0869	0.78	1.00
GO:0018724	<i>4-phenanthrol sulfotransferase activity</i>	0.000 %		-1.0869	0.78	1.00
GO:0018722	<i>1-phenanthrol sulfotransferase activity</i>	0.000 %		-1.0869	0.78	1.00
GO:0043849	Ras palmitoyltransferase activity	0.000 %		-1.1360	0.75	0.64
GO:0018721	trans-9R,10R-dihydrodiolphenanthrene sulfotransferase activity	0.000 %		-1.0869	0.80	0.65
GO:0018725	trans-3,4-dihydrodiolphenanthrene sulfotransferase activity	0.000 %		-1.0869	0.80	0.65
GO:0019111	phenanthrol sulfotransferase activity	0.000 %		-1.0869	0.80	0.65
GO:0034604	pyruvate dehydrogenase (NAD+) activity	0.012 %		-1.7409	0.92	0.66
GO:0031406	carboxylic acid binding	0.887 %		-3.0716	0.94	0.68
GO:0051287	NAD binding	1.108 %		-1.3928	0.94	0.68
GO:0050694	galactose 3-O-sulfotransferase activity	0.001 %		-1.0431	0.79	0.68
GO:0008374	O-acyltransferase activity	0.256 %		-1.1060	0.67	0.69

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Frequent keywords within your set of GO terms:

metabolism multicellular heterocycle up-regulation single-organism enzyme state ribose expression secretion ribonucleoside transform production il-1
compound g1/s cascade stimulus **sulphotransferase** individual reactions cell lipid **repetition** metabolic **organic** response
biopolymer frequency **sulfotransferase** unfolded non-encoded sparingly **coash** modulates degradative rate organonitrogen upregulation ribosomes
chemical change leucocyte **activation** surroundings tgf-b1 organism molecules level purine **tca** biochemical stimulation regulation organismal succinate-coa tensile

simply substances result leukocyte **upr** immune extent **macromolecule** movement pathways **process cellular** macromolecules



Keywords that correlate with the value you provided alongside GO terms:

schwann sizes 40-100 occupied **considerable** parental **been** lumen-facing **coated after** oligodendrocytes electrically sheath **limiting** fluid **varying participation**
trnas fusion taken proper **exosome** lectin **alternative virtually shapes considerably simply** concomitant **promote** microvesicles foreign rnas endotoxins
iga gel-like igm self **semiautonomous notably** nucleic insulating **antigen- igg concerned disposal capacity** supply myelin **properdin fine globulin**
encodes stroma direct those glial surrounds **self-reproducing** microparticles **exosomes invaginated** astrocyte **multivesicular antibody-coated material**
microbes replicating endosomal microparticle oligodendrocyte microvesicle folded **coding**

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