

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 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.

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 %		0.99	0.00
GO:0002377	immunoglobulin production	0.005 %		0.84	0.00
... GO:0002474	<i>antigen processing and presentation of peptide antigen via MHC class I</i>	0.060 %		0.82	0.72
... GO:0016064	<i>immunoglobulin mediated immune response</i>	0.007 %		0.68	0.62
... GO:0042590	<i>antigen processing and presentation of exogenous peptide antigen via MHC class I</i>	0.001 %		0.85	0.76
... GO:0030449	<i>regulation of complement activation</i>	0.067 %		0.38	1.00
... GO:0001798	<i>positive regulation of type IIa hypersensitivity</i>	0.000 %		0.53	0.83
... GO:0050776	<i>regulation of immune response</i>	0.265 %		0.50	0.89
... GO:0019882	<i>antigen processing and presentation</i>	0.131 %		0.82	0.61
... GO:0019886	<i>antigen processing and presentation of exogenous peptide antigen via MHC class II</i>	0.001 %		0.85	0.93
... GO:0002367	<i>cytokine production involved in immune response</i>	0.004 %		0.59	0.94
... GO:0045087	<i>innate immune response</i>	0.137 %		0.61	0.83
...					

GO:0002250	adaptive immune response	0.073 %		0.65	0.73
GO:0006958	complement activation, classical pathway	0.001 %		0.53	0.90
GO:0006955	immune response	0.380 %		0.62	0.83
GO:0006956	complement activation	0.069 %		0.43	0.77
GO:0007155	cell adhesion	0.564 %		0.96	0.00
GO:0031295	T cell costimulation	0.001 %		0.56	1.45
GO:0016337	single organismal cell-cell adhesion	0.020 %		0.91	0.64
GO:0042102	positive regulation of T cell proliferation	0.005 %		0.53	1.57
GO:0007160	cell-matrix adhesion	0.015 %		0.96	0.62
GO:0034116	positive regulation of heterotypic cell-cell adhesion	0.001 %		0.67	0.82
GO:0045581	negative regulation of T cell differentiation	0.002 %		0.51	1.58
GO:0045582	positive regulation of T cell differentiation	0.004 %		0.46	1.66
GO:0045059	positive thymic T cell selection	0.001 %		0.64	0.83
GO:0043372	positive regulation of CD4-positive, alpha-beta T cell differentiation	0.001 %		0.48	1.46
GO:0070527	platelet aggregation	0.002 %		0.54	0.91
GO:0008283	cell proliferation	0.105 %		0.95	0.00
GO:0014823	response to activity	0.001 %		0.81	0.00
GO:0019835	cytolysis	0.185 %		0.97	0.00
GO:0019953	sexual reproduction	0.051 %		0.98	0.00
GO:0030212	hyaluronan metabolic process	0.003 %		0.96	0.00
GO:0032092	positive regulation of protein binding	0.003 %		0.81	0.00
GO:0070814	hydrogen sulfide biosynthetic process	0.072 %		0.95	0.02
GO:0007010	cytoskeleton organization	0.151 %		0.92	0.02
GO:0051258	protein polymerization	0.107 %		0.93	0.86
GO:0000422	mitochondrion degradation	0.001 %		0.88	0.52
GO:0010506	regulation of autophagy	0.078 %		0.75	0.74
GO:0000045	autophagosome assembly	0.003 %		0.66	0.79
GO:0006461	protein complex assembly	0.564 %		0.92	0.52
GO:0042359	vitamin D metabolic process	0.001 %		0.94	0.03
GO:0042369	vitamin D catabolic process	0.000 %		0.91	0.86
GO:0032620	interleukin-17 production	0.002 %		0.83	0.03
GO:2000343	positive regulation of chemokine (C-X-C motif) ligand 2 production	0.000 %		0.64	0.55
GO:0061000	negative regulation of dendritic spine development	0.000 %		0.64	0.64
GO:0032911	negative regulation of transforming growth factor beta1 production	0.000 %		0.70	0.55
GO:0010575	positive regulation of vascular endothelial growth factor production	0.001 %		0.62	0.59
GO:0001817	regulation of cytokine production	0.125 %		0.65	0.84
GO:0050726	positive regulation of interleukin-1 alpha biosynthetic process	0.000 %		0.66	0.75
GO:0050663	cytokine secretion	0.010 %		0.75	0.66
GO:0032651	regulation of interleukin-1 beta production	0.002 %		0.71	0.66
GO:0032743	positive regulation of interleukin-2 production	0.001 %		0.63	0.58
GO:0000082	G1/S transition of mitotic cell cycle	0.010 %		0.92	0.04
GO:1901991	negative regulation of mitotic cell cycle phase transition	0.013 %		0.73	0.94
GO:0007050	cell cycle arrest	0.011 %		0.74	0.57
GO:0031659	positive regulation of cyclin-dependent protein serine/threonine kinase activity involved in G1/S transition of mitotic cell cycle	0.001 %		0.64	0.86
GO:0006977	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	0.001 %		0.53	1.04
GO:0007568	aging	0.013 %		0.88	0.04
GO:0006869	lipid transport	0.093 %		0.91	0.04
GO:0010884	positive regulation of lipid storage	0.001 %		0.67	0.75
GO:0006928	movement of cell or subcellular component	0.492 %		0.92	0.07
GO:0031639	plasminogen activation	0.009 %		0.92	0.08
GO:0008635	activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c	0.000 %		0.62	0.81
GO:0006915	apoptotic process	0.247 %		0.84	0.09
GO:2001243	negative regulation of intrinsic apoptotic signaling pathway	0.004 %		0.55	0.89
GO:2001238	positive regulation of extrinsic apoptotic signaling pathway	0.004 %		0.48	0.91
GO:2000352	negative regulation of endothelial cell apoptotic process	0.001 %		0.72	0.99
GO:0043065	positive regulation of apoptotic process	0.021 %		0.60	0.81
GO:0043066	negative regulation of apoptotic process	0.047 %		0.68	0.86
GO:0008637	apoptotic mitochondrial changes	0.006 %		0.83	0.75
GO:0008631	intrinsic apoptotic signaling pathway in response to oxidative stress	0.002 %		0.55	0.81
GO:0008630	intrinsic apoptotic signaling pathway in response to DNA damage	0.007 %		0.60	0.87
GO:1902172	regulation of keratinocyte apoptotic process	0.000 %		0.78	0.90
GO:1903912	negative regulation of endoplasmic reticulum stress-induced eIF2 alpha phosphorylation	0.013 %		0.52	0.92
GO:1903898	negative regulation of PERK-mediated unfolded protein response	0.000 %		0.56	0.73
GO:0042981	regulation of apoptotic process	0.129 %		0.71	0.93
GO:1902042	negative regulation of extrinsic apoptotic signaling pathway via death domain receptors	0.001 %		0.57	0.84
GO:0072577	endothelial cell apoptotic process	0.002 %		0.87	0.70
GO:0097192	extrinsic apoptotic signaling pathway in absence of ligand	0.005 %		0.61	0.77
GO:0070059	intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress	0.002 %		0.61	0.70
GO:0043280	positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	0.006 %		0.58	0.93
GO:0006919	activation of cysteine-type endopeptidase activity involved in apoptotic process	0.005 %		0.58	0.98
GO:0006402	mRNA catabolic process	0.113 %		0.91	0.09
	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	0.003 %		0.92	0.75

GO:000288				
GO:1900153	positive regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	0.001 %		0.670.80
GO:0010508	positive regulation of autophagy	0.006 %		0.640.83
GO:0031086	nuclear-transcribed mRNA catabolic process, deadenylation-independent decay	0.000 %		0.930.58
GO:0051603	proteolysis involved in cellular protein catabolic process	0.218 %		0.870.69
GO:0045732	positive regulation of protein catabolic process	0.007 %		0.630.91
GO:0043101	purine-containing compound salvage	0.157 %		0.940.15
GO:0042632	cholesterol homeostasis	0.004 %		0.810.16
GO:0051209	release of sequestered calcium ion into cytosol	0.004 %		0.680.96
GO:0051281	positive regulation of release of sequestered calcium ion into cytosol	0.001 %		0.591.03
GO:0042593	glucose homeostasis	0.010 %		0.800.62
GO:0002906	negative regulation of mature B cell apoptotic process	0.000 %		0.630.96
GO:0007204	positive regulation of cytosolic calcium ion concentration	0.009 %		0.770.64
GO:0051480	cytosolic calcium ion homeostasis	0.009 %		0.770.95
GO:0042985	negative regulation of amyloid precursor protein biosynthetic process	0.000 %		0.760.16
GO:0032026	response to magnesium ion	0.000 %		0.760.19
GO:0042542	response to hydrogen peroxide	0.057 %		0.660.82
GO:0070301	cellular response to hydrogen peroxide	0.052 %		0.620.67
GO:0051592	response to calcium ion	0.005 %		0.730.66
GO:0045943	positive regulation of transcription from RNA polymerase I promoter	0.000 %		0.690.19
GO:0032967	positive regulation of collagen biosynthetic process	0.001 %		0.610.50
GO:0045429	positive regulation of nitric oxide biosynthetic process	0.002 %		0.670.53
GO:0006910	phagocytosis, recognition	0.001 %		0.890.19
GO:0008038	neuron recognition	0.002 %		0.770.78
GO:0050853	B cell receptor signaling pathway	0.003 %		0.490.82
GO:0048259	regulation of receptor-mediated endocytosis	0.003 %		0.730.62
GO:0038096	Fc-gamma receptor signaling pathway involved in phagocytosis	0.000 %		0.500.75
GO:0031623	receptor internalization	0.004 %		0.870.56
GO:0045807	positive regulation of endocytosis	0.005 %		0.610.91
GO:0002092	positive regulation of receptor internalization	0.001 %		0.610.85
GO:2000427	positive regulation of apoptotic cell clearance	0.000 %		0.650.80
GO:0006911	phagocytosis, engulfment	0.001 %		0.880.78
GO:0070493	thrombin receptor signaling pathway	0.001 %		0.680.20
GO:0016477	cell migration	0.069 %		0.870.20
GO:0030335	positive regulation of cell migration	0.017 %		0.590.83
GO:0050900	leukocyte migration	0.014 %		0.750.68
GO:0002548	monocyte chemotaxis	0.002 %		0.570.81
GO:0090023	positive regulation of neutrophil chemotaxis	0.001 %		0.430.93
GO:0072679	thymocyte migration	0.000 %		0.790.85
GO:0072678	T cell migration	0.002 %		0.760.73
GO:0048247	lymphocyte chemotaxis	0.001 %		0.570.94
GO:0060326	cell chemotaxis	0.016 %		0.600.82
GO:0030593	neutrophil chemotaxis	0.004 %		0.550.90
GO:0051085	chaperone mediated protein folding requiring cofactor	0.013 %		0.920.20
GO:0001666	response to hypoxia	0.019 %		0.760.22
GO:0071456	cellular response to hypoxia	0.004 %		0.670.92
GO:0070588	calcium ion transmembrane transport	0.036 %		0.890.24
GO:0036149	phosphatidylinositol acyl-chain remodeling	0.000 %		0.930.26
GO:0051365	cellular response to potassium ion starvation	0.000 %		0.750.27
GO:0007584	response to nutrient	0.004 %		0.720.60
GO:0010468	regulation of gene expression	9.331 %		0.710.29
GO:0014065	phosphatidylinositol 3-kinase signaling	0.005 %		0.660.29
GO:0006508	proteolysis	3.705 %		0.920.30
GO:0007529	establishment of synaptic specificity at neuromuscular junction	0.000 %		0.920.31
GO:0006475	internal protein amino acid acetylation	0.018 %		0.900.31
GO:0009607	response to biotic stimulus	0.465 %		0.750.32
GO:0007166	cell surface receptor signaling pathway	0.621 %		0.580.75
GO:0007165	signal transduction	3.804 %		0.530.69
GO:0006950	response to stress	4.119 %		0.710.52
GO:0071236	cellular response to antibiotic	0.001 %		0.720.33
GO:0043418	homocysteine catabolic process	0.000 %		0.920.34
GO:1990441	negative regulation of transcription from RNA polymerase II promoter in response to endoplasmic reticulum stress	0.000 %		0.710.34
GO:0043488	regulation of mRNA stability	0.003 %		0.790.35
GO:0001934	positive regulation of protein phosphorylation	0.039 %		0.590.88
GO:0045860	positive regulation of protein kinase activity	0.026 %		0.600.95
GO:0010628	positive regulation of gene expression	0.200 %		0.620.93
GO:0045893	positive regulation of transcription, DNA-templated	0.193 %		0.590.89
GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	0.009 %		0.620.89
GO:0043547	positive regulation of GTPase activity	0.130 %		0.620.84
GO:0061158	3'-UTR-mediated mRNA destabilization	0.000 %		0.750.84
GO:0010951	negative regulation of endopeptidase activity	0.083 %		0.660.80
GO:0043410	positive regulation of MAPK cascade	0.024 %		0.450.95

GO:0006417	regulation of translation	0.496 %		0.69	0.67
GO:0006469	negative regulation of protein kinase activity	0.074 %		0.66	0.92
GO:0045727	positive regulation of translation	0.047 %		0.60	0.80
GO:0034976	response to endoplasmic reticulum stress	0.011 %		0.75	0.35
GO:0050936	xanthophore differentiation	0.000 %		0.87	0.35
GO:0048757	pigment granule maturation	0.001 %		0.68	1.00
GO:0035646	endosome to melanosome transport	0.001 %		0.65	0.77
GO:0007259	JAK-STAT cascade	0.007 %		0.66	0.36
GO:0007260	tyrosine phosphorylation of STAT protein	0.003 %		0.65	0.36
GO:0043491	protein kinase B signaling	0.009 %		0.66	0.37
GO:0009395	phospholipid catabolic process	0.023 %		0.89	0.39
GO:0030198	extracellular matrix organization	0.015 %		0.90	0.39
GO:0003342	proepicardium development	0.000 %		0.82	0.39
GO:0060509	Type I pneumocyte differentiation	0.001 %		0.79	0.52
GO:0038066	p38MAPK cascade	0.001 %		0.64	0.40
GO:0046330	positive regulation of JNK cascade	0.004 %		0.48	0.89
GO:1900745	positive regulation of p38MAPK cascade	0.001 %		0.51	0.75
GO:0070371	ERK1 and ERK2 cascade	0.010 %		0.62	0.72
GO:0009611	response to wounding	0.111 %		0.75	0.40
GO:2000680	regulation of rubidium ion transport	0.000 %		0.79	0.40
GO:1900182	positive regulation of protein localization to nucleus	0.005 %		0.64	0.58
GO:2000778	positive regulation of interleukin-6 secretion	0.000 %		0.59	0.67
GO:0002792	negative regulation of peptide secretion	0.002 %		0.73	0.52
GO:0090277	positive regulation of peptide hormone secretion	0.003 %		0.58	0.88
GO:0010828	positive regulation of glucose transport	0.002 %		0.66	0.57
GO:0072703	cellular response to methyl methanesulfonate	0.000 %		0.72	0.40
GO:0046327	glycerol biosynthetic process from pyruvate	0.000 %		0.92	0.40
GO:0010866	regulation of triglyceride biosynthetic process	0.001 %		0.80	0.83
GO:0001558	regulation of cell growth	0.021 %		0.76	0.40
GO:0030308	negative regulation of cell growth	0.008 %		0.72	0.89
GO:0042060	wound healing	0.025 %		0.74	0.40
GO:0001970	positive regulation of activation of membrane attack complex	0.000 %		0.51	0.60
GO:0072378	blood coagulation, fibrin clot formation	0.000 %		0.60	0.83
GO:0050727	regulation of inflammatory response	0.080 %		0.56	0.88
GO:0042730	fibrinolysis	0.001 %		0.52	0.86
GO:0002248	connective tissue replacement involved in inflammatory response wound healing	0.000 %		0.67	0.63
GO:0007596	blood coagulation	0.015 %		0.55	0.79
GO:0030168	platelet activation	0.007 %		0.54	0.95
GO:0030193	regulation of blood coagulation	0.005 %		0.51	0.93
GO:0071409	cellular response to cycloheximide	0.000 %		0.71	0.42
GO:0071364	cellular response to epidermal growth factor stimulus	0.001 %		0.68	0.59
GO:0071404	cellular response to low-density lipoprotein particle stimulus	0.000 %		0.70	0.50
GO:0097067	cellular response to thyroid hormone stimulus	0.001 %		0.68	0.56
GO:0007265	Ras protein signal transduction	0.101 %		0.61	0.43
GO:0016601	Rac protein signal transduction	0.004 %		0.67	0.71
GO:0043113	receptor clustering	0.002 %		0.87	0.44
GO:2001020	regulation of response to DNA damage stimulus	0.044 %		0.59	0.44
GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB signaling	0.011 %		0.51	0.72
GO:0070374	positive regulation of ERK1 and ERK2 cascade	0.007 %		0.48	0.84
GO:0034136	negative regulation of toll-like receptor 2 signaling pathway	0.000 %		0.51	0.54
GO:1903378	positive regulation of oxidative stress-induced neuron intrinsic apoptotic signaling pathway	0.000 %		0.53	0.61
GO:0009968	negative regulation of signal transduction	0.177 %		0.52	0.70
GO:0000186	activation of MAPKK activity	0.004 %		0.49	0.79
GO:0045745	positive regulation of G-protein coupled receptor protein signaling pathway	0.001 %		0.54	0.52
GO:0046597	negative regulation of viral entry into host cell	0.001 %		0.75	0.44
GO:0010760	negative regulation of macrophage chemotaxis	0.000 %		0.50	0.71
GO:0010759	positive regulation of macrophage chemotaxis	0.000 %		0.46	0.93
GO:0006954	inflammatory response	0.099 %		0.73	0.45
GO:0071222	cellular response to lipopolysaccharide	0.009 %		0.62	0.95
GO:0050829	defense response to Gram-negative bacterium	0.007 %		0.73	0.83
GO:0032496	response to lipopolysaccharide	0.014 %		0.65	0.87
GO:0006957	complement activation, alternative pathway	0.000 %		0.54	0.51
GO:0006953	acute-phase response	0.002 %		0.77	0.58
GO:0042742	defense response to bacterium	0.075 %		0.70	0.73
GO:0035456	response to interferon-beta	0.001 %		0.71	0.45
GO:0070741	response to interleukin-6	0.001 %		0.71	0.60
GO:0043200	response to amino acid	0.005 %		0.68	0.79
GO:0001961	positive regulation of cytokine-mediated signaling pathway	0.001 %		0.46	0.65
GO:0034341	response to interferon-gamma	0.004 %		0.58	0.68
GO:0032869	cellular response to insulin stimulus	0.008 %		0.64	0.97
GO:0032868	response to insulin	0.010 %		0.67	0.98
GO:0019221	cytokine-mediated signaling pathway	0.088 %		0.49	0.84

GO:0071356	cellular response to tumor necrosis factor	0.005 %		0.66	0.70
GO:0071375	cellular response to peptide hormone stimulus	0.010 %		0.63	0.98
GO:0071385	cellular response to glucocorticoid stimulus	0.002 %		0.66	0.96
GO:0051384	response to glucocorticoid	0.004 %		0.68	0.73
GO:0071320	cellular response to cAMP	0.002 %		0.66	0.94
GO:1901653	cellular response to peptide	0.011 %		0.64	0.98
GO:0071346	cellular response to interferon-gamma	0.003 %		0.57	0.67
GO:0071347	cellular response to interleukin-1	0.004 %		0.66	0.65
GO:0032526	response to retinoic acid	0.005 %		0.68	0.73
GO:0071549	cellular response to dexamethasone stimulus	0.001 %		0.67	0.96
GO:0009725	response to hormone	0.077 %		0.64	0.83
GO:0043434	response to peptide hormone	0.013 %		0.66	0.85
GO:0032570	response to progesterone	0.001 %		0.70	0.65
GO:0034097	response to cytokine	0.100 %		0.65	0.82
GO:0060337	type I interferon signaling pathway	0.063 %		0.41	0.96
GO:0035691	macrophage migration inhibitory factor signaling pathway	0.000 %		0.62	0.53
GO:0051591	response to cAMP	0.003 %		0.68	0.67
GO:0070098	chemokine-mediated signaling pathway	0.009 %		0.54	0.85
GO:0010803	regulation of tumor necrosis factor-mediated signaling pathway	0.001 %		0.56	0.89
GO:0070542	response to fatty acid	0.001 %		0.70	0.51
GO:0014070	response to organic cyclic compound	0.061 %		0.66	0.67
GO:0002606	positive regulation of dendritic cell antigen processing and presentation	0.000 %		0.65	0.45
GO:0042493	response to drug	0.207 %		0.68	0.45
GO:0006935	chemotaxis	0.336 %		0.63	0.69
GO:0045661	regulation of myoblast differentiation	0.002 %		0.73	0.45
GO:1901741	positive regulation of myoblast fusion	0.000 %		0.62	0.82
GO:0045600	positive regulation of fat cell differentiation	0.002 %		0.61	0.65
GO:0071332	cellular response to fructose stimulus	0.000 %		0.71	0.46
GO:0097403	cellular response to raffinose	0.001 %		0.68	0.77
GO:0032474	otolith morphogenesis	0.000 %		0.81	0.46
GO:0061075	positive regulation of neural retina development	0.000 %		0.67	0.53
GO:0021915	neural tube development	0.012 %		0.79	0.89
GO:0001701	in utero embryonic development	0.022 %		0.79	0.67
GO:0061402	positive regulation of transcription from RNA polymerase II promoter in response to acidic pH	0.000 %		0.64	0.46
GO:0008285	negative regulation of cell proliferation	0.034 %		0.73	0.46
GO:0008284	positive regulation of cell proliferation	0.044 %		0.63	0.91
GO:0048146	positive regulation of fibroblast proliferation	0.003 %		0.67	0.77
GO:0002576	platelet degranulation	0.001 %		0.89	0.46
GO:0051639	actin filament network formation	0.000 %		0.91	0.47
GO:2000249	regulation of actin cytoskeleton reorganization	0.001 %		0.79	0.58
GO:0002507	tolerance induction	0.001 %		0.71	0.47
GO:0036035	osteoclast development	0.001 %		0.69	0.59
GO:0050871	positive regulation of B cell activation	0.004 %		0.57	0.91
GO:0030890	positive regulation of B cell proliferation	0.002 %		0.57	0.93
GO:0045657	positive regulation of monocyte differentiation	0.000 %		0.54	0.72
GO:0045577	regulation of B cell differentiation	0.001 %		0.58	0.86
GO:0045579	positive regulation of B cell differentiation	0.001 %		0.52	0.83
GO:0030183	B cell differentiation	0.006 %		0.65	0.75
GO:0007605	sensory perception of sound	0.008 %		0.82	0.47
GO:0045907	positive regulation of vasoconstriction	0.001 %		0.61	0.71
GO:1900134	negative regulation of renin secretion into blood stream	0.000 %		0.65	0.83
GO:0051930	regulation of sensory perception of pain	0.001 %		0.73	0.62
GO:0003105	negative regulation of glomerular filtration	0.000 %		0.70	0.65
GO:0048873	homeostasis of number of cells within a tissue	0.002 %		0.72	0.48
GO:0071361	cellular response to ethanol	0.000 %		0.69	0.48
GO:0033280	response to vitamin D	0.001 %		0.68	0.72
GO:0032355	response to estradiol	0.003 %		0.68	0.79
GO:0070561	vitamin D receptor signaling pathway	0.001 %		0.58	0.91
GO:0050667	homocysteine metabolic process	0.009 %		0.91	0.49
GO:0019343	cysteine biosynthetic process via cystathionine	0.005 %		0.90	0.53
GO:0006535	cysteine biosynthetic process from serine	0.128 %		0.89	0.80
GO:0006563	L-serine metabolic process	0.264 %		0.90	0.63
GO:0071223	cellular response to lipoteichoic acid	0.001 %		0.68	0.49
GO:0031100	organ regeneration	0.001 %		0.81	0.49
GO:2000347	positive regulation of hepatocyte proliferation	0.000 %		0.60	0.85
GO:0014004	microglia differentiation	0.000 %		0.70	0.78
GO:0001889	liver development	0.006 %		0.79	0.57
GO:0045595	regulation of cell differentiation	0.090 %		0.69	0.69
GO:0001525	angiogenesis	0.026 %		0.78	0.63
GO:0045766	positive regulation of angiogenesis	0.006 %		0.57	0.89
GO:0048709	oligodendrocyte differentiation	0.005 %		0.77	0.57
GO:0007229	integrin-mediated signaling pathway	0.015 %		0.63	0.50

... GO:1900746	regulation of vascular endothelial growth factor signaling pathway	0.001 %		0.57	0.74
... GO:0048008	platelet-derived growth factor receptor signaling pathway	0.003 %		0.66	0.81
... GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	0.040 %		0.61	0.61
... GO:0007186	G-protein coupled receptor signaling pathway	0.368 %		0.57	0.75
GO:0035690	cellular response to drug	0.004 %		0.70	0.50

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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.

 Hide/show dispensable GO terms

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term ID	description	frequency	pin?	uniqueness	dispensability
GO:0005576	extracellular region	4.572 %		0.97	0.00
GO:0005615	extracellular space	0.249 %		0.85	0.00
GO:0005623	cell	64.133 %		0.99	0.00
GO:0005911	cell-cell junction	0.091 %		0.94	0.00
GO:0005925	<i>focal adhesion</i>	0.016 %		0.94	0.82
GO:0016020	membrane	51.720 %		0.98	0.00
GO:0030054	cell junction	0.154 %		0.96	0.00
GO:0031252	cell leading edge	0.034 %		0.94	0.00
GO:0035693	NOS2-CD74 complex	0.000 %		0.87	0.00
GO:0005901	caveola	0.008 %		0.78	0.02
GO:0009986	cell surface	0.186 %		0.94	0.02
GO:0048471	perinuclear region of cytoplasm	0.050 %		0.83	0.02
GO:0042995	cell projection	1.485 %		0.93	0.03
GO:0031094	platelet dense tubular network	0.001 %		0.80	0.05
GO:0005622	intracellular	46.136 %		0.93	0.06
GO:0016021	integral component of membrane	35.230 %		0.91	0.12
GO:0097136	Bcl-2 family protein complex	0.001 %		0.86	0.18
GO:0035692	macrophage migration inhibitory factor receptor complex	0.000 %		0.84	0.18
GO:0005764	lysosome	0.049 %		0.71	0.23
GO:0043202	<i>lysosomal lumen</i>	0.001 %		0.73	0.76

GO:0005765	lysosomal membrane	0.024 %		0.65	0.94
GO:0043235	receptor complex	0.050 %		0.84	0.23
GO:0005938	cell cortex	0.094 %		0.76	0.24
GO:0002102	podosome	0.002 %		0.71	0.25
GO:0031410	cytoplasmic vesicle	0.167 %		0.67	0.26
GO:0070062	extracellular exosome	0.300 %		0.58	1.04
GO:0031089	platelet dense granule lumen	0.000 %		0.65	0.55
GO:0031091	platelet alpha granule	0.002 %		0.65	0.69
GO:1903561	extracellular vesicle	0.510 %		0.61	0.92
GO:0042470	melanosome	0.004 %		0.68	0.65
GO:0031301	integral component of organelle membrane	0.076 %		0.71	0.30
GO:0005768	endosome	0.077 %		0.66	0.30
GO:0000139	Golgi membrane	0.090 %		0.62	0.76
GO:0031902	late endosome membrane	0.006 %		0.64	0.78
GO:0030660	Golgi-associated vesicle membrane	0.025 %		0.56	0.87
GO:0005770	late endosome	0.019 %		0.67	0.63
GO:0097487	multivesicular body, internal vesicle	0.000 %		0.66	0.65
GO:0005794	Golgi apparatus	0.265 %		0.64	0.75
GO:0022625	cytosolic large ribosomal subunit	0.008 %		0.70	0.31
GO:0030529	ribonucleoprotein complex	6.088 %		0.77	0.32
GO:0005886	plasma membrane	13.934 %		0.82	0.32
GO:0005654	nucleoplasm	0.221 %		0.70	0.38
GO:0043231	intracellular membrane-bounded organelle	8.847 %		0.68	0.51
GO:0009897	external side of plasma membrane	0.032 %		0.77	0.39
GO:0009898	cytoplasmic side of plasma membrane	0.051 %		0.76	0.86
GO:0005579	membrane attack complex	0.002 %		0.70	0.57
GO:0005887	integral component of plasma membrane	1.253 %		0.74	0.54
GO:0042613	MHC class II protein complex	0.123 %		0.65	0.80
GO:0031234	extrinsic component of cytoplasmic side of plasma membrane	0.014 %		0.75	0.92
GO:0042612	MHC class I protein complex	0.126 %		0.65	1.04
GO:0035631	CD40 receptor complex	0.001 %		0.70	0.63
GO:0072562	blood microparticle	0.012 %		0.84	0.46
GO:0019815	B cell receptor complex	0.001 %		0.69	0.94
GO:0005577	fibrinogen complex	0.002 %		0.76	0.60
GO:0034364	high-density lipoprotein particle	0.003 %		0.75	1.28
GO:0034361	very-low-density lipoprotein particle	0.002 %		0.75	0.60
GO:0042571	immunoglobulin complex, circulating	0.000 %		0.76	0.54

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term ID	description	frequency	pin?	uniqueness	dispensability
GO:0004550	nucleoside diphosphate kinase activity	0.046 %		0.96	0.00
GO:0004860	protein kinase inhibitor activity	0.005 %		0.89	0.00
... GO:0005096	<i>GTPase activator activity</i>	0.075 %		0.88	0.63
... GO:0004866	<i>endopeptidase inhibitor activity</i>	0.084 %		0.87	0.80
... GO:0004867	<i>serine-type endopeptidase inhibitor activity</i>	0.030 %		0.88	0.93
... GO:0004857	<i>enzyme inhibitor activity</i>	0.161 %		0.88	0.79
GO:0004871	signal transducer activity	2.025 %		0.93	0.00
... GO:0004896	<i>cytokine receptor activity</i>	0.014 %		0.93	0.60
... GO:0004888	<i>transmembrane signaling receptor activity</i>	0.371 %		0.93	0.80
GO:0005262	calcium channel activity	0.018 %		0.97	0.00
GO:0070026	nitric oxide binding	0.000 %		0.94	0.00
GO:0050421	nitrite reductase (NO-forming) activity	0.005 %		0.96	0.01
GO:0004122	cystathionine beta-synthase activity	0.006 %		0.96	0.01
GO:0004623	phospholipase A2 activity	0.011 %		0.95	0.01
GO:0070025	carbon monoxide binding	0.000 %		0.93	0.02
GO:0035718	macrophage migration inhibitory factor binding	0.000 %		0.72	0.02
GO:0005537	mannose binding	0.001 %		0.93	0.02
GO:0035925	mRNA 3'-UTR AU-rich region binding	0.000 %		0.92	0.02
GO:0003823	antigen binding	0.064 %		0.93	0.03
GO:0001540	beta-amyloid binding	0.002 %		0.91	0.03
...					

GO:0042605	<i>peptide antigen binding</i>	0.062 %		0.89	0.76
GO:0008144	drug binding	0.260 %		0.92	0.04
GO:0030246	carbohydrate binding	0.825 %		0.92	0.05
GO:0005515	protein binding	2.482 %		0.91	0.06
GO:0031406	carboxylic acid binding	0.887 %		0.90	0.07
GO:0008403	25-hydroxycholecalciferol-24-hydroxylase activity	0.000 %		0.93	0.14
GO:0030342	<i>1-alpha,25-dihydroxyvitamin D3 24-hydroxylase activity</i>	0.000 %		0.93	0.95
GO:0043565	sequence-specific DNA binding	1.944 %		0.90	0.15
GO:0004197	cysteine-type endopeptidase activity	0.102 %		0.94	0.15
GO:0004252	<i>serine-type endopeptidase activity</i>	0.675 %		0.94	0.66
GO:0005509	calcium ion binding	0.365 %		0.90	0.15
GO:0004731	purine-nucleoside phosphorylase activity	0.056 %		0.96	0.15
GO:0008201	heparin binding	0.013 %		0.90	0.18
GO:0043395	<i>heparan sulfate proteoglycan binding</i>	0.002 %		0.66	0.51
GO:0070180	large ribosomal subunit rRNA binding	0.084 %		0.90	0.27
GO:0001965	G-protein alpha-subunit binding	0.001 %		0.70	0.28
GO:0030145	manganese ion binding	0.545 %		0.90	0.29
GO:0034987	immunoglobulin receptor binding	0.000 %		0.68	0.29
GO:0043015	gamma-tubulin binding	0.002 %		0.69	0.31
GO:0004613	phosphoenolpyruvate carboxykinase (GTP) activity	0.010 %		0.96	0.31
GO:0033897	ribonuclease T2 activity	0.018 %		0.95	0.32
GO:0051219	phosphoprotein binding	0.004 %		0.68	0.34
GO:0045296	cadherin binding	0.003 %		0.67	0.35
GO:0005178	<i>integrin binding</i>	0.004 %		0.62	0.90
GO:0019955	cytokine binding	0.006 %		0.67	0.36
GO:0017124	SH3 domain binding	0.006 %		0.67	0.37
GO:0001948	glycoprotein binding	0.006 %		0.67	0.37
GO:0019903	protein phosphatase binding	0.006 %		0.66	0.37
GO:0019901	<i>protein kinase binding</i>	0.053 %		0.62	0.76
GO:0044389	<i>ubiquitin-like protein ligase binding</i>	0.019 %		0.64	0.67
GO:0008022	protein C-terminus binding	0.009 %		0.66	0.38
GO:0050839	cell adhesion molecule binding	0.010 %		0.66	0.39
GO:0044822	poly(A) RNA binding	0.135 %		0.90	0.39
GO:0001848	complement binding	0.018 %		0.65	0.40
GO:0031715	C5L2 anaphylatoxin chemotactic receptor binding	0.000 %		0.67	0.41
GO:0005518	collagen binding	0.014 %		0.64	0.41
GO:0042289	MHC class II protein binding	0.001 %		0.66	0.44
GO:0042658	<i>MHC class II protein binding, via antigen binding groove</i>	0.000 %		0.65	0.86
GO:0005172	vascular endothelial growth factor receptor binding	0.001 %		0.65	0.45
GO:0008009	<i>chemokine activity</i>	0.006 %		0.61	0.88
GO:0048020	<i>CCR chemokine receptor binding</i>	0.001 %		0.64	0.68
GO:0031731	<i>CCR6 chemokine receptor binding</i>	0.000 %		0.66	0.74
GO:0046982	protein heterodimerization activity	0.108 %		0.62	0.47
GO:0005102	<i>receptor binding</i>	0.416 %		0.60	0.60
GO:0032403	<i>protein complex binding</i>	0.146 %		0.62	0.54
GO:0042803	<i>protein homodimerization activity</i>	0.122 %		0.62	0.72

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Frequent keywords within your set of GO terms:

multicellular **results** up-regulation single-organism up enzyme state triacylglycerols stress-activated **expression** secretion transform **production** il-1
g1/s **cascade** **stimulus** individual **cell** wounding apoptotic **stress-induced** **repetition** organic **response** biopolymer **frequency** unfolded sparingly
modulates **rate** tissues **positive** organonitrogen upregulation change leucocyte organs transduction **activation** surroundings **organism** death level
encapsulating **stimulation** **regulation** increases **organismal** activates **external** tensile substances **result** **leukocyte** lymphocyte solvents stress
immune **extent** macromolecule phagocytes intracellular **humidity** movement **process** sapk **cellular** macromolecules internal

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