

While parsing your file, I found some errors:

Go term 102336 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.


Go term 102337 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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interpretation of the coordinate axes?

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

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term ID	description	frequency	pin?	log ₁₀ p-value	uniqueness	dispensability
GO:0002376	immune system process	0.625 %		-1.0665	0.98	0.00
GO:0006956	complement activation	0.069 %		-5.1904	0.62	0.00
... GO:0050861	<i>positive regulation of B cell receptor signaling pathway</i>	0.000 %		-1.0545	0.70	0.82
... GO:0050853	<i>B cell receptor signaling pathway</i>	0.003 %		-1.6050	0.68	0.70
... GO:0045087	<i>innate immune response</i>	0.137 %		-1.3832	0.73	0.80
... GO:0051607	<i>defense response to virus</i>	0.321 %		-1.2605	0.70	0.84
... GO:0006957	<i>complement activation, alternative pathway</i>	0.000 %		-4.9747	0.69	0.70
... GO:0006958	<i>complement activation, classical pathway</i>	0.001 %		-5.3429	0.69	0.76
... GO:0006955	<i>immune response</i>	0.380 %		-1.2406	0.75	0.89
GO:0008152	metabolic process	82.183 %		-6.5452	1.00	0.00
GO:0019835	cytolysis	0.185 %		-3.9318	0.96	0.00
GO:0032392	DNA geometric change	0.428 %		-1.3142	0.93	0.02

GO:0002576	platelet degranulation	0.001 %		-2.8268	0.90	0.03
GO:0007568	aging	0.013 %		-1.3210	0.91	0.03
GO:0006636	unsaturated fatty acid biosynthetic process	0.007 %		-4.6799	0.76	0.07
GO:0030212	hyaluronan metabolic process	0.003 %		-3.7328	0.92	0.08
GO:0006629	lipid metabolic process	3.094 %		-4.3002	0.89	0.10
GO:0043691	reverse cholesterol transport	0.001 %		-1.6170	0.91	0.15
GO:0030301	<i>cholesterol transport</i>	0.005 %		-1.2793	0.90	0.92
GO:0046166	glyceraldehyde-3-phosphate biosynthetic process	0.000 %		-1.0238	0.88	0.16
GO:0050892	intestinal absorption	0.001 %		-1.4859	0.87	0.16
GO:0019255	glucose 1-phosphate metabolic process	0.000 %		-1.3796	0.94	0.16
GO:0019442	tryptophan catabolic process to acetyl-CoA	0.000 %		-4.3904	0.82	0.18
GO:0042632	cholesterol homeostasis	0.004 %		-3.9431	0.83	0.19
GO:0055089	<i>fatty acid homeostasis</i>	0.001 %		-1.5270	0.85	0.87
GO:0035356	<i>cellular triglyceride homeostasis</i>	0.000 %		-2.3064	0.81	0.83
GO:0070328	<i>triglyceride homeostasis</i>	0.002 %		-1.0759	0.84	0.92
GO:0055114	oxidation-reduction process	15.044 %		-7.8327	0.88	0.21
GO:0006147	guanine catabolic process	0.013 %		-1.3142	0.85	0.22
GO:0006953	acute-phase response	0.002 %		-2.3394	0.81	0.25
GO:0030521	androgen receptor signaling pathway	0.003 %		-1.1955	0.76	0.25
GO:0010951	negative regulation of endopeptidase activity	0.083 %		-1.9971	0.75	0.26
GO:0043154	<i>negative regulation of cysteine-type endopeptidase activity involved in apoptotic process</i>	0.005 %		-1.1611	0.76	1.22
GO:0070373	<i>negative regulation of ERK1 and ERK2 cascade</i>	0.002 %		-1.2854	0.66	0.74
GO:0071499	cellular response to laminar fluid shear stress	0.000 %		-1.0238	0.83	0.26
GO:0071222	cellular response to lipopolysaccharide	0.009 %		-2.6236	0.73	0.27
GO:0048545	<i>response to steroid hormone</i>	0.034 %		-1.2944	0.76	0.86
GO:0051384	<i>response to glucocorticoid</i>	0.004 %		-2.2803	0.78	0.76
GO:0006544	glycine metabolic process	0.250 %		-3.8665	0.78	0.29
GO:0006563	<i>L-serine metabolic process</i>	0.264 %		-1.6413	0.78	0.84
GO:0097192	extrinsic apoptotic signaling pathway in absence of ligand	0.005 %		-1.0869	0.74	0.31
GO:0052695	cellular glucuronidation	0.000 %		-2.0175	0.84	0.33
GO:0019805	quinolinate biosynthetic process	0.031 %		-1.2793	0.78	0.33
GO:0042572	retinol metabolic process	0.001 %		-4.1267	0.72	0.33
GO:0042574	<i>retinal metabolic process</i>	0.001 %		-1.8707	0.83	0.91
GO:0006508	proteolysis	3.705 %		-1.5162	0.90	0.35
GO:0042158	lipoprotein biosynthetic process	0.093 %		-1.1095	0.89	0.36
GO:0042157	lipoprotein metabolic process	0.098 %		-1.1955	0.92	0.36
GO:0006641	triglyceride metabolic process	0.005 %		-2.6108	0.82	0.36
GO:0046327	<i>glycerol biosynthetic process from pyruvate</i>	0.000 %		-1.5526	0.78	0.82
GO:0090107	regulation of high-density lipoprotein particle assembly	0.000 %		-1.3796	0.80	0.38
GO:0033622	integrin activation	0.001 %		-1.0238	0.94	0.39
GO:0008206	bile acid metabolic process	0.001 %		-3.5702	0.76	0.40
GO:0008203	<i>cholesterol metabolic process</i>	0.007 %		-3.1198	0.78	0.75
GO:0006694	<i>steroid biosynthetic process</i>	0.030 %		-1.8880	0.78	0.88
GO:0006695	<i>cholesterol biosynthetic process</i>	0.002 %		-2.3231	0.77	0.89
GO:0060136	embryonic process involved in female pregnancy	0.000 %		-1.0545	0.87	0.41
GO:0007584	response to nutrient	0.004 %		-1.9971	0.79	0.44
GO:1902904	negative regulation of fibril organization	0.000 %		-1.4573	0.81	0.44
GO:0034625	fatty acid elongation, monounsaturated fatty acid	0.000 %		-2.1981	0.78	0.44
GO:0034626	<i>fatty acid elongation, polyunsaturated fatty acid</i>	0.000 %		-2.1490	0.78	0.95
GO:0072318	clathrin coat disassembly	0.000 %		-1.1639	0.88	0.45
GO:0007586	digestion	0.006 %		-1.0137	0.88	0.46
GO:0042761	very long-chain fatty acid biosynthetic process	0.001 %		-2.4529	0.78	0.47
GO:0045444	fat cell differentiation	0.011 %		-1.1091	0.89	0.47
GO:0035999	tetrahydrofolate interconversion	0.102 %		-1.7374	0.78	0.47
GO:0016062	adaptation of rhodopsin mediated signaling	0.000 %		-1.5526	0.73	0.48
GO:0006911	phagocytosis, engulfment	0.001 %		-1.8836	0.89	0.48
GO:0006910	<i>phagocytosis, recognition</i>	0.001 %		-1.3923	0.88	0.78
GO:1900034	regulation of cellular response to heat	0.000 %		-1.1450	0.76	0.48
GO:0001771	immunological synapse formation	0.000 %		-2.0590	0.84	0.51
GO:0050871	<i>positive regulation of B cell activation</i>	0.004 %		-1.5934	0.76	0.71
GO:0006631	fatty acid metabolic process	0.867 %		-3.3152	0.71	0.51
GO:0006644	<i>phospholipid metabolic process</i>	1.014 %		-1.6987	0.77	0.76
GO:0006633	<i>fatty acid biosynthetic process</i>	0.629 %		-3.1785	0.70	0.75
GO:0006103	2-oxoglutarate metabolic process	0.010 %		-1.0441	0.82	0.51
GO:0061402	positive regulation of transcription from RNA polymerase II promoter in response to acidic pH	0.000 %		-1.1639	0.75	0.52
GO:0042493	response to drug	0.207 %		-1.2606	0.78	0.53
GO:0006107	oxaloacetate metabolic process	0.017 %		-1.1450	0.82	0.53
GO:0006990	positive regulation of transcription from RNA polymerase II promoter involved in unfolded protein response	0.000 %		-1.2577	0.67	0.53
GO:0006656	phosphatidylcholine biosynthetic process	0.002 %		-1.7272	0.75	0.54
GO:1902807	negative regulation of cell cycle G1/S phase transition	0.004 %		-1.4573	0.80	0.54
GO:0097053	L-kynurenine catabolic process	0.004 %		-1.7194	0.80	0.54
GO:0016480	negative regulation of transcription from RNA polymerase III promoter	0.002 %		-1.0877	0.79	0.54
GO:0043124	negative regulation of I-kappaB kinase/NF-kappaB signaling	0.002 %		-1.6308	0.69	0.55

GO:0006089	lactate metabolic process	0.034 %		-1.1240	0.77	0.58
GO:0002418	immune response to tumor cell	0.001 %		-3.8268	0.79	0.58
GO:0002357	<i>defense response to tumor cell</i>	0.000 %	+	-3.5272	0.82	0.92
GO:0006954	inflammatory response	0.099 %		-1.5422	0.79	0.58
GO:0006520	cellular amino acid metabolic process	6.437 %		-1.1310	0.75	0.58
GO:0010977	negative regulation of neuron projection development	0.002 %		-1.3999	0.72	0.60
GO:0071638	<i>negative regulation of monocyte chemotactic protein-1 production</i>	0.000 %	+	-1.0545	0.79	0.77
GO:0032715	<i>negative regulation of interleukin-6 production</i>	0.001 %	+	-1.0869	0.77	0.76
GO:0055088	lipid homeostasis	0.006 %		-1.1766	0.85	0.60
GO:0051365	cellular response to potassium ion starvation	0.000 %		-1.1240	0.79	0.60
GO:0034354	'de novo' NAD biosynthetic process from tryptophan	0.008 %		-1.2646	0.82	0.60
GO:0034516	response to vitamin B6	0.000 %		-1.6760	0.79	0.61
GO:0006936	muscle contraction	0.018 %		-1.2334	0.87	0.62
GO:0071333	cellular response to glucose stimulus	0.003 %		-1.1611	0.66	0.63
GO:0071332	<i>cellular response to fructose stimulus</i>	0.000 %	+	-1.0238	0.80	0.85
GO:0071347	cellular response to interleukin-1	0.004 %		-1.5776	0.77	0.63
GO:0006536	glutamate metabolic process	0.272 %		-1.1698	0.77	0.63
GO:0032088	negative regulation of NF-kappaB transcription factor activity	0.004 %		-1.0739	0.78	0.64
GO:0070327	thyroid hormone transport	0.000 %		-1.9782	0.84	0.64
GO:0019915	lipid storage	0.006 %		-1.0739	0.83	0.65
GO:0043420	anthranilate metabolic process	0.008 %		-1.2502	0.78	0.67
GO:0050728	negative regulation of inflammatory response	0.005 %		-1.4778	0.68	0.67
GO:0007596	<i>blood coagulation</i>	0.015 %	+	-1.4130	0.67	0.73
GO:0001970	positive regulation of activation of membrane attack complex	0.000 %		-1.2081	0.67	0.68
GO:0034435	cholesterol esterification	0.001 %		-1.0877	0.82	0.68
GO:0032869	cellular response to insulin stimulus	0.008 %		-1.2008	0.75	0.68
GO:0032868	<i>response to insulin</i>	0.010 %	+	-1.0808	0.77	0.96
GO:0046098	guanine metabolic process	0.013 %		-1.3142	0.85	0.68
GO:0007275	multicellular organismal development	0.460 %		-1.1744	0.84	0.69
GO:0006569	tryptophan catabolic process	0.044 %		-3.9626	0.77	0.69
GO:0019441	<i>tryptophan catabolic process to kynurenine</i>	0.029 %	+	-2.9497	0.77	0.97
GO:0014070	response to organic cyclic compound	0.061 %		-1.2430	0.77	0.70

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Make R script for plotting

term ID	description	frequency	pin?	log ₁₀ p-value	uniqueness	dispensability
GO:0005576	extracellular region	4.572 %		-5.2069	0.95	0.00
GO:0005925	focal adhesion	0.016 %		-1.1476	0.94	0.00
GO:0016020	membrane	51.720 %		-2.9286	0.97	0.00
GO:0070062	extracellular exosome	0.300 %		-20.2048	0.51	0.00
GO:0031410	cytoplasmic vesicle	0.167 %		-1.4370	0.61	0.88
GO:0097447	dendritic tree	0.006 %		-2.9596	0.84	0.00
GO:0043025	neuronal cell body	0.028 %		-1.1674	0.84	0.78
GO:0005579	membrane attack complex	0.002 %		-1.9891	0.83	0.02
GO:0043209	myelin sheath	0.005 %		-1.5779	0.92	0.02
GO:0048471	perinuclear region of cytoplasm	0.050 %		-1.2460	0.72	0.02
GO:0017053	transcriptional repressor complex	0.014 %		-1.8271	0.90	0.23
GO:0044194	cytolytic granule	0.000 %		-2.4728	0.68	0.24
GO:0005764	lysosome	0.049 %		-1.4918	0.61	0.76
GO:0005829	cytosol	0.807 %		-1.1590	0.68	0.28
GO:0005777	peroxisome	0.063 %		-1.3348	0.63	0.33
GO:0005789	endoplasmic reticulum membrane	0.136 %		-3.2874	0.45	0.35
GO:0032580	Golgi cisterna membrane	0.012 %		-1.3141	0.52	0.71
GO:0005768	endosome	0.077 %		-1.8775	0.50	0.72
GO:0000139	Golgi membrane	0.090 %		-1.0534	0.47	0.83

GO:0030176	<i>integral component of endoplasmic reticulum membrane</i>	0.034 %		-1.9889	0.49	0.90
GO:0005783	<i>endoplasmic reticulum</i>	0.299 %		-2.4584	0.46	0.84
GO:0005794	<i>Golgi apparatus</i>	0.265 %		-2.5372	0.46	0.79
GO:0005791	<i>rough endoplasmic reticulum</i>	0.007 %		-1.2765	0.54	0.72
GO:0009897	<i>external side of plasma membrane</i>	0.032 %		-1.6288	0.88	0.36
GO:0005759	<i>mitochondrial matrix</i>	0.055 %		-3.0660	0.58	0.38
GO:0005654	<i>nucleoplasm</i>	0.221 %		-1.6849	0.58	0.77
GO:0072562	<i>blood microparticle</i>	0.012 %		-6.5935	0.83	0.46
GO:0031904	<i>endosome lumen</i>	0.000 %		-2.2775	0.59	0.49
GO:0043231	<i>intracellular membrane-bounded organelle</i>	8.847 %		-2.0474	0.56	0.53
GO:0031089	<i>platelet dense granule lumen</i>	0.000 %		-1.4426	0.53	0.58
GO:0005615	<i>extracellular space</i>	0.249 %		-7.4318	0.84	0.58
GO:0034364	<i>high-density lipoprotein particle</i>	0.003 %		-2.2028	0.76	0.62
GO:0034361	<i>very-low-density lipoprotein particle</i>	0.002 %		-1.3655	0.76	1.28
GO:0030118	<i>clathrin coat</i>	0.051 %		-1.0096	0.66	0.62
GO:0042470	<i>melanosome</i>	0.004 %		-1.6985	0.62	0.69
GO:0001917	<i>photoreceptor inner segment</i>	0.003 %		-1.5669	0.84	0.69

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 Hide/show dispensable GO terms

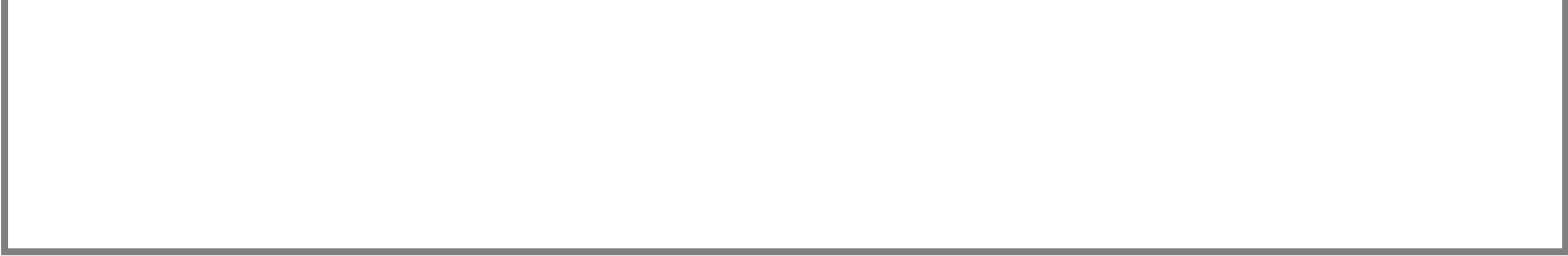
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GO:0003713	transcription coactivator activity	0.025 %		-1.9430	0.96	0.00
GO:0003824	catalytic activity	69.295 %		-4.2933	0.99	0.00
GO:0004745	retinol dehydrogenase activity	0.001 %		-4.4237	0.91	0.00
GO:0004867	serine-type endopeptidase inhibitor activity	0.030 %		-6.7100	0.93	0.00
 GO:0004866	<i>endopeptidase inhibitor activity</i>	0.084 %		-4.9706	0.93	0.93
GO:0005044	scavenger receptor activity	0.013 %		-3.8601	0.96	0.00
GO:0008201	heparin binding	0.013 %		-3.2048	0.92	0.00
GO:0022829	wide pore channel activity	0.137 %		-3.3098	0.96	0.00
GO:0009922	fatty acid elongase activity	0.000 %		-3.3747	0.93	0.01
GO:0004658	propionyl-CoA carboxylase activity	0.003 %		-2.9921	0.92	0.01
 GO:0003989	<i>acetyl-CoA carboxylase activity</i>	0.129 %		-1.0677	0.91	0.78
GO:0004252	serine-type endopeptidase activity	0.675 %		-2.7086	0.90	0.01
 GO:0008236	<i>serine-type peptidase activity</i>	1.044 %		-1.5270	0.90	0.94
GO:0016853	isomerase activity	3.154 %		-1.1245	0.95	0.03
GO:0005178	integrin binding	0.004 %		-2.3147	0.77	0.03
GO:0044822	poly(A) RNA binding	0.135 %		-2.1140	0.92	0.03

GO:0030247	polysaccharide binding	0.035 %		-1.1237	0.93	0.04
GO:0003823	antigen binding	0.064 %		-1.9639	0.93	0.04
GO:0016491	oxidoreductase activity	14.657 %		-4.5331	0.95	0.04
GO:0005515	protein binding	2.482 %		-1.4808	0.92	0.05
GO:0016787	hydrolase activity	21.764 %		-1.2116	0.95	0.07
GO:0016740	transferase activity	22.118 %		-1.0060	0.95	0.07
GO:0048037	cofactor binding	6.702 %		-1.2820	0.92	0.08
GO:0020037	heme binding	1.765 %		-1.6958	0.91	0.09
GO:0015020	glucuronosyltransferase activity	0.003 %		-2.4828	0.91	0.10
GO:0005506	iron ion binding	2.467 %		-2.0605	0.90	0.12
GO:0004372	glycine hydroxymethyltransferase activity	0.056 %		-2.3218	0.93	0.13
GO:0008301	DNA binding, bending	0.001 %		-1.4689	0.93	0.13
GO:0008398	sterol 14-demethylase activity	0.001 %		-1.0891	0.93	0.14
GO:0030429	kynureninase activity	0.006 %		-1.8408	0.93	0.16
GO:0004623	phospholipase A2 activity	0.011 %		-1.2388	0.93	0.17
GO:0030170	pyridoxal phosphate binding	1.703 %		-2.4502	0.90	0.19
GO:0004000	adenosine deaminase activity	0.061 %		-1.6441	0.91	0.19
GO:0008892	<i>guanine deaminase activity</i>	0.015 %		-1.3156	0.91	0.71
GO:0031177	phosphopantetheine binding	0.062 %		-1.1121	0.91	0.22
GO:0000166	nucleotide binding	20.353 %		-1.2834	0.90	0.27
GO:0004607	phosphatidylcholine-sterol O-acyltransferase activity	0.000 %		-1.1254	0.93	0.28
GO:0052650	NADP-retinol dehydrogenase activity	0.000 %		-1.0559	0.92	0.31
GO:0035615	clathrin adaptor activity	0.000 %		-1.1653	0.81	0.31
GO:0034186	apolipoprotein A-I binding	0.000 %		-1.4587	0.80	0.31
GO:0050733	RS domain binding	0.000 %		-1.2095	0.80	0.32
GO:0004467	long-chain fatty acid-CoA ligase activity	0.016 %		-1.1981	0.93	0.33
GO:0005509	calcium ion binding	0.365 %		-1.1575	0.91	0.34
GO:0002020	protease binding	0.004 %		-1.8831	0.78	0.36
GO:0001848	complement binding	0.018 %		-2.1519	0.77	0.39
GO:0016616	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	1.929 %		-1.5353	0.89	0.47
GO:0042802	identical protein binding	0.154 %		-2.0553	0.74	0.48
GO:0034987	immunoglobulin receptor binding	0.000 %		-1.6198	0.79	0.48
GO:0031072	heat shock protein binding	0.070 %		-1.4781	0.75	0.52
GO:0003831	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase activity	0.000 %		-2.3093	0.91	0.54
GO:0008378	galactosyltransferase activity	0.025 %		-2.1787	0.91	0.55
GO:0042803	protein homodimerization activity	0.122 %		-1.3803	0.74	0.55
GO:0005125	cytokine activity	0.020 %		-1.0974	0.75	0.59
GO:0046983	protein dimerization activity	0.735 %		-1.7487	0.72	0.63
GO:0019899	enzyme binding	0.221 %		-1.1584	0.74	0.65
GO:0005102	receptor binding	0.416 %		-1.0810	0.73	0.69
GO:0016901	oxidoreductase activity, acting on the CH-OH group of donors, quinone or similar compound as acceptor	0.136 %		-1.2592	0.90	0.70

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Export data to text table (CSV).



Make R script for plotting treemaps



Frequent keywords within your set of GO terms:

metabolism activitory results heterocycle systematic single-organism apolipoproteins enzyme neurites state triacylglycerols expression secretion
transform production -cooh aged compound mapk3 mapk1 membrane-enclosed non-living purposes cascade **similarly** ccl2 lipids stimulus individual
reactions **repetition** metabolic organic response **biopolymer** attack object **non-encoded** alditols fatty-acid **shear** kynurenine peptidolysis
organonitrogen erk1/2 vacuoles mcp-1 acidity chemical **non-protein** acidic organism tcc encapsulating stoichiometric biochemical mac
simply neurogenesis 3-(2-aminobenzoyl)-alanine abiotic result **subcomponent** macromolecule nucleic pathways protein-lipid **process**
cellular macromolecules



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

proceeds **40-100 occupied** serpin encapsulating parental outermost after proteases substrates removal
limiting replication participation catalyze parasite **fusion** derived repair **exosome** others platelets hydrolyzes
alternative steps size mdr **simply** covers **concomitant** promote microvesicles microsomal outside catalytically
endotoxins iga endoproteinase becomes igm endothelial **protons** space antigen- igg surroundings transform desaturation
disposal a1 **successive** properdin globulin **electrons** direct microparticles refers living antibody-coated retinene
antagonizes altered walls **inhibits** microbes endopeptidases microparticle reversible microvesicle nonterminal

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