



click empty space and and drag to zoom

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interpretation of the coordinate axes?



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term ID	description	frequency	pin?	log ₁₀ p-value	uniqueness	dispensability
GO:0030970	retrograde protein transport, ER to cytosol	0.000 %		-4.2464	0.58	0.00
GO:0030433	<i>ER-associated ubiquitin-dependent protein catabolic process</i>	0.003 %		-1.4196	0.59	0.79
GO:0043666	regulation of phosphoprotein phosphatase activity	0.004 %		-3.1361	0.84	0.01
GO:0031247	actin rod assembly	0.000 %		-4.1931	0.86	0.04
GO:0019227	neuronal action potential propagation	0.001 %		-1.5219	0.82	0.04
GO:0008380	RNA splicing	0.097 %		-1.8359	0.74	0.08
GO:0042359	vitamin D metabolic process	0.001 %		-1.6748	0.85	0.08
GO:0055114	oxidation-reduction process	15.044 %		-2.1353	0.86	0.08
GO:0043066	negative regulation of apoptotic process	0.047 %		-1.2290	0.82	0.19
GO:0006457	protein folding	0.863 %		-4.0348	0.73	0.21
GO:0001666	response to hypoxia	0.019 %		-1.4153	0.77	0.29
GO:0035754	B cell chemotaxis	0.000 %		-1.7786	0.64	0.32
GO:0000209	protein polyubiquitination	0.010 %		-1.0789	0.77	0.32
GO:0006465	signal peptide processing	0.023 %		-1.0442	0.73	0.34
GO:0030490	maturation of SSU-rRNA	0.001 %		-1.0578	0.76	0.38
GO:0006869	lipid transport	0.093 %		-1.2263	0.81	0.39
GO:0000380	alternative mRNA splicing, via spliceosome	0.003 %		-1.3938	0.75	0.40
GO:0006958	complement activation, classical pathway	0.001 %		-1.7691	0.60	0.40
GO:0006956	<i>complement activation</i>	0.069 %		-1.0310	0.54	0.76
GO:0071318	cellular response to ATP	0.000 %		-2.8774	0.71	0.46
GO:0002244	hematopoietic progenitor cell differentiation	0.010 %		-1.5860	0.67	0.48
GO:0051028	mRNA transport	0.053 %		-1.0956	0.84	0.53

GO:0006957	complement activation, alternative pathway	0.000 %	-1.2170	0.61	0.58
GO:0033280	response to vitamin D	0.001 %	-1.2380	0.72	0.62
GO:0001649	osteoblast differentiation	0.013 %	-1.3455	0.80	0.64
GO:0006397	mRNA processing	0.373 %	-1.2397	0.72	0.65

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term ID	description	frequency	pin?	log ₁₀ p-value	uniqueness	dispensability
GO:0005576	extracellular region	4.572 %		-1.0535	0.86	0.00
GO:0016235	aggresome	0.003 %		-2.2397	0.79	0.00
GO:0070062	extracellular exosome	0.300 %		-4.6459	0.48	0.00
GO:0030496	midbody	0.014 %		-1.8058	0.82	0.02
GO:0030424	axon	0.032 %		-1.0629	0.82	0.02
GO:0005886	plasma membrane	13.934 %		-1.5423	0.82	0.03
GO:0048471	perinuclear region of cytoplasm	0.050 %		-2.0421	0.70	0.05
GO:0005788	endoplasmic reticulum lumen	0.007 %		-4.6440	0.46	0.28
 GO:0005789	<i>endoplasmic reticulum membrane</i>	<i>0.136 %</i>		<i>-1.1598</i>	<i>0.44</i>	<i>0.81</i>
GO:0043231	intracellular membrane-bounded organelle	8.847 %		-1.7912	0.52	0.53
GO:0016607	nuclear speck	0.012 %		-1.4424	0.56	0.57
GO:0005615	extracellular space	0.249 %		-1.2687	0.77	0.58
GO:0034663	endoplasmic reticulum chaperone complex	0.000 %		-2.9736	0.53	0.59
GO:0042470	melanosome	0.004 %		-1.1353	0.56	0.69

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term ID	description	frequency	pin?	log ₁₀ p-value	uniqueness	dispensability
GO:0008403	25-hydroxycholecalciferol-24-hydroxylase activity	0.000 %		-2.3435	0.81	0.00
GO:0030342	1-alpha,25-dihydroxyvitamin D3 24-hydroxylase activity	0.000 %		-2.3435	0.81	0.95
GO:0051082	unfolded protein binding	0.451 %		-3.2487	0.85	0.00
GO:0004252	serine-type endopeptidase activity	0.675 %		-1.1507	0.89	0.01
GO:0008766	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate-D-alanyl-D-alanine ligase activity	0.043 %		-1.1453	0.56	0.02
GO:0046790	virion binding	0.000 %		-3.0177	0.89	0.03
GO:0016491	oxidoreductase activity	14.657 %		-1.6966	0.90	0.03
GO:0044822	poly(A) RNA binding	0.135 %		-2.3544	0.85	0.04
GO:0008144	drug binding	0.260 %		-1.4577	0.89	0.05
GO:0005506	iron ion binding	2.467 %		-2.0808	0.88	0.06
GO:0016705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	0.772 %		-1.1412	0.87	0.17
GO:0003723	RNA binding	5.860 %		-1.0801	0.86	0.25
GO:0036002	pre-mRNA binding	0.001 %		-1.2522	0.86	0.29
GO:0043774	coenzyme F420-2 alpha-glutamyl ligase activity	0.000 %		-1.1369	0.65	0.41
GO:0050750	low-density lipoprotein particle receptor binding	0.001 %		-1.3970	0.86	0.43
GO:0070738	tubulin-glycine ligase activity	0.000 %		-1.1369	0.56	0.45
GO:0070737	protein-glycine ligase activity, elongating	0.000 %		-1.1205	0.56	0.86
GO:0070736	protein-glycine ligase activity, initiating	0.000 %		-1.1125	0.54	0.92
GO:0070735	protein-glycine ligase activity	0.000 %		-1.0896	0.62	0.49
GO:0043773	coenzyme F420-0 gamma-glutamyl ligase activity	0.005 %		-1.1205	0.58	0.59
GO:0018169	ribosomal S6-glutamic acid ligase activity	0.005 %		-1.1205	0.55	0.59
GO:0070740	tubulin-glutamic acid ligase activity	0.000 %		-1.0679	0.60	0.82
GO:0070739	protein-glutamic acid ligase activity	0.005 %		-1.1125	0.58	0.59

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Frequent keywords within your set of GO terms:

modifications **single-organism** triacylglycerols subcellular exposures **f420-2** polynucleotides pre-translation
slitlike transform microbes non-apoptotic **c-24** exons membrane-enclosed culminates plastids transmitted deteriorating cease
biopolymer reticulum-associated **interdependent** markedly vital extra-nucleolar elastase 25-hydroxycholecalciferol
immunological tagging **gamma-carboxyl** group(s) peptidolysis objective aggregated organonitrogen vacuoles disposal
glycylase protein-glycine ribosomes dislocation gradually microscopy expanded disaggregate leucine-rich
glutamylase encapsulating organismal 24-hydroxylase protoplast **simply** 25-hydroxyvitamin abiotic triad glycoprotein-specific
halting ergocalciferol phosphorus regularly subcomponent immunogenic macromolecule outermost organelle oxygen-containing housed nucleoplasm
modification-dependent macromolecules posttranslational co-translational



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

grp94 **dislocation** pdi **40-100** cyclophilin envelope histone-specific polypeptides covalent tertiary
correct **limiting** retrotranslocation located **fusion** tubules **exosome** viral co-
chaperonin **cisterna** co-chaperone virion multisubunit composed chaperonin erp72 **lumen**
beta-tubulin disulfide **cisternal** rod **simply** bip arranged **called** phosphatase folding
retrograde erdj3 glycoprotein-specific non-chaperonin complex actin assembly chaperone
translocon udp-glucosyltransferase through cytosol network **vesicular** released
noncovalent cabp1 atpase chaperonin-mediated sdf2-l1 grp170 **hexagonally** tubulin-specific modulates
vesicle formation parallel **diameter** fimbrium-specific **exosomes**
phosphoprotein unfolded multichaperone **multivesicular** rods alpha-tubulin
endosomal volume isomerase capsid assisting **nm**

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