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term ID	description	frequency	pin?	uniqueness	dispensability
GO:0006950	response to stress	4.119 %		0.80	0.00
GO:0008152	metabolic process	82.183 %		0.99	0.00
GO:0016192	vesicle-mediated transport	0.381 %		0.88	0.00
GO:0016311	dephosphorylation	0.777 %		0.90	0.00
GO:0042157	lipoprotein metabolic process	0.098 %		0.85	0.01
GO:0031247	actin rod assembly	0.000 %		0.83	0.02
GO:0007050	cell cycle arrest	0.011 %		0.71	0.04
GO:0043066	negative regulation of apoptotic process	0.047 %	⚑	0.69	0.55
GO:2001238	positive regulation of extrinsic apoptotic signaling pathway	0.004 %	⚑	0.61	0.75
GO:0040020	regulation of meiotic nuclear division	0.003 %	⚑	0.71	0.66
GO:0008380	RNA splicing	0.097 %		0.82	0.11
GO:0006397	mRNA processing	0.373 %	⚑	0.80	0.56
GO:0000380	alternative mRNA splicing, via spliceosome	0.003 %	⚑	0.83	0.65
GO:0043666	regulation of phosphoprotein phosphatase activity	0.004 %		0.79	0.20
GO:0051028	mRNA transport	0.053 %		0.86	0.22
GO:0000209	protein polyubiquitination	0.010 %		0.83	0.23
GO:0019217	regulation of fatty acid metabolic process	0.029 %		0.77	0.23

GO:0006898	receptor-mediated endocytosis	0.166 %		0.88	0.24
GO:0006465	signal peptide processing	0.023 %		0.81	0.25
GO:1900034	regulation of cellular response to heat	0.000 %		0.70	0.27
GO:0071318	cellular response to ATP	0.000 %		0.77	0.28
GO:0090398	cellular senescence	0.002 %		0.73	0.32
GO:0006457	protein folding	0.863 %		0.80	0.34
GO:0002502	peptide antigen assembly with MHC class I protein complex	0.000 %		0.82	0.34
GO:0045727	positive regulation of translation	0.047 %		0.62	0.36
GO:2000510	positive regulation of dendritic cell chemotaxis	0.000 %	⚐	0.57	0.53
GO:0002244	hematopoietic progenitor cell differentiation	0.010 %		0.77	0.43
GO:1900026	positive regulation of substrate adhesion-dependent cell spreading	0.001 %	⚐	0.63	0.72
GO:0045665	negative regulation of neuron differentiation	0.004 %	⚐	0.67	0.60
GO:0032211	negative regulation of telomere maintenance via telomerase	0.000 %		0.63	0.43
GO:0032212	positive regulation of telomere maintenance via telomerase	0.000 %	⚐	0.63	0.96
GO:0048387	negative regulation of retinoic acid receptor signaling pathway	0.001 %		0.64	0.45
GO:0033144	negative regulation of intracellular steroid hormone receptor signaling pathway	0.002 %	⚐	0.64	0.60
GO:0006957	complement activation, alternative pathway	0.000 %		0.61	0.47
GO:0036498	IRE1-mediated unfolded protein response	0.000 %		0.67	0.48
GO:0030970	retrograde protein transport, ER to cytosol	0.000 %	⚐	0.59	0.79
GO:0030433	ER-associated ubiquitin-dependent protein catabolic process	0.003 %	⚐	0.65	0.78
GO:0034504	protein localization to nucleus	0.025 %		0.83	0.49
GO:0051168	nuclear export	0.078 %	⚐	0.82	0.52
GO:0051170	nuclear import	0.098 %	⚐	0.81	0.90

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GO:0005576	extracellular region	4.572 %		0.91	0.00
GO:0005615	extracellular space	0.249 %		0.82	0.00
GO:0005925	focal adhesion	0.016 %		0.91	0.00
GO:0016020	membrane	51.720 %		0.95	0.00
GO:0019013	viral nucleocapsid	0.446 %		0.91	0.00
GO:0030496	midbody	0.014 %		0.89	0.00
GO:0031012	extracellular matrix	0.156 %		0.91	0.00
GO:0016235	aggresome	0.003 %		0.85	0.02
GO:0005844	polysome	0.004 %		0.82	0.05
GO:0048471	perinuclear region of cytoplasm	0.050 %		0.73	0.05
GO:0033018	sarcoplasmic reticulum lumen	0.000 %		0.57	0.16
GO:0042824	MHC class I peptide loading complex	0.000 %	🚩	0.53	0.54
GO:0043231	intracellular membrane-bounded organelle	8.847 %	🚩	0.60	0.53
GO:0034663	endoplasmic reticulum chaperone complex	0.000 %	🚩	0.54	0.54
GO:0005788	endoplasmic reticulum lumen	0.007 %	🚩	0.52	0.64
GO:0005783	endoplasmic reticulum	0.299 %	🚩	0.50	0.52
GO:0005789	endoplasmic reticulum membrane	0.136 %	🚩	0.44	0.81
GO:0042470	melanosome	0.004 %		0.61	0.20
GO:0030669	clathrin-coated endocytic vesicle membrane	0.004 %	🚩	0.55	0.66
GO:0070062	extracellular exosome	0.300 %	🚩	0.54	0.69
GO:0005829	cytosol	0.807 %		0.70	0.28
GO:0034361	very-low-density lipoprotein particle	0.002 %		0.77	0.41

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term ID	description	frequency	pin?	uniqueness	dispensability
GO:0005044	scavenger receptor activity	0.013 %		0.89	0.00
GO:0016901	oxidoreductase activity, acting on the CH-OH group of donors, quinone or similar compound as acceptor	0.136 %		0.89	0.00
GO:0046790	virion binding	0.000 %		0.85	0.00
GO:0098505	G-rich strand telomeric DNA binding	0.000 %		0.83	0.02
GO:0003924	GTPase activity	0.935 %		0.87	0.02
GO:0005537	mannose binding	0.001 %		0.85	0.02
GO:0050750	low-density lipoprotein particle receptor binding	0.001 %		0.81	0.02
GO:0042277	peptide binding	0.093 %		0.84	0.03
GO:0008201	heparin binding	0.013 %		0.82	0.03
GO:0030246	carbohydrate binding	0.825 %		0.83	0.04
GO:0036002	pre-mRNA binding	0.001 %		0.79	0.08
GO:0005509	calcium ion binding	0.365 %		0.78	0.10
GO:0016208	AMP binding	0.024 %		0.76	0.22
GO:0004252	serine-type endopeptidase activity	0.675 %		0.86	0.25
GO:0000166	nucleotide binding	20.353 %		0.79	0.26
GO:0044822	poly(A) RNA binding	0.135 %		0.76	0.29
GO:0005506	iron ion binding	2.467 %		0.77	0.34
GO:0003729	mRNA binding	0.070 %		0.76	0.39
GO:0051082	unfolded protein binding	0.451 %		0.79	0.43

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Frequent keywords within your set of GO terms:

membrane-bounded multicellular erad modifications single-organism oxoacid subcellular macromolecular transform history aged non-apoptotic cell-substrate exons membrane-enclosed anhydride culminates topologically plastids individual repetition deteriorating cease biopolymer telomeric reticulum adhesion-dependent young unfolded markedly vital later telomere tagging monitors internally organonitrogen vacuoles ribosomes gradually multiple surroundings rar molecules level encapsulating lectin anhydrides responses organismal low endoplasmic simply neurogenesis protein-coding infectious triad halting substances phosphorus regularly macromolecule organelle humidity nucleobase-containing clathrin-coated lengthening cellular macromolecules inactions

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