

ONTOLOGY	ID	Description	pvalue	p.adjust	qvalue
BP	GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process	7.31E-13	4.50E-09	3.88E-09
BP	GO:0042176	regulation of protein catabolic process	9.51E-12	2.93E-08	2.53E-08
BP	GO:0016049	cell growth	5.30E-10	1.05E-06	9.05E-07
BP	GO:0007179	transforming growth factor beta receptor signaling pathway	6.82E-10	1.05E-06	9.05E-07
BP	GO:0001558	regulation of cell growth	1.80E-08	2.22E-05	1.91E-05
BP	GO:0017015	regulation of transforming growth factor beta receptor signaling pathway	2.16E-08	2.22E-05	1.91E-05
BP	GO:1903844	regulation of cellular response to transforming growth factor beta stimulus	4.09E-08	3.60E-05	3.10E-05
BP	GO:0071560	cellular response to transforming growth factor beta stimulus	5.63E-08	3.87E-05	3.34E-05
BP	GO:0071559	response to transforming growth factor beta	5.65E-08	3.87E-05	3.34E-05
BP	GO:0045732	positive regulation of protein catabolic process	8.03E-08	4.95E-05	4.27E-05
BP	GO:0072594	establishment of protein localization to organelle	8.88E-08	4.98E-05	4.29E-05
BP	GO:1903320	regulation of protein modification by small protein conjugation or removal	1.13E-07	5.43E-05	4.67E-05
BP	GO:0061136	regulation of proteasomal protein catabolic process	1.14E-07	5.43E-05	4.67E-05
BP	GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	3.16E-07	0.000139	0.00012
BP	GO:0034976	response to endoplasmic reticulum stress	4.06E-07	0.000167	0.000144
BP	GO:1903050	regulation of proteolysis involved in protein catabolic process	5.38E-07	0.000207	0.000178
BP	GO:0032386	regulation of intracellular transport	9.42E-07	0.000341	0.000294
BP	GO:0008380	RNA splicing	1.27E-06	0.000435	0.000375
BP	GO:0032434	regulation of proteasomal ubiquitin-dependent protein catabolic process	1.47E-06	0.000464	0.0004
BP	GO:1903829	positive regulation of protein localization	1.52E-06	0.000464	0.0004
BP	GO:2000058	regulation of ubiquitin-dependent protein catabolic process	1.67E-06	0.000464	0.0004
BP	GO:0032535	regulation of cellular component size	1.70E-06	0.000464	0.0004
BP	GO:0035088	establishment or maintenance of apical/basal cell polarity	1.81E-06	0.000464	0.0004
BP	GO:0061245	establishment or maintenance of bipolar cell polarity	1.81E-06	0.000464	0.0004
BP	GO:0048193	Golgi vesicle transport	1.94E-06	0.000478	0.000412
BP	GO:0090287	regulation of cellular response to growth factor stimulus	2.40E-06	0.000567	0.000489
BP	GO:0042177	negative regulation of protein catabolic process	2.49E-06	0.000567	0.000489
BP	GO:0043484	regulation of RNA splicing	3.26E-06	0.000701	0.000604
BP	GO:0090092	regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	3.33E-06	0.000701	0.000604
BP	GO:0031396	regulation of protein ubiquitination	3.41E-06	0.000701	0.000604
BP	GO:0034504	protein localization to nucleus	4.86E-06	0.000965	0.000832
BP	GO:0034315	regulation of Arp2/3 complex-mediated actin nucleation	5.18E-06	0.000985	0.000849
BP	GO:0051222	positive regulation of protein transport	5.28E-06	0.000985	0.000849
BP	GO:0042326	negative regulation of phosphorylation	7.01E-06	0.001272	0.001095
BP	GO:0003158	endothelium development	7.60E-06	0.001337	0.001152
BP	GO:1902903	regulation of supramolecular fiber organization	9.35E-06	0.001593	0.001372
BP	GO:0045197	establishment or maintenance of epithelial cell apical/basal polarity	9.56E-06	0.001593	0.001372
BP	GO:0007517	muscle organ development	1.32E-05	0.002146	0.001849

BP	GO:1904951	positive regulation of establishment of protein localization	1.49E-05	0.002359	0.002032
BP	GO:0007163	establishment or maintenance of cell polarity	1.58E-05	0.002433	0.002096
BP	GO:0045446	endothelial cell differentiation	1.70E-05	0.002557	0.002203
BP	GO:0001933	negative regulation of protein phosphorylation	1.80E-05	0.002645	0.002279
BP	GO:0016032	viral process	2.34E-05	0.003359	0.002893
BP	GO:0008631	intrinsic apoptotic signaling pathway in response to oxidative stress	2.67E-05	0.00371	0.003196
BP	GO:1901800	positive regulation of proteasomal protein catabolic process	2.71E-05	0.00371	0.003196
BP	GO:0010906	regulation of glucose metabolic process	2.82E-05	0.003773	0.003251
BP	GO:0097193	intrinsic apoptotic signaling pathway	3.23E-05	0.004241	0.003653
BP	GO:0062197	cellular response to chemical stress	3.52E-05	0.004521	0.003895
BP	GO:0045862	positive regulation of proteolysis	3.61E-05	0.004529	0.003902
BP	GO:0045936	negative regulation of phosphate metabolic process	3.67E-05	0.004529	0.003902
BP	GO:0007015	actin filament organization	3.76E-05	0.004546	0.003916
BP	GO:0010563	negative regulation of phosphorus metabolic process	3.99E-05	0.004624	0.003983
BP	GO:0090083	regulation of inclusion body assembly	4.05E-05	0.004624	0.003983
BP	GO:0048024	regulation of mRNA splicing, via spliceosome	4.05E-05	0.004624	0.003983
BP	GO:2001233	regulation of apoptotic signaling pathway	4.31E-05	0.00483	0.004161
BP	GO:2000060	positive regulation of ubiquitin-dependent protein catabolic process	4.84E-05	0.005251	0.004524
BP	GO:0006997	nucleus organization	4.94E-05	0.005251	0.004524
BP	GO:0034314	Arp2/3 complex-mediated actin nucleation	4.94E-05	0.005251	0.004524
BP	GO:0032436	positive regulation of proteasomal ubiquitin-dependent protein catabolic process	5.55E-05	0.005794	0.004992
BP	GO:0006888	endoplasmic reticulum to Golgi vesicle-mediated transport	5.65E-05	0.005806	0.005002
BP	GO:0070972	protein localization to endoplasmic reticulum	5.84E-05	0.005901	0.005084
BP	GO:0006606	protein import into nucleus	6.64E-05	0.006553	0.005645
BP	GO:0036503	ERAD pathway	6.83E-05	0.006553	0.005645
BP	GO:0006111	regulation of gluconeogenesis	6.86E-05	0.006553	0.005645
BP	GO:0048545	response to steroid hormone	6.91E-05	0.006553	0.005645
BP	GO:0007176	regulation of epidermal growth factor-activated receptor activity	7.20E-05	0.006725	0.005794
BP	GO:2001242	regulation of intrinsic apoptotic signaling pathway	7.48E-05	0.006858	0.005908
BP	GO:1903052	positive regulation of proteolysis involved in protein catabolic process	7.67E-05	0.006858	0.005908
BP	GO:0007626	locomotory behavior	7.68E-05	0.006858	0.005908
BP	GO:0060537	muscle tissue development	7.85E-05	0.006911	0.005954
BP	GO:0050890	cognition	8.08E-05	0.007015	0.006043
BP	GO:0070302	regulation of stress-activated protein kinase signaling cascade	8.66E-05	0.007415	0.006388
BP	GO:0006942	regulation of striated muscle contraction	9.68E-05	0.008171	0.00704
BP	GO:0050708	regulation of protein secretion	0.000101	0.008407	0.007242
BP	GO:0031667	response to nutrient levels	0.000102	0.008407	0.007242
BP	GO:0032933	SREBP signaling pathway	0.000104	0.008407	0.007242
BP	GO:0070482	response to oxygen levels	0.000105	0.008422	0.007256

BP	GO:0001885	endothelial cell development	0.000108	0.008563	0.007377
BP	GO:0051170	import into nucleus	0.000113	0.008781	0.007565
BP	GO:0072599	establishment of protein localization to endoplasmic reticulum	0.000115	0.008781	0.007565
BP	GO:0050804	modulation of chemical synaptic transmission	0.000118	0.008781	0.007565
BP	GO:0050684	regulation of mRNA processing	0.000119	0.008781	0.007565
BP	GO:0030433	ubiquitin-dependent ERAD pathway	0.00012	0.008781	0.007565
BP	GO:0006605	protein targeting	0.00012	0.008781	0.007565
BP	GO:0000209	protein polyubiquitination	0.000124	0.008909	0.007675
BP	GO:0099177	regulation of trans-synaptic signaling	0.000127	0.008909	0.007675
BP	GO:0051960	regulation of nervous system development	0.000127	0.008909	0.007675
BP	GO:0032922	circadian regulation of gene expression	0.000127	0.008909	0.007675
BP	GO:0048675	axon extension	0.000135	0.009286	0.008
BP	GO:0001756	somitogenesis	0.000136	0.009286	0.008
BP	GO:0008361	regulation of cell size	0.000137	0.009286	0.008
BP	GO:0051125	regulation of actin nucleation	0.00014	0.009351	0.008056
BP	GO:0070997	neuron death	0.000146	0.009551	0.008228
BP	GO:0071692	protein localization to extracellular region	0.000146	0.009551	0.008228
BP	GO:0045047	protein targeting to ER	0.000147	0.009551	0.008228
BP	GO:0050714	positive regulation of protein secretion	0.000158	0.010076	0.00868
BP	GO:1900180	regulation of protein localization to nucleus	0.000159	0.010076	0.00868
BP	GO:0044262	cellular carbohydrate metabolic process	0.00018	0.011311	0.009744
BP	GO:0071501	cellular response to sterol depletion	0.000186	0.011584	0.00998
BP	GO:2001243	negative regulation of intrinsic apoptotic signaling pathway	0.000194	0.011849	0.010208
BP	GO:0006898	receptor-mediated endocytosis	0.000195	0.011849	0.010208
BP	GO:0006109	regulation of carbohydrate metabolic process	0.000196	0.011849	0.010208
BP	GO:0051047	positive regulation of secretion	0.000202	0.012054	0.010385
BP	GO:0046879	hormone secretion	0.00021	0.012054	0.010385
BP	GO:0023061	signal release	0.00021	0.012054	0.010385
BP	GO:1903322	positive regulation of protein modification by small protein conjugation or removal	0.00021	0.012054	0.010385
BP	GO:0030511	positive regulation of transforming growth factor beta receptor signaling pathway	0.000211	0.012054	0.010385
BP	GO:1903846	positive regulation of cellular response to transforming growth factor beta stimulus	0.000211	0.012054	0.010385
BP	GO:0009306	protein secretion	0.000214	0.012099	0.010424
BP	GO:1903532	positive regulation of secretion by cell	0.000217	0.012142	0.010461
BP	GO:0062012	regulation of small molecule metabolic process	0.000223	0.012383	0.010668
BP	GO:0008154	actin polymerization or depolymerization	0.000227	0.012491	0.010761
BP	GO:0035592	establishment of protein localization to extracellular region	0.000232	0.012651	0.010899
BP	GO:0090307	mitotic spindle assembly	0.000236	0.012732	0.010969
BP	GO:0031098	stress-activated protein kinase signaling cascade	0.000241	0.012903	0.011116
BP	GO:0061028	establishment of endothelial barrier	0.000251	0.013098	0.011284

BP	GO:0043153	entrainment of circadian clock by photoperiod	0.000252	0.013098	0.011284
BP	GO:1902175	regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	0.000252	0.013098	0.011284
BP	GO:0007611	learning or memory	0.000253	0.013098	0.011284
BP	GO:0009914	hormone transport	0.000257	0.013213	0.011383
BP	GO:0032872	regulation of stress-activated MAPK cascade	0.000265	0.013509	0.011638
BP	GO:0019319	hexose biosynthetic process	0.000278	0.013931	0.012001
BP	GO:0061053	somite development	0.000278	0.013931	0.012001
BP	GO:0090101	negative regulation of transmembrane receptor protein serine/threonine kinase signaling	0.000295	0.014645	0.012616
BP	GO:1903573	negative regulation of response to endoplasmic reticulum stress	0.000325	0.015831	0.013639
BP	GO:0071901	negative regulation of protein serine/threonine kinase activity	0.000325	0.015831	0.013639
BP	GO:0032970	regulation of actin filament-based process	0.000326	0.015831	0.013639
BP	GO:0007254	JNK cascade	0.000351	0.016888	0.014549
BP	GO:0030512	negative regulation of transforming growth factor beta receptor signaling pathway	0.00036	0.017056	0.014693
BP	GO:0046328	regulation of JNK cascade	0.00036	0.017056	0.014693
BP	GO:0034764	positive regulation of transmembrane transport	0.000363	0.017056	0.014693
BP	GO:0031647	regulation of protein stability	0.000381	0.017778	0.015316
BP	GO:1901879	regulation of protein depolymerization	0.000394	0.018133	0.015622
BP	GO:0110053	regulation of actin filament organization	0.000398	0.018133	0.015622
BP	GO:0051656	establishment of organelle localization	0.000402	0.018133	0.015622
BP	GO:0022604	regulation of cell morphogenesis	0.000402	0.018133	0.015622
BP	GO:0034329	cell junction assembly	0.000403	0.018133	0.015622
BP	GO:0016051	carbohydrate biosynthetic process	0.00041	0.018327	0.015789
BP	GO:0036473	cell death in response to oxidative stress	0.000422	0.018707	0.016116
BP	GO:0010675	regulation of cellular carbohydrate metabolic process	0.00044	0.019232	0.016569
BP	GO:0006937	regulation of muscle contraction	0.000442	0.019232	0.016569
BP	GO:0006094	gluconeogenesis	0.000445	0.019232	0.016569
BP	GO:0016570	histone modification	0.000446	0.019232	0.016569
BP	GO:0010720	positive regulation of cell development	0.000468	0.02002	0.017247
BP	GO:0031056	regulation of histone modification	0.000495	0.020853	0.017965
BP	GO:0050821	protein stabilization	0.000503	0.020853	0.017965
BP	GO:0050767	regulation of neurogenesis	0.000504	0.020853	0.017965
BP	GO:0030308	negative regulation of cell growth	0.000504	0.020853	0.017965
BP	GO:0006991	response to sterol depletion	0.00051	0.020853	0.017965
BP	GO:0032873	negative regulation of stress-activated MAPK cascade	0.000521	0.020853	0.017965
BP	GO:0070303	negative regulation of stress-activated protein kinase signaling cascade	0.000521	0.020853	0.017965
BP	GO:1901799	negative regulation of proteasomal protein catabolic process	0.000521	0.020853	0.017965
BP	GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	0.000525	0.020853	0.017965
BP	GO:0000398	mRNA splicing, via spliceosome	0.000525	0.020853	0.017965
BP	GO:0034599	cellular response to oxidative stress	0.000527	0.020853	0.017965

BP	GO:0031397	negative regulation of protein ubiquitination	0.000529	0.020853	0.017965
BP	GO:0006979	response to oxidative stress	0.000531	0.020853	0.017965
BP	GO:0046364	monosaccharide biosynthetic process	0.00055	0.021468	0.018495
BP	GO:0032387	negative regulation of intracellular transport	0.000563	0.021662	0.018662
BP	GO:1903321	negative regulation of protein modification by small protein conjugation or removal	0.000565	0.021662	0.018662
BP	GO:0043244	regulation of protein-containing complex disassembly	0.000566	0.021662	0.018662
BP	GO:0042886	amide transport	0.000583	0.022051	0.018997
BP	GO:0032984	protein-containing complex disassembly	0.000583	0.022051	0.018997
BP	GO:0035601	protein deacylation	0.000633	0.02377	0.020478
BP	GO:0090150	establishment of protein localization to membrane	0.000644	0.024068	0.020735
BP	GO:0002790	peptide secretion	0.00066	0.02426	0.0209
BP	GO:0048638	regulation of developmental growth	0.000664	0.02426	0.0209
BP	GO:0043967	histone H4 acetylation	0.000672	0.02426	0.0209
BP	GO:0016050	vesicle organization	0.000672	0.02426	0.0209
BP	GO:0006613	cotranslational protein targeting to membrane	0.000673	0.02426	0.0209
BP	GO:0051443	positive regulation of ubiquitin-protein transferase activity	0.000673	0.02426	0.0209
BP	GO:0016358	dendrite development	0.000681	0.024385	0.021008
BP	GO:0006984	ER-nucleus signaling pathway	0.000688	0.024385	0.021008
BP	GO:0008542	visual learning	0.000688	0.024385	0.021008
BP	GO:0090084	negative regulation of inclusion body assembly	0.000694	0.024455	0.021068
BP	GO:0060048	cardiac muscle contraction	0.000698	0.024455	0.021068
BP	GO:0043254	regulation of protein-containing complex assembly	0.000713	0.024818	0.021381
BP	GO:0000375	RNA splicing, via transesterification reactions	0.000717	0.024818	0.021381
BP	GO:1990138	neuron projection extension	0.000723	0.024897	0.021449
BP	GO:1901215	negative regulation of neuron death	0.000745	0.025506	0.021974
BP	GO:0030072	peptide hormone secretion	0.000771	0.026108	0.022493
BP	GO:0033157	regulation of intracellular protein transport	0.000771	0.026108	0.022493
BP	GO:0044065	regulation of respiratory system process	0.00081	0.027112	0.023357
BP	GO:0007632	visual behavior	0.000815	0.027112	0.023357
BP	GO:0051403	stress-activated MAPK cascade	0.000818	0.027112	0.023357
BP	GO:0050730	regulation of peptidyl-tyrosine phosphorylation	0.000818	0.027112	0.023357
BP	GO:0006913	nucleocytoplasmic transport	0.000896	0.029388	0.025318
BP	GO:0051169	nuclear transport	0.000896	0.029388	0.025318
BP	GO:0009648	photoperiodism	0.000904	0.02948	0.025397
BP	GO:0045010	actin nucleation	0.000923	0.029935	0.02579
BP	GO:0010970	transport along microtubule	0.000944	0.03033	0.026129
BP	GO:0006941	striated muscle contraction	0.000948	0.03033	0.026129
BP	GO:0036293	response to decreased oxygen levels	0.000953	0.03033	0.026129
BP	GO:0046883	regulation of hormone secretion	0.000955	0.03033	0.026129

BP	GO:0043242	negative regulation of protein-containing complex disassembly	0.000993	0.03129	0.026956
BP	GO:0006006	glucose metabolic process	0.000995	0.03129	0.026956
BP	GO:0005996	monosaccharide metabolic process	0.001	0.03129	0.026956
BP	GO:0035065	regulation of histone acetylation	0.001011	0.0314	0.027052
BP	GO:0070841	inclusion body assembly	0.001014	0.0314	0.027052
BP	GO:0051402	neuron apoptotic process	0.00102	0.031427	0.027074
BP	GO:0018108	peptidyl-tyrosine phosphorylation	0.00103	0.03143	0.027077
BP	GO:0002793	positive regulation of peptide secretion	0.00103	0.03143	0.027077
BP	GO:0098732	macromolecule deacylation	0.001042	0.031629	0.027248
BP	GO:0002791	regulation of peptide secretion	0.001052	0.031772	0.027372
BP	GO:0007612	learning	0.001083	0.032441	0.027948
BP	GO:0071900	regulation of protein serine/threonine kinase activity	0.00109	0.032441	0.027948
BP	GO:0045926	negative regulation of growth	0.001091	0.032441	0.027948
BP	GO:0090257	regulation of muscle system process	0.001111	0.032441	0.027948
BP	GO:0019318	hexose metabolic process	0.001115	0.032441	0.027948
BP	GO:0048588	developmental cell growth	0.001115	0.032441	0.027948
BP	GO:1901214	regulation of neuron death	0.001119	0.032441	0.027948
BP	GO:0071383	cellular response to steroid hormone stimulus	0.00112	0.032441	0.027948
BP	GO:0009895	negative regulation of catabolic process	0.001121	0.032441	0.027948
BP	GO:0031398	positive regulation of protein ubiquitination	0.001139	0.032803	0.02826
BP	GO:0006469	negative regulation of protein kinase activity	0.001156	0.032928	0.028368
BP	GO:0010975	regulation of neuron projection development	0.001164	0.032928	0.028368
BP	GO:0018212	peptidyl-tyrosine modification	0.001181	0.032928	0.028368
BP	GO:1990182	exosomal secretion	0.001184	0.032928	0.028368
BP	GO:0006457	protein folding	0.001189	0.032928	0.028368
BP	GO:0050808	synapse organization	0.00119	0.032928	0.028368
BP	GO:0046329	negative regulation of JNK cascade	0.001194	0.032928	0.028368
BP	GO:0071634	regulation of transforming growth factor beta production	0.001194	0.032928	0.028368
BP	GO:0009649	entrainment of circadian clock	0.001197	0.032928	0.028368
BP	GO:0086004	regulation of cardiac muscle cell contraction	0.001197	0.032928	0.028368
BP	GO:0019058	viral life cycle	0.001203	0.032955	0.028391
BP	GO:0014706	striated muscle tissue development	0.001208	0.032955	0.028391
BP	GO:0022411	cellular component disassembly	0.001233	0.033468	0.028833
BP	GO:0002087	regulation of respiratory gaseous exchange by nervous system process	0.001252	0.033537	0.028893
BP	GO:0003157	endocardium development	0.001252	0.033537	0.028893
BP	GO:0090435	protein localization to nuclear envelope	0.001252	0.033537	0.028893
BP	GO:1901880	negative regulation of protein depolymerization	0.001286	0.034234	0.029493
BP	GO:0090087	regulation of peptide transport	0.001289	0.034234	0.029493
BP	GO:0099170	postsynaptic modulation of chemical synaptic transmission	0.001296	0.034272	0.029526

BP	GO:0003012	muscle system process	0.001302	0.034278	0.029531
BP	GO:0003007	heart morphogenesis	0.001314	0.034455	0.029683
BP	GO:1900024	regulation of substrate adhesion-dependent cell spreading	0.001361	0.035536	0.030615
BP	GO:0061097	regulation of protein tyrosine kinase activity	0.001382	0.03595	0.030972
BP	GO:0043491	protein kinase B signaling	0.001389	0.035957	0.030977
BP	GO:0008064	regulation of actin polymerization or depolymerization	0.001442	0.037189	0.032039
BP	GO:0043434	response to peptide hormone	0.00147	0.037761	0.032531
BP	GO:0090276	regulation of peptide hormone secretion	0.001509	0.038518	0.033184
BP	GO:0000266	mitochondrial fission	0.001526	0.038518	0.033184
BP	GO:1903115	regulation of actin filament-based movement	0.001526	0.038518	0.033184
BP	GO:0032102	negative regulation of response to external stimulus	0.001529	0.038518	0.033184
BP	GO:0032388	positive regulation of intracellular transport	0.001531	0.038518	0.033184
BP	GO:0046822	regulation of nucleocytoplasmic transport	0.001548	0.03862	0.033271
BP	GO:0031331	positive regulation of cellular catabolic process	0.001548	0.03862	0.033271
BP	GO:0009266	response to temperature stimulus	0.001571	0.039018	0.033614
BP	GO:0060560	developmental growth involved in morphogenesis	0.001586	0.039018	0.033614
BP	GO:0051258	protein polymerization	0.001591	0.039018	0.033614
BP	GO:0008306	associative learning	0.001593	0.039018	0.033614
BP	GO:0030218	erythrocyte differentiation	0.001607	0.039018	0.033614
BP	GO:0045471	response to ethanol	0.001607	0.039018	0.033614
BP	GO:0048511	rhythmic process	0.001612	0.039018	0.033614
BP	GO:0033673	negative regulation of kinase activity	0.001614	0.039018	0.033614
BP	GO:0006476	protein deacetylation	0.001665	0.040072	0.034523
BP	GO:0051924	regulation of calcium ion transport	0.001696	0.04066	0.035029
BP	GO:0097062	dendritic spine maintenance	0.001718	0.04088	0.035219
BP	GO:0097734	extracellular exosome biogenesis	0.001718	0.04088	0.035219
BP	GO:0001666	response to hypoxia	0.001733	0.041048	0.035363
BP	GO:2001235	positive regulation of apoptotic signaling pathway	0.001738	0.041048	0.035363
BP	GO:0048738	cardiac muscle tissue development	0.001756	0.041316	0.035594
BP	GO:0005976	polysaccharide metabolic process	0.001765	0.041349	0.035622
BP	GO:2000756	regulation of peptidyl-lysine acetylation	0.001797	0.04194	0.036132
BP	GO:1903201	regulation of oxidative stress-induced cell death	0.001835	0.042512	0.036624
BP	GO:0032271	regulation of protein polymerization	0.001845	0.042512	0.036624
BP	GO:0090277	positive regulation of peptide hormone secretion	0.00185	0.042512	0.036624
BP	GO:0097581	lamellipodium organization	0.00185	0.042512	0.036624
BP	GO:0061564	axon development	0.001856	0.042512	0.036624
BP	GO:0045216	cell-cell junction organization	0.001895	0.043253	0.037263
BP	GO:1903169	regulation of calcium ion transmembrane transport	0.001906	0.04334	0.037338
BP	GO:0044089	positive regulation of cellular component biogenesis	0.001931	0.043743	0.037685

BP	GO:0051016	barbed-end actin filament capping	0.001951	0.044036	0.037938
BP	GO:0030832	regulation of actin filament length	0.001978	0.044499	0.038336
BP	GO:0034446	substrate adhesion-dependent cell spreading	0.002007	0.044973	0.038744
BP	GO:0001569	branching involved in blood vessel morphogenesis	0.002016	0.045024	0.038788
BP	GO:0043268	positive regulation of potassium ion transport	0.002035	0.045141	0.038889
BP	GO:0031929	TOR signaling	0.002036	0.045141	0.038889
BP	GO:0035865	cellular response to potassium ion	0.002095	0.046285	0.039875
BP	GO:0045814	negative regulation of gene expression, epigenetic	0.002132	0.046919	0.040421
BP	GO:0000380	alternative mRNA splicing, via spliceosome	0.00214	0.046931	0.040431
BP	GO:0034101	erythrocyte homeostasis	0.002183	0.047713	0.041105
BP	GO:0010821	regulation of mitochondrion organization	0.002204	0.047831	0.041207
BP	GO:0031023	microtubule organizing center organization	0.002204	0.047831	0.041207
BP	GO:0072583	clathrin-dependent endocytosis	0.002235	0.048337	0.041643
BP	GO:0030041	actin filament polymerization	0.002286	0.049259	0.042437
BP	GO:0019932	second-messenger-mediated signaling	0.002317	0.049759	0.042867
BP	GO:0018205	peptidyl-lysine modification	0.002328	0.049808	0.04291
BP	GO:0035282	segmentation	0.002345	0.050005	0.04308
BP	GO:0019080	viral gene expression	0.002403	0.051071	0.043998
BP	GO:0071604	transforming growth factor beta production	0.002421	0.051267	0.044167
BP	GO:1905897	regulation of response to endoplasmic reticulum stress	0.002486	0.052466	0.045199
BP	GO:0016482	cytosolic transport	0.002522	0.052863	0.045542
BP	GO:1904064	positive regulation of cation transmembrane transport	0.002522	0.052863	0.045542
BP	GO:0032435	negative regulation of proteasomal ubiquitin-dependent protein catabolic process	0.002571	0.053704	0.046267
BP	GO:0043410	positive regulation of MAPK cascade	0.002596	0.054041	0.046557
BP	GO:0036296	response to increased oxygen levels	0.002626	0.054311	0.046789
BP	GO:0042026	protein refolding	0.002626	0.054311	0.046789
BP	GO:0042306	regulation of protein import into nucleus	0.002649	0.054523	0.046972
BP	GO:0033522	histone H2A ubiquitination	0.002654	0.054523	0.046972
BP	GO:0031960	response to corticosteroid	0.002678	0.054836	0.047241
BP	GO:0031057	negative regulation of histone modification	0.002743	0.055975	0.048223
BP	GO:1900407	regulation of cellular response to oxidative stress	0.002804	0.056979	0.049088
BP	GO:2001234	negative regulation of apoptotic signaling pathway	0.002811	0.056979	0.049088
BP	GO:0003208	cardiac ventricle morphogenesis	0.002843	0.057451	0.049494
BP	GO:0016197	endosomal transport	0.00286	0.057564	0.049592
BP	GO:0015833	peptide transport	0.002877	0.057564	0.049592
BP	GO:0008088	axo-dendritic transport	0.002877	0.057564	0.049592
BP	GO:0007635	chemosensory behavior	0.002919	0.057836	0.049827
BP	GO:0045721	negative regulation of gluconeogenesis	0.002919	0.057836	0.049827
BP	GO:0045945	positive regulation of transcription by RNA polymerase III	0.002919	0.057836	0.049827

CC	GO:0030055	cell-substrate junction	4.79E-08	2.43E-05	1.93E-05
CC	GO:0005925	focal adhesion	6.66E-08	2.43E-05	1.93E-05
CC	GO:0016607	nuclear speck	9.79E-08	2.43E-05	1.93E-05
CC	GO:0031252	cell leading edge	1.83E-06	0.00034	0.000269
CC	GO:0099572	postsynaptic specialization	3.77E-06	0.000559	0.000442
CC	GO:0016605	PML body	4.49E-06	0.000559	0.000442
CC	GO:0032279	asymmetric synapse	6.17E-06	0.00061	0.000483
CC	GO:0014069	postsynaptic density	6.55E-06	0.00061	0.000483
CC	GO:0030135	coated vesicle	1.62E-05	0.001341	0.001062
CC	GO:0098984	neuron to neuron synapse	1.80E-05	0.001341	0.001062
CC	GO:0043197	dendritic spine	3.21E-05	0.00218	0.001726
CC	GO:0044309	neuron spine	3.68E-05	0.002185	0.00173
CC	GO:0005769	early endosome	3.81E-05	0.002185	0.00173
CC	GO:0031965	nuclear membrane	7.11E-05	0.003788	0.002998
CC	GO:0030133	transport vesicle	7.88E-05	0.003917	0.003101
CC	GO:0016234	inclusion body	8.92E-05	0.004159	0.003292
CC	GO:0005905	clathrin-coated pit	9.72E-05	0.004263	0.003375
CC	GO:0005798	Golgi-associated vesicle	0.000129	0.005366	0.004248
CC	GO:0030016	myofibril	0.000156	0.006132	0.004854
CC	GO:0031307	integral component of mitochondrial outer membrane	0.000165	0.006144	0.004863
CC	GO:0043292	contractile fiber	0.000199	0.00707	0.005597
CC	GO:0000775	chromosome, centromeric region	0.000227	0.007071	0.005597
CC	GO:0005677	chromatin silencing complex	0.000236	0.007071	0.005597
CC	GO:0005635	nuclear envelope	0.000239	0.007071	0.005597
CC	GO:0000922	spindle pole	0.000241	0.007071	0.005597
CC	GO:0031306	intrinsic component of mitochondrial outer membrane	0.000246	0.007071	0.005597
CC	GO:0005912	adherens junction	0.000259	0.007147	0.005657
CC	GO:0000791	euchromatin	0.000294	0.007823	0.006193
CC	GO:0030018	Z disc	0.000308	0.007921	0.00627
CC	GO:0031674	I band	0.000333	0.008278	0.006553
CC	GO:0005775	vacuolar lumen	0.000384	0.00924	0.007315
CC	GO:0098687	chromosomal region	0.000398	0.009273	0.00734
CC	GO:0005819	spindle	0.000469	0.010597	0.008388
CC	GO:0044304	main axon	0.00055	0.012063	0.009549
CC	GO:0043202	lysosomal lumen	0.000586	0.012496	0.009891
CC	GO:0043025	neuronal cell body	0.00068	0.014101	0.011162
CC	GO:0044232	organelle membrane contact site	0.000715	0.014413	0.011409
CC	GO:0030027	lamellipodium	0.000825	0.015785	0.012495
CC	GO:0030496	midbody	0.000825	0.015785	0.012495

CC	GO:0098685	Schaffer collateral - CA1 synapse	0.001026	0.01914	0.015151
CC	GO:0098978	glutamatergic synapse	0.001114	0.020265	0.016041
CC	GO:0062023	collagen-containing extracellular matrix	0.001195	0.021224	0.016801
CC	GO:0030017	sarcomere	0.001235	0.021432	0.016965
CC	GO:0005788	endoplasmic reticulum lumen	0.001308	0.021687	0.017168
CC	GO:0005938	cell cortex	0.001308	0.021687	0.017168
CC	GO:0098857	membrane microdomain	0.001386	0.022478	0.017794
CC	GO:0030120	vesicle coat	0.001507	0.023021	0.018223
CC	GO:0016327	apicolateral plasma membrane	0.001512	0.023021	0.018223
CC	GO:0044233	mitochondria-associated endoplasmic reticulum membrane	0.001512	0.023021	0.018223
CC	GO:0005796	Golgi lumen	0.00182	0.027153	0.021494
CC	GO:0001726	ruffle	0.001897	0.027743	0.021961
CC	GO:0045177	apical part of cell	0.002112	0.02902	0.022972
CC	GO:0045121	membrane raft	0.002139	0.02902	0.022972
CC	GO:0016580	Sin3 complex	0.00214	0.02902	0.022972
CC	GO:0070822	Sin3-type complex	0.00214	0.02902	0.022972
CC	GO:0030134	COPII-coated ER to Golgi transport vesicle	0.002214	0.029488	0.023343
CC	GO:0000779	condensed chromosome, centromeric region	0.002469	0.032309	0.025575
CC	GO:0000792	heterochromatin	0.002701	0.034747	0.027505
CC	GO:0042470	melanosome	0.003012	0.035791	0.028332
CC	GO:0048770	pigment granule	0.003012	0.035791	0.028332
CC	GO:0043220	Schmidt-Lanterman incisure	0.003023	0.035791	0.028332
CC	GO:0071203	WASH complex	0.003023	0.035791	0.028332
CC	GO:0099091	postsynaptic specialization, intracellular component	0.003023	0.035791	0.028332
CC	GO:1904813	ficolin-1-rich granule lumen	0.003412	0.039766	0.031479
CC	GO:0034399	nuclear periphery	0.003866	0.044371	0.035124
CC	GO:0071782	endoplasmic reticulum tubular network	0.003992	0.045124	0.03572
CC	GO:0000118	histone deacetylase complex	0.004162	0.046338	0.036681
CC	GO:0016363	nuclear matrix	0.004248	0.046604	0.036891
CC	GO:0000793	condensed chromosome	0.004798	0.051246	0.040566
CC	GO:0031301	integral component of organelle membrane	0.004816	0.051246	0.040566
CC	GO:0033270	paranode region of axon	0.005021	0.051246	0.040566
CC	GO:1903293	phosphatase complex	0.005026	0.051246	0.040566
CC	GO:0034451	centriolar satellite	0.005089	0.051246	0.040566
CC	GO:0002102	podosome	0.005097	0.051246	0.040566
CC	GO:0030117	membrane coat	0.005244	0.051246	0.040566
CC	GO:0048475	coated membrane	0.005244	0.051246	0.040566
CC	GO:0044322	endoplasmic reticulum quality control compartment	0.005289	0.051246	0.040566
CC	GO:0031901	early endosome membrane	0.005557	0.052694	0.041712

CC	GO:0030136	clathrin-coated vesicle	0.00558	0.052694	0.041712
CC	GO:0120111	neuron projection cytoplasm	0.00595	0.055161	0.043665
CC	GO:0031256	leading edge membrane	0.006015	0.055161	0.043665
CC	GO:0030662	coated vesicle membrane	0.006063	0.055161	0.043665
CC	GO:0098791	Golgi apparatus subcompartment	0.006191	0.055645	0.044048
CC	GO:0101002	ficolin-1-rich granule	0.006569	0.058004	0.045915
CC	GO:0044291	cell-cell contact zone	0.006672	0.058004	0.045915
CC	GO:0150034	distal axon	0.006731	0.058004	0.045915
CC	GO:0034774	secretory granule lumen	0.0068	0.058004	0.045915
CC	GO:0031968	organelle outer membrane	0.006842	0.058004	0.045915
CC	GO:0030140	trans-Golgi network transport vesicle	0.007271	0.060594	0.047965
CC	GO:0031300	intrinsic component of organelle membrane	0.00731	0.060594	0.047965
CC	GO:0031209	SCAR complex	0.007802	0.062586	0.049542
CC	GO:0042405	nuclear inclusion body	0.007802	0.062586	0.049542
CC	GO:0044615	nuclear pore nuclear basket	0.007802	0.062586	0.049542
CC	GO:0019867	outer membrane	0.00789	0.062615	0.049565
MF	GO:0045296	cadherin binding	3.85E-07	0.000302	0.000282
MF	GO:0044389	ubiquitin-like protein ligase binding	5.64E-07	0.000302	0.000282
MF	GO:0060090	molecular adaptor activity	1.02E-06	0.000302	0.000282
MF	GO:0031625	ubiquitin protein ligase binding	1.06E-06	0.000302	0.000282
MF	GO:0046332	SMAD binding	3.70E-05	0.008437	0.007875
MF	GO:0008022	protein C-terminus binding	0.000128	0.024367	0.022745
MF	GO:0030674	protein-macromolecule adaptor activity	0.000157	0.025609	0.023904
MF	GO:0003924	GTPase activity	0.000215	0.030614	0.028576
MF	GO:0005525	GTP binding	0.000422	0.050526	0.047161
MF	GO:0017124	SH3 domain binding	0.000444	0.050526	0.047161
MF	GO:0033218	amide binding	0.000493	0.051051	0.047652
