
p < 0.01
p < 0.05
p < 0.1
5/18 'de novo' protein folding
28/75 protein folding
2/8 'de novo' posttranslational protein folding
14/26 chaperone−mediated protein folding
13/42 positive regulation of multi−organism process
40/143 regulation of multi−organism process
19/53 regulation of symbiosis, encompassing mutualism through parasitism
35/100 RNA catabolic process
22/35 nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
60/217 organic cyclic compound catabolic process
191/771 cellular catabolic process
2/9 histone mRNA catabolic process
2/10 exonucleolytic nuclear−transcribed mRNA catabolic process involved in deadenylation−dependent decay
102/313 mRNA metabolic process
19/23 translational initiation
3/5 cap−independent translational initiation
23/60 regulation of RNA splicing
6/20 regulation of alternative mRNA splicing, via spliceosome
11/24 negative regulation of mRNA processing
25/82 mRNA splicing, via spliceosome
1/8 alternative mRNA splicing, via spliceosome
114/400 RNA processing
32/113 RNA splicing
8/44 RNA modification
1/22 tRNA processing
6/14 tRNA aminoacylation for protein translation
8/41 tRNA metabolic process
36/134 ncRNA processing
3/11 maturation of 5.8S rRNA
35/106 rRNA metabolic process
2/10 rRNA modification
179/679 RNA metabolic process
56/233 ncRNA metabolic process
3/5 maturation of LSU−rRNA from tricistronic rRNA transcript (SSU−rRNA, 5.8S rRNA, LSU−rRNA)
5/29 maturation of SSU−rRNA
3/15 maturation of SSU−rRNA from tricistronic rRNA transcript (SSU−rRNA, 5.8S rRNA, LSU−rRNA)
4/33 RNA phosphodiester bond hydrolysis
2/22 cleavage involved in rRNA processing
26/40 translation
11/13 cytoplasmic translation
110/380 macromolecule biosynthetic process
4/5 cell fate commitment involved in formation of primary germ layer
6/23 RNA secondary structure unwinding
3/6 regulation of translational elongation
3/9 cargo loading into vesicle
91/283 cellular macromolecular complex assembly
2/6 cargo loading into COPII−coated vesicle
26/84 vesicle organization
9/24 vesicle coating
5/11 proteasome assembly
26/84 ribonucleoprotein complex subunit organization
4/11 ribosomal large subunit assembly
4/17 protein transmembrane transport
41/193 transmembrane transport
2/12 intracellular protein transmembrane import
17/62 protein import
12/47 mitochondrial transport
118/368 cytoplasmic transport
16/52 nuclear import
38/109 establishment of protein localization to organelle
21/28 protein targeting to membrane
29/71 protein targeting
98/278 intracellular protein transport
207/651 intracellular transport
19/25 protein targeting to ER
37/95 nucleobase−containing compound transport
2/14 nuclear pore organization
4/23 mitochondrial membrane organization
27/116 mitochondrion organization
5/21 apoptotic mitochondrial changes
2/15 cellular response to corticosteroid stimulus
3/6 amino acid import
3/24 protein complex biogenesis
3/13 mitochondrial respiratory chain complex I assembly
9/53 cellular component biogenesis
5/24 ribonucleoprotein complex biogenesis
29/80 positive regulation of cell adhesion
6/11 positive regulation of cell−cell adhesion
16/30 Golgi to plasma membrane transport
5/10 paranodal junction assembly
115/325 localization
78/224 cellular macromolecule localization
39/121 single−organism cellular localization
24/68 protein localization to plasma membrane
36/99 plasma membrane organization
6/13 regulation of cardiac muscle cell action potential
33/86 maintenance of protein location
5/10 cytoskeletal anchoring at plasma membrane
35/98 maintenance of location
5/14 regulation of cardiac muscle contraction by calcium ion signaling
9/25 regulation of heart rate
8/16 regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum
13/33 regulation of calcium ion transport into cytosol
181/554 regulation of transport
12/24 regulation of release of sequestered calcium ion into cytosol
4/7 regulation of peptidyl−cysteine S−nitrosylation
130/424 regulation of cellular localization
4/6 regulation of growth hormone secretion
43/115 positive regulation of secretion
72/233 regulation of secretion
28/61 cell junction assembly
9/17 cell−substrate junction assembly
36/86 cell junction organization
31/71 cell projection assembly
162/464 cell projection organization
7/20 cilium organization
133/411 anatomical structure formation involved in morphogenesis
25/74 cellular component assembly involved in morphogenesis
13/17 lamellipodium organization
57/172 cilium morphogenesis
100/298 cell part morphogenesis
3/6 hindbrain development
21/37 establishment of cell polarity
36/86 establishment or maintenance of cell polarity
7/12 polarized epithelial cell differentiation
4/5 spindle midzone assembly
116/293 microtubule−based process
144/329 cytoskeleton organization
63/162 microtubule cytoskeleton organization
15/25 cytoplasmic microtubule organization
18/46 microtubule organizing center organization
6/15 centrosome cycle
5/6 centrosome separation
165/531 cell cycle process
24/54 G2/M transition of mitotic cell cycle
35/145 cell cycle phase transition
36/88 cytokinesis
24/62 mitotic cytokinesis
101/317 cell division
123/366 cell cycle
7/13 positive regulation of cytokinesis
15/28 regulation of cytokinesis
39/110 regulation of cell division
225/667 single−organism organelle organization
9/18 chromosome condensation
19/36 actomyosin structure organization
15/29 actin filament−based movement
71/148 actin filament−based process
8/15 actin−mediated cell contraction
13/25 actin cytoskeleton reorganization
6/10 endothelial cell development
84/272 cell development
4/5 establishment of endothelial intestinal barrier
177/579 positive regulation of molecular function
20/63 positive regulation of protein binding
20/47 positive regulation of GTPase
8/17 regulation of peptidyl−threonine phosphorylation
171/548 regulation of phosphorylation
210/681 regulation of phosphorus metabolic process
58/198 regulation of protein serine/threonine kinase
81/248 positive regulation of transferase
115/371 regulation of transferase
36/118 activation of protein kinase
115/377 positive regulation of phosphate metabolic process
9/30 regulation of interleukin−2 production
21/59 regulation of peptidyl−serine phosphorylation
220/672 positive regulation of response to stimulus
6/10 detection of bacterium
8/16 detection of biotic stimulus
200/608 regulation of intracellular signal transduction
6/14 positive regulation of TOR signaling
16/54 regulation of intrinsic apoptotic signaling pathway
4/5 cellular response to X−ray
19/75 ossification
11/27 regulation of cytokine production involved in inflammatory response
57/189 regulation of sequence−specific DNA binding transcription factor
11/26 negative regulation of NIK/NF−kappaB signaling
20/65 regulation of NIK/NF−kappaB signaling
18/60 regulation of interleukin−6 production
213/579 intracellular signal transduction
13/47 I−kappaB kinase/NF−kappaB signaling
12/34 negative regulation of immune response
28/93 negative regulation of immune system process
20/62 negative regulation of defense response
20/51 negative regulation of I−kappaB kinase/NF−kappaB signaling
19/53 regulation of fibroblast proliferation
166/590 regulation of cell proliferation
11/30 negative regulation of fibroblast proliferation
30/73 negative regulation of epithelial cell proliferation
8/13 epithelial structure maintenance
18/47 cell−substrate adhesion
79/273 protein phosphorylation
58/165 regulation of cell adhesion
27/65 regulation of cell−substrate adhesion
10/27 regulation of cell junction assembly
7/17 regulation of establishment or maintenance of cell polarity
62/193 positive regulation of locomotion
123/354 regulation of locomotion
3/5 regulation of lamellipodium morphogenesis
66/194 positive regulation of cell projection organization
111/316 regulation of cell projection organization
38/102 regulation of axonogenesis
75/187 regulation of cell morphogenesis involved in differentiation
154/470 regulation of cell development
5/19 axon midline choice point recognition
9/38 neuron recognition
109/303 positive regulation of cell differentiation
57/134 positive regulation of cell development
19/45 positive regulation of axonogenesis
137/431 positive regulation of developmental process
145/409 regulation of anatomical structure morphogenesis
21/49 regulation of cell shape
104/258 regulation of cell morphogenesis
3/11 regulation of glial cell proliferation
111/338 regulation of neurogenesis
1/7 negative regulation of glial cell proliferation
37/109 negative regulation of response to external stimulus
192/624 negative regulation of response to stimulus
6/17 negative regulation of behavior
31/87 negative regulation of locomotion
49/98 regulation of small GTPase mediated signal transduction
27/47 regulation of Rho protein signal transduction
8/19 positive regulation of small GTPase mediated signal transduction
4/12 positive regulation of Rho protein signal transduction
24/82 homophilic cell adhesion
139/415 biological adhesion
47/142 cell−cell adhesion
11/28 heterophilic cell−cell adhesion
17/54 leukocyte migration
138/409 locomotion
46/137 neuron projection guidance
224/588 cellular component movement
7/24 motor neuron axon guidance
6/11 nuclear migration
4/16 regulation of nitric oxide biosynthetic process
91/191 regulation of cytoskeleton organization
33/66 regulation of protein polymerization
13/16 regulation of actin filament depolymerization
32/58 regulation of actin filament length
49/124 regulation of anatomical structure size
4/6 barbed−end actin filament capping
8/11 actin filament capping
27/65 negative regulation of protein complex assembly
12/24 negative regulation of protein polymerization
136/377 regulation of cellular component biogenesis
26/51 negative regulation of cytoskeleton organization
111/312 negative regulation of cellular component organization
15/25 regulation of protein depolymerization
66/125 regulation of actin filament−based process
9/10 negative regulation of actin filament bundle assembly
23/35 regulation of actin filament bundle assembly
6/7 negative regulation of stress fiber assembly
25/68 regulation of cell projection assembly
17/26 actin polymerization or depolymerization
57/97 actin filament organization
13/17 actin filament polymerization
6/10 actin filament depolymerization
16/30 protein polymerization
198/630 regulation of protein modification process
16/26 regulation of histone methylation
6/10 regulation of histone H3−K4 methylation
10/17 positive regulation of histone methylation
79/187 positive regulation of organelle organization
169/438 regulation of organelle organization
8/13 peptidyl−lysine trimethylation
9/19 peptidyl−lysine methylation
5/6 histone H3−K4 trimethylation
11/24 histone lysine methylation
16/27 Rho protein signal transduction
40/74 small GTPase mediated signal transduction
3/6 Cdc42 protein signal transduction
6/7 Rac protein signal transduction
7/9 skin morphogenesis
19/41 skeletal system development
80/273 system development
6/8 response to catecholamine
9/13 protein heterotrimerization
16/44 protein heterooligomerization
25/68 blood vessel development
17/50 response to retinoic acid
21/64 embryonic organ morphogenesis
84/234 organ morphogenesis
5/6 notochord morphogenesis
68/194 tissue development
15/31 epidermis development
4/6 Wnt signaling pathway, planar cell polarity pathway
6/12 non−canonical Wnt signaling pathway
89/319 embryonic morphogenesis
21/55 regulation of embryonic development
16/40 establishment of planar polarity
57/197 tissue morphogenesis
10/18 branching involved in ureteric bud morphogenesis
4/7 regulation of integrin activation
23/60 specification of symmetry
72/214 pattern specification process
38/124 regionalization
21/57 anterior/posterior pattern specification
5/7 dorsal/ventral neural tube patterning
176/569 organ development
46/135 heart development
14/41 camera−type eye development
18/60 embryonic organ development
137/412 cellular component morphogenesis
45/135 cell morphogenesis
4/6 lung cell differentiation
14/38 epithelial cell proliferation
15/37 palate development
8/16 bone trabecula formation
13/29 trabecula formation
17/56 appendage morphogenesis
5/10 hormone−mediated signaling pathway
11/75 miRNA metabolic process
78/266 enzyme linked receptor protein signaling pathway
14/82 neural tube development
13/88 regulation of neural precursor cell proliferation
16/111 protein autoubiquitination
26/71 regulated secretory pathway
32/88 cell activation involved in immune response
5/7 acute−phase response
8/19 regulation of cellular amine metabolic process
28/96 protein modification by small protein removal
24/53 antigen processing and presentation
12/23 antigen processing and presentation of peptide antigen via MHC class I
8/19 antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP−dependent
12/23 regulation of hematopoietic stem cell differentiation
12/45 regulation of RNA stability
8/20 regulation of transcription from RNA polymerase II promoter in response to hypoxia
30/112 response to oxygen levels
17/60 cellular response to oxygen levels
13/33 regulation of DNA−templated transcription in response to stress
40/212 protein catabolic process
8/27 SCF−dependent proteasomal ubiquitin−dependent protein catabolic process
90/373 macromolecule catabolic process
6/26 anaphase−promoting complex−dependent proteasomal ubiquitin−dependent protein catabolic process
57/287 proteolysis
37/203 proteolysis involved in cellular protein catabolic process
11/36 positive regulation of ligase
21/83 positive regulation of protein ubiquitination
7/21 positive regulation of ubiquitin−protein ligase involved in mitotic cell cycle
20/65 negative regulation of protein ubiquitination
189/512 positive regulation of cellular component organization
2/6 positive regulation of RNA polymerase II transcriptional preinitiation complex assembly
4/13 regulation of DNA−templated transcription, initiation
82/261 cellular homeostasis
7/23 cellular iron ion homeostasis
2/9 copper ion homeostasis
17/38 cell redox homeostasis
2/8 cellular response to low−density lipoprotein particle stimulus
6/11 cellular response to fatty acid
32/104 nervous system development
23/73 dephosphorylation
19/53 protein dephosphorylation
4/22 lysosome organization
9/57 vacuole organization
2/22 oligosaccharide metabolic process
1/8 N−glycan processing
53/257 carbohydrate metabolic process
44/170 organophosphate biosynthetic process
1/5 nucleotide−sugar biosynthetic process
33/138 carbohydrate derivative biosynthetic process
25/93 nucleoside phosphate biosynthetic process
7/32 nucleoside monophosphate biosynthetic process
102/429 organic cyclic compound biosynthetic process
33/130 purine−containing compound metabolic process
17/49 purine nucleoside triphosphate metabolic process
17/55 nucleoside triphosphate metabolic process
5/12 ATP biosynthetic process
12/29 nucleoside triphosphate biosynthetic process
12/24 ribonucleoside triphosphate biosynthetic process
3/7 ATP synthesis coupled proton transport
74/300 organophosphate metabolic process
24/94 glycosyl compound metabolic process
13/41 glycosyl compound biosynthetic process
9/22 ATP metabolic process
12/46 nucleoside monophosphate metabolic process
46/194 nucleobase−containing small molecule metabolic process
2/15 purine nucleobase metabolic process
61/271 carbohydrate derivative metabolic process
4/13 cAMP metabolic process
108/475 single−organism biosynthetic process
10/21 monosaccharide biosynthetic process
3/12 ATP hydrolysis coupled proton transport
15/82 monovalent inorganic cation transport
6/20 proton transport
7/53 cofactor biosynthetic process
26/114 cofactor metabolic process
2/6 myeloid cell homeostasis
91/361 organic acid metabolic process
2/5 malate metabolic process
169/643 small molecule metabolic process
18/96 sulfur compound metabolic process
17/68 cellular amino acid biosynthetic process
57/261 organonitrogen compound biosynthetic process
3/7 L−serine metabolic process
48/178 cellular amino acid metabolic process
125/551 organonitrogen compound metabolic process
31/126 alpha−amino acid metabolic process
7/16 one−carbon metabolic process
14/59 cellular amino acid catabolic process
34/127 small molecule catabolic process
1/7 aromatic amino acid family catabolic process
2/11 aromatic amino acid family metabolic process
37/184 organonitrogen compound catabolic process
3/8 glyoxylate metabolic process
6/19 cellular aldehyde metabolic process
44/153 monocarboxylic acid metabolic process
5/36 detection of stimulus involved in sensory perception
2/20 DNA replication initiation