



- 26/43 **modification of morphology or physiology of other organism**
- 20/24 **cell killing**
- 90/151 **multi-organism cellular process**
- 10/12 **pathogenesis**
- 67/115 **negative regulation of protein modification process**
- 311/58 **regulation of phosphorylation**
- 10/11 **regulation of ubiquitin–protein ligase involved in mitotic cell cycle**
- 116/203 **negative regulation of protein metabolic process**
- 9/14 *negative regulation of ubiquitin–protein ligase*
- 16/23 **regulation of ligase**
- 51/72 **positive regulation of cell cycle process**
- 15/21 **positive regulation of cell cycle arrest**
- 21/34 *antigen processing and presentation*
- 13/17 **antigen processing and presentation of peptide antigen via MHC class I**
- 59/96 **proteasomal protein catabolic process**
- 44/79 **proteolysis**
- 14/72 *ER-associated ubiquitin–dependent protein catabolic process*
- 77/130 **protein catabolic process**
- 11/12 **anaphase–promoting complex–dependent proteasomal ubiquitin–depende**
- 114/189 **proteolysis involved in cellular protein catabolic process**
- 239/401 **protein modification by small protein conjugation or removal**
- 11/23 **protein ubiquitination**
- 26/50 **protein ubiquitination involved in ubiquitin–dependent protein catabolic process**
- 5/6 **regulation of DNA–dependent DNA replication initiation**
- 12/14 **DNA replication initiation**
- 288/454 **cell cycle**
- 55/85 **mitotic cell cycle**
- 52/81 *DNA conformation change*
- 7/7 *DNA unwinding involved in DNA replication*
- 6/8 **DNA replication checkpoint**
- 38/54 **meiotic nuclear division**
- 183/259 **organelle fission**
- 10/14 **ribosomal metabolic process**
- 4/5 **protein localization to kinetochore**
- 6/7 *spindle checkpoint*
- 32/48 **chromosome segregation**
- 27/37 **regulation of nuclear division**
- 9/18 *camera-type eye development*
- 45/77 **brain development**
- 47/81 **rhythmic process**
- 13/23 *ovulation cycle process*
- 83/147 **regulation of cell projection organization**
- 6/8 **negative regulation of axon extension**
- 13/23 **regulation of extent of cell growth**
- 37/67 **regulation of developmental growth**
- 97/76 **regulation of neurogenesis**
- 23/45 **regulation of dendrite development**
- 162/218 **regulation of cell development**
- 41/86 **positive regulation of cell projection organization**
- 20/32 **regulation of chemotaxis**
- 30/46 **regulation of behavior**
- 13/18 *positive regulation of chemotaxis*
- 255/457 **cellular component movement**
- 32/42 **neuron migration**
- 130/238 **cell motility**
- 161/285 **locomotion**
- 13/16 **axonal fasciculation**
- 21/31 **positive regulation of angiogenesis**
- 37/67 **positive regulation of vasculature development**
- 76/296 **regulation of anatomical structure morphogenesis**
- 20/29 **regulation of epithelial to mesenchymal transition**
- 122/212 **negative regulation of developmental process**
- 9/17 *negative regulation of angiogenesis*
- 6/10 *nerve development*
- 5/6 *cranial nerve development*
- 168/309 **system development**
- 97/187 **nervous system development**
- 267/437 **response to endogenous stimulus**
- 48/91 **response to fibroblast growth factor**
- 96/187 **response to growth factor**
- 144/262 **enzyme linked receptor protein signaling pathway**
- 505/900 **cell surface receptor signaling pathway**
- 8/13 *ephrin receptor signaling pathway*
- 35/64 **protein autoubiquitination**
- 61/104 *response to peptide*
- 63/112 **peptidyl–tyrosine phosphorylation**
- 278/510 **phosphorylation**
- 45/85 **protein autophosphorylation**
- 253/429 **regulation of cell differentiation**
- 20/27 *regulation of myeloid leukocyte differentiation*
- 370/531 **regulation of developmental process**
- 166/273 **positive regulation of developmental process**
- 8/12 **regulation of osteoblast proliferation**
- 43/69 **regulation of ossification**
- 31/50 *regulation of osteoblast differentiation*
- 31/47 **ossification**
- 49/78 **regulation of canonical Wnt signaling pathway**
- 66/112 **regulation of Wnt signaling pathway**
- 7/9 **establishment of planar polarity of embryonic epithelium**
- 74/137 **Wnt signaling pathway**
- 16/23 **inner ear receptor stereocilium organization**
- 11/36 **cell projection organization**
- 14/40 *negative regulation of transforming growth factor beta receptor signaling pathway*
- 199/359 **negative regulation of response to stimulus**
- 18/27 **negative regulation of cellular response to growth factor stimulus**
- 223/395 **regulation of cell proliferation**
- 129/216 **positive regulation of cell proliferation**
- 7/8 *positive regulation of cardiac muscle cell proliferation*
- 22/35 **regulation of muscle organ development**
- 27/49 **morphogenesis of a branching structure**
- 5/8 **pericardium morphogenesis**
- 11/1 **morphogenesis of an epithelial sheet**
- 37/57 **multicellular organismal development**
- 525/899 **regulation of cell communication**
- 6/9 *heart valve morphogenesis*
- 249/450 **regulation of transcription from RNA polymerase II promoter**
- 99/180 **negative regulation of transcription from RNA polymerase II promoter**
- 140/262 **negative regulation of transcription from RNA polymerase II promoter**
- 328/580 **negative regulation of metabolic process**
- 17/17 *negative regulation of gene expression, epigenetic*
- 240/441 **negative regulation of biosynthetic process**
- 191/339 **negative regulation of nitrogen compound metabolic process**
- 5/9 *negative regulation of fat cell differentiation*
- 11/18 *regulation of fat cell differentiation*
- 58/106 **negative regulation of phosphate metabolic process**
- 49/93 **neuron differentiation**
- 22/45 **skeletal system morphogenesis**
- 108/189 **organ morphogenesis**
- 328/575 **anatomical structure morphogenesis**
- 13/23 *epithelial to mesenchymal transition*
- 9/10 *neural crest formation*
- 133/248 **cellular component morphogenesis**
- 105/183 **pattern specification process**
- 61/103 **regionalization**
- 32/54 *anterior/posterior pattern specification*
- 13/25 *embryonic pattern specification*
- 19/29 **convergent extension**
- 131/236 **embryonic morphogenesis**
- 80/141 **tissue morphogenesis**
- 29/46 **embryonic heart tube morphogenesis**
- 10/13 **regulation of planar cell polarity pathway involved in neural tube closure**
- 37/65 **tube morphogenesis**
- 18/29 **cardiac septum development**
- 21/37 **maintenance of organ identity**
- 27/51 **specification of symmetry**
- 258/440 **organ development**
- 44/72 **kidney development**
- 26/46 **lung development**
- 32/69 **cilium morphogenesis**
- 19/36 **photoreceptor cell maintenance**
- 44/71 **establishment or maintenance of cell polarity**
- 15/25 **epithelial cilium movement**
- 21/38 **cilium movement**
- 169/295 *microtubule–based process*
- 80/153 *microtubule–based movement*
- 10/12 *epithelial cilium movement involved in determination of left/right asymmetry*
- 23/42 **regulation of embryonic development**
- 6/11 *neural tube formation*
- 9/16 **embryonic epithelial tube formation**
- 26/54 **tube formation**
- 11/15 **execution phase of apoptosis**
- 21/46 *muscle tissue development*
- 108/186 **tissue development**
- 5/8 *activation of adenylate cyclase*
- 156/290 **regulation of nucleotide metabolic process**
- 388/679 **regulation of phosphorus metabolic process**
- 44/73 **regulation of cyclic nucleotide metabolic process**
- 19/34 **regulation of cyclase**
- 8/16 *positive regulation of lyase*
- 28/51 **regulation of purine nucleotide biosynthetic process**
- 17/27 **positive regulation of nucleotide metabolic process**
- 235/488 **positive regulation of biosynthetic process**
- 9/19 **regulation of vasodilation**
- 9/15 **regulation of cAMP–dependent protein kinase**
- 71/113 **neuropeptide signaling pathway**
- 38/72 **regulation of Ras protein signal transduction**
- 23/40 *regulation of Rho protein signal transduction*
- 55/98 **regulation of small GTPase mediated signal transduction**
- 12/21 *positive regulation of Rac GTPase*
- 37/66 *regulation of Rho GTPase*
- 65/103 **regulation of binding**
- 47/74 **regulation of protein binding**
- 31/258 **positive regulation of molecular function**
- 11/45 **positive regulation of binding**
- 509/901 **regulation of molecular function**
- 14/23 *regulation of lipase*
- 39/65 **positive regulation of MAP kinase**
- 178/234 **positive regulation of phosphate metabolic process**
- 149/245 **positive regulation of intracellular signal transduction**
- 441/752 **regulation of protein metabolic process**
- 60/97 **activation of protein kinase**
- 117/184 **positive regulation of transferase**
- 17/16 **regulation of NIK/NF–kappaB signaling**
- 126/208 **positive regulation of protein phosphorylation**
- 483/805 **positive regulation of metabolic process**
- 211/341 **positive regulation of protein metabolic process**
- 61/96 **positive regulation of protein serine/threonine kinase**
- 217/358 **regulation of protein phosphorylation**
- 54/94 **regulation of MAP kinase**
- 101/164 **regulation of protein serine/threonine kinase**
- 5/5 **interleukin–1–mediated signaling pathway**
- 22/33 **positive regulation of stress–activated protein kinase signaling cascade**
- 53/81 **regulation of stress–activated protein kinase signaling cascade**
- 141/232 **regulation of MAPK cascade**
- 270/463 **regulation of intracellular signal transduction**
- 32/59 **tube development**
- 15/23 **respiratory tube development**
- 169/297 **regulation of response to stress**
- 4/5 *macropinocytosis*
- 93/156 **regulation of cellular response to stress**
- 7/8 **bone remodeling**
- 246/459 **regulation of cell death**
- 39/65 **regulation of I–kappaB kinase/NF–kappaB signaling**
- 61/111 **regulation of sequence–specific DNA binding transcription factor**
- 41/45 *immune response–activating cell surface receptor signaling pathway*
- 38/67 **positive regulation of sequence–specific DNA binding transcription factor**
- 61/105 **synaptic transmission**
- 146/237 **cell communication**
- 4/7 *synaptic transmission, cholinergic*
- 99/168 **single organism signaling**
- 16/22 **response to nicotine**
- 143/232 **response to nitrogen compound**
- 31/45 *response to alkaloid*
- 21/33 **negative regulation of cytokine production**
- 64/100 **regulation of cytokine production**
- 10/13 **negative regulation of tumor necrosis factor production**
- 415/727 **regulation of multicellular organismal process**
- 15/18 **regulation of tumor necrosis factor production**
- 9/10 **regulation of interleukin–6 production**
- 71/10 *positive regulation of cytokine biosynthetic process*
- 9/14 **regulation of cytokine biosynthetic process**
- 128/221 **immune response**
- 9/14 **adaptive immune response**
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- 30/44 *positive regulation of cytokine production*
- 41/83 *leukocyte differentiation*
- 9/10 **mature B cell differentiation**
- 385/684 **cell differentiation**
- 6/7 *mature B cell differentiation involved in immune response*
- 50/96 **immune effector process**
- 7/9 *lymphocyte mediated immunity*
- 8/13 **leukocyte mediated immunity**
- 20/41 **T cell activation**
- 9/14 **regulation of interferon–beta production**
- 15/26 **regulation of type I interferon production**
- 173/291 **defense response**
- 28/49 *positive regulation of defense response*
- 279/469 **positive regulation of response to stimulus**
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- 59/107 **positive regulation of immune system process**
- 45/77 **positive regulation of immune response**
- 41/45 *immune response–activating cell surface receptor signaling pathway*
- 47/79 **immune response–regulating signaling pathway**
- 119/212 **regulation of immune system process**
- 21/41 **immune response–regulating cell surface receptor signaling pathway**
- 66/121 **regulation of immune response**
- 10/17 *regulation of leukocyte mediated immunity*
- 27/45 **regulation of immune effector process**
- 9/13 **regulation of NF–kappaB import into nucleus**
- 66/111 **regulation of intracellular transport**
- 143/245 **regulation of cellular localization**
- 29/61 *regulation of nucleocytoplasmic transport*
- 33/76 **negative regulation of transport**
- 6/8 **negative regulation of endocytosis**
- 25/37 **reactive oxygen species metabolic process**
- 10/16 *superoxide metabolic process*
- 551/932 **response to chemical**
- 6/9 *response to superoxide*
- 10/13 **cellular response to amino acid stimulus**
- 8/10 **actin–mediated cell contraction**
- 4/6 *actin–myosin filament sliding*
- 67/111 **embryo development**
- 49/80 **embryo development ending in birth or egg hatching**
- 8/10 **blood circulation**
- 29/45 **circulatory system process**
- 23/43 **muscle system process**
- 231/388 **system process**
- 54/81 *sensory perception of light stimulus*
- 112/184 **sensory perception**
- 175/289 **neurological system process**
- 38/63 **sensory perception of mechanical stimulus**
- 84/138 **single–organism behavior**
- 24/41 *adult behavior*
- 4/6 *behavioral response to ethanol*
- 35/56 **locomotory behavior**
- 120/201 **behavior**
- 12/20 **associative learning**
- 56/92 **cognition**
- 52/80 **response to alcohol**
- 19/30 **response to ethanol**
- 186/303 **metal ion transport**
- 36/72 **sodium ion transport**
- 23/43 **sodium ion transmembrane transport**
- 266/418 **cation transport**
- 446/739 **transmembrane transport**
- 51/78 **potassium ion transport**
- 124/203 **monovalent inorganic cation transport**
- 14/15 **energy coupled proton transmembrane transport, against electrochemical g**
- 46/61 **hydrogen transport**
- 238/369 **ion transmembrane transport**
- 9/12 *membrane depolarization during action potential*
- 77/111 **regulation of transmembrane transport**
- 350/605 **regulation of localization**
- 4/5 *regulation of acetylcholine secretion, neurotransmission*
- 107/160 **regulation of ion transport**
- 254/433 **regulation of transport**
- 19/37 *membrane depolarization*
- 5/10 *neuronal action potential*
- 11/19 *action potential*
- 49/78 **regulation of membrane potential**
- 7/15 *response to pain*
- 92/1 *multicellular organismal response to stress*
- 71/101 **calcium ion transmembrane transport**
- 95/145 **divalent inorganic cation transport**
- 14/30 *detection of chemical stimulus*
- 64/110 **detection of stimulus**
- 112/16 *detection of chemical stimulus involved in sensory perception*
- 16/36 **detection of stimulus involved in sensory perception**
- 30/55 **detection of mechanical stimulus**
- 238/404 **response to abiotic stimulus**
- 278/472 **response to external stimulus**
- 7/8 *mechanosensory behavior*
- 58/101 **response to mechanical stimulus**
- 9/14 **phospholipase C–activating G–protein coupled receptor signaling pathway**
- 186/324 **G–protein coupled receptor signaling pathway**
- 8/19 **adenergic receptor signaling pathway**
- 19/40 **regulation of heart contraction**
- 13/18 **regulation of heart rate**
- 6/8 **positive regulation of heart rate**
- 56/109 **regulation of system process**
- 6/12 **positive regulation of heart contraction**
- 10/15 **regulation of cardiac muscle contraction**
- 13/22 **regulation of smooth muscle contraction**
- 28/48 **regulation of muscle system process**
- 6/10 *positive regulation of smooth muscle contraction*
- 6/11 **reflex**
- 6/10 *adult heart development*
- 48/90 **heart development**
- 61/26 *positive regulation of synaptic transmission*
- 60/101 **regulation of synaptic transmission**
- 5/6 **regulation of action potential**
- 12/15 **regulation of tissue remodeling**
- 52/98 *regulation of homeostatic process*
- 95/162 **ion homeostasis**
- 48/80 **divalent inorganic cation homeostasis**
- 125/217 **chemical homeostasis**
- 77/114 **cellular chemical homeostasis**
- 22/53 **cytosolic calcium ion homeostasis**
- 152/1 *developmental cell growth*
- 29/43 **cell growth**
- 23/38 *post–embryonic development*
- 41/59 **neuron development**
- 39/59 **cell–cell adhesion**
- 39/42 **cell–cell adhesion**
- 6/8 **cum–dependent cell–cell adhesion**
- 29/51 **peptidyl–tyrosine dephosphorylation**
- 44/84 **protein dephosphorylation**
- 6/10 *lung cell differentiation*
- 11/21 *establishment of spindle localization*
- 73/103 **protein folding**
- 21/25 **protein peptidyl–prolyl isomerization**
- 28/38 **peptidyl–proline modification**
- 14/16 **chaperone–mediated protein folding**
- 6/7 *de novo protein folding*
- 22/31 **peptidyl–asparagine modification**
- 205/364 **peptidyl–amino acid modification**
- 24/44 **protein N–linked glycosylation**
- 5/8 **COP11 vesicle coating**
- 29/49 **post–translational protein modification**
- 8/10 **cell–cell recognition**
- 61/17 *intracellular protein transmembrane transport*
- 149/249 **intracellular protein transport**
- 337/593 **establishment of protein localization**
- 21/36 **mitochondrial transport**
- 116/164 *membrane organization*
- 156/142 **cellular macromolecular complex assembly**
- 16/20 *spliceosomal snRNP assembly*
- 7/11 *mRNA splice site selection*
- 38/55 *protein–DNA complex subunit organization*
- 27/37 **protein–DNA complex assembly**
- 12/18 **chromatin assembly or disassembly**
- 47/80 **peptidyl–lysine modification**
- 90/159 *covalent chromatin modification*
- 6/12 *transcription from RNA polymerase I promoter*
- 465/873 **RNA biosynthetic process**
- 111/226 *ncRNA metabolic process*
- 33/73 *RNA metabolic process*
- 202/366 *RNA processing*
- 145/210 **translation**
- 12/15 **formation of translation preinitiation complex**
- 34/53 **translational initiation**
- 19/23 **translational elongation**
- 22/32 **multicellular organismal metabolic process**
- 61/100 **cellular component disassembly**
- 5/7 *actin nucleation*
- 42/71 **regulation of protein polymerization**
- 4/5 *cobalamin metabolic process*
- 32/35 **digestion**
- 86/152 *carbohydrate derivative biosynthetic process*
- 32/57 *glycosyl compound biosynthetic process*
- 30/45 **nucleoside monophosphate biosynthetic process**
- 37/104 *nucleoside phosphate biosynthetic process*
- 317/513 **single–organism biosynthetic process**
- 9/14 **ATP biosynthetic process**
- 267/466 *carbohydrate derivative catabolic process*
- 22/29 **nucleobase metabolic process**
- 16/21 **purine nucleobase metabolic process**
- 315/541 **nucleobase–containing small molecule metabolic process**
- 4/6 *purine metabolic process*
- 21/34 *pigment metabolic process*
- 268/508 **intracellular signal transduction**
- 23/39 *second–messenger–mediated signaling*
- 6/8 *intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress*
- 71/2 *cAMP metabolic process*
- 14/10 **cyclic nucleotide metabolic process**
- 171/261 **cellular amino acid metabolic process**
- 5/6 **L–serine biosynthetic process**
- 175/104 **cellular amino acid biosynthetic process**
- 156/426 **small molecule biosynthetic process**
- 30/44 *aspartate family amino acid metabolic process*
- 173/278 **organonitrogen compound biosynthetic process**
- 7/8 **pteridine–containing compound biosynthetic process**
- 24/37 **cellular modified amino acid biosynthetic process**
- 40/18 **cellular modified amino acid metabolic process**
- 17/28 **glutathione metabolic process**
- 36/56 **peptide metabolic process**
- 54/84 **cellular amide metabolic process**
- 403/679 **single–organism catabolic process**
- 8/10 *monovalent inorganic cation catabolic process*
- 87/146 **small molecule catabolic process**
- 32/55 *cellular lipid catabolic process*
- 526/894 **cellular catabolic process**
- 21/29 *nuclear–transcribed mRNA catabolic process, nonsense–mediated decay*
- 5/7 *anthranilate metabolic process*
- 19/14 **aromatic amino acid family catabolic process**
- 302/509 **organonitrogen compound catabolic process**
- 52/80 **cellular amino acid catabolic process**
- 5/6 **tryptophan catabolic process to kynurenine**
- 9/11 **tryptophan catabolic process**
- 191/181 **alpha–amino acid metabolic process**
- 10/14 **benzene–containing compound metabolic process**
- 293/490 *lipid metabolic process*
- 18/24 **terpenoid metabolic process**
- 198/335 **cellular lipid metabolic process**
- 23/24 *cellular hormone metabolic process*
- 436/643 **oxidation–reduction process**
- 17/21 **primary alcohol metabolic process**
- 61/2 *prostaglandin metabolic process*
- 80/136 **fatty acid metabolic process**
- 81/24 *pyruvate metabolic process*
- 324/551 **organic acid metabolic process**
- 133/220 **monocarboxylic acid metabolic process**
- 45/77 **sulfur compound biosynthetic process**
- 91/150 **sulfur compound metabolic process**
- 4/6 *acetyl–CoA biosynthetic process*
- 81/2 **acetyl–CoA metabolic process**
- 15/29 **thioester metabolic process**
- 78/136 **cofactor metabolic process**
- 23/31 **tricarboxylic acid cycle**
- 15/21 **cellular aldehyde metabolic process**
- 53/76 *cellular carbohydrate metabolic process*
- 53/76 **cellular carbohydrate metabolic process**
- 242/394 **carbohydrate metabolic process**
- 23/29 *polysaccharide catabolic process*
- 36/49 **polysaccharide metabolic process**
- 26/58 *carbohydrate biosynthetic process*
- 91/7 **oligosaccharide metabolic process**
- 14/21 **amino sugar catabolic process**
- 29/44 **amino sugar metabolic process**
- 20/30 **chitin metabolic process**
- 41/67 **aminoglycan metabolic process**
- 45/78 **organophosphate metabolic process**
- 30/49 **single–organism carbohydrate catabolic process**
- 49/74 **carbohydrate catabolic process**
- 33/50 **glucose metabolic process**
- 59/87 **monosaccharide metabolic process**
- 8/10 *Nucleic acid metabolism*
- 176/293 **single–organism carbohydrate metabolic process**
- 8/11 **pentose metabolic process**
- 20/29 **pyridine–containing compound metabolic process**
- 10/16 **NADP metabolic process**
- 21/24 *oxidoreduction coenzyme metabolic process*
- 32/46 **cell redox homeostasis**
- 17/31 **chloride transport**
- 88/165 *anion transport*
- 26/43 **inorganic anion transport**
- 6/16 *negative amino acid transport*
- 5/5 **plasminogen activation**
- 11/19 **negative regulation of coagulation**
- 8/8 **regulation of fibrinolysis**
- 64/119 **DNA integration**
- 86/149 **RNA–dependent DNA replication**

p < 0.01
p < 0.05
p < 0.1