



- 200/402 regulation of catabolic process
- 133/268 regulation of nucleoside metabolic process
- 5/6 negative regulation of neural precursor cell proliferation
- 9/14 oligodendrocyte development
- 5/11 negative regulation of ERK1 and ERK2 cascade
- 73/142 positive regulation of cell death
- 217/442 regulation of cell cycle
- 96/205 regulation of cell cycle process
- 19/29 regulation of cell cycle arrest
- 14/21 positive regulation of cell cycle arrest
- 39/81 positive regulation of cell cycle process
- 294/610 intracellular signal transduction
- 37/57 positive regulation of protein ubiquitination
- 54/88 regulation of protein ubiquitination
- 20/26 regulation of ligase
- 7/10 regulation of cellular amino acid metabolic process
- 506/881 proteolysis
- 11/15 anaphase–promoting complex–dependent proteasomal ubiquitin–dependent protein catabolic proc
- 124/234 negative regulation of protein metabolic process
- 74/135 negative regulation of protein modification process
- 11/14 regulation of ubiquitin–protein ligase involved in mitotic cell cycle
- 204/419 cellular response to DNA damage stimulus
- 35/85 regulation of cell division
- 257/509 negative regulation of biosynthetic process
- 343/683 negative regulation of metabolic process
- 203/402 negative regulation of nitrogen compound metabolic process
- 12/16 negative regulation of lipid metabolic process
- 268/519 regulation of transcription from RNA polymerase II promoter
- 114/206 negative regulation of transcription from RNA polymerase II promoter
- 13/17 circadian regulation of gene expression
- 31/70 regulation of chromosome organization
- 23/43 regulation of chromatin organization
- 145/308 regulation of organelle organization
- 52/111 positive regulation of organelle organization
- 14/23 histone ubiquitination
- 87/180 covalent chromatin modification
- 431/879 single–organism organelle organization
- 25/55 chromatin remodeling
- 164/339 chromatin organization
- 42/95 peptidyl–lysine modification
- 522/1054 RNA biosynthetic process
- 112/230 methylation
- 29/62 protein methylation
- 53/114 macromolecule methylation
- 15/28 regulation of ERBB signaling pathway
- 16/26 positive regulation of canonical Wnt signaling pathway
- 20/36 positive regulation of Wnt signaling pathway
- 43/85 regulation of epithelial cell proliferation
- 7/13 face morphogenesis
- 418/732 multicellular organismal development
- 7/13 establishment of planar polarity of embryonic epithelium
- 369/702 anatomical structure morphogenesis
- 43/64 ossification
- 83/160 gamete generation
- 204/421 peptidyl–amino acid modification
- 10/19 protein hydroxylation
- 23/39 peptidyl–proline modification
- 31/56 positive regulation of intracellular transport
- 59/126 regulation of intracellular transport
- 37/82 regulation of intracellular protein transport
- 34/71 regulation of nucleocytoplasmic transport
- 306/696 establishment of protein localization
- 113/285 intracellular protein transport
- 265/574 intracellular transport
- 80/177 response to other organism
- 131/256 response to biotic stimulus
- 85/153 actin filament–based process
- 17/29 establishment of cell polarity
- 46/87 cilium organization
- 67/130 cellular component assembly involved in morphogenesis
- 76/159 organelle assembly
- 63/123 cell projection assembly
- 216/412 cell projection organization
- 6/8 filopodium assembly
- 14/26 microtubule bundle formation
- 71/148 microtubule cytoskeleton organization
- 168/328 cytoskeleton organization
- 9/18 axoneme assembly
- 161/343 microtubule–based process
- 31/67 cytokinesis
- 95/198 RNA splicing
- 200/446 RNA processing
- 154/324 mRNA metabolic process
- 74/132 calcium ion transmembrane transport
- 235/466 ion transmembrane transport
- 53/99 potassium ion transport
- 269/520 cation transport
- 198/379 metal ion transport
- 106/200 regulation of ion transport
- 15/24 neuron–neuron synaptic transmission
- 166/306 cell communication
- 121/219 single organism signaling
- 19/28 glutamate receptor signaling pathway
- 13/24 regulation of vasodilation
- 52/95 regulation of cyclic nucleotide metabolic process
- 7/9 G–protein coupled acetylcholine receptor signaling pathway
- 228/458 G–protein coupled receptor signaling pathway
- 9/17 hair cell differentiation
- 20/37 epidermal cell differentiation
- 13/23 mechanoreceptor differentiation
- 56/114 sensory perception of light stimulus
- 256/498 system process
- 27/46 cell–matrix adhesion
- 350/613 biological adhesion
- 8/10 regulation of syncytium formation by plasma membrane fusion
- 8/10 trypsinogen activation
- 97/163 extracellular structure organization
- 27/53 extracellular matrix disassembly
- 37/52 modification of morphology or physiology of other organism
- 11/15 positive regulation of blood coagulation
- 39/59 multi–organism behavior
- 13/21 negative regulation of coagulation
- 249/493 DNA replication
- 478/966 DNA metabolic process
- 197/353 RNA–dependent DNA replication
- 143/265 DNA integration
- 159/330 nucleic acid phosphodiester bond hydrolysis
- 296/633 organic cyclic compound catabolic process
- 309/654 nucleobase–containing small molecule metabolic process
- 19/35 oxidoreduction coenzyme metabolic process
- 79/152 cofactor metabolic process
- 30/51 vitamin metabolic process
- 52/98 monosaccharide metabolic process
- 94/162 small molecule catabolic process
- 8/12 serine family amino acid catabolic process
- 630/1253 organic substance catabolic process
- 21/37 aminoglycan catabolic process
- 5/5 secondary metabolite catabolic process
- 76/126 steroid metabolic process
- 35/64 steroid biosynthetic process
- 322/620 single–organism biosynthetic process
- 5/6 arachidonic acid metabolite production involved in inflammatory response
- 10/18 retinol metabolic process
- 14/25 primary alcohol metabolic process
- 425/779 oxidation–reduction process
- 5/7 malate metabolic process
- 33/55 cell redox homeostasis
- 28/36 digestion
- 18/24 tRNA aminoacylation for protein translation
- 133/215 translation

p < 0.01  
p < 0.05  
p < 0.1